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Appendix A: Tool Installation Guide

This appendix details the basic system requirements and the steps needed to install and uninstall the Bighorn Sheep Risk of Contact (RoC) Tool.

A.1 System requirements

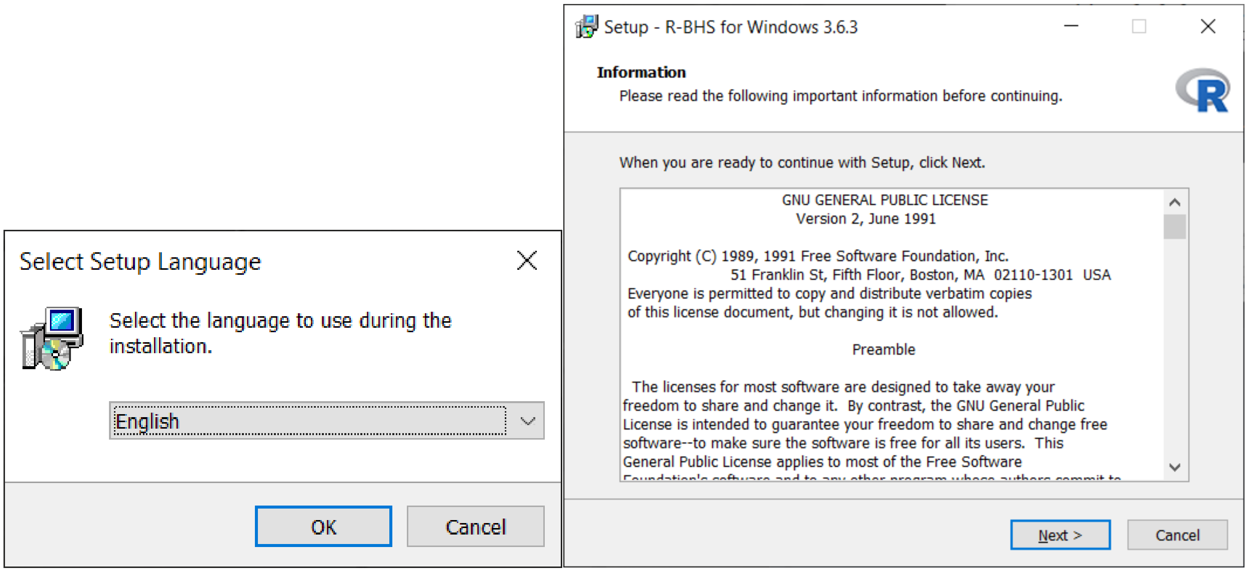
The RoC Tool can be installed on any computer that is running a 64-bit version of the Windows operating system. The only additional requirement is that the computer must be equipped with a web browser (preferably Chrome, Firefox, or Microsoft Edge), which the Tool will use to display its user interface. The Tool does **not** require an active internet connection (though without an internet connection, the Tool's Map tab will not display the background map layer that shows political and land management boundaries, municipalities, roads, lakes, streams, mountains, and other physical features).

A.2 Installing the RoC Tool

The RoC Tool is implemented using the free, open source programming language **R**. Both the geospatial computations used to produce the core herd home range and risk of contact estimates and the user interface are coded for in **R** and rely on a variety of **R** packages. The RoCT installer (`RoCT-GUI-v15-R-3.6.3-win.exe`) installs **R-3.6.3** and all of these packages along with desktop and Start menu shortcuts that can be used to launch the Tool.

To launch the installer, double click on the file `RoCT-GUI-v15-R-3.6.3-win.exe`. This will open a splash screen or dialog box asking whether you want to allow this program from an unknown publisher to make changes to your computer. To proceed, answer **Yes**.

You will next be presented with a series of dialog boxes, the first two of which are shown in FIGURE A.1. After clicking **OK** on the first box to accept English as the default language, click **Next** on the subsequent boxes (shown in FIGURE A.2, FIGURE A.3, and FIGURE A.4) to accept all of the default settings and proceed to installation.



Select the language to use during the installation.

Please read the following important information before continuing.

When you are ready to continue with Setup, click Next.

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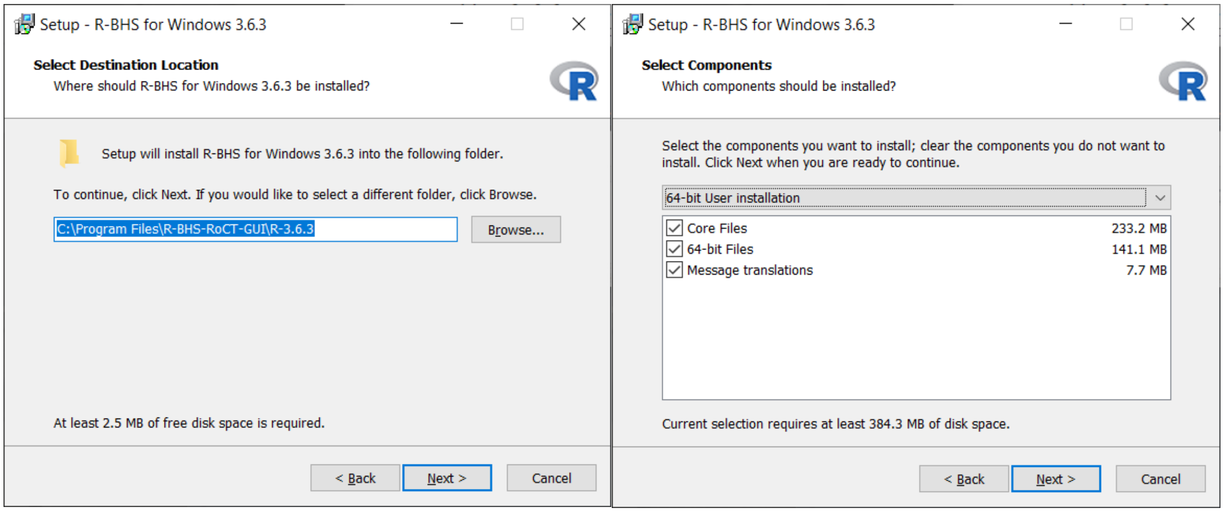
Preamble

The licenses for most software are designed to take away your freedom to share and change it. By contrast, the GNU General Public License is intended to guarantee your freedom to share and change free software--to make sure the software is free for all its users. This General Public License applies to most of the Free Software

FIGURE A.1. FIRST AND SECOND DIALOG BOXES LAUNCHED BY RoCT INSTALLER

While progressing through the dialog boxes, it is **strongly** recommended that users accept all default settings. However, if necessary, a user may choose a different install path in the **Select Destination Location** dialog box (FIGURE A.2). Likewise, accepting the defaults on the **Startup options** dialog box (FIGURE A.3) is recommended but not strictly required; selecting "Yes (customized startup)" will guide the user through two additional dialog boxes that configure components of the **R** graphical user interface that are not used by and therefore do not affect the Risk of Contact Tool. Otherwise, all default settings are required.



Setup - R-BHS for Windows 3.6.3

Select Destination Location

Where should R-BHS for Windows 3.6.3 be installed?

Setup will install R-BHS for Windows 3.6.3 into the following folder.

To continue, click Next. If you would like to select a different folder, click Browse.

C:\Program Files\R-BHS-RoCT-GUI\R-3.6.3

At least 2.5 MB of free disk space is required.

Setup - R-BHS for Windows 3.6.3

Select Components

Which components should be installed?

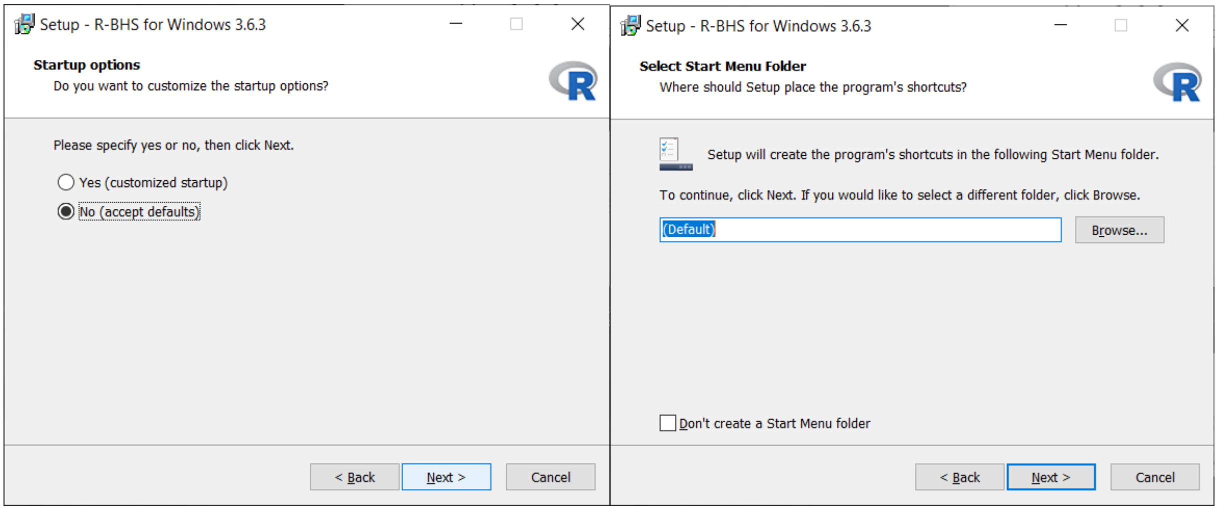
Select the components you want to install; clear the components you do not want to install. Click Next when you are ready to continue.

64-bit User installation

☑ Core Files	233.2 MB
☑ 64-bit Files	141.1 MB
☑ Message translations	7.7 MB

Current selection requires at least 384.3 MB of disk space.

FIGURE A.2. THIRD AND FOURTH DIALOG BOXES LAUNCHED BY RoCT INSTALLER



Setup - R-BHS for Windows 3.6.3

Startup options

Do you want to customize the startup options?

Please specify yes or no, then click Next.

○ Yes (customized startup)

● No (accept defaults)

Setup - R-BHS for Windows 3.6.3

Select Start Menu Folder

Where should Setup place the program's shortcuts?

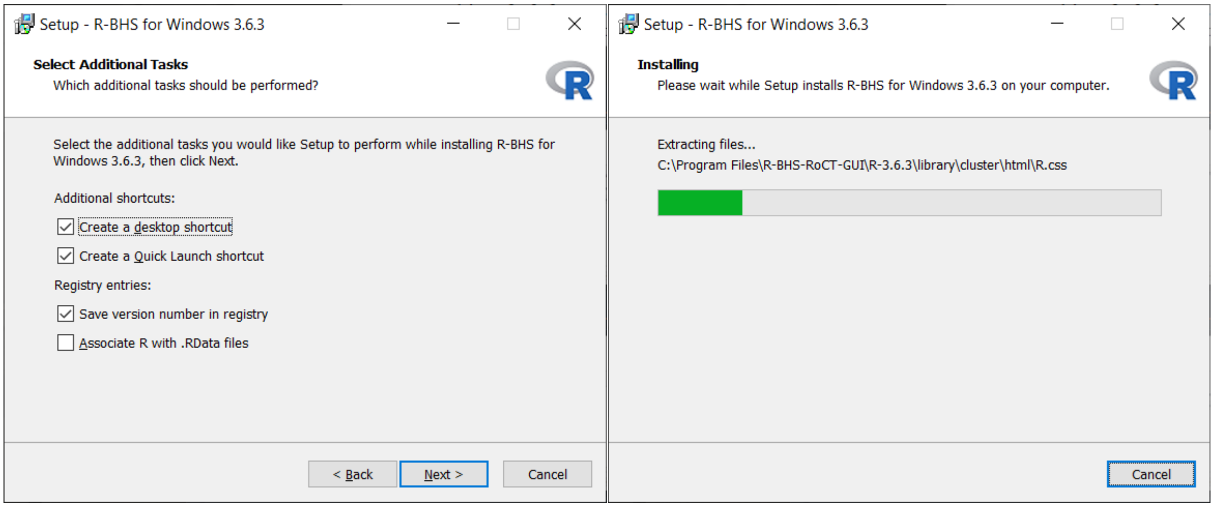
Setup will create the program's shortcuts in the following Start Menu folder.

To continue, click Next. If you would like to select a different folder, click Browse.

(Default)

☐ Don't create a Start Menu folder

FIGURE A.3. FIFTH AND SIXTH DIALOG BOXES LAUNCHED BY RoCT INSTALLER



Setup - R-BHS for Windows 3.6.3

Select Additional Tasks

Which additional tasks should be performed?

Select the additional tasks you would like Setup to perform while installing R-BHS for Windows 3.6.3, then click Next.

Additional shortcuts:

☑ Create a desktop shortcut

☑ Create a Quick Launch shortcut

Registry entries:

☑ Save version number in registry

☐ Associate R with .RData files

Setup - R-BHS for Windows 3.6.3

Installing

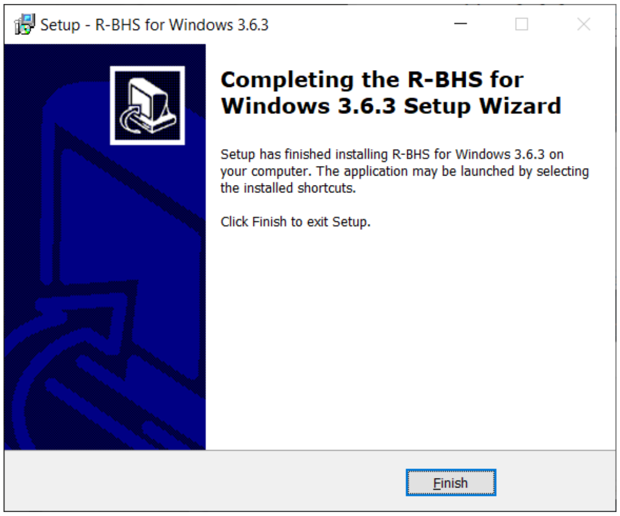
Please wait while Setup installs R-BHS for Windows 3.6.3 on your computer.

Extracting files...

C:\Program Files\R-BHS-RoCT-GUI\R-3.6.3\library\cluster\html\R.css

FIGURE A.4 SEVENTH DIALOG BOX LAUNCHED BY RoCT INSTALLER AND INSTALL PROGRESS INDICATOR

When installation is complete, you will be presented with the box in FIGURE A.5 below. Click **Finish** to exit the install wizard.



Completing the R-BHS for Windows 3.6.3 Setup Wizard

Setup has finished installing R-BHS for Windows 3.6.3 on your computer. The application may be launched by selecting the installed shortcuts.

Click Finish to exit Setup.

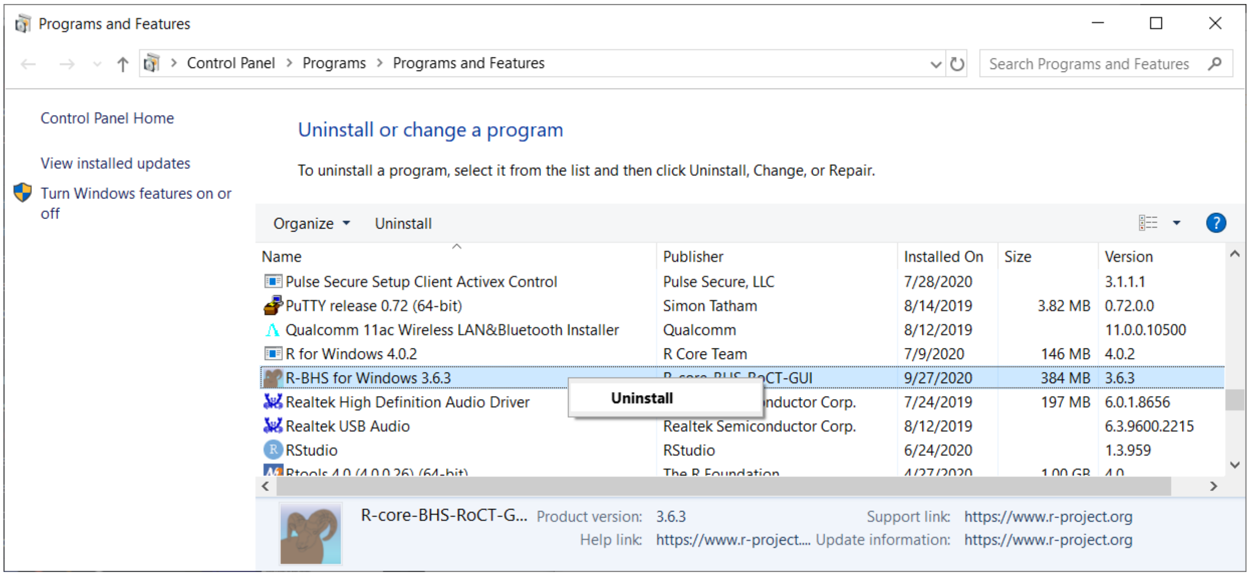
FIGURE A.5. DIALOG BOX INDICATING THAT RoCT INSTALLATION IS COMPLETE

NOTE FOR THOSE WHO USE R FOR OTHER PROJECTS/ANALYSES:

The **R** executable and **R** packages installed by running `RoCT-GUI-v15-R-3.6.3-win.exe` are entirely isolated and will not interfere with nor be interfered with by any other versions of **R** installed on your machine.

A.3 Uninstalling the RoC Tool

To completely uninstall the RoC Tool (including all registry entries and the desktop and Start menu shortcuts), use the same “Uninstall or change a program” window as you would for any other Windows program. To launch it, click the Start button (displayed as a Windows icon) on the bottom left of your screen, type “Program Features” and then select “Uninstall or change a program”. You should be presented with a window like the one in FIGURE A.6. Find the entry for “R-BHS for Windows 3.6.3”, right click anywhere on it, and click **Uninstall**.



Uninstall or change a program

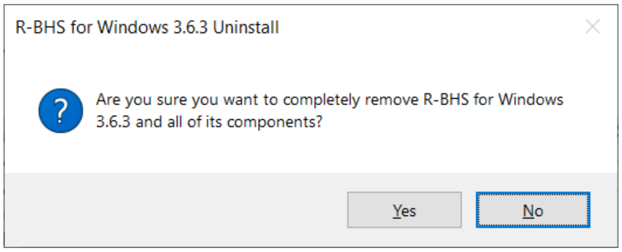
To uninstall a program, select it from the list and then click Uninstall, Change, or Repair.

Name	Publisher	Installed On	Size	Version
Pulse Secure Setup Client Activex Control	Pulse Secure, LLC	7/28/2020		3.1.1.1
PuTTY release 0.72 (64-bit)	Simon Tatham	8/14/2019	3.82 MB	0.72.0.0
Qualcomm 11ac Wireless LAN&Bluetooth Installer	Qualcomm	8/12/2019		11.0.0.10500
R for Windows 4.0.2	R Core Team	7/9/2020	146 MB	4.0.2
R-BHS for Windows 3.6.3	R-core-BHS-RoCT-GUI	9/27/2020	384 MB	3.6.3
Realtek High Definition Audio Driver	nductor Corp.	7/24/2019	197 MB	6.0.1.8656
Realtek USB Audio	Realtek Semiconductor Corp.	8/12/2019		6.3.9600.2215
RStudio	RStudio	6/24/2020		1.3.959
Rtools 4.0 (4.0.0.26) (64-bit)	The R Foundation	4/27/2020	1.00 GB	4.0

R-core-BHS-RoCT-G... Product version: 3.6.3 Support link: https://www.r-project.org
Help link: https://www.r-project.... Update information: https://www.r-project.org

FIGURE A.6. UNINSTALL OR CHANGE A PROGRAM DIALOG

To confirm that you do indeed want to uninstall the program, click **Yes** on the dialog box shown in FIGURE A.7. Successful uninstallation will be announced with one more dialog box and can be verified by checking that the shortcuts to the Tool have been removed from the desktop and Start menu.



R-BHS for Windows 3.6.3 Uninstall

Are you sure you want to completely remove R-BHS for Windows 3.6.3 and all of its components?

FIGURE A.7. DIALOG TO CONFIRM UNINSTALL

Appendix B: Distance Distribution File Format

This appendix describes the format of files used to supply ram and ewe foray distance distributions to the Risk of Contact Tool. To demonstrate the expected format, TABLE 1 below shows the contents of the default ram distance distribution file that is distributed with the RoC Tool. The values in that file were derived from a 12-year record of telemetry observations from 104 radio-collared rams in 12 Hells Canyon area bighorn herds.

Each ram or ewe foray distance distribution should be supplied as a *.csv file with columns named "Distance" and "ForayProb". The "Distance" column should contain integers running sequentially from 1 to the maximum distance in km at which a foraying animal was observed. The "ForayProb" column gives the proportion of animals on forays that reach rings at each distance (in km) from the CHHR. It should have a value of 1 for its first entry (since 100% of animals that leave the CHHR on a foray enter the first 1 km wide ring surrounding the CHHR) with subsequent values dropping monotonically towards 0 with increasing distance from the CHHR.

Distance	ForayProb
1	1
2	0.9511509
3	0.9019131
4	0.8519672
5	0.8011736
6	0.7496466
7	0.6977936
8	0.6463024
9	0.5960646
10	0.5480446
11	0.5031165
12	0.4619105
13	0.4247026
14	0.3913743
15	0.3614454
16	0.3341694
17	0.3086657
18	0.2840673
19	0.2596598
20	0.2349892
21	0.2099244
22	0.184658
23	0.159647
24	0.1355072
25	0.1128867
26	0.092346
27	0.074272
28	0.0588345
29	0.0459911
30	0.0355299
31	0.0271359
32	0.0204613
33	0.0151823
34	0.0110316
35	0.0078033

TABLE 1. DEFAULT RAM FORAY DISTANCE DISTRIBUTION

Appendix C: Finding the RoC Tool's Install Location

This appendix describes how to find the path of the directory that contains the software underlying the Risk of Contact Tool. Knowing this location is important if you need to rerun an analysis stored in an archive directory (see Appendices E and F) or would for some other reason like to inspect (or directly use) the R packages that the Tool uses to compute CHHR and Risk of Contact estimates.

The `RoCT-GUI-v15-R-3.6.3-win.exe` installer by default installs a copy of **R** and all required **R** packages into the directory `C:\Program Files\BHS-RoCT-GUI\R-3.6.3`. Assuming that is the path on your machine as well, the version of **R** used by the RoC Tool can be launched by double clicking on the `Rgui.exe` executable found at `C:\Program Files\BHS-RoCT-GUI\R-3.6.3\bin\x64\Rgui.exe`.

If the Tool has been installed to a different location, you can find it by following the numbered steps in FIGURE C.1, first typing "BHS-RoCT" in the start menu, then right-clicking on the BHS-RoCT shortcut icon, and finally clicking **Properties** on the pop-up context menu. The install path is given by the "Start in" field in the Properties dialog, as shown in FIGURE C.2.

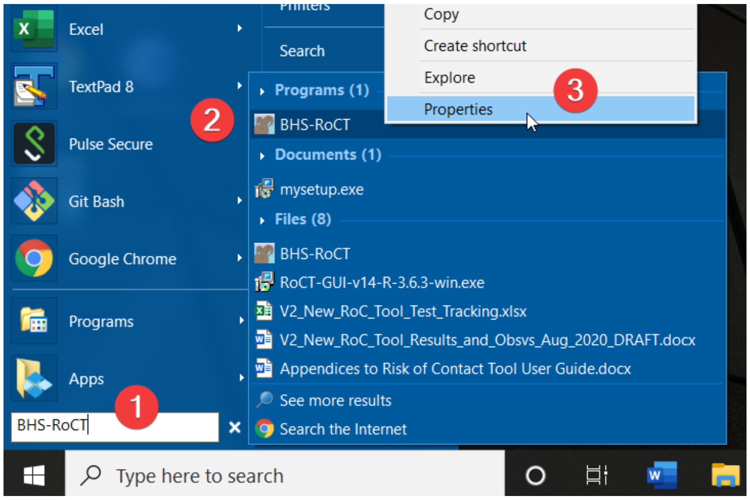
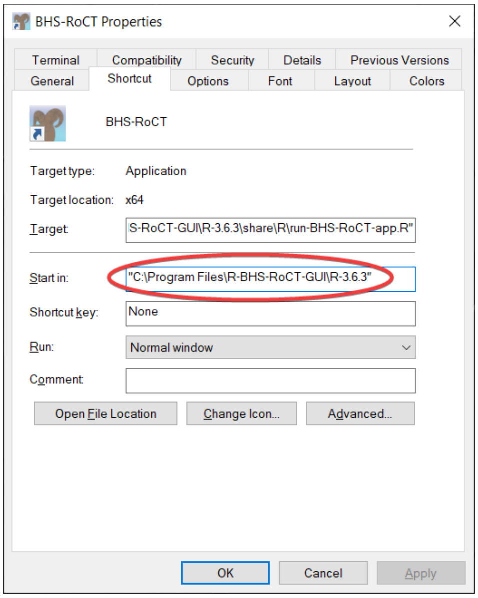


FIGURE C.1. EXAMINING START MENU BHS-RoCT SHORTCUT PROPERTIES



Target type: Application

Target location: x64

Target: S-RoCT-GUI\R-3.6.3\share\R\run-BHS-RoCT-app.R"

Start in: "C:\Program Files\R-BHS-RoCT-GUI\R-3.6.3"

Shortcut key: None

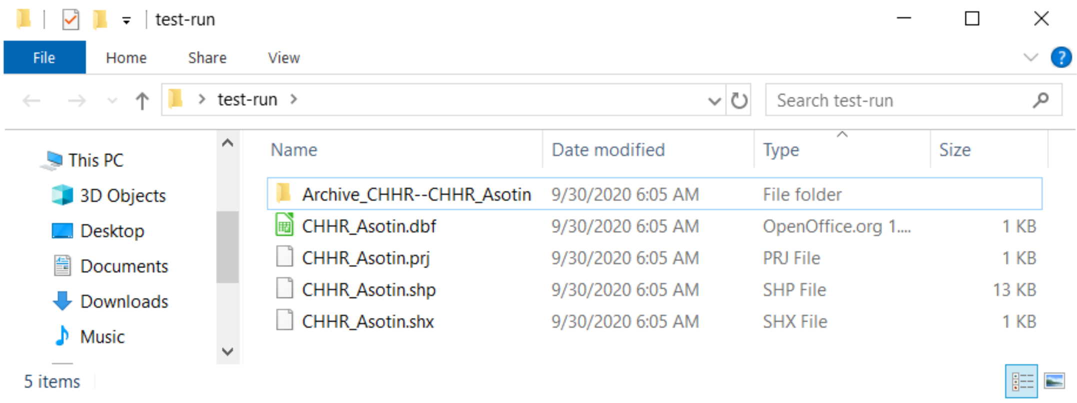
Run: Normal window

Comment:

FIGURE C.2. FINDING INSTALL PATH FROM RoCT START MENU SHORTCUT PROPERTIES

Appendix D: Core Herd Home Range Estimation Archive

If a user selects the “Archive inputs” option on the “Compute CHHR” sidebar tab, an additional archive subdirectory will be added to the output directory. This archive contains copies of all the data needed to reproduce the analyses performed when clicking the Tool’s “Compute CHHR” button, along with instructions on how to do so. The archive directory’s name incorporates the user-supplied name for the CHHR so that, for example, the archive for a CHHR named “Asotin” will be placed in a subdirectory named `Archive_CHHR--Asotin`.



Name	Date modified	Type	Size
Archive_CHHR--CHHR_Asotin	9/30/2020 6:05 AM	File folder	
CHHR_Asotin.dbf	9/30/2020 6:05 AM	OpenOffice.org 1....	1 KB
CHHR_Asotin.prj	9/30/2020 6:05 AM	PRJ File	1 KB
CHHR_Asotin.shp	9/30/2020 6:05 AM	SHP File	13 KB
CHHR_Asotin.shx	9/30/2020 6:05 AM	SHX File	1 KB

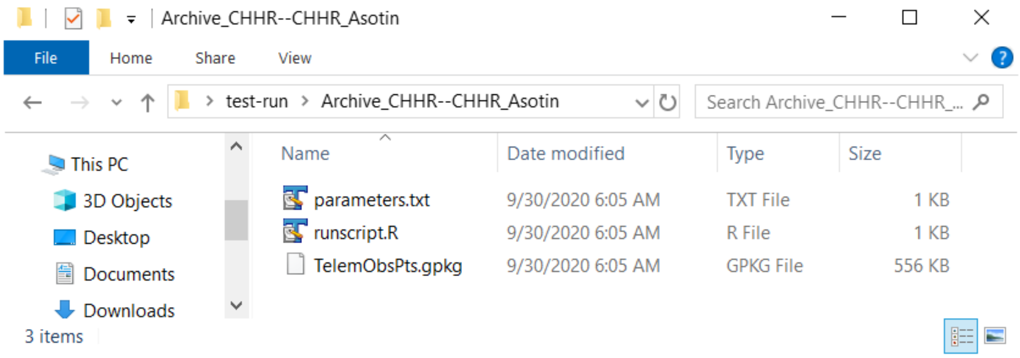
FIGURE D.1. OUTPUT DIRECTORY STRUCTURE FOLLOWING CHHR ESTIMATION

The archive directory (example in FIGURE D.2) contains the following three files:

- **`TelemObsPts.gpkg`** is a geopackage file (a modern, nonproprietary geospatial file format) that stores the telemetry or other animal location observations that were used to estimate the CHHR.

- **`parameters.txt`** is a text file, written in a structured YAML format, that records the paths to all geospatial inputs along with all other parameters used in estimating the CHHR. For a more detailed description of its contents, see Section D.1 below.

- **`runscript.R`** is also a text file, containing an **R** script that can be run to reproduce the analysis used to estimate the CHHR. For a more detailed description of its contents, see the section below.

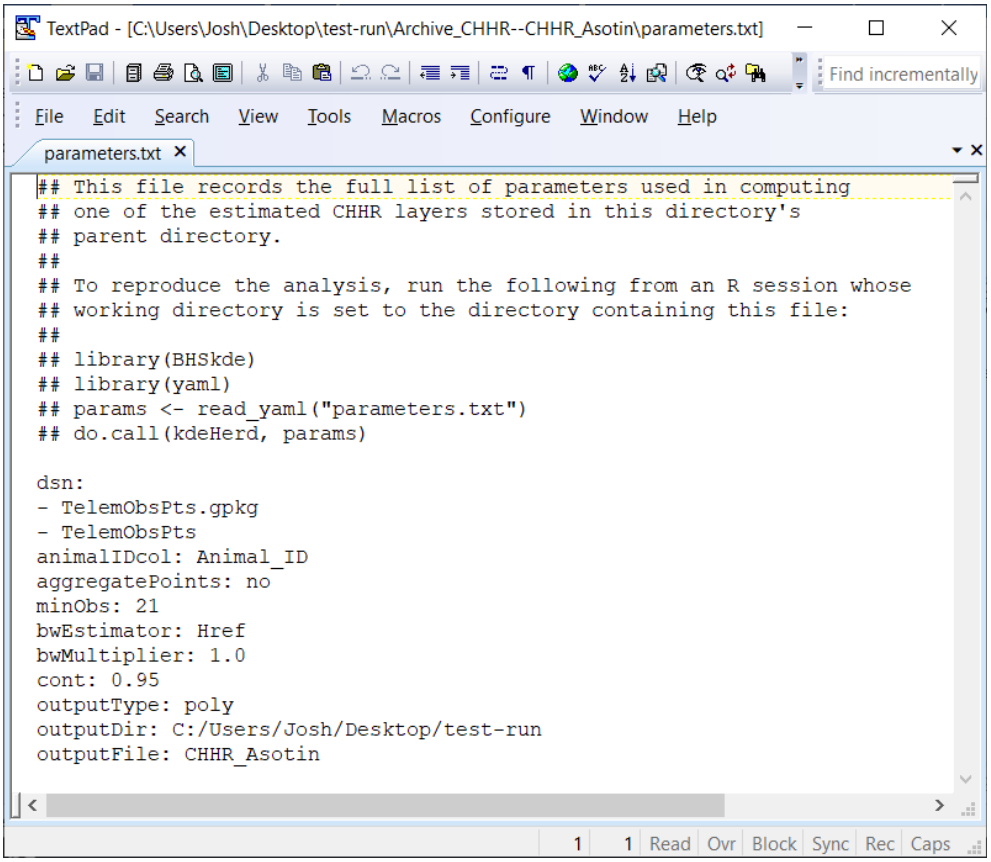


Name	Date modified	Type	Size
parameters.txt	9/30/2020 6:05 AM	TXT File	1 KB
runscript.R	9/30/2020 6:05 AM	R File	1 KB
TelemObsPts.gpkg	9/30/2020 6:05 AM	GPKG File	556 KB

FIGURE D.2. CHHR ESTIMATION ARCHIVE DIRECTORY STRUCTURE

D.1 The "`parameters.txt`" File

While using the RoC Tool to estimate a core herd home range, users interact with various widgets (file upload dialogs, pull-down menus, numeric entry fields, etc.) to set the parameters of the analysis. Behind the scenes, these parameters are collected into a list that is eventually passed on to the **R** package that directs the actual CHHR estimation computations. The archive's `parameters.txt` file records the values of all those user-selected parameters, printing parameter-value pairs in a standardized YAML format (see FIGURE D.3). As a result, the `parameters.txt` file can be used to reproduce the estimated CHHR that it documents.



```
## This file records the full list of parameters used in computing
## one of the estimated CHHR layers stored in this directory's
## parent directory.
##
## To reproduce the analysis, run the following from an R session whose
## working directory is set to the directory containing this file:
##
## library(BHSkde)
## library(yaml)
## params <- read_yaml("parameters.txt")
## do.call(kdeHerd, params)

dsn:
- TelemObsPts.gpkg
- TelemObsPts
animalIDcol: Animal_ID
aggregatePoints: no
minObs: 21
bwEstimator: Href
bwMultiplier: 1.0
cont: 0.95
outputType: poly
outputDir: C:/Users/Josh/Desktop/test-run
outputFile: CHHR_Asotin
```

FIGURE D.3. "parameters.txt" FILE FROM CHHR ESTIMATION ARCHIVE

To view a help file that precisely describes the meaning of the parameters recorded in `parameters.txt` or to reproduce the estimated CHHR, follow these instructions:

1. Use `Rgui.exe` to launch the version of **R** installed by the RoCT installer. (For instructions on how to find the proper version of `Rgui.exe`, see Appendix C above.)

2. In **R**, change the working directory to the archive directory containing `parameters.txt`. One way to do so from the **R** GUI launched in Step 1 is to select **File** then **Change dir…** from the GUI's toolbar.

3. To view the help file that documents the meaning of the parameters recorded in `parameters.txt`, type `?BHSkde::kdeHerd` in the R GUI console and the press **Return.**

4. To reproduce the estimated CHHR, copy and paste these lines into the R GUI command line, then press **Return**:

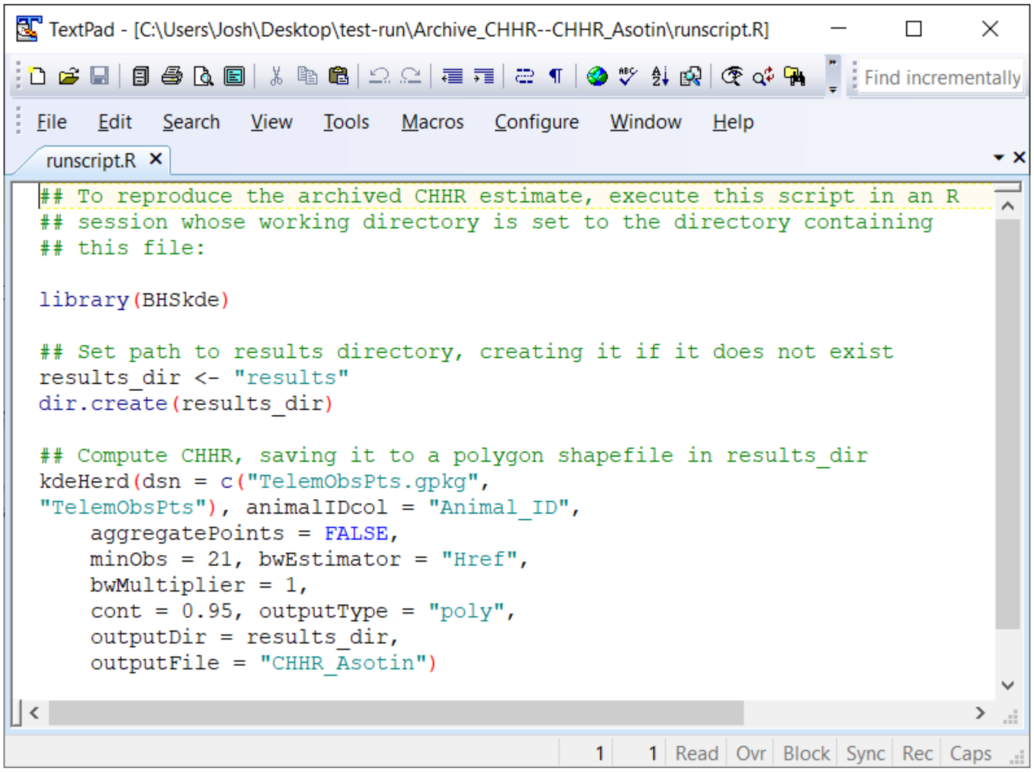
```
library(BHSkde)
library(yaml)
params <- read_yaml("parameters.txt")
do.call(kdeHerd, params)
```

D.2 The “runscript.R” File

Much like the `parameters.txt` file described in Section D.1 above, `runscript.R` is a text file that records the values of the parameters used to estimate a CHHR. It may be opened and viewed using any plain text editor (such as Notepad, WordPad, or TextPad) by right-clicking on the file and using **Open with** to select the editor.

Unlike `parameters.txt`, `runscript.R` records the parameters in an **R** script. If sourced or copy-and-pasted into an **R** session whose working directory is set to be the archive directory containing the script, it will reproduce the estimated CHHR, writing it to a shapefile in a newly created new directory named `results`.

Importantly, the script can be used as a template by managers who need to run a large number of analyses and would prefer to do so from the command line (rather than using the GUI to repeatedly enter all parameters, once for each run).



```
## To reproduce the archived CHHR estimate, execute this script in an R
## session whose working directory is set to the directory containing
## this file:

library(BHSkde)

## Set path to results directory, creating it if it does not exist
results_dir <- "results"
dir.create(results_dir)

## Compute CHHR, saving it to a polygon shapefile in results_dir
kdeHerd(dsn = c("TelemObsPts.gpkg",
"TelemObsPts"), animalIDcol = "Animal_ID",
    aggregatePoints = FALSE,
    minObs = 21, bwEstimator = "Href",
    bwMultiplier = 1,
    cont = 0.95, outputType = "poly",
    outputDir = results_dir,
    outputFile = "CHHR_Asotin")
```

FIGURE D.4. "runscript.R" FILE FROM CHHR ESTIMATION ARCHIVE

To reproduce the estimated CHHR using `runscript.R`, follow these instructions:

1. Use `Rgui.exe` to launch the version of **R** installed by the RoCT installer. (For instructions on how to find the proper version of `Rgui.exe`, see Appendix C above.)

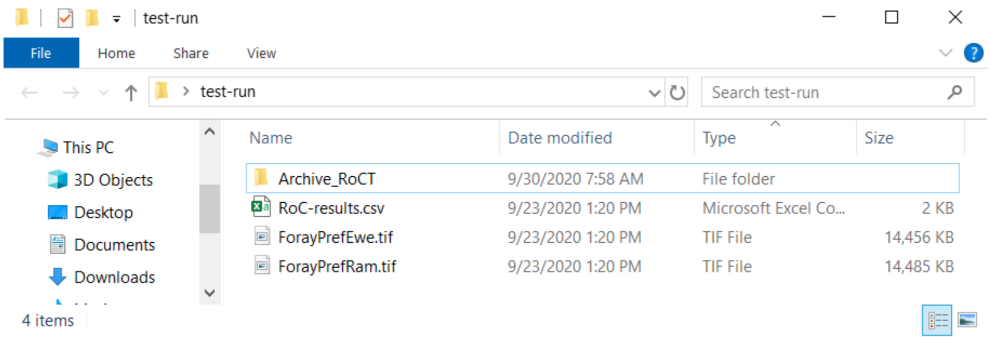
2. In **R**, change the working directory to the archive directory containing `runscript.R`. One way to do so from the **R** GUI launched in Step 1 is to select **File** then **Change dir…** from the GUI’s toolbar.

3. To reproduce the estimated CHHR, either copy and paste the contents of `runscript.R` into the **R** console (and then press **Return**), or type the following line at the **R** GUI command line and then press **Return**:

```
source("runscript.R")
```

Appendix E: Risk of Contact Estimation Archive

If a user selects the “Archive inputs” option on the “Compute RoCT” sidebar tab, an additional subdirectory named `Archive_RoCT` will be added to the output directory. This archive contains copies of all the data needed to reproduce the analyses performed when clicking the Tool’s “Compute RoCT” button, along with instructions on how to do so.

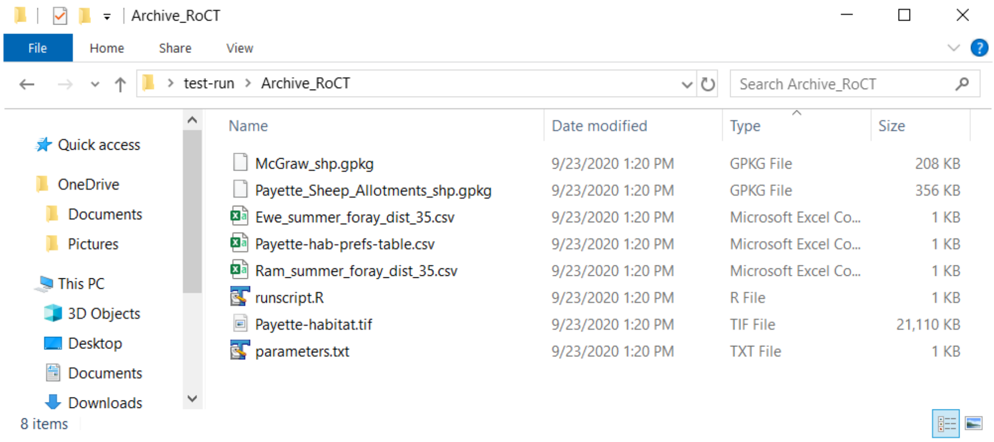


Name	Date modified	Type	Size
Archive_RoCT	9/30/2020 7:58 AM	File folder	
RoC-results.csv	9/23/2020 1:20 PM	Microsoft Excel Co...	2 KB
ForayPrefEwe.tif	9/23/2020 1:20 PM	TIF File	14,456 KB
ForayPrefRam.tif	9/23/2020 1:20 PM	TIF File	14,485 KB

FIGURE E.1. OUTPUT DIRECTORY STRUCTURE FOLLOWING CHHR ESTIMATION

The archive directory (example in FIGURE E.2) contains the following files:

- **Two `*.gpkg` files**, geopackage files, one containing the CHHR polygon feature and the other containing the allotments polygon feature used in the RoC analysis. The file names reflect the names of the features selected for the analysis.
- **One `*.tif` file,** containing the habitat preference raster used in the RoC analysis.
- **Three `*.csv` files**, two of them recording the ram and ewe foray distance distributions and the third recording the habitat preference value assigned to each habitat class in the habitat preference raster.
- **`parameters.txt`**, a text file, written in a structured YAML format, that records the paths to all geospatial inputs along with all other parameters used in estimating the RoC. For a more detailed description of its contents, see Section D.1 below.
- **`runscript.R`**, also a text file, containing an **R** script that can be run to reproduce the analysis used to estimate the RoC. For a more detailed description of its contents, see the section below.

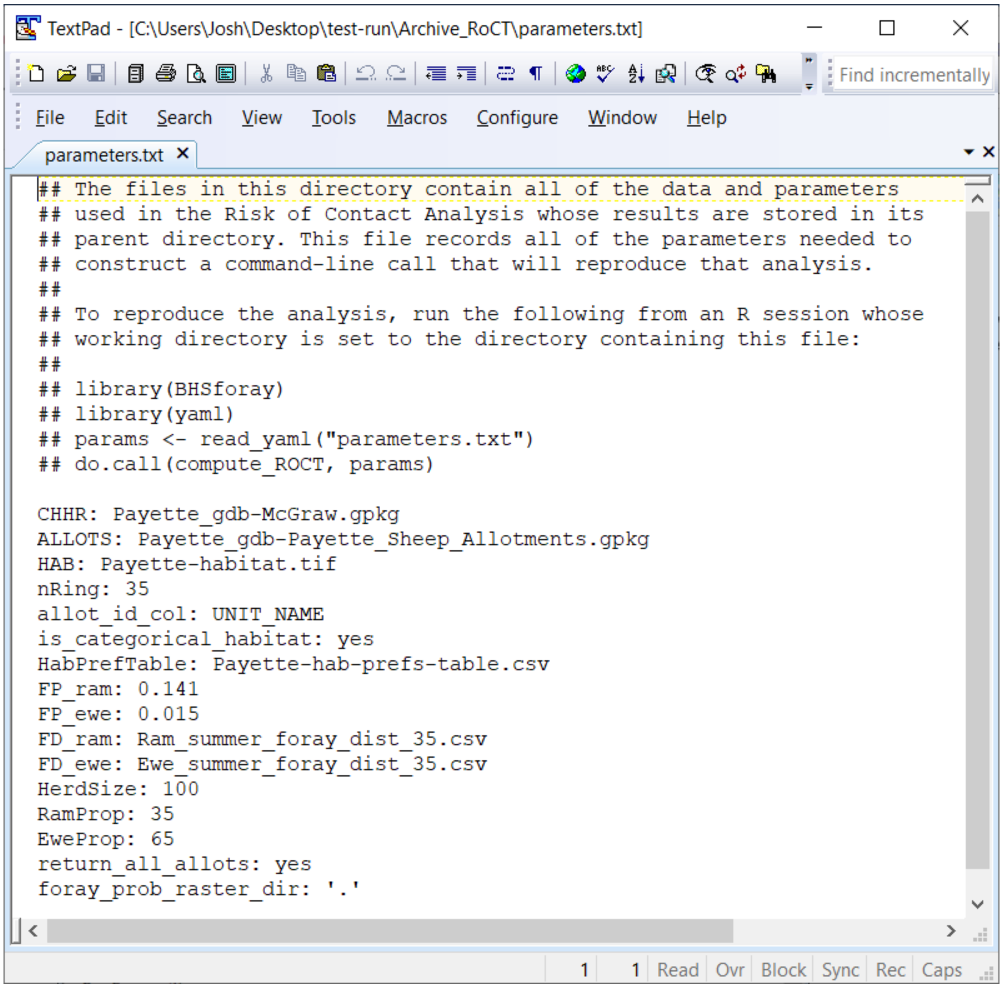


Name	Date modified	Type	Size
McGraw_shp.gpkg	9/23/2020 1:20 PM	GPKG File	208 KB
Payette_Sheep_Allotments_shp.gpkg	9/23/2020 1:20 PM	GPKG File	356 KB
Ewe_summer_foray_dist_35.csv	9/23/2020 1:20 PM	Microsoft Excel Co...	1 KB
Payette-hab-prefs-table.csv	9/23/2020 1:20 PM	Microsoft Excel Co...	1 KB
Ram_summer_foray_dist_35.csv	9/23/2020 1:20 PM	Microsoft Excel Co...	1 KB
runscript.R	9/23/2020 1:20 PM	R File	1 KB
Payette-habitat.tif	9/23/2020 1:20 PM	TIF File	21,110 KB
parameters.txt	9/23/2020 1:20 PM	TXT File	1 KB

FIGURE E.2. RoCT ESTIMATION ARCHIVE DIRECTORY STRUCTURE

E.1 The “`parameters.txt`” File

Like the `parameters.txt` file described in Section D.1 above, the RoCT archive’s `parameters.txt` file (see FIGURE E.3) records the values of all parameters selected by a user in the course of an analysis. It writes parameter-value pairs in a standardized YAML format that can, as a result, be used to reproduce the estimated CHHR that it documents.



```
## The files in this directory contain all of the data and parameters
## used in the Risk of Contact Analysis whose results are stored in its
## parent directory. This file records all of the parameters needed to
## construct a command-line call that will reproduce that analysis.
##
## To reproduce the analysis, run the following from an R session whose
## working directory is set to the directory containing this file:
##
## library(BHSforay)
## library(yaml)
## params <- read_yaml("parameters.txt")
## do.call(compute_ROCT, params)

CHHR: Payette_gdb-McGraw.gpkg
ALLOTS: Payette_gdb-Payette_Sheep_Allotments.gpkg
HAB: Payette-habitat.tif
nRing: 35
allot_id_col: UNIT_NAME
is_categorical_habitat: yes
HabPrefTable: Payette-hab-prefs-table.csv
FP_ram: 0.141
FP_ewe: 0.015
FD_ram: Ram_summer_foray_dist_35.csv
FD_ewe: Ewe_summer_foray_dist_35.csv
HerdSize: 100
RamProp: 35
EweProp: 65
return_all_allots: yes
foray_prob_raster_dir: '.'
```

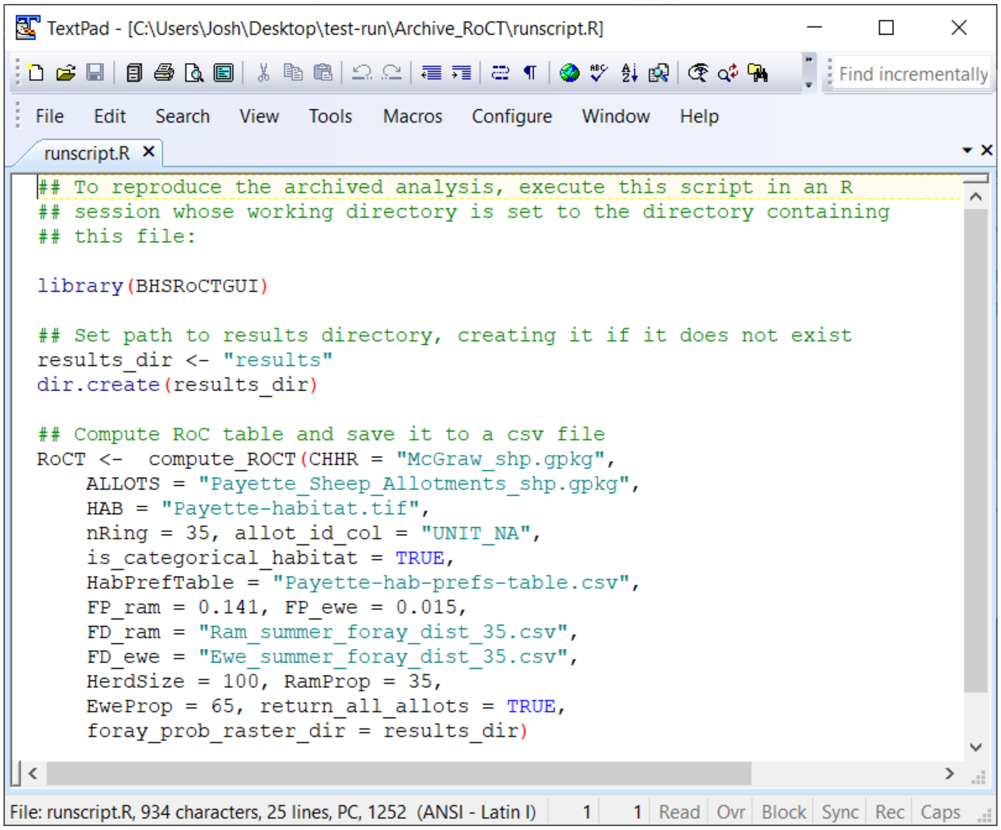
FIGURE E.3. "parameters.txt" FILE FROM RoCT ESTIMATION ARCHIVE

To view a help file that precisely describes the meaning of the parameters recorded in `parameters.txt` or to reproduce the estimated RoCT, follow the instructions given in Section D.1. The only minor modification to those instructions is that in this case, one will need to run all code from within the RoCT estimation archive rather than from within the CHHR archive.

E.2 The “runscript.R” File

Like the file described in Section D.2 above, `runscript.R` is a text file that records the values of the parameters used in a Risk of Contact analysis. It may be opened and viewed using any plain text editor (such as Notepad, WordPad, or TextPad) by right-clicking on the file and using **Open with** to select the editor.

Importantly (and also like the file described in Section D.2) the script can be used as a template by managers who need to run a large number of analyses and would prefer to do so from the command line. For instructions on how to use a `runscript.R` file like that shown in FIGURE E.4 to reproduce a RoC analysis, see Section D.2. The only minor modification to those instructions is that in this case, one will need to run all code from within the RoCT estimation archive rather than from within the CHHR archive.

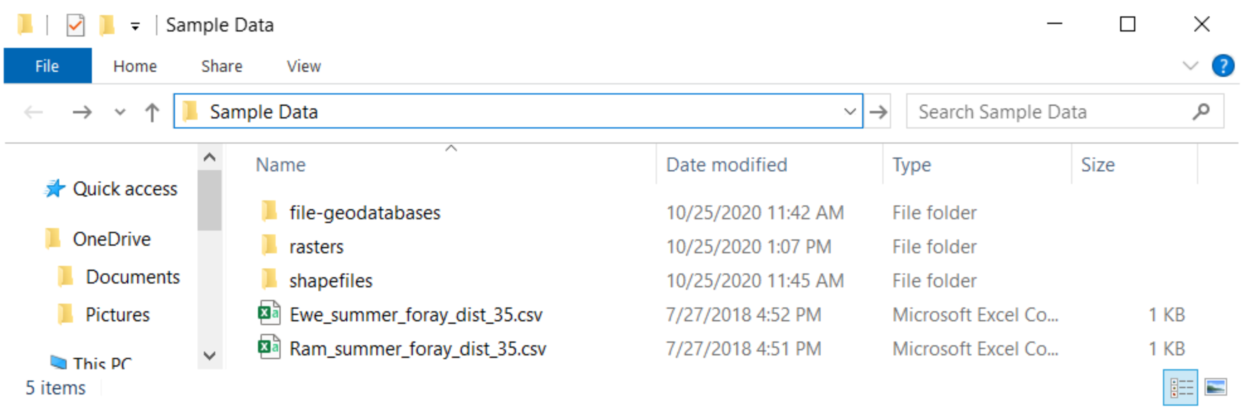


```
## To reproduce the archived analysis, execute this script in an R
## session whose working directory is set to the directory containing
## this file:

library(BHSRoCTGUI)

## Set path to results directory, creating it if it does not exist
results_dir <- "results"
dir.create(results_dir)

## Compute RoC table and save it to a csv file
RoCT <-  compute_ROCT(CHHR = "McGraw_shp.gpkg",
    ALLOTS = "Payette_Sheep_Allotments_shp.gpkg",
    HAB = "Payette-habitat.tif",
    nRing = 35, allot_id_col = "UNIT_NA",
    is_categorical_habitat = TRUE,
    HabPrefTable = "Payette-hab-prefs-table.csv",
    FP_ram = 0.141, FP_ewe = 0.015,
    FD_ram = "Ram_summer_foray_dist_35.csv",
    FD_ewe = "Ewe_summer_foray_dist_35.csv",
    HerdSize = 100, RamProp = 35,
    EweProp = 65, return_all_allots = TRUE,
    foray_prob_raster_dir = results_dir)
```

FIGURE E.4. "runscript.R" FILE FROM RoC ESTIMATION ARCHIVE

Appendix F: Sample Data Folder

The Risk of Contact Tool is distributed with a complete set of sample data, collected in the **`Sample Data`** folder (FIGURE F.1). The data, from Oregon, Washington, and Idaho, are a subset of those used in the 2010 Payette National Forest (NF) risk of contact analysis (USDA-FS, 2010; O'Brien et al., 2014) that formed the basis of the model implemented by the current Risk of Contact Tool. They may used to test the Tool's functionality or as examples of the type of data and the data formats required for the Tool's spatial and non-spatial inputs.



Name	Date modified	Type	Size
file-geodatabases	10/25/2020 11:42 AM	File folder	
rasters	10/25/2020 1:07 PM	File folder	
shapefiles	10/25/2020 11:45 AM	File folder	
Ewe_summer_foray_dist_35.csv	7/27/2018 4:52 PM	Microsoft Excel Co...	1 KB
Ram_summer_foray_dist_35.csv	7/27/2018 4:51 PM	Microsoft Excel Co...	1 KB

FIGURE F.1. "Sample Data" FOLDER DISTRIBUTED WITH THE RoCT TOOL

The `Sample Data` folder contains the following subdirectories and files:

- The **`file-geodatabases`** directory contains two file geodatabases. The first, `Asotin-telemetry-points.gdb`, contains a points feature consisting of telemetry points collected from bighorn sheep in a herd near Asotin, Washington. These points may be used as inputs to a CHHR estimation analysis by uploading them to the **Load bighorn locations** tab.as described in Section 4.4.1. The second, `Payette-polygons.gdb`, contains 15 polygon features. One of those, labeled "Payette_Sheep_Allotments", records allotment boundaries on the Payette NF, suitable for upload to the **Load allotments** tab (Section 4.5.3). The other 14 record CHHR boundaries of herds in the Hells Canyon and Snake River metapopulation, suitable for upload to the **Load CHHR** tab (Section 4.5.2).

- The **`rasters`** directory contains two files. `Payette-habitat.tif` is the habitat class raster used in the RoC analysis shown in the User's Guide, and may be uploaded using the **Upload habitat raster GeoTiff** button (Section 4.5.3). `Payette-hab-prefs-table.csv` is a "habitat preference file" associated with `Payette-habitat.tif`. It may be uploaded to the Tool by clicking on the radio button labeled "Habitat **classes**, with class preferences from a CSV file" shown in **Error! Reference source not found.**.

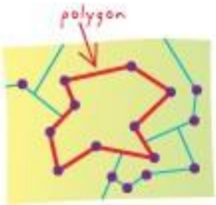
- The **`shapefiles`** directory contains the same spatial features as the **`file-geodatabases`** directory described above, stored in 16 separate shapefiles. `Asotin-telemetry-points.shp` is the points feature that may be used in the CHHR estimation workflow and `Payette_Sheep_Allotments.shp` records the Forest's sheep allotment boundaries. The remaining 14 shapefiles contain CHHR boundaries.

- The files `Ewe_summer_foray_dist_35.csv` and `Ram_summer_foray_dist_35.csv` are foray distance distribution files of the type described in Appendix B. They may be uploaded to the Tool using the **Input foray behavior** tab as described in Section 4.5.5.

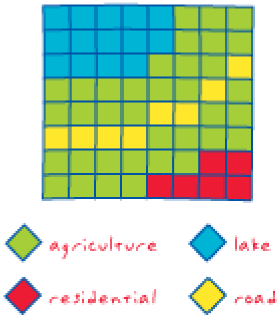
Appendix G: Glossary

Below are definitions for terms used in this document. For a complete listing of GIS terms, refer to the online ESRI GIS Dictionary.

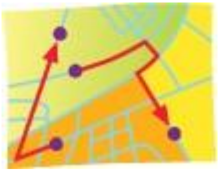
For additional information visit: https://desktop.arcgis.com/en/arcmap

dataset	Any collection of related data, usually grouped or stored together.
extension	In ArcGIS, an optional software module that adds specialized tools and functionality to ArcGIS Desktop. ArcGIS Network Analyst, ArcGIS StreetMap, and ArcGIS Business Analyst are examples of ArcGIS extensions.
feature	A representation of a real-world object on a map. 
floating points	Numbers that contain floating decimal points. For example, the numbers 5.5, 0.001, and –2,345.6789 are floating point numbers.
integer	A whole number (not a fraction) that can be positive, negative, or zero.
isopleth	An isoline drawn according to known values that can only be recorded for areas not points. Examples include population per square mile or the ratio of residential land to total land for an area. 
polygon	On a map, a closed shape defined by a connected sequence of x,y coordinate pairs, where the first and last coordinate pair are the same and all other pairs are unique. 
quantile	In a data distribution, a value representing a class break where classes contain approximately equal numbers of observations. The p-th quantile, where p is between 0 and 1, is that value that has a proportion p of the data below the value. For theoretical distributions, the p-th quantile is the value that has p probability below the value.
raster	A spatial data model that defines space as an array of equally sized cells arranged in rows and columns and composed of single or multiple bands. Each cell contains an attribute value and location coordinates. Unlike a vector structure, which stores

coordinates explicitly, raster coordinates are contained in the ordering of the matrix. Groups of cells that share the same value represent the same type of geographic feature.



shapefile	A vector data storage format for storing the location, shape, and attributes of geographic features. A shapefile is stored in a set of related files and contains one feature class.
telemetry	A technology that allows data measurements to be made at a distance.
vector	A coordinate-based data model that represents geographic features as points, lines, and polygons. Each point feature is represented as a single coordinate pair, while line and polygon features are represented as ordered lists of vertices. Attributes are associated with each vector feature, as opposed to a raster data model, which associates attributes with grid cells.



Appendix H: Frequently Asked Question (FAQs)

H.1 Model structure

Q: Does the Tool model attraction between bighorn sheep (BHS) and domestic sheep (DS)?

No. The Tool only models the probability that foraying bighorn sheep will reach allotments. It does not model the possible role of DS in attracting BHS to occupied allotments, nor does it model the interaction between BHS and DS occupying those allotments. The probability of contact with an allotment is based solely on the habitat suitability, BHS foray behavior, and distance of the allotment from the Core Herd Home Range (CHHR). The presence or absence of domestic sheep in an allotment plays no role (in the model) in the probability that bighorn sheep will reach that allotment. However, this does not mean that managers shouldn't consider the known attraction of the species for one another.

Q: How does the Tool take into account the amount of time BHS and DS are within contact of each other?

As explained in the previous answer, the Tool models the probability that foraying bighorn sheep will reach allotments. It does not directly model their interactions with domestic sheep occupying those allotments, nor the amount of time they spend in them.

However, if it is known that an allotment is only occupied by domestic sheep during a limited but definable period, the analysis should specify that period and the model inputs should be adjusted accordingly. The May-October "summer season" model reflected the period when domestic sheep were on NFS lands, and the 14% ram foray probability was based on that time window.

Q: What about the possibility of pathogen transmission from straying domestic sheep?

Stray domestic sheep have been implicated in several die-off's, and in many settings may pose a risk of transmission as large as or greater than do foraying bighorn sheep. Although the Tool does not model this factor, managers should also consider the risk of transmission due to straying domestic sheep.

Q: Did you investigate cost-surface models?

Cost-surface models of animal movement attempt to represent a landscape's permeability (or resistance) to animal movements. Each pixel of the landscape is assigned a resistance value: preferred habitat types have low resistance values, while high values are given to areas that are not preferred or are actively avoided. Locations that can only be reached by long journeys through non-habitat will have the highest path costs, and the lowest probabilities of being reached.

During the early model-development phase, the possibility of using cost-surface models was explored. Although a well-parameterized cost-surface model might be more realistic, the available data were not sufficient to adequately parameterize such a model. Even among the 1300+ animal years of data in the Hells Canyon telemetry data set, just 44 ram forays were observed, and in those, observations were typically at two-week intervals, so the actual paths travelled by foraying animals were simply unknown. Given that sheep on forays do seem to exhibit different behavior and habitat preferences than they do while inside the home range, there were simply not enough data to support a cost-surface analysis.

H.2 Data inputs and default parameter values

Q: What is the cell size of the draft habitat class raster layer developed by the Forest Service?

The habitat layers produced by the Forest Service for each of the western states are composed of 30 meter by 30 meter grid cells.

***Q:* How many animals (and how many points per animal) are needed to estimate a CHHR?**

A cutoff of 21 points per animal was used in the Payette NF analysis, but there is no hard rule. Like the rest of the model, the CHHR delineation should not be carried out in a vacuum, and the reasonableness of its estimated boundaries should by examined by an informed wildlife biologist.

Also, the number of points in a telemetry dataset is only one measure of its quality. Just as important is how representative of whole-year (or whole-season) use patterns those points are. In general, it's better to have a smaller number of records well distributed through the year than it is to have many "non-independent" points collected over a short time interval.

***Q:* Where do the default habitat preference values come from? Were they arbitrary ("just SWAGs" in the words of one questioner)?**

The values were derived from the Hells Canyon Bighorn Sheep Restoration Committee telemetry data set (approximately 54,000 data points). Preference values were based on a use/availability model which compares the proportion of telemetry points falling within a given habitat type to the proportion of the landscape composed of that habitat type (See Payette FSEIS Appendix L, p. L-32).

For example, while outside of the CHHR, Hells Canyon bighorn sheep exhibited relative habitat preferences of 1.00 for habitat and 0.177 for connectivity area. This implies that a given acre of habitat is nearly 6 times more likely to be visited or occupied by a bighorn sheep than the same area of connectivity area. Likewise, an allotment completely composed of habitat will be estimated to have nearly 6 times the contact rate as it would were it fully composed of connectivity area.

***Q:* How should habitat preferences be adjusted based on the amount of habitat and non-habitat? Do you recommend using the habitat preferences in the User Guide?**

Use/availability habitat preferences are expressed on a per area basis, so they may be applied without modification in landscapes with differing amounts of habitat and non-habitat.

The habitat preferences in the User Guide were based on actual observations of habitat use by Hells Canyon-area animals. In areas where enough telemetry data exist, it is possible (and maybe advisable) to calculate observed preferences of local bighorn sheep.

The Tool is also set up to use regionally appropriate habitat preference models wherever they are available. The Tool's habitat layer input field will accept any integer or real-valued GeoTIFF raster file with extension "tif" or "tiff". (See Section 3.2.3 of the User Guide for more details.)

***Q:* Is the risk of contact sensitive to herd size? Do users need to have good quality information about herd size and sex ratios?**

The estimated risk of contact is sensitive to herd size. In fact, the relationship between the two is linear, meaning that, e.g., doubling the number of animals in a herd will double the herd's expected annual contact rates with surrounding allotments.

Because rams are much more likely than ewes to leave the CHHR (i.e., to engage in foray movements), and tend to travel farther from the CHHR when they do, a herd's sex ratio also plays an important role in determining estimated contact rates. For a good first approximation, a herd's rate of contact is determined by the number of rams it contains.

In the prior analyses, estimates of herd size and sex ratio were primarily based on annual counts conducted by the Idaho, Oregon and Washington wildlife agencies responsible for Hells Canyon bighorn sheep. In some cases, herd-specific counts were available, while in others, counts were at the level of hunting units. In 11 Oregon and Washington bighorn sheep herds examined in the 2010 Payette NF analysis, observed ram:ewe ratios clustered tightly around 35:65, forming the empirical basis for the Tool's default value (USDA, 2010; Technical Appendix, p. L-41). Sex ratio data for other areas (e.g., state census data) can be used if available.

***Q:* Can all BHS in an administrative unit be analyzed at once, or does each BHS herd need to be analyzed separately? Is there a minimum distance between distinct herds?**

The Tool is designed to calculate risk of contact on a herd-by-herd basis. The CHHR should delineate the area typically used by members of a herd, from the borders of which any animal in the herd might make a foray movement. Forests or Districts encompassing several distinct herds should thus run the Tool several times, once for each identifiable herd. Where delineating the boundaries between herds is difficult or impossible, we advise consulting with both state and federal wildlife biologists and the bighorn sheep working group, who have some experience with this issue.

H.3 Scope/range of model's applicability

***Q:* What about seasonality of the model? (e.g., what to do in a desert setting where considerable variation in movement patterns between breeding and non-breeding seasons is known to exist?)**

Knowledge of local bighorn sheep's behavior and/or domestic sheep grazing patterns will lead to the choice of different seasons of analysis. The recommended workflow is to run the Tool once for each season of interest and to then aggregate the estimated rates of contact during each season. (Care should be taken to adjust foray probabilities to match the length of each season: all else being equal, foray probabilities will be higher during a six-month period than during a one- month period.)

***Q:* Can the Tool be used to model interactions between bighorn and cattle (or any animals other than domestic sheep)? Are there any known cases of pathogen transmission from cattle to sheep?**

Yes and yes. The Tool certainly could be applied to contact with other species or even with other herds of BHS. The Tool models probability of forays reaching different parts of a landscape, irrespective of what activities are occurring there. It could just as well be used to model probability of contact with cattle-occupied allotments (or roads, or areas of ORV use) as it can be used to model probability of contact with domestic sheep occupied allotments. The management implications of these "other types" of contacts would clearly be very different.

Although there are a few documented cases of pathogen transmission from cattle to bighorn sheep, contact with cattle is normally not a concern. Bighorn sheep and domestic sheep are attracted to one another and have behavioral and physiological similarities, unlike the situation with cattle. The few known instances involved extreme circumstances such as drought or hard winters that brought the two in close proximity. These unusual events can be prevented by not watering or salting near bighorn sheep.

***Q:* Could the model be used to evaluate relative suitability of different potential reintroduction sites in a landscape containing numerous private domestic sheep flocks?**

Yes, that would be an excellent setting in which to use the model.

***Q:* What about impacts of domestic sheep on private/State/other non-Federal lands?**

The Tool can be used to calculate the risk of contact with any polygon defining an area within which domestic sheep are found. The risk of contact with private sheep and goat farm flocks, as well as with other adjacent federal or State land located near CHHRs should be considered as a part of cumulative effects analysis.

H.4 Management Implications

***Q:* What is the suggested size of a single analysis area? Allotment? Ranger District? Field Office? District Office? State? Region?**

This may vary by agency regulatory requirements and the purpose of the individual analysis. The model could be applied to any of these. For Forest Planning (i.e. viability-related issues at Forest Plan scale) the National Forest might be an appropriate analysis area. For analyses of possible allotment management plan revisions, the allotment scale might be more appropriate. While carrying out allotment-level analyses, it is important to keep in mind that what matters, biologically-speaking, to a bighorn sheep herd, is its overall, landscape-level, rate of contact with domestic sheep. That landscape-wide rate, not its rate of contact with a single allotment, is what will determine the frequency of interspecies pathogen transmission and the herd's long-term prospects for viability.

The National Forest Management Act (NFMA) and the Forest Service's interpretive regulations require that habitats be managed to support viable populations of species at a Forest scale. Hence, the Payette Forest Plan analysis area incorporated bighorn sheep populations potentially affected by management at the Forest scale.

For BLM administered lands, The Federal Land Policy and Management Act of 1976 (FLPMA) states "the Secretary (of Interior) shall by regulation or otherwise, take action necessary to prevent unnecessary or undue degradation of the (public) lands." FLPMA also requires the BLM to manage its lands for multiple use and sustained yield. According to the Act, sustained yield means "the achievement and maintenance in perpetuity of a high-level annual or regular periodic output of the various renewable resources of the public lands consistent with multiple use" (43 USC § 1701 Sec. 103(h)).

For both the Forest Service and the BLM, the National Environmental Policy Act (NEPA) also prohibits the agencies from making an irreversible or irretrievable commitment of resources until those recognized risks are analyzed. See 42 U.S.C. § 4332.

Q: How should users deal with allotments that intersect the CHHR?

The Risk of Contact model focuses on the risk of contact due to relatively infrequent forays by bighorn sheep outside of their CHHR. Where an allotment directly overlaps the CHHR, it may be contacted by any adult or juvenile bighorn sheep using that part of the CHHR, not just those engaged in infrequent and relatively brief forays. Although the model doesn't quantify the rate of interspecies contact expected with allotments intersecting the CHHR, the rate is likely to be quite high. Barring strong evidence to the contrary, users should assume multiple contacts per year with allotments that overlap the CHHR.

Users can use the CHHR to clip the allotment so that only parts of it lying outside of the CHHR are considered. A knowledgeable wildlife biologist should be consulted before this type of manipulation is carried out.

Q: What is an acceptable level (probability or rate) of contact? Do you have any suggestions about how to translate the output of the Tool into management recommendations? What are recommended courses of action?

Obviously, the greater the rate of contact, the more likely that contact will result in pathogen transmission and a disease outbreak in a bighorn sheep population. In the Payette NF analysis, the rate of contact with allotments was used as one element in a complex disease model which estimated extirpation probabilities for various herds.

The FSEIS also estimated disease return intervals (in years) under risk scenarios that varied in the likelihood of a disease outbreak given contact with an allotment (see Payette EIS Table W- 29). Estimated disease return intervals help managers assess the possible impacts of outbreaks on bighorn sheep populations. Chapter 3 of the Payette EIS discusses the ramifications of various disease return intervals. We recommend that model users refer to the Payette EIS for examples of how this and other metrics may assist decision makers in interpreting the model's results.

The development team is considering next steps for how the probability and rates of contacts from the Risk of Contact Model can be used for near-term management recommendations. One step is to develop an output table that converts contact rates to estimated disease outbreak intervals given various risk assumptions that a contact with an allotment will result in a disease outbreak event. This information, along with other metrics used for the model, can be used to inform decision-makers on risks associated with different alternative management actions.

Q: Will using a Payette-style analysis lead to Payette-type conclusions?

The model is an adaptation of the Payette-style analysis that will be executed using site-specific information to derive site-specific results. It is one tool, in addition to other biological, social and economic factors, used by line officers in making an informed, science-based decisions.

Q: Is the model "conservative" with respect to estimating the risk of contact?

The model is intended to be neither conservative, nor liberal, in its risk of contact estimate. It provides a realistic framework for characterizing likely bighorn sheep movements across landscapes given what we understand about their behavior and habitat suitability. Obviously, the more data one has on populations and movement patterns and distances, the more accurate the model will be. The Hell's Canyon telemetry data points fit the habitat model with 92% of the telemetry points within modeled suitable habitat. The telemetry data points supplied by the State of Colorado had similar results after modification of canopy closure levels. The probabilities that sheep will reach each point on the landscape are mathematically derived using observed foray frequencies and distances and habitat preferences. Hence, the risk of contact model is likely not an overreach. The additional factor of known attraction between the two species is not modeled so from that perspective, it might be considered conservative.

Estimating the probability that contact with an allotment will result in a disease outbreak is a different question. Obviously, the more contacts, the more likely pathogen transmission and subsequent outbreak will occur. One can evaluate the rates of contact, relative to the risks of a contact resulting in a disease outbreak. One approach to quantifying pathogen transmission risk is addressed in the response to the previous question "What is an acceptable level (probability or rate) of contact?"

Q: How should managers account for risk of contact with domestic sheep occupying areas that are not administered by their agency? What does the model imply about the likely persistence/viability of disjunct "island" populations surrounded by domestic sheep that are not grazing on NF lands, but are within easy foray distance of the bighorn sheep?

Federal and state agencies need to consider the contributions of all land ownerships to bighorn sheep recovery. Private and state lands with domestic sheep are a pathogen transmission concern to be addressed with state, federal and NGO partners to minimize interspecies contact.

Agencies are responsible for management on their own lands. The courts have usually ruled that regardless of threats to species on other ownerships, agencies still must demonstrate management that is consistent with their regulations (e.g. viability). The management of salmon/steelhead populations on NFS lands is a good example: even though the vast majority of impacts occur off NFS lands, there is still a clear responsibility that agencies must provide conservation measures for habitats on public lands.

Q: What do the rates in the contact model's output table represent, and how can they be described in narrative form?

This frequently asked question does not ask for direction on the management actions that should be taken based on the results in the output table. Instead, it seeks clarification regarding the precise meaning of the values in the table.

The Payette NF's FSEIS' discussion of alternatives (especially the section beginning on its page 3-55) provides one example of how the model's contact rate and probability estimates may be described in narrative form. Another example is included below, in the text following Table H-1.

Table H-1 displays estimated contact rates from a single bighorn sheep herd ("Herd S15") to two nearby domestic sheep allotments. Herd S15 consists of 200 adult animals — 70 rams and 130 ewes. Its columns have been renamed and reformatted, as they might be in a report, but the values in them directly correspond to the values in the `RoC-results.csv` file in the output directory produced by using the Tool to run a Risk of Contact analysis. (This same table is also displayed in the browser at the conclusion of a Risk of Contact analysis (Figure 4.54).)

The **Single ram** and **Single ewe** columns (corresponding to columns labeled **"**ramContactProb**"** and **"**eweContactProb**"** in `RoC-results.csv`) display the annual/seasonal probability that a given ram or ewe **will leave the CHHR and then go on to contact an allotment**. These per-individual contact rates for ewes are much lower than those for rams, largely because ewes are much less likely to make any foray movement in a year than are rams. (The default annual/seasonal foray probabilities are 14.1% for rams, and 1.5% for ewes.)

The columns **All rams** and **All ewes** (corresponding to the columns labeled "allRamsContactRate" and "allEwesContactRate" in `RoC-results.csv`) display the expected annual/seasonal number of rams and ewes

that will foray outside of herd S15's home range and contact each of the allotments. For both rams and ewes, the total contact rate is equal to the per-individual contact probability multiplied by the number of animals. Looking just at the Fisher Mountain Pasture, for example, the number of expected contacts for all rams is 0.009308 contacts/ram/yr * 70 rams = 0.651553 contacts/yr.
Similarly, for all ewes, the number is expected contacts 0.000472 contacts/ewe/yr * 130 ewes = 0.06139 contacts/yr.

The final column (corresponding to the "herdContactRate" column in `RoC-results.csv`) gives the total herd contact rate, the sum of the rates for all rams and all ewes. For the Fisher Mountain allotment, the total rate is 0.651553 + 0.06139 = 0.712944 contacts/yr.

TABLE H-1: ESTIMATED ANNUAL CONTACT RATES OF HERD S15 ANIMALS (70 RAMS AND 130 EWES) WITH IVY CREEK AND FISHER MOUNTAIN PASTURES.

	Estimated annual contact rates via foray				
Pasture	**Single ram**	**Single ewe**	**All rams**	**All ewes**	**All animals (Herd)**
Ivy Creek	0.002446	0.000138	0.171236	0.017934	0.189169
Fisher Mtn	0.009308	0.000472	0.651553	0.06139	0.712944

The following bullets give one example of how the rates in Table H-1 might be described in narrative form:

- **Single Ram Contact Rate:** Annual/Seasonal probability that a typical ram will leave its Core Herd Home Range (CHHR) and contact this pasture.

Fisher Mtn. Example: There is an estimated 0.93% probability that any given ram will leave the S15 herd's CHHR and contact the Fisher Mtn. pasture in any given year/season.

- **Single Ewe Contact Rate:** Annual/Seasonal probability that a typical ewe will leave its Core Herd Home Range (CHHR) and contact this pasture.

Fisher Mtn. Example: There is a 0.047% probability that any given ewe will leave its CHHR and contact this pasture each year/season.

- **All Rams Contact Rate:** Expected number of rams contacting the pasture each year/season.

Fisher Mtn. Example: Based on the number of rams (70) and their individual contact probabilities (0.93%), it is estimated that Herd S15 rams will foray from the CHHR and make contact with this pasture at a rate of 0.65 times per season (= 70 *0.93%). In other words, one ram contact with the Fisher Mtn. pasture is expected every 1.5 (= 1 / 0.65) years/seasons.

- **All Ewes Contact Rate:** Expected number of ewes contacting pasture each year/season.

Fisher Mtn. Example: Based on the number of ewes (130) and their individual contact probabilities (0.047%), it is estimated that Herd S15 ewes will foray from the CHHR and make contact with this pasture at a rate of 0.06 (= 130 * 0.047%) times per year/season. In other words, one ewe contact with the pasture is expected to occur every 16 (= 1 / 0.06) years/seasons.

- **Total Herd Contact Rate:** Average number of adult bighorn sheep (rams plus ewes) expected to foray from the CHHR and contact this pasture each year/season.

Fisher Mtn. Example: Based on the aggregate ram and ewe contact rates (0.65 and 0.06 contacts/year respectively), it is expected that a bighorn sheep will foray from the core herd range and make contact with this pasture at an average rate of 0.71 times per year/season equating to a rate of approximately 7 contacts every 10 years.

Using a conservative assumption that one in four contacts results in pathogen transmission and a subsequent outbreak, a disease outbreak would be expected to occur every 10 years if not sooner. If, instead, just one in 10 contacts results in an outbreak, disease outbreaks would still be expected every 14 years, on average. Outbreaks at this level would mean that the population is consistently exposed to ongoing pathogen transmission and resultant disease outbreaks. The population would likely be extirpated as a result of consistent exposure to interspecies contact.

Q: Is there a realistic minimum viable population size for bighorn herds?

The model does not recommend a minimum population. Our planning regulations definition for a viable population is: “A population of a species that continues to persist over the long term with sufficient distribution to be resilient and adaptable to stressors and likely future environments”. The literature suggests a range from 100-188 animals to provide for bighorn sheep population persistence.

Q: What other considerations go into interpreting contact rates and their possible impacts on bighorn sheep persistence?

The Risk of Contact Model provides outcomes that reflect contact rates between bighorn sheep and domestic sheep allotment boundaries. This may, or may not, equate to interspecies contact. Nothing in the available literature provides an estimate of bighorn sheep contacts with an allotment and real interspecies contact rates in wildland environments. To account for this uncertainty an array of probabilities that contact with an allotment would result in actual interspecies contact that would in turn result in pathogen transmission and a subsequent disease outbreak can be evaluated. The Payette analysis defined a “moderate” rate of contact with an allotment resulting in a disease outbreak at 0.25, or that 1 in 4 contacts with an allotment would result in interspecies contact, pathogen transmission, and a disease outbreak. Scenarios with probabilities above and below this value were evaluated; i.e. from 0.05 (1 in 20) and 1.0 (every) contacts with an allotment resulting in a disease outbreak event. This approach allows the relative comparison of alternatives while recognizing uncertainties associated with these assumptions.

Although the mechanisms of pathogen transmission and resulting disease outbreaks in bighorn sheep following interspecies contact are not fully understood, there is compelling evidence from the literature indicating the need to prevent interspecies contact and associated management guidance that these species be kept separate (WAFWA 2012). The Risk of Contact model does provide the probability and rates of contact between bighorn sheep and allotments where they potentially can contact domestic sheep. This is a logical surrogate to address separation.

The effects of respiratory disease outbreaks on bighorn sheep populations are often severe (see Besser et al. (2012a), Table 1 and Besser et al. (2012b), Table 1). Controlled pen experiments identified in Besser et al. (2012a) resulted in complete or nearly complete die-offs of bighorn sheep following contact with domestic sheep. Besser et al. (2012b), Coggins and Matthews (1992), and Foreyt (1990) also document that disease perturbations can affect lamb recruitment for several years following severe population declines resulting from disease epizootics. Hence, when bighorn sheep disease die-offs occur, there is a substantial immediate mortality (population decline) and subsequent delayed population recovery due to poor lamb recruitment, that follows in the aftermath for many years.

Although there is no guidance on the number of decades required to recover from a disease outbreak, observations of herds that have experienced pneumonic events indicate it likely requires many decades, if the herd recovers at all. Given the severity of respiratory die-offs and the potential link to domestic sheep as a causal factor in outbreaks, management scenarios should allow for long periods of time without interspecies contact. Population recovery is unlikely where interspecies contact, potentially resulting in pathogen transmission and subsequent disease outbreaks, occurs within a few decades of each other.

As an example, if the model output is 0.08 contacts (combined ram and ewe) with an allotment per year, and the assumed probability of a contact with an allotment resulting in an interspecies pathogen transmission and subsequent disease event is one in four (0.25), the average disease outbreak period would be 50 years (1 / [0.08 contacts / yr * 0.25 outbreaks / contact]). Although we still lack empirical data to make recommendations on the periodicity of outbreaks and the effects on bighorn sheep, this might be a good benchmark to ensure population persistence until better data are available.

Appendix I: References

Besser, T. E., E. F. Cassirer, C. Yamada, K. A. Potter, C. Herndan, W. J. Foreyt, D. P. Knowles, and S. Srikumaran. 2012a. Survival of bighorn sheep (*Ovis canadensis*) comingled with domestic sheep (*Ovis aries*) in the absence of *Mycoplasma ovipneumoniae*. Journal of Wildlife Diseases 48(1): 168–172.

Besser, T. E., M. A. Highland, K. Baker, E. F. Cassirer, N. J. Anderson, J. M. Ramsey, K. Mansfield, D. L. Bruning, P. Wolff, J. B. Smith, and J. A. Jenks. 2012b. Causes of pneumonia epizootics among bighorn sheep, 2008-2010. Emerging Infectious Diseases 18(3):406–414.

Coggins, V. L., and P. E. Matthews. 1992. Lamb survival and herd status of the Lostine bighorn herd following a Pasteurella die-off. Proceedings of the Biennial Symposium of the Northern Wild Sheep and Goat Council 8:147–154.

Fieberg, W. J. 1990. Kernel density estimators of home range: Smoothing and the autocorrelation red herring. Ecology. 88(4):1059-1066.

Foreyt, W. J. 1990. Pneumonia in bighorn sheep: effects of *Pasteurella haemolytica* from domestic sheep and effects on survival and long-term reproduction. Proceedings of the Biennial Symposium of the Northern Wild Sheep and Goat Council 7:92–101.

Holtrip, J. 2011. Letter: Bighorn Sheep Analysis for NEPA Documents, August 19, 2011

O'Brien, J. M., C. S. O'Brien, C. M. McCarthy, and T. E. Carpenter. 2014. Incorporating foray behavior into models estimating contact risk between bighorn sheep and areas occupied by domestic sheep. Wildlife Society Bulletin 38(2):321–331.

Sheather, S.J. and Jones, M.C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. Journal of the Royal Statistical Society, B. 53:683-690.

U.S. Department of Agriculture, Forest Service [USDA-FS]. 2010. Final supplement to the final environmental impact statement for the Southwest Idaho Ecogroup Land and Resource Management Plans. U.S. Department of Agriculture, Forest Service, Intermountain Region, Payette National Forest, Ogden, Utah, USA.

Weldon, L. 2012. Letter: Bighorn Sheep Analysis for NEPA Documents, June 11, 2012

Western Association of Fish and Wildlife Agencies [WAFWA]. 2012. Recommendations for Domestic Sheep and Goat Management in Wild Sheep Habitat. WAFWA Wild Sheep Working Group. 24 pp.

Appendix J: Payette FSEIS, Chapter 3

This appendix contains “Chapter 3. Affected Environment and Environmental Consequences” from the Payette National Forest’s 2010 Final Supplemental Environmental Impact Statement, in which they reported the results of their bighorn sheep risk of contact analysis (USDA-FS, 2010). It is included here as an example of how the model and its results have been incorporated in an environmental impact statement.

The first half of the chapter includes an extensive review of the literature available in 2010 implicating domestic sheep and goats in transmission of respiratory disease to bighorn sheep. It then moves on to an introductory discussion of the risk of contact model. In the chapter’s second half, the section titled “Environmental Consequences” is devoted a comparison of several proposed alternative management scenarios with respect to their likely impacts on pathogen transmission to bighorn sheep herds.

Chapter 3.
Affected Environment and Environmental Consequences

Terrestrial Wildlife Habitat and Species

Consistent with 36 CFR §219.20(a), these paragraphs will supplement the Management Indicator Species section, page 3-281 through 3-282, of the Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement.

CURRENT CONDITION

Management Indicator Species

Proposed Management Indicator Species

White-headed Woodpecker (*Picoides albolarvatus*)—The effects analysis for threatened, endangered and sensitive species can be found in the *Biological Evaluation* (Appendix K). The white-headed woodpecker is a management indicator species for the Payette National Forest. Given the habitat requisites of this species (i.e., forested habitats), changes in domestic sheep grazing to conserve bighorn sheep habitats will have negligible effects on habitats and populations of this species (Terrestrial Management Indicator Species for the Payette National Forests in Appendix F).

Pileated Woodpecker (*Dryocopus pileated*)—The pileated woodpecker is a management indicator species for the Payette National Forest. Given the habitat requisites of this species (i.e., forested habitats), changes in domestic sheep grazing to conserve bighorn sheep habitats will have negligible effects on habitats and populations of this species (Terrestrial Management Indicator Species for the Payette National Forests in Appendix F).

Consistent with 36 CFR §219.20(a), the bighorn sheep discussion in the Current Conditions, Species of Special Interest section, pages 3-286 through 3-287, of the Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement will be deleted. The following pages will supplement the Current Conditions, Sensitive Species section, page 3-277, and Table W-2 will replace the corresponding table, pages 3-268 though 3-269, of the Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement.

CURRENT CONDITIONS

Sensitive Species

At present, 19 terrestrial vertebrate species (1 amphibian, 13 birds, and 7 mammals) within the Ecogroup are on the U.S. Forest Service, Intermountain Region sensitive species list (see Table W-2). The bighorn sheep was added to this list by the Regional Forester on July 29, 2009.

Table W-2. Sensitive Terrestrial Species of the Ecogroup

Type	Common Name	Forest*	Global Rank	PVGs[a] or Cover Types Used by the Species	PVGs or Cover Types that Provide Primary Habitat	Management Considerations
Mammals	Wolverine	All 3	G4T4	All	All	Vulnerability during denning
	fisher	All 3	G5	3, 4, 5, 6, 7, 8, 9, 10	3, 4, 5, 6, 7, 8, 9	Habitat fragmentation, snags and logs
	Townsend's big-eared bat	All 3	G4	NA	NA	Vulnerability to disruption
	spotted bat	All 3	G4	NA	NA	Vulnerability to disruption
	Bighorn sheep	All 3	G4	Non Forested	Non Forested	Vulnerable to disease
	Southern Idaho ground squirrel	Boise	G2	Non Forested	Non Forested	Habitat fragmentation
	gray wolf	All 3	G4	All	All	Human caused mortality

Type	Common Name	Forest*	Global Rank	PVGs[a] or Cover Types Used by the Species	PVGs or Cover Types that Provide Primary Habitat	Management Considerations
Birds	northern goshawk	All 3	G5	All	2, 3, 4, 5, 6, 7, 8, 9	Nest stand, prey availability
	white-headed woodpecker	All 3	G4	1, 2, 3, 5	1, 2, 3, 5	Large Snags, low crown density
	flammulated owl	All 3	G4	1 ,2 3, 5, 7	1, 2, 3, 5, 7	Large snags and trees
	harlequin duck	Payette	G4	Large streams in forest setting	Large streams in forest setting	Forest Riparian
	mountain quail	Payette, Boise	G5	1	1	Shrubby Riparian
	boreal owl	All 3	G5	3, 6, 7, 8, 9, 11	3, 6, 7, 8, 9, 11	Large snags
	northern three-toed woodpecker	All 3	G5	3, 7, 8, 9, 10, 11	3, 7, 8, 9, 10, 11	Abundant snags
	great gray owl	All 3	G5	9, 10	9, 10	Forested areas with meadows
	Columbian sharp-tailed grouse	Sawtooth	G5T3	Native shrub/ grass lands	Native shrub/ grass lands	Shrubby wintering areas
	common loon	Sawtooth	G5	Natural lakes	Natural lakes	Vulnerability during nesting, abundant small fish for prey
	peregrine falcon	All 3	G4T3	High cliffs	High cliffs	Vulnerability during nesting, prey abundance
	yellow-billed cuckoo	None	G5	Riparian	Riparian	Habitat fragmentation
	bald eagle	All 3	G5	Riparian	Riparian	nest stand, prey availability
Amphibian	Columbia spotted frog	All 3	G4Q	Riparian areas	Riparian Areas	Still or ponded water

[a] PVGs are Potential Vegetation Groups

Bighorn Sheep (*Ovis canadensis*)

History

Prior to the mid-1800s, bighorn sheep were abundant and widely distributed throughout the western United States. Bighorn sheep in North America were estimated to number approximately 1.5–2 million (Buechner 1960, Queen et al. 1994). Large declines in both bighorn sheep abundance and distribution occurred during the late 1800s and early 1900s due to overharvest, habitat loss, and competition for forage with and disease transmission from domestic livestock (Goodson 1982, Valdez and Krausman 1999). Bighorn sheep occur at less than 10 percent of historic numbers and the current distribution is estimated at less than 33 percent of historic distribution, with most existing within relatively small and isolated populations despite recurring recovery efforts (Berger 1990, Singer et al. 2000b).

Bighorn sheep were abundant in Idaho prior to the mid-1800s (Smith 1954, Toweill and Geist 1999), and included both California bighorn sheep (*O. c. californiana*) in the southwest portion of the state, and Rocky Mountain bighorn sheep (*O. c. canadensis*) northeast of the Snake River Plains. European settlement of Idaho in the mid-1800s increased bighorn sheep harvest and introduced domestic sheep onto these landscapes. Historic accounts of major die-offs of bighorn sheep in the Salmon River Mountains began in approximately 1870 (Smith 1954). In 1969, Idaho began reintroducing Rocky Mountain bighorn sheep into historic habitats and increased their numbers to nearly 4,000 sheep by 1989. That number had decreased to 1,710 by 1998, with population declines attributed to disease outbreaks (Toweill and Geist 1999).

History of Bighorn Sheep on the Payette National Forest

Two Rocky Mountain bighorn sheep metapopulations occur on the Payette National Forest, one within the Hells Canyon of the Snake River and the other among the Salmon River Mountains (USDA Forest Service 2003b). Historically, these populations were likely connected by suitable habitats between the two major drainages and may have functioned as one metapopulation. More than 10,000 bighorn sheep may have once lived in the Hells Canyon and surrounding mountains, but they were extirpated by the mid-1940s by competition for forage with domestic livestock, disease, and unregulated hunting (HCBSRC 2005). Reintroduction efforts in Hells Canyon began in 1971 and 474 bighorn sheep were transplanted into Hells Canyon between 1971 and 2004 (HCBSRC 2005). In 2005, the Hells Canyon Bighorn Sheep Restoration Committee estimated 875 bighorn sheep were located within Hells Canyon (HCBSRC 2005). This number represents a positive population growth since 1971, although seven bighorn sheep die-offs have been reported since 1971 (HCBSRC 1997).

The Salmon River metapopulation was never extirpated (Toweill and Geist 1999) although the population has experienced periodic die-offs. Recent winter population surveys document at least 567bighorn sheep within the big game management units 14, 19, 19A, 20, 20A, 26 and 27of the Salmon River; in 2006 and 2007, and an additional 137 bighorn sheep were surveyed in the South Fork Salmon River and main Salmon River (IDFG 2008). Current estimates of bighorn sheep in hunting units in and around the Payette National Forest have decreased 47 percent since the 1981 Idaho Fish and Game surveys—(IDFG 1985)

Bighorn Sheep Populations and Movement

Bighorn sheep are typically structured in metapopulations. Each metapopulation is composed of discrete local populations that interact with each other as a result of limited movement between the local populations (Bleich et al. 1996, Singer et al. 2000a). The fragmented nature of sheep habitat and the relatively small size of most bighorn sheep herds suggest that bighorn sheep evolved with a metapopulation structure where small populations would not persist without movement and reproduction between herds (Gilpin and Hanski 1989, Berger 1990, Bleich et al. 1990). The term “population” is used loosely here: a large amount of contact and exchange of individuals may occur between some of the populations named in this document, while other populations are fairly isolated. For the purpose of this document, the term population will be used, recognizing that distinct populations within a metapopulation of bighorn sheep are not always clearly delineated.

The metapopulation structure of bighorn sheep and long-distance periodic movements between populations are well documented. For example, sheep with geographically separate winter ranges have been observed sharing summer ranges (Akenson and Akenson 1992). These interactions can have positive effects, such as population augmentation, colonization, and enhancement of genetic diversity; however, negative effects, such as disease transmission, can also occur. Bighorn sheep ewes can travel as far as 24.8 miles from winter ranges to lambing areas. On Bureau of Land Management (BLM) lands in Idaho, bighorn sheep rams were documented to have traveled up to nearly 50 miles through towns and across major rivers (Coggins 2002). Telemetry data has shown that desert bighorn sheep regularly cross the broad valleys that separate the majority of desert mountain ranges (Ough and deVos 1984, Schwartz et al. 1986, Jaeger 1994). These complex spatial and temporal range use patterns occur between populations of sheep with resulting effects on forage and vulnerability to disease and parasite transmission (Akenson and Akenson 1992). Telemetry and observational data of bighorn sheep herds in the Hells Canyon and the Salmon River drainages document movement from canyon-bottom winter ranges to high-elevation summer ranges. The presence of dispersal corridors between suitable patches of habitat, and the ability of sheep to move between patches, influences their ability to disperse into suitable, but unoccupied, habitats (Noss 1987, Simberloff and Cox 1987, Hudson 1991, Douglas and Leslie 1999).

Hells Canyon Metapopulation

The Hells Canyon metapopulation contains 12 populations, largely defined by reintroduced cohorts that established in specific areas within Hells Canyon. The Hells Canyon bighorn sheep restoration project covers 5,617,062 acres in the Snake River drainage in Washington, Oregon, and Idaho (HCBSRC 2005). When the Hells Canyon bighorn sheep restoration project was established, it was believed that sheep would not cross from the Oregon side of Hells Canyon to the Idaho side; however, that has not been the case and bighorn sheep have been observed swimming across the reservoir and walking on Brownlee Dam (Vic Coggins, personal communication, 2008). Winter range is limited at the higher elevations of the Wallowa and Seven Devils mountains but is extensive within the Snake River portion of the project area (HCBSRC 1997). Extent of habitat does not appear to currently limit the number of bighorn sheep since they do not occupy much of the suitable habitat; however, habitat quality such as forage species composition and nutritional value may affect herd size, productivity, and distribution (HCBSRC 1997).

Salmon River Metapopulation

Native populations of bighorn sheep were never extirpated from the Salmon River Mountains, making them important native genetic stock: loss of the genetic diversity of these populations could affect bighorn sheep persistence and restoration at scales much larger than the Payette National Forest. The Salmon River metapopulation has several populations distributed along the South Fork Salmon River, main Salmon River Canyon, and Middle Fork Salmon River. Of these populations, the only ones known within the boundaries of the Payette National Forest are the Main Salmon River, South Fork Salmon River, Upper Main Salmon River, and Big Creek herds (Akenson and Akenson 1992). Several observations of bighorn sheep have been made in the Little Salmon River over multiple years. These observations suggest a degree of site fidelity for this area; however, neither telemetry data nor enough observations exist to determine if an established herd is in this area. The uncertainty of bighorn sheep status in the Little Salmon River has lead to analyzing this area as an area of concern. This area of concern is analyzed similar to a herd; however, the population size has been limited to four animals as this is the number reported in the area. Due to the nature of a metapopulation and the high vagility characteristics of this species, bighorn sheep adjacent to the Payette National Forest may affect or be affected by management on the Payette National Forest. The main Salmon River populations may overlap the Payette National Forest, with the Middle Fork Salmon River populations just east and adjacent to the Payette National Forest.

Review of Disease Transmission and Bighorn Sheep

Free-ranging bighorn sheep are susceptible to many diseases. The most important of these is bronchopneumonia, which is usually associated with bacteria in the genera *Pasteurella* and *Mannheimia* (Bunch et al. 1999, Miller 2001). Pneumonia caused by these bacteria has produced partial to complete die-offs of herds across the species’ range, with the frequency of die-offs being particularly high in the northwestern US (Monello et al. 2001). The current abundance and distribution of the species appears to be largely limited by recurrent pasteurellosis epidemics (Hobbs and Miller 1992, Jorgenson et al. 1997, McCarty and Miller 1998).

A long history of large-scale, rapid, all-age die-offs in bighorn sheep has been documented across Canada and the United States, many presumed associated with domestic animal contact (Shackleton 1999). Although limited knowledge of transmission dynamics exists (Garde et al. 2005), extensive scientific literature supports a relationship between disease in bighorn sheep populations and contact with domestic sheep. The literature includes both circumstantial evidence linking bighorn die-offs in the wild to contact with domestic animals, and controlled experiments where healthy bighorn sheep exposed to domestic sheep displayed subsequently high mortality rates (Foreyt 1989, 1990, 1992 a,b; Foreyt et al. 1994; Onderka et al. 1988; Onderka and Wishart 1988; Garde et al. 2005). While much of the evidence for disease transmission from domestic sheep to free-ranging bighorn sheep is circumstantial, a large literature base has emerged that documents bighorn sheep die-offs near domestic sheep. These die-offs have prompted management decisions to eliminate shared use of ranges by bighorn and domestic sheep by Federal land management agencies and State wildlife departments (Goodson 1982).

Respiratory Disease Outbreaks in Bighorn Sheep

Early evidence of an association of domestic sheep with die-offs was largely anecdotal. Since at least 1937, multiple die-offs of bighorn sheep throughout North America have been documented in literature and *Pasteurella* spp. were often cited as the cause (Potts 1937, Marsh 1938, Post 1962, Foreyt and Jessup 1982, Onderka and Wishart 1984, Spraker et al. 1984, Hobbs and Miller 1992, Ryder et al. 1992, McCarty and Miller 1998). As with other native North American wild ruminants, epidemics in bighorn sheep typically followed the settlement and establishment of domestic livestock grazing and may have reflected an historical introduction of novel pathogens into native wildlife populations by the late 1800s (Grinnell 1928, Skinner 1928, Honess and Frost 1942, Miller 2001). Limited understanding and/or access to bacteriological techniques probably precluded diagnoses of pasteurellosis in many early field investigations, thus the role of *Pasteurella* spp. in bighorn sheep epidemics was probably underestimated in studies reported prior to 1980 (Frank et al. 2004).

Although various stressors and organisms are implicated in outbreaks of bacterial pneumonia in bighorn sheep, the most commonly associated organisms are bacteria in the genera *Pasteurella* and *Mannheimia*, in particular *Mannheimia haemolytica* (formerly *Pasteurella haemolytica*[1]) and *Bibersteinia trehalosi* (formerly *P. haemolytica* biotype T) (Foreyt 1990). Both genera belong to the *Pasteurellaceae* — an incredibly large and diverse group of bacteria that continues to undergo reclassification (Garde et al. 2005). *Pasteurella* and *Mannheimia* spp. infect most mammalian families, as well as many if not all non-vertebrates (Miller 2001). They are common commensals on the mucous membranes of animal species in all climatic zones, most of whom are asymptomatic carriers (Biberstein 1979).

Despite being ubiquitous among mammals, including native North American ruminants (Biberstein 1979, Thorne 1982, Jaworski et al. 1998), these bacteria cause only sporadic cases of pasteurellosis (usually associated with *Pasteurella multocida*) in bison, elk, moose, mountain goats, mule deer, and pronghorn (Thorne 1982). And while pasteurellosis is one of the most common bacterial infections of domestic sheep, the most severe outbreaks kill 2.5 percent of the domestic sheep in a herd, not even close to the mortality seen in die-offs of bighorn sheep (Gilmour and Gilmour 1989, Donachie 2007, Miller 2001).

In contrast to most other wild and domesticated mammal species, bighorn sheep are notable in their extreme susceptibility to some strains of *Pasteurellaceae* (Miller 2001). Pneumonia associated with *Pasteurella* causes die-offs that can kill some, many, or all adult bighorn sheep in a herd (Bunch et al. 1999). Outbreaks of pneumonia are often followed by several years of decreased recruitment; lambs are born healthy but then sicken and die after several weeks, presumably after the loss of protection via passive immunity from their mother’s colostrum (Foreyt 1990). Elevated mortality of lambs can continue for several years – up to 15 – further impairing population recovery and stability (Foreyt 1990, McCarty and Miller 1998, Miller et al. 2000, Cassirer et al. 2001, Miller 2001, Cassirer and Sinclair 2007, George et al. 2008, Frank et al. 2004). It has been speculated that once *Pasteurella* spp. have been introduced to bighorn sheep populations, they may become endemic and continue cycling for decades (Miller et al. 1991, Hobbs and Miller 1992, Miller et al. 1995).

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[1] Future references to *Pasteurella* spp. include both *Pasteurella* spp. and *Mannheimia haemolytica.*

Although a high propensity for bighorn sheep mortality following direct contact with domestic sheep exists, domestic sheep appear to be refractory to most wild sheep pathogens (Martin et al. 1996, Schommer and Woolever 2001). Furthermore, domestic sheep are often carriers of *Pasteurella* spp. but do not exhibit clinical signs.

The physiological and cellular causes of bighorn sheep's susceptibility to *Pasteurella* spp. are an area of active research. On a general level, bighorn sheep did not co-evolve with the same set of pathogens as domestic sheep (Dubay et al. 2002), and domestic animals have likely been selected for disease resistance (Jessup 1985). Divergences in host–parasite co-evolutionary paths may explain observed differences in defense mechanisms between bighorn and domestic sheep (Silflow et al.1989).

Phenotypic traits of *Pasteurella* spp. isolated from bighorn sheep are similar to those of isolates from domestic ruminants, so the susceptibility of bighorn sheep is due to the biology of the animals (Frank et al. 2004). Physiologically, domestic and bighorn sheep have different alveolar macrophage function and arachidonic acid metabolism, which may cause increased sensitivity of bighorn sheep to respiratory disease (Silflow et al. 1991). Furthermore, *in vitro* studies have revealed a reduced capacity of bighorn sheep immune systems to kill bacteria compared with domestic sheep immune systems (Dubay et al. 2002). Silflow and Foreyt (1994) found that bighorn sheep neutrophils were more susceptible to cytotoxin damage than domestic sheep neutrophils. All ruminant leukocytes are particularly susceptible to cytolysis by the *M. haemolytica* leukotoxin (Shanthalingam and Srikumaran 2009). Leukotoxin secreted by *M. haemolytica* appears to be its main virulence factor in bighorn sheep, indicating that the basis of bighorn sheep's susceptibility to the bacteria may lie in the details of the interaction between leukotoxin and their leukocytes. (Dassanayake et al. 2009).

Developing immunity to pasteurellosis in bighorn sheep is complex and poorly understood (Miller 2001) and vaccines to protect bighorn sheep have proven ineffective (Foreyt 1992a, Foreyt 1998, Foreyt and Silflow 1996).

Evidence of Disease Transmission from Domestic Sheep

In the past 25 years, much research has been devoted to the question of whether healthy contact with healthy domestic sheep leads to die-offs of bighorn sheep populations, due to the transmission of organisms that are non-pathogenic in domestic sheep, but deadly in bighorn sheep. Evidence contributing to an answer to that question takes a variety of forms, each of which has its own inherent limitations. The next four sections discuss several types of evidence, derived from controlled experiments and field observations. The discussion notes the limitations of each type of observation, and is structured to show how each one complements the others so that together they point towards a common conclusion that contact with domestic sheep does pose a risk to free-ranging bighorn sheep populations.

Inoculation experiments

Inoculation experiments have been used to test the hypothesis that healthy domestic sheep carry pneumonia-causing bacteria that can kill bighorn sheep. In one series of experiments, isolates of a particular strain of *M. haemolytica* from healthy domestic sheep were intratracheally inoculated into eight bighorn sheep and seven domestic sheep. Seven of the eight bighorn sheep died within 48 hours, whereas all seven domestic sheep remained asymptomatic (Foreyt et al. 1994). In two similar experiments inoculation with *M. haemolytica* cultures from domestic sheep resulted in the death of five of five bighorn sheep (Foreyt and Silflow 1996, Onderka et al. 1988).

More recently, Dassanayake et al. (2009) isolated from domestic sheep a particular strain of the A1 serotype of *M. haemolytica*, that they thought would be fatal in bighorn sheep. (While they typically carry both A1 and A2 serotypes, A2 serotypes are the primary cause of pneumonia in domestic sheep (Dassanayake et al. 2009)). All four bighorn sheep injected with the strain died within 48 hours, while none of the domestic sheep were apparently affected by the bacteria. In addition, by injecting some bighorn sheep with a mutant of serotype A1 from which the leukotoxin gene had been deleted, the researchers succeeded in pinpointing the single gene that is the primary virulence factor of *M. haemolytica*.

These inoculation experiments together indicate that domestic sheep carry at least some strains of bacteria that are not pathogenic to them, but are highly lethal to bighorn sheep. Inoculation experiments themselves, however, cannot show whether such bacteria can be transmitted by contact between domestic and bighorn sheep.

Pen experiments

Pen experiments are designed to test the hypothesis that contact can lead to transmission of disease from domestic sheep to bighorn sheep. In a pen experiment, healthy bighorn sheep are put in contact or close proximity with healthy individuals of other species, and are watched for the development of disease. In six independent pen studies since 1982, 44 of 46 bighorn sheep have died of pneumonia or become so sick that they were euthanized (Foreyt and Jessup 1982, Onderka and Wishart 1988, Foreyt 1989, Foreyt 1994, Callan et al. 1991, Lawrence et al. Forthcoming).

For example, Foreyt (1989) raised six Rocky Mountain bighorn sheep in captivity, five from birth and one that was taken from the wild as a lamb. He kept all six in captivity for 1 year. Six clinically normal domestic sheep were then placed on the 2 hectares of pasture with the bighorn sheep. *M. haemolytica* was isolated from swab specimens from four of the six domestic sheep but none from the bighorn sheep. All six bighorn sheep died within 4 to 71 days of exposure to the domestic sheep. *M. haemolytica* was isolated from the respiratory tract tissue of the bighorn sheep at the time of death. None of the domestic sheep were clinically ill during the study, but three of the six were later euthanized, and *M. haemolytica* was isolated from two of them.

To test the possibility that it is only the stress of being housed with other animals (and not the transmission of pathogens) that causes bighorn sheep to fall ill, researchers have conducted pen experiments in which bighorn sheep are co-housed with other animals. Of 39 bighorn sheep in three studies, housed with elk, deer, domestic goats, mountain goats, llamas, cattle, horses, and steers, only one died of pneumonia (Foreyt 1992b, Foreyt et al. 1994, Foreyt and Lagerquist 1996). These studies provide evidence that stress is not the sole factor causing disease in bighorn sheep when they are penned with domestic sheep.

A recent pen experiment definitively demonstrated a case in which a deadly pathogen was transferred from domestic sheep to bighorn sheep (Lawrence et al. Forthcoming). Four isolates of *M. haemolytica* were obtained from domestic sheep, and were tagged with a plasmid carrying genes for a green fluorescent protein and for resistance to the antibiotic ampicillin. The tagged bacteria were put back into four domestic sheep, who then entered a pen experiment with four bighorn sheep. The bighorn sheep all contracted pneumonia and died or were euthanized. More informatively, tagged bacteria, which glowed green and grew even in the presence of ampicillin, were isolated from all four bighorn sheep. The study shows unambiguously that transmission of *M. haemolytica* from domestic sheep to bighorn sheep occurs, and that it can result in pneumonia and death of the bighorn sheep.

Commingling of domestic and bighorn sheep under experimental conditions clearly results in transmission of fatal pneumonia to bighorn sheep. However, pen experiments cannot by themselves shed light on whether transmission of fatal disease between domestic sheep and bighorn sheep actually occurs in the wild.

Observations of outbreaks following contact between domestic and free-ranging bighorn sheep

Given the evidence from pen experiments, it is certainly plausible that transmission of pneumophilic bacteria could also occur in the wild. Bighorn sheep and domestic sheep are attracted to each other, particularly during rut, which increases the probability that they will make the close contact necessary for disease transmission when they are in the vicinity of one another (Onderka et al. 1988, Foreyt 1989, Ward et al. 1997, Dubay et al. 2002).

Evidence that disease transmission and subsequent die-offs may occur in the wild comes from numerous observations of die-offs following soon after contact of free-ranging bighorn sheep with domestic livestock (e.g. Onderka and Wishart 1984, Coggins 1988, Callan et al. 1991, George et al. 2008). Onderka and Wishart (1984) describe a major die-off of bighorn that began in southeaster British Columbia after bighorn sheep were observed mixing with domestic sheep, and proceeded to spread south over the course of three winters, eventually reaching Glacier Park. Coggins (1988) reports a die-off that killed two-thirds of a herd of 100 animals in the Wallowa Mountains of northeastern Oregon. Almost two months before the outbreak, two bighorn rams and ewe had been observed with a domestic ewe. In December 1997, on Sugarloaf Mountain in Colorado, George et al. (2008) observed a single domestic ram grazing with a group of bighorn sheep, 14 kilometers (km) from the nearest herd of domestic sheep. It was the first and only time during a 10-year study that the authors saw domestic sheep associating with bighorn sheep, and it coincided with the beginning of an outbreak that eventually spread to two additional herds.

These observations and others like them (Martin et al. 1996) are consistent with the hypothesis that disease spread by domestic sheep cause die-offs of bighorn sheep herds, but they are by themselves essentially anecdotal. On the one hand, they don’t include definitive evidence that transmission of a fatal pathogen occurred – evidence that is only possible in a carefully controlled experimental setting. On the other hand, they lack generality – even if disease transmission has occurred in one or a few cases, is it really a general phenomenon?

Analyses Correlating Bighorn Population Performance with Distance From Domestic Sheep

The few attempts to quantitatively test whether contact with domestic sheep poses a general risk of die-off or extirpation of bighorn sheep populations have examined the correlation between population performance and distance from domestic sheep. Monello et al. (2001) analyzed population records of 99 bighorn sheep herds ranging from the southwestern US to Alaska, in an investigation designed to discover the ecological correlates of pneumonia epizootics. They found that bighorn sheep populations that had suffered a pneumonia-induced-die-off were located on average significantly closer to domestic sheep allotments (24.1 ± 11.5 km) than either those that had not suffered a die-off (39.6 ± 8.5 km) or those that had suffered a die-off not induced by pneumonia.

Singer et al. (2000d) analyzed factors contributing to the success of 100 translocations of bighorn sheep in six western states, and found that the 30 unsuccessful translocations were on average significantly closer to domestic sheep (6 ± km) than either modestly successful or successful translocations. Finally, based on an analysis of 24 herds, Singer et al. (2001) found that the persistence of bighorn sheep populations was significantly correlated with the presence of domestic sheep: populations located closer to domestic sheep were smaller and had lower population growth rates than bighorn populations located farther from domestic sheep.

While these analyses indicate that bighorn sheep populations perform more poorly when they are closer to domestic sheep, they typically don't even include observations of contact, let alone the transmission of a pathogen from domestic sheep to bighorn sheep.

Summary

No one form of evidence can or does conclusively demonstrate that contact with domestic sheep frequently leads to die-offs off bighorn sheep populations. Taken together, however, the experiments and observations from the lab and the field do indicate that contact of wild bighorn populations with domestic sheep does pose a risk of disease transmission and die-offs in the free-ranging bighorn populations. Lab experiments elucidate the particular sensitivity of bighorn sheep to some pneumonia causing bacteria. The controlled conditions available in inoculation and pen experiments show that healthy domestic sheep often carry bacteria that are fatal to bighorn sheep, and that they can transmit those bacteria through close contact. Finally, nearly a century of observations in the field supports the view that proximity to domestic sheep is a risk factor for bighorn sheep, quite plausibly due in part to disease transmission from domestic sheep to bighorn sheep.

In a summary of risk to wild sheep from *Pasteurella* spp. and *Mannheimia* spp., Garde et al. (2005) offers the following conclusions:

- These bacteria can cause pneumonia in bighorn sheep, but there are benign commensal strains in the upper respiratory tract.
- Pathogens that are benign in domestic sheep can be lethal in bighorn sheep.
- The transference of pathogens from domestic to bighorn sheep has been documented in laboratory settings with resulting mortality in bighorn sheep.
- Domestic sheep, goats, and llamas have been reported with these bacteria species.
- Wild sheep and mountain goats have been reported with these bacteria species.
- Transmission is by direct contact and aerosolization.
- These bacteria species do not persist in the environment.
- Acute-to-chronic die-offs in bighorn sheep can result in low-to-100 percent mortality, although they can be present in healthy sheep.
- These bacteria are considered opportunistic and can result in pneumonia outbreaks.
- These bacteria can cause clinical disease in domestic sheep and goats but are rarely primary pathogens.

In summary, field observations suggest that bighorn sheep have a high probability of contracting fatal pneumonia following contact with domestic sheep, which has led to numerous independent experiments. These experiments provide strong corroboration that bighorn sheep have a high probability of contracting fatal pneumonia following contact with domestic sheep.

The impact of disease on bighorn sheep conservation is likely to increase as habitat loss and fragmentation restrict their movement and concentrate them into smaller areas, increasing contact rates and the spread of disease (Scott 1988, Levins et al. 1994, Schrag and Wiener 1995). Several agencies and experts have weighed in on the issue. U.S. Department of Agriculture (USDA) Forest Service Region 2 identified the following threats to the long-term viability of their bighorn sheep: the risk of disease outbreaks resulting from contact with domestic sheep and goats is identified as the most significant threat facing bighorn sheep in both Region 2 and across their range, followed by lack of connectivity and/or loss of genetic fitness due to habitat fragmentation; habitat loss; human disturbance; competition with domestic livestock; and predation on small, isolated herds (Beecham et al. 2007). Given the substantial concern raised in the published literature over the last 30 years, management guidance has focused on the separation of these species to prevent disease transmission from domestic to bighorn sheep.

Other factors / Stressors

Recent research suggest that the interaction of disease outbreaks with other stressors (both disease and otherwise) in bighorn sheep populations is poorly understood. Recent research (Tomassini et al. 2009, Dassanayake et al. 2010, and Lawrence et al. Forthcoming) suggest the complex interactions of disease agents themselves increases uncertainty in diagnosis and may also predispose bighorn sheep to secondary disease events. For example, Tomassini et al. (2009) suggests that pathogens typically associated with bighorn sheep mortality are secondary pathogens, indicating that there are likely other pathogens involved in primary infections that have yet to be identified. Dassanayake et al. (2010) found in laboratory tests that *Bibersteinia trelahosi* would overgrow and inhibit *M. haemolytica*, suggesting the difficulty in isolating the latter in wildland disease investigations. This may be why routine isolation of *Pasteurella* spp. and *M.* spp. in wildland environments is uncommon (Foreyt 1989). Additional research is needed on the interactions of disease pathogens, but it is reasonable to expect that these factors potentially predispose bighorn sheep to diseases caused by multiple pathogens that result in multiple disease cycles (e.g. *Mycoplasma ovipneumoniae*, viruses, internal and external parasites and other bacterial taxa). Some combination of disease agents with other stressors may cause the organism to shift from being a commensal to pathogenic (Srikumaran 2007). Although the exact mechanism for developing pneumonia and other diseases in bighorn sheep following association with domestic sheep is unknown, experimental and field data indicate the two species are not compatible on sympatric ranges (Foreyt 1992a,b).

Additional stressors include overcrowding on limited range; loss of escape cover; harassment by dogs; encroachment by humans; heavy snowfall and other weather stressors (Bunch et al. 1999); parasitism; poor nutrition; predation; and other human disturbances such as roads, habitat degradation, noise, genetics, high population densities; capture and restraint techniques; breeding behavior; the presence of other wildlife and high dust levels (Festa-Bianchet 1988, Jenkins et al. 2000, Jones and Worley 2004, Foreyt 1998, Monello et al. 2001). These stressors may reduce the ability of bighorn sheep to resist disease (Garde et al. 2005).

Alternative Arguments

There are scientists and others, primarily from agricultural disciplines, who contend disease transmission between bighorn sheep and domestic sheep is not a relevant factor in bighorn sheep distribution and population declines. The following contentions are summarized from comments received during the public scoping process and public meetings:

- The mechanisms and causal agents leading to epizootic disease events in bighorn sheep are not completely understood.
- The hypothesis that bighorn sheep have a high likelihood of contracting fatal respiratory disease following contact with domestic sheep has not been scientifically demonstrated in wildland conditions.
- Bighorn sheep die-offs have occurred in the absence of domestic sheep.
- Evidence that domestic sheep contact with bighorn sheep will result in a disease transmission does not exist.
- Sources of error or omission and data limitations have not been presented by those advocating that disease transmission does occur between the species.
- The peer review process does not support the contention that disease transmission occurs between the species.
- Research evaluating disease transmission between the species lacks proper experimental design that is not accounted for in the results.
- Current, ambient levels of pathogens occur in bighorn sheep, regardless of how those pathogens were introduced, making separation from domestic sheep irrelevant.
- Given the probabilities of contact from off-forest private lands sources, excluding domestic sheep on Federal lands is futile.

Some of these contentions are accurate. We do not understand all of the mechanisms involved in potential disease transmission between the species. For example, Ward et al. (1997) could not conclusively attribute a bighorn sheep die-off in Nevada to disease transmission, although he did note that the die-off occurred after domestic sheep were detected on those ranges. The study did find *Pasteurella* spp. isolates in both species and suggests a disease transmission event. They further advise separation of the species given the propensity for contact and disease transmission.

We have learned a tremendous amount from recent research on pathogen transfer between the species, and the fact that some pathogens that are non-lethal in domestic sheep have high lethality in bighorn sheep (Dassanaye et al. 2009). We also know that specific pathogens are transmitted from domestic sheep to bighorn sheep, resulting in bighorn sheep mortality (Lawrence et al. Forthcoming).

Alternative arguments criticize publications where findings very clearly infer disease transmission between the species, citing improper experimental design or other flaws in research design. However, the referenced papers are published in widely recognized scientific publications and underwent rigorous peer review prior to publication.

Some contend a lack of evidence of disease transmission between domestic sheep and bighorn sheep in wildland environments. Arguably, much of the evidence is circumstantial; however, the compilation of cases throughout several decades does contribute to an increasing body of evidence that overwhelmingly demonstrates bighorn sheep near domestic sheep are at risk for disease transmission, even though "contact" may not have actually been observed.
Monello et al. (2001) state that bighorn sheep herds classified in a "pneumonia induced die-off" category were located significantly closer (<15 miles) to domestic sheep allotments than those in

a non-die-off category (>25 miles). George et al. (2008) document a winter die-off in Colorado that affected three bighorn sheep herds that was traced to contact with a single domestic ewe.

Additional arguments state that since disease pathogens have already been transferred to domestic sheep, separation at this point is moot, or that private lands provide risks to bighorn sheep that cannot be offset, regardless of actions taken on Federal lands. These contentions claim that management on Federal lands to provide separation will not be effective due to changed conditions that cannot be offset. The uncertainty in these contentions poses all of the risk to be borne by bighorn sheep. They do not consider that pathogens likely evolve as they move within and between species, or existing or new diseases that are virulent to bighorn sheep (e.g., mycoplasms) may still be transferred between domestic and bighorn sheep. Recent serological research (Dassanayake et al. 2009) demonstrates that pathogens, in this case *Mannheimia haemolytica* serotype A1, which are not lethal to domestic sheep, are transferrable to bighorn sheep and highly lethal to them. In another recent experiment, pathogens were tagged and followed as they passed from domestic to bighorn sheep and resulted in bighorn sheep mortality (Lawrence et al. Forthcoming).

The disease review sections of this document, consider a large body of peer reviewed and published literature, spanning several decades, that addresses the allegations. While there clearly are gaps in the knowledge base on the causal factors and mechanisms of bighorn sheep die-offs and disease transmission between these species, the vast majority of literature supports the potential for disease transmission between the species, documents bighorn sheep die-offs near domestic sheep, and supports the management option of keeping these species separate to prevent disease transmission. Further, there is no peer reviewed literature that suggests bighorn sheep can be grazed with domestic sheep without concern for disease transmission between the species. Scientists from both sides of the issue also recommend that the species be kept separate until the disease transmission science is better understood.

The analysis conducted in this document recognizes these uncertainties but clearly focuses on the Forest Service's responsibility to provide habitats that support viable populations of bighorn sheep, particularly given the risks that the species currently faces relative to the devastating impacts of disease.

History of Pneumonia Infections near the Payette National Forest

Hells Canyon Metapopulation

At least seven population die-offs have been reported since reintroductions were initiated in Hells Canyon in 1971 (HCBSRC 1997). *Pasteurella multocida* was associated with a major die-off in Hells Canyon in 1995–1996 (Frank et al. 2004). During this time, over 300 bighorn sheep died of pasteurellosis (pneumonia) in Hells Canyon, possibly caused by contact with one goat (Cassirer et al. 1996, Coggins 2002). During this period of die-off, bighorn sheep on the Idaho side of the river showed signs of respiratory disease, but no die-off was documented (Cassirer et al. 1996). Five die-offs within the Hells Canyon metapopulation have been circumstantially linked to domestic sheep (Coggins 1988). Cassirer and Sinclair (2007) describe the effects of chronic, repeated pneumonia outbreaks on bighorn sheep populations in Hells Canyon, and their potential adverse effects on bighorn sheep population recovery and persistence.

Five bighorn sheep populations of the Hells Canyon metapopulation have occurred near domestic sheep allotments on the westside of the Payette National Forest since 2000: Muir Creek, Myers Creek, McGraw, Upper Hells Canyon, and Sheep Mountain. One of these, the McGraw population, is no longer considered extant (IDFG 2004b). The other populations have had periodic pneumonia outbreaks that have resulted in substantial mortality as indicated by bighorn sheep population trends in Hells Canyon (Figure W-0a). Disease has reduced the population growth rate of the Hells Canyon metapopulation by at least 40 percent (HCBSRC 1997). Population counts in Big Game Management Unit (BGMU) 18 (Figure W-0b) corroborate the aforementioned discussion of population declines associated with respiratory disease in this part of Hells Canyon (Figure W-0c).

Figure W-0a. Population Trends for Bighorn Sheep by Herd in Hells Canyon from population census data collected by Washington Department of Fish and Wildlife, Oregon Department of Fish and Wildlife, and Idaho Department of Fish and Game

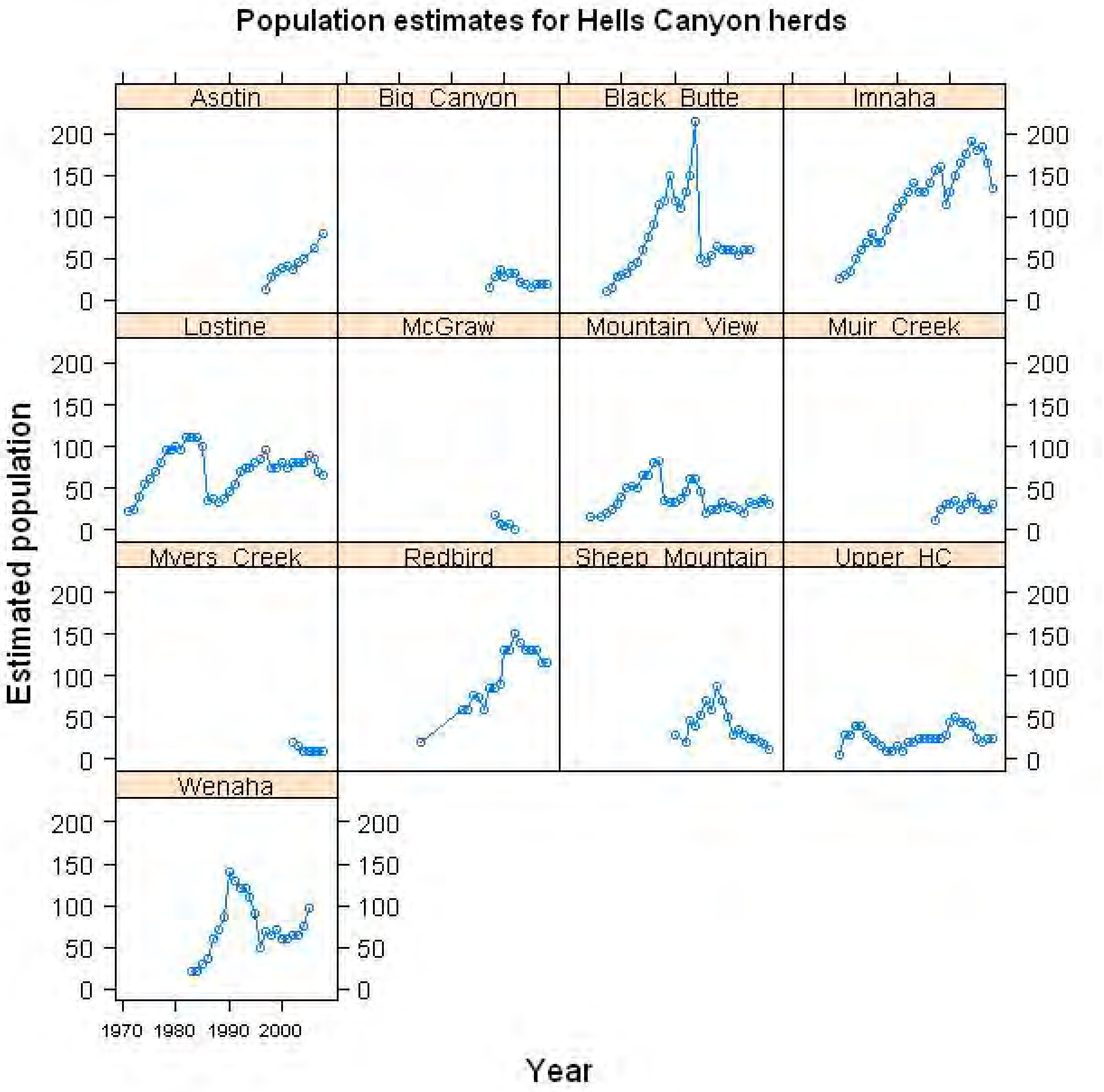


Figure W-0b. Bighorn Sheep Populations on and Adjacent to the Payette National Forest by Idaho Department of Fish and Game Big Game Management Units

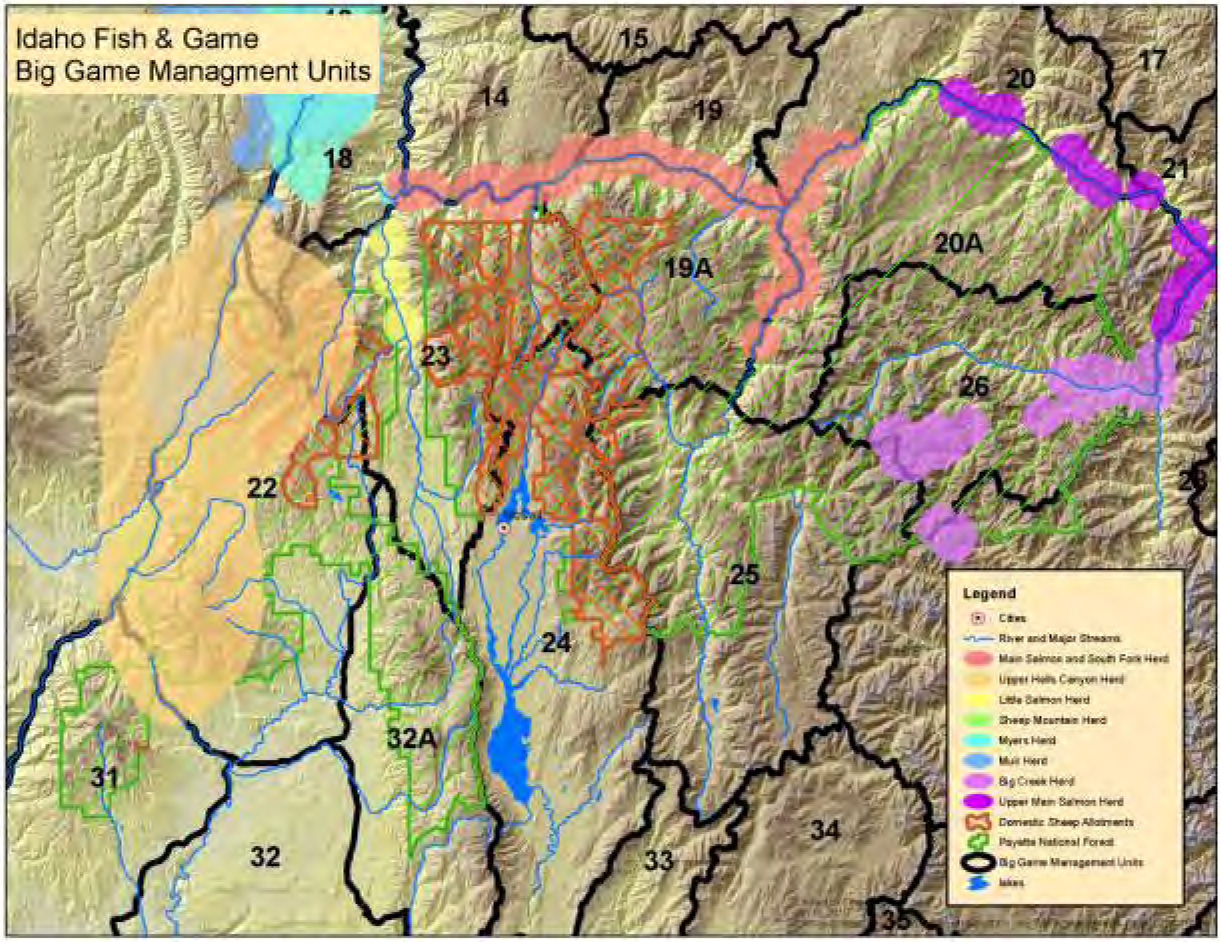
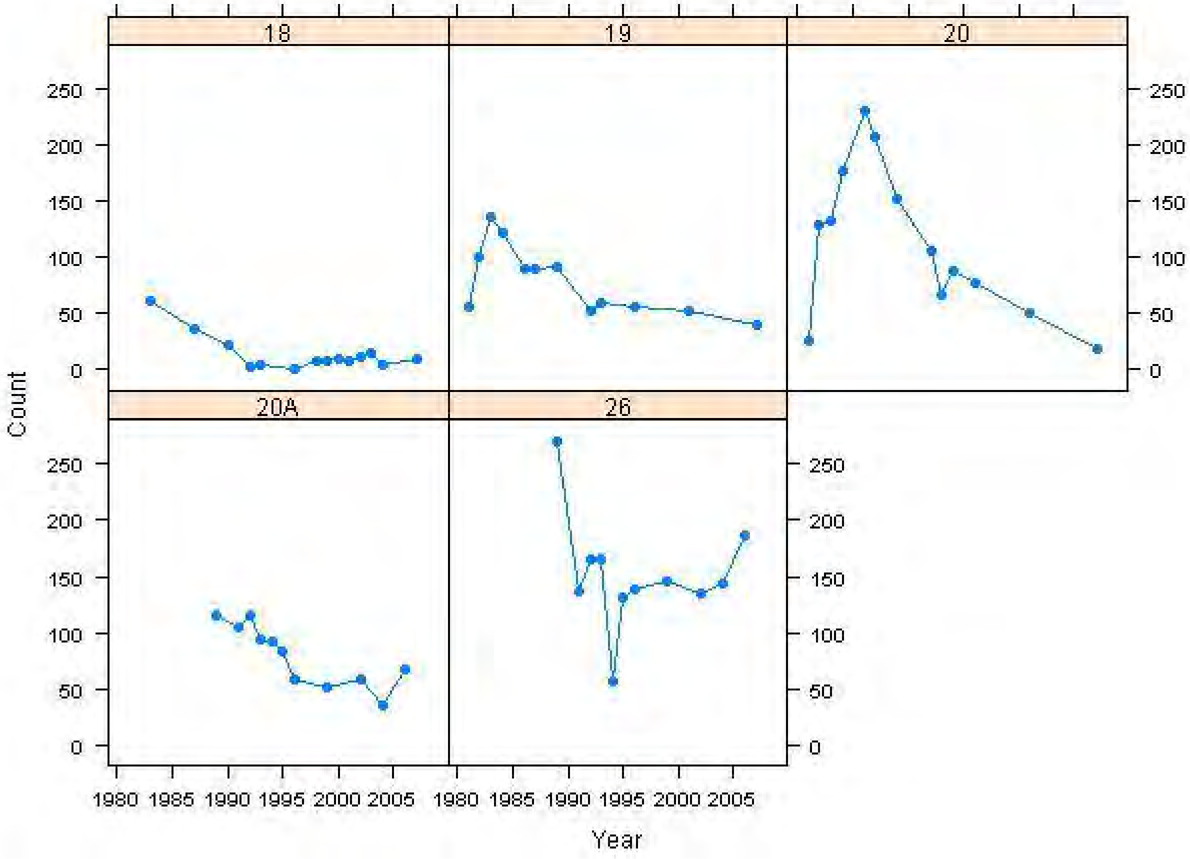


Figure W-0c. Population Trends for Bighorn Sheep in Idaho Big Game Management Units that Overlap the Payette National Forest (from population census data collected by the Idaho Department of Fish and Game)



Salmon River Metapopulation

Population count summaries for BGMUs 18, 19, 20, and 20a (Figure W-0c), suggest significant recent declines in several of these bighorn sheep populations. Evidence suggests that disease has had severe implications on the South Fork Salmon River population, main Salmon River population, and Big Creek populations of the Salmon River Mountains metapopulation on the eastside of the Payette National Forest (IDFG 2004a, 2006).

The small numbers of bighorn sheep within the South Fork Salmon River raise concern about the viability of this population. From 1987 to 1991, a population on Big Creek experienced 5 years of low lamb-to-ewe ratios and an all-age die-off in 1990 (Akenson and Akenson 1992). Research conducted in April 2000 found a highly virulent strain of *Pasteurella* spp. in the Big Creek population (IDFG 2004a, 2006).

Risks of Contact between Domestic Sheep and Bighorn Sheep on the Payette National Forest

As stated in the 2003 *Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement* (FEIS), a principal assumption from the published literature is that direct contact between domestic sheep and bighorn sheep results in a high likelihood of disease transmission to bighorn sheep and disease outbreaks in local bighorn sheep herds. Risk factors include distance between domestic sheep allotments and the nearest bighorn sheep populations; amount of bighorn sheep habitat within, and between, domestic sheep allotments and the nearest bighorn sheep herd; the amount and quality of bighorn sheep habitat; the presence of incidental bighorn sheep in or near domestic sheep allotments (i.e., bighorn sheep forays); bighorn sheep distribution and movement near the allotments; and characteristics of each domestic sheep allotment.

Resiliency of Bighorn Sheep on the Payette National Forest to Climate Change

Recent, rapid climate change has raised concern over the ability of some species to adapt to landscape changes associated with this phenomenon. Diaz and Eischeid (2007) found an average increase of approximately 1.0 °F over the last 20 years in the western United States, with the highest increases at high elevations. They contend that changes in annual shrub phenology (earlier flowering), increases in significant forest pest infestations, earlier spring runoff, intensified wildfires, and the disappearance of alpine and tundra ecosystems illustrate rapid changes in the hydrological, phenological, and biological indicators of western ecosystems that are a result of climate warming. Research findings (Westerling et al. 2006, Gedaloff et al. 2005) document increases in large western wildfires beginning in the mid-1980s and correlated climate variables including increased spring and summer temperatures and early spring snow melt.

The vulnerability of wildlife species to these changes is largely related to environmental exposure (potential changes in habitat continuity and availability) and species sensitivity (ecological elasticity) to climate change. NatureServe recently developed a Climate Change Vulnerability Index model (Young et al. 2009) that utilizes these concepts to assess species that are potentially vulnerable to climate change. Factors contributing to a species vulnerability to environmental exposure and its sensitivity to climate change are evaluated in light of climate data summarized for specific geographic areas. Although the model is geared towards a rapid assessment to identify species that are vulnerable to climate change, the concepts can be used to assess environmental conditions and species life history traits that allow evaluating climate change effects on a given species.

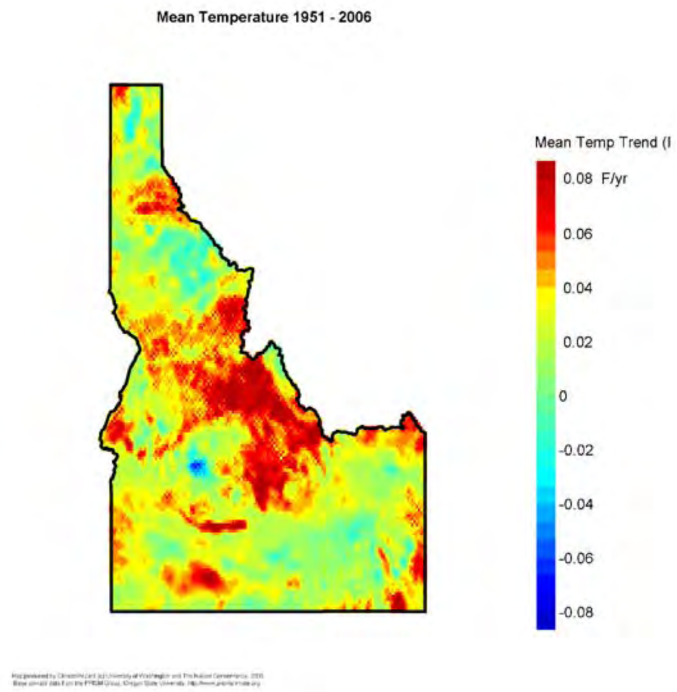
Climate data for the last 55 years (1951–2006) (www.climatewizard.com) reveal that on average, temperatures in Idaho have increased 0.031 °F per year, and precipitation has increased 0.085 percent per year (Figure W-0d). Consistent with findings by Diaz and Eischeid (2007), the temperature increases have been more severe at higher elevations, which likely include bighorn sheep summer source habitats.

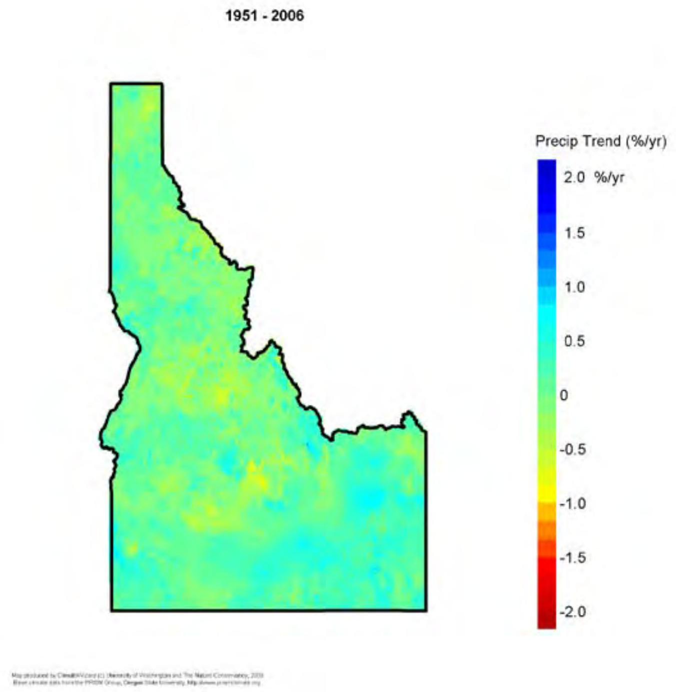
A species’ vulnerability to environmental exposure reflects its ability to acquire new habitats as climate change reduces or alters current habitats. Factors such as geographical barriers and anthropogenic barriers contribute to environmental exposure. Source habitats for the Hells Canyon and Salmon River metapopulations are well connected and still capable of supporting robust bighorn sheep populations. Anthropogenic changes in landscapes over the last 150 years have resulted in loss of wintering habitats at lower elevations as a result of agricultural development, urbanization, and incursion of land uses, such as domestic sheep grazing, that potentially put bighorn sheep at risk. Conversely, recent large-scale fires may have resulted in additional bighorn sheep summer foraging habitat.

Factors that influence species sensitivity include the dispersal ability of a species, sensitivity to temperature and precipitation changes, habitat specificity, dependence on interspecific interactions, migration and movement patterns, genetic limitations, and the ability to respond to changing seasonal temperature and precipitation regimes. As a species, bighorn sheep are a highly vagile species capable of exploring and acquiring suitable habitats. However, some populations may be at risk, particularly if suitable habitats are fragmented and isolated. Climate change phenomena may be more pronounced in species or populations that (1) face greater threats from environmental exposure and (2) lack life history traits that allow greater resilience to these changes. Epps et al. (2004) found that climate change correlated with the extirpation of desert bighorn sheep populations (*O. c. nelsoni*) in California desert habitats, and that current bighorn sheep herds in low elevation, low precipitation areas had higher probabilities of extinction.

The unique geomorphology and vegetation of the Hells Canyon and Salmon River areas currently provide extensive, contiguous habitats for bighorn sheep. Noss (2001) argues that climate change is not the greatest threat to today’s forests (ecosystems) but is an additional stressor and recommends management practices that retain biodiversity and ecological function, particularly those that provide climatic refugia and connectivity of habitats. Conservation management that contributes to the resilience and connectivity of these ecosystems (Shaffer et al. 2002) should also benefit bighorn sheep habitats in central Idaho. As discussed in much of this SEIS, the most significant threat faced by bighorn sheep in these two metapopulations is the potential for disease transmission resulting from contact with domestic sheep. Providing conditions that allow bighorn sheep to occupy suitable and available habitats in central Idaho and reducing the likelihood of disease contagion will likely provide for populations that can withstand the effects of climate change.

Figure W-0d. Average Temperature and Precipitation Changes for Idaho from 1951–2006 (Source: www.climatewizard.org).





Model Analysis

Three models were developed to better understand bighorn sheep habitat suitability, the potential for contact between bighorn sheep and domestic sheep, and the inferences for disease transmission between the species: (1) a bighorn sheep source habitat model; (2) a risk-of-contact model, which utilizes a bighorn sheep core herd home range (CHHR) analysis and bighorn sheep foray analysis; and (3) a disease model. A detailed description of these models can be found in the *Bighorn Sheep Supplemental Environmental Impact Statement Analysis: Modeling and Analysis Technical Report* (Appendix L). Outputs from these models were used to describe current conditions on the Payette National Forest and adjacent areas and as a basis for alternative comparison. Models used in this document updated the previous analyses conducted for the *Southwest Idaho Ecogroup Land and Resource Management Plans Draft Environmental Impact Statement* (DEIS). Detailed rationales for these changes are discussed in the *Bighorn Sheep Supplemental Environmental Impact Statement Analysis: Modeling Technical Report* (Appendix L) and summarized in Chapter 2.

Source Habitat Model

Bighorn sheep occupy rugged canyons, foothills, and mountainous terrain at elevations ranging from 1,450 to 10,500 feet. Key habitat features include steep, rugged “escape” terrain; grasses and forbs for forage; and a limited amount of tall vegetation. Native bunchgrasses and forbs are important components of forage (IDFG 2005).

Visibility is an important habitat variable for bighorn sheep: vegetation height and structure are probably more important than plant species composition for predator detection (Risenhoover and Bailey 1985, Wakelyn 1987), and a negative correlation between forest cover and bighorn sheep occurrence has been observed (Bentz and Woodard 1988). Open habitat provides good visibility for detecting predators and communicating with other herd members (Risenhoover et al. 1988). Post-fire habitats can benefit bighorn sheep by improving forage quality (McWhirter et al. 1992) and increasing visibility (Bentz and Woodard 1988). Seasonal use of different slopes and aspects results in the use of a mosaic of plant communities and phenological patterns, providing foraging and security opportunities for bighorn sheep (Valdez and Krausman 1999).

Source habitats are those characteristics of macrovegetation that contribute to positive population growth for a species in a specified area and time (Wisdom et al. 2000, Raphael et al. 2001). Source habitats contribute to source environments, which represent the composite of all environmental conditions that result in stationary or positive population growth in a specified area and within a specified time (Wisdom et al. 2000, Raphael et al. 2001). Wisdom et al. (2000) describe source habitats for bighorn sheep in alpine, subalpine, upland shrubland, and upland herbland community groups. Alpine and subalpine community groups are primarily summer range, while upland herbland and shrubland are used in both seasons, depending on elevation (Wisdom et al. 2000). Old-forest and stand initiation stages of whitebark pine and the stand initiation stages of other forested cover types are other contributors to source habitat.

Escape terrain is so critical for ewes during lambing (Blood 1961, Kornet 1978, Hall 1981) that they will sacrifice access to high-quality forage for security (Festa-Bianchet 1989, Cook 1990, Bleich et al. 1997). Escape terrain must contain the following characteristics (HCBSRC 2004):

- 300 meter[2] buffer of all areas with a slope between 31 and 85 degrees
- if two or more pieces of escape terrain are within 1,000 meters (m), they are buffered so that their total area is connected
- an area of least 1.6 hectares

Source habitat for bighorn sheep falls within suitable rangeland on the Payette National Forest. Suitable rangelands include lands suitable for grazing cattle or sheep. Although impacts to habitat from historic livestock grazing have been substantially reduced under current practices, livestock grazing can still cause localized areas of damage, including changes in understory vegetation from livestock foraging, trampling of reproducing tree seedlings, soil erosion, and other habitat degradation. Damage can result in the subsequent introduction and spread of invasive weeds and other non-natives, disruption of ecological and physical processes, and changes in historic fire regimes. Bighorn sheep have been found to actively avoid habitats occupied by cattle (Wilson 1968, McQuivey 1978, Jones 1980, Dodd and Brady 1986, Steinkamp 1990). Overgrazing by domestic livestock reduces the overall carrying capacity of bighorn sheep range and may lead to more predation by increasing cover for predators. Succession of grassland to shrub communities may also increase competition with deer and increase cougar populations, the major predator of bighorn sheep (Beecham et al. 2007). Competition with domestic sheep and goats is considered even more serious than with cattle because of their similar preferences in forage and topography, and the higher potential for disease transmission between the species (Beecham et al. 2007).

The existing vegetation layer from the national LANDFIRE layer (The National Map LANDFIRE 2006) was used to assess the current source habitat available for bighorn sheep. This information was utilized because it allows analyzing landscapes that extend beyond but include the Payette National Forest, and can be used to address habitat connectivity issues at broader scales. The vegetative cover types used by the Hells Canyon Restoration Committee (HCBSRC 2004) and Wisdom et al. (2000) were crosswalked into the LANDFIRE ecological systems (NatureServe 2004) to identify summer and winter source habitat. Winter source habitat is a subset of summer source habitat in that it encompasses only those areas below 4,500 feet on southerly aspects.

For this source habitat model, a component was added to the escape terrain to filter out areas that have the steepness but not the ruggedness that contributes to source habitat capacity. A ruggedness surface was created using an ArcGIS script (Sappington et al. 2007), then the telemetry and observations were overlaid to create a histogram of the ruggedness with a range from 0 to 3,455. Based on the histogram, areas with a ruggedness value of 310 or less were excluded from the map of source habitat capacity to limit over mapping. Vegetation is not considered a component of source habitat capacity since vegetation will vary in response to successional and disturbance processes, while escape terrain remains constant. Therefore, while source habitat capacity is constant, source habitat will vary spatially and temporally across the landscape.

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[2] Data pertaining to the models or model development is given in metric units.

On the Payette National Forest, 369,641 acres of summer source habitat and 156,919 acres of winter source habitat exist, representing 15.4 percent and 6.5 percent, respectively of the Payette National Forest (Figures W-0e and W-0f). Outside of wilderness areas, the percentages are 14.4 percent and 5.7 percent, respectively. Source habitat for bighorn sheep is distributed across the Payette National Forest, and bighorn sheep habitat is considered contiguous although not all of it is currently known to be occupied.

This mid-scale habitat modeling may not represent finer-scale conditions. For example, not all special habitat features may be delineated and invasions by exotic plants, forage quality, and human disturbance factors may not be detectible. Changes in the patch and pattern of range mosaics have changed since historical times as fire suppression has resulted in an increased density of trees in formerly open stands, with a resultant loss of foraging quantity, quality, and open habitat (Wisdom et al. 2000). Fire-suppressed stands have created barriers between historical winter and summer range, preventing occupancy of the total range although each isolated range may be suitable (Wakelyn 1987). In other cases, fires have opened up forested areas and increased habitat. Mixed-lethal fire regimes may have followed historical patch and pattern, but the same may not be true for non-lethal fire regimes. Although the effects of the 2007 fires within the Payette National Forest on bighorn sheep habitat and movement are unknown, these fires may have opened up additional movement corridors and summer habitats for bighorn sheep. Disruption of hydrological regimes from a variety of sources has also resulted in the loss of riparian vegetation in many foraging areas (Wisdom et al. 2000).

Figure W-0e. Modeled Bighorn Sheep Summer Source Habitats on and Adjacent to the Payette National Forest

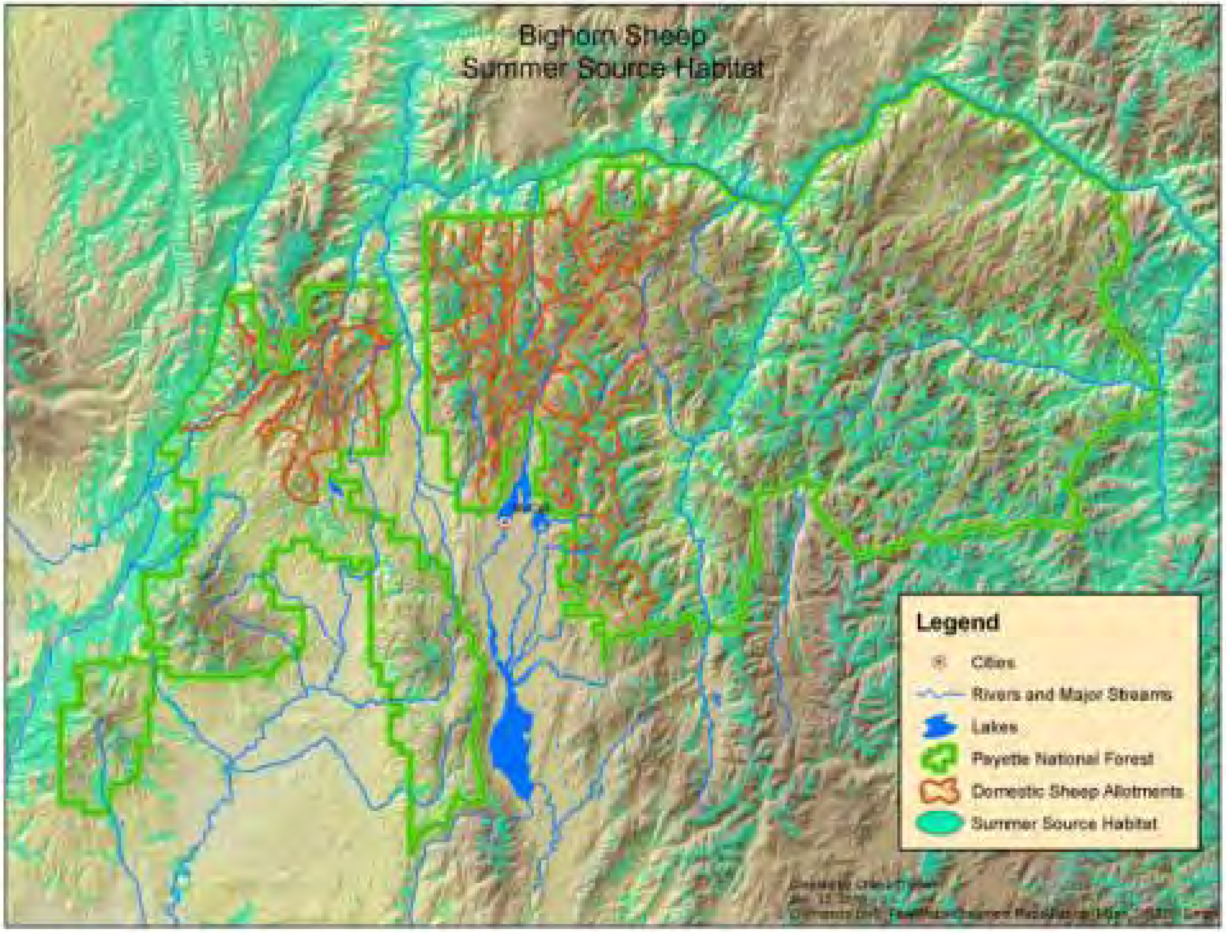
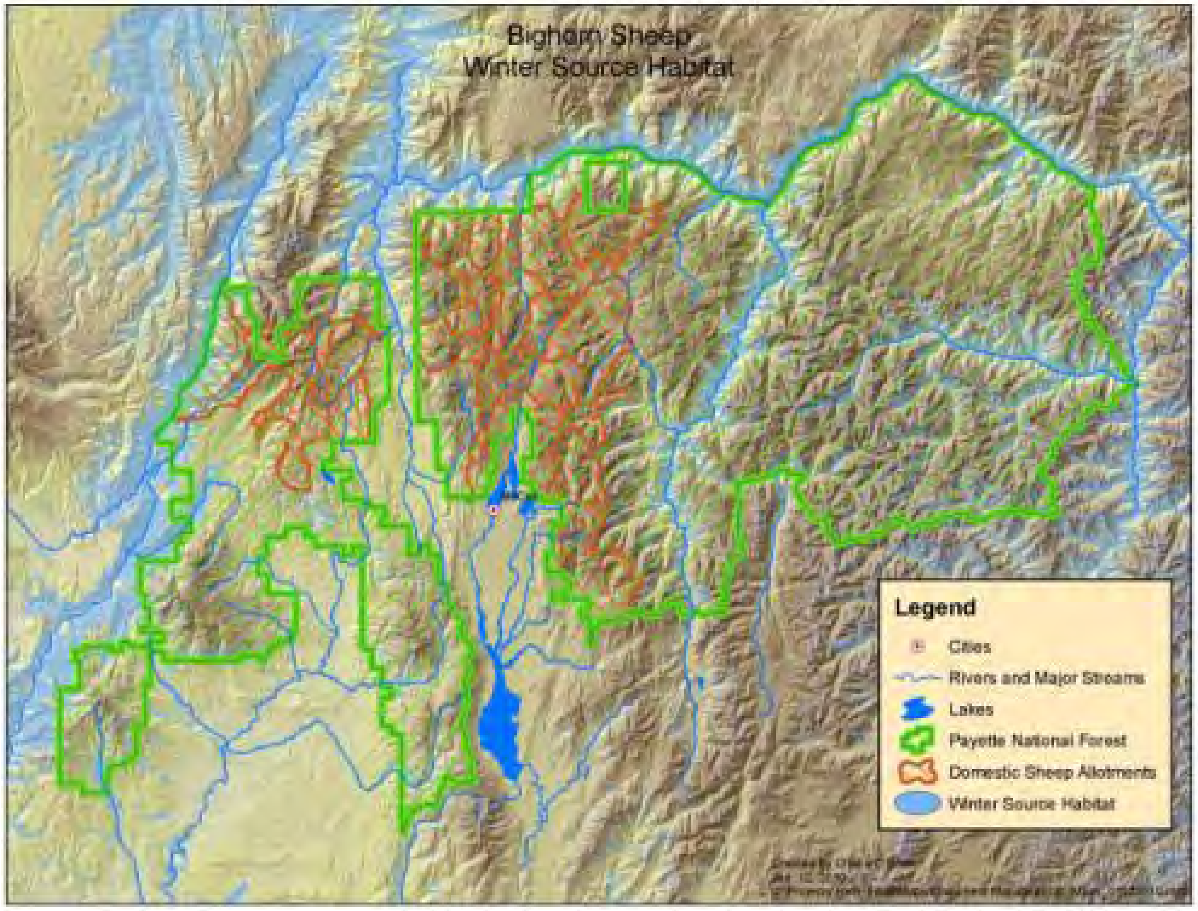


Figure W-0f. Modeled Bighorn Sheep Winter Source Habitats on and Adjacent to the Payette National Forest



Risk of Contact Model

The sequence of events by which a disease outbreak could result from contact between a bighorn sheep and a domestic sheep in an active allotment located outside of bighorn sheep home range can be broken down into a number of steps. First, to reach an occupied allotment, a bighorn sheep must (1) leave the CHHR; (2) travel far enough to reach the allotment; and (3) intersect the allotment (i.e., rather than some other area at the same distance from the CHHR). For disease transmission to occur, the bighorn sheep must (4) come into contact with domestic sheep in the allotment and (5) contract the disease from the domestic sheep. Finally, for an outbreak to affect the animal’s home herd, the infected bighorn sheep must (6) make its way back to the CHHR and (7) transmit the disease to other members of the herd.

The contact model described in this section aims to determine the probability that a bighorn sheep will reach an occupied allotment, steps 1–3 above. Steps 4–7, which are also necessary for an outbreak to results from such a movement, are discussed below as part of disease model.

The contact model is based on an analysis of 12 years of bighorn sheep telemetry data from the Hells Canyon and Salmon River populations, and its construction involves two distinct analyses. First, the analysis is used to delineate areas where most animals in each herd spend most of their time. Such areas are designated as the CHHR. Then, the analysis examines the characteristics of bighorn sheep movements or “forays” outside of the CHHR. This foray analysis examines how frequently and at what season foray movements occur, as well as how far beyond the CHHR animals are likely to travel. Together, the habitat, CHHR, and foray models are used to estimate the probability that a ewe or a ram in any of the herds will reach any of the open allotments in a given year.

Telemetry Data

Telemetry and observational data for Hells Canyon were collected by the Hells Canyon Initiative (HCI) and overlapped with the Payette National Forest (Figure W-0g). The HCI is a tri-state coordination group that has been focused on restoring bighorn sheep populations to Hells Canyon and is comprised of the fish and wildlife agencies of Idaho, Oregon, and Washington, the Forest Service, and other private entities. These data include more than 54,000 telemetry points, representing approximately 400 individuals from 12 Hells Canyon herds and 3 Salmon River herds. With one exception, the data were collected from March 1997 through December 2008. Telemetry and observation data for the Salmon River metapopulation was collected from multiple sources. Telemetry data for the Main Salmon/South Fork Herd was collected from 2008 to 2009 by the Nez Perce Tribe under contract by the Payette National Forest. Telemetry data for the Big Creek Herd was collected from 1989 to 1990 by University of Idaho researchers. The rest of the observations were collected on many different dates.

These telemetry data suggest that bighorn sheep utilize habitats within allotments managed by the Payette National Forest. Figures W-0h and W-0i display telemetry points of bighorn sheep documented on the allotments on the west and east sides of the Payette National Forest in Hells Canyon.

Figure W-0g. Telemetry Data and Observations of Bighorn Sheep near the Payette National Forest

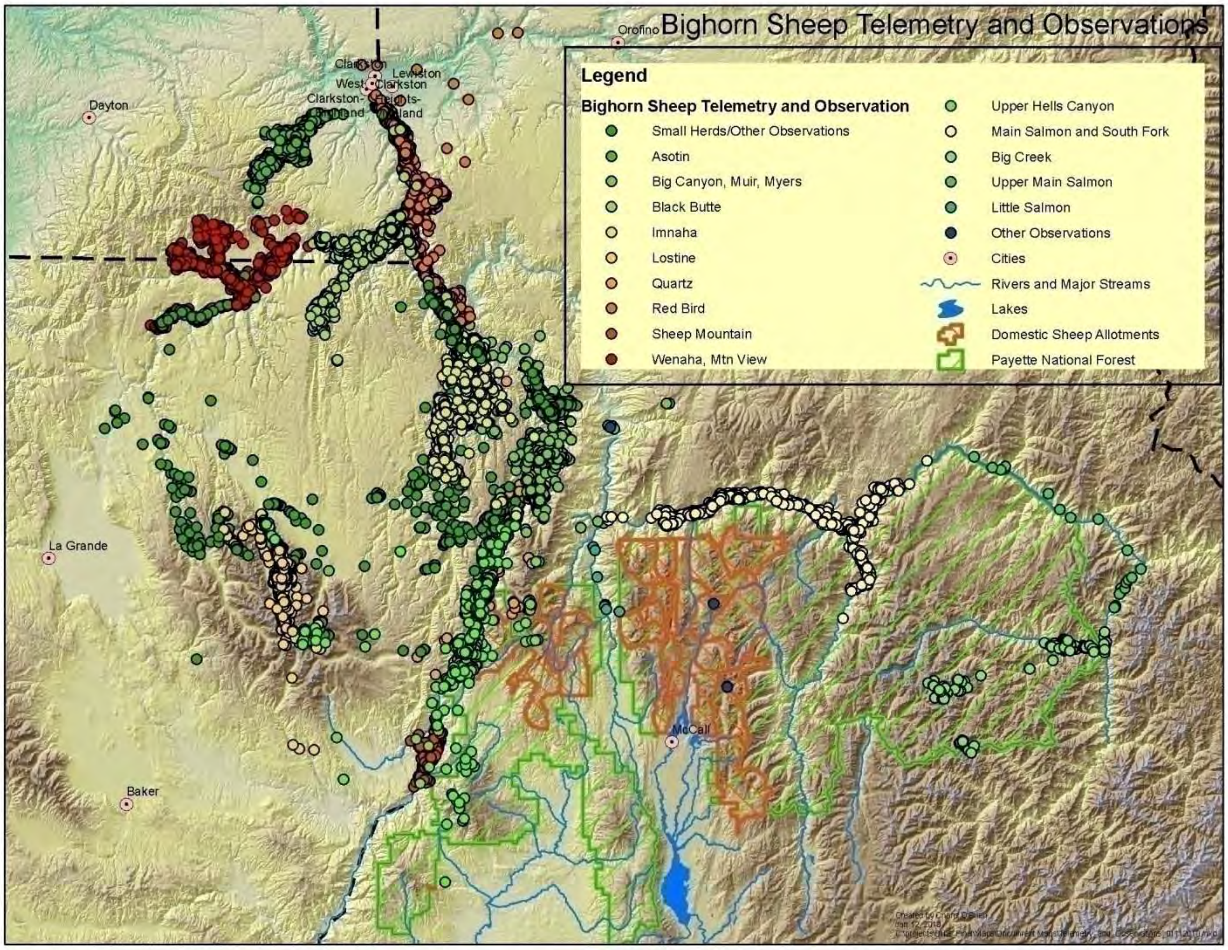


Figure W-0h. Telemetry and Observation Points for Bighorn Sheep on the Westside of the Payette National Forest

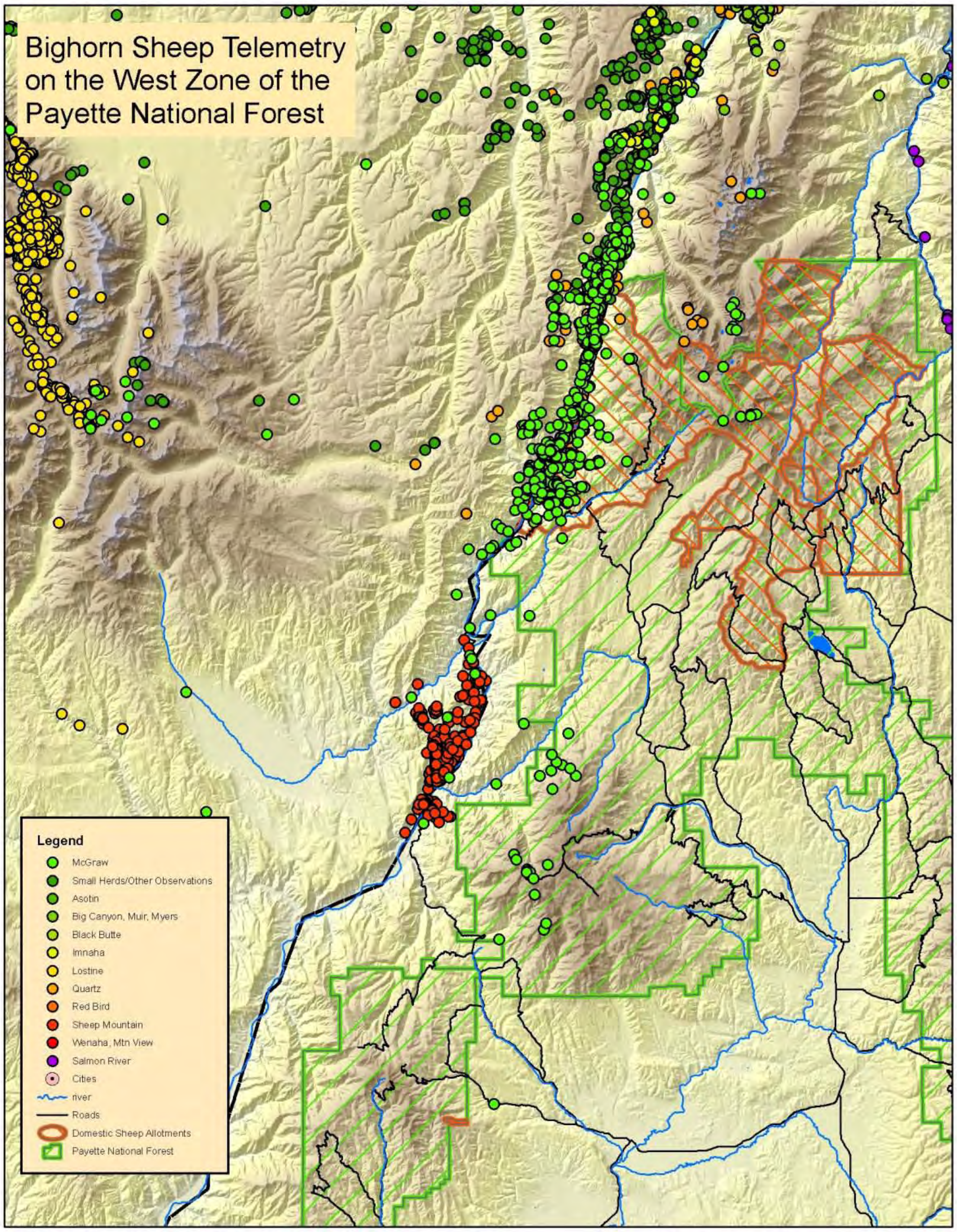
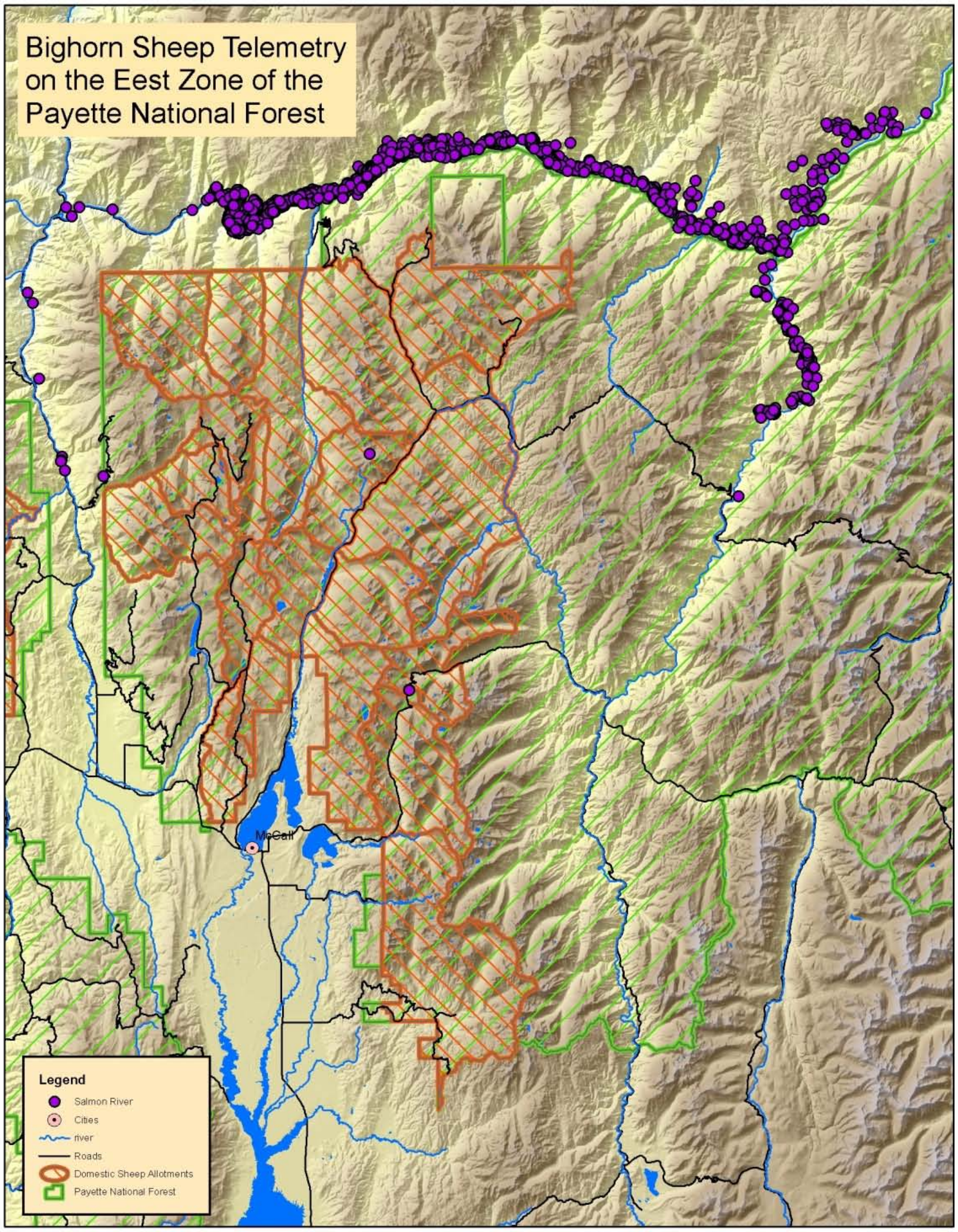


Figure W-0i. Telemetry and Observation Points for Bighorn Sheep on the Eastside of the Payette National Forest



Hells Canyon Metapopulation

The Hells Canyon telemetry data used for modeling have been collected as part of the HCI by the Idaho Department of Fish and Game (IDFG), Oregon Department of Fish and Wildlife (ODFW), and Forest Service. In any given year, approximately 150 animals have telemetry collars. Between 1999 and 2004, radio-collared bighorn sheep were detected within the Smith Mountain Allotment on 319 occasions and within 1–4 miles of the Curren Hill Allotment on 22 occasions. These telemetry data account for 22 individuals: 7 rams and 15 ewes. Of these 22 individuals, 18 (7 rams and 11 ewes) entered the allotments when domestic sheep were present (May–October), with a total of 163 telemetry points from those 18 individuals within that time period. All of these recorded individuals are now deceased. It is unknown how many bighorn sheep without telemetry collars entered the allotments when domestic sheep were present.

A 6,567-acre area of the Smith Mountain Allotment is within the boundaries of the Hells Canyon National Recreation Area (HCNRA). The Curren Hill Allotment also contains portions of the HCNRA.

Salmon River Metapopulation

Only a limited telemetry data set is available for analysis of the Salmon River metapopulation. Hence, uncertainty about the risk of contact and potential subsequent disease transmission is relatively high on the eastside of the Payette National Forest.

The Payette National Forest, IDFG, and Nez Perce Tribe have a cooperative project (the Salmon River Bighorn Sheep Project [SRBSP]) that is placing Global Positioning System (GPS) collars on Salmon River Mountain bighorn sheep. Fifteen sheep were collared in fall 2007 and spring 2008. One of those collared sheep was lethally removed by IDFG in early 2008 due to contact with domestic goats. Eighteen more sheep were collared in fall 2008. One collared sheep was lethally removed in spring 2009 after suspected contact with domestic sheep. One collared sheep was harvested by a hunter and one other collared sheep was killed by a mountain lion. This information has provided additional bighorn sheep movement data on the eastside of the Payette National Forest. Forested area and large rivers, which bighorn sheep do not prefer for movement and which serve as partial barriers to bighorn sheep movement (Singer et al. 2000b), are located between bighorn sheep habitat on the South Fork Salmon River and the eastside allotments. Bighorn sheep have, however, been observed swimming large rivers and have been found in locales at which they arrived via unknown routes.

Akenson and Akenson’s (1992) 5-year study of bighorn sheep in the Big Creek drainage, which included observations of 12 radio-collared ewes, provides an additional source of information about bighorn sheep movements on the Payette National Forest. They observed ewes from different parts of the winter range utilizing four different drainages for lambing and three separate summer ranges, indicating a high degree of movement for this population. They also observed ewes traveling more than 50 miles in less than 3 days, and pregnant ewes swimming Big Creek during flood stage to begin spring migration. Ewes followed rock outcrops and broken open terrain, but the migration corridor also included forested ridges and a snow covered pass (Akenson and Akenson 1992). Big Creek bighorn sheep had separate winter ranges from the Middle Fork Salmon River bighorn sheep but did share some summer range, which would increase the risk of disease transmission between populations of the Salmon River Mountains metapopulation (Akenson and Akenson 1992).

Several incidental observations show that at least some bighorn sheep in the Salmon River metapopulation reach areas far from the mapped CHHRs. One bighorn ram that was caught in a leg-hold trap was observed within the Josephine Allotment. On the North Fork Lick Creek Allotment, three ewes were sighted in one year and the following year, two ewes were seen along the border with the Lake Fork Allotment. These individuals entered the allotments when domestic sheep were present (May–October). The lack of more extensive telemetry data makes it impossible to know how frequently other bighorn sheep utilize domestic sheep allotments. An added complication is that unlike re-introduced sheep in Hells Canyon, these native sheep are considered migratory, and historical migration routes are important to their population dynamics (Dale Toweill, IDFG, personal communication).

Core Herd Home Range Analysis

Home range modeling was conducted as part of the analysis of herds in the Hells Canyon and Salmon River metapopulations. Modeling the CHHR enabled Payette National Forest managers to analyze the impacts of domestic sheep grazing on the Payette National Forest on the broader bighorn sheep metapopulations. The analysis also highlighted the extent of the overlap and possible interaction between the different herds throughout the Hells Canyon Complex and the main and South Fork Salmon Rivers.

The first step in developing the CHHR model was to separately calculate the home range of each individual animal. Occasional movement outside of the area could be exploratory in nature and was not considered part of the CHHR. However, these excursions—or forays—were of great interest to the modelers and were analyzed separately in the foray model (see Foray Analysis section below).

The tools and processes used to complete this analysis are common to home range analyses used for many other species. The analysis consisted of a fixed-kernel home range model conducted with the observations and telemetry data collected by the HCI from 1997 to 2008. These telemetry data were used by HCI to divide the bighorn sheep populations into herds. The following herd assignments were based on transplant cohorts to specific locations and breeding groups of ewes that shared the same range: Asotin, Big Canyon, Black Butte, Imnaha, Lostine, Upper Hells Canyon, Mountain View, Muir Creek, Myers Creeks, Redbird, Sheep Mountain, and Wenaha. Several small herds had too few points to accurately create a CHHR or were transplants that had telemetry data but failed to form a herd; thus, home range modeling was not conducted on the following herds: 05IMREL, Lower Hells Canyon, Saddle Creek, Quartz Creek, Minam, and Sheep Creek. The bighorn sheep in the Salmon River metapopulation are endemic rather than reintroduced, so herds divisions were defined differently. Named herds in the Salmon River were based on the type of observations available for describing their locations: the Main Salmon/South Fork included animals radio-collared as a part of the Salmon River study in 2008-2009; the Big Creek population included animals radio-collared by Akenson and Akenson (1992) in 1989 and 1990, and the Upper Salmon; and the Upper Main Salmon was comprised of animals in the Salmon River Canyon between the Upper Main Salmon/South Fork and Big Creek populations, for which no telemetry data at all were available.

Home range modeling was completed using the Home Range Extension version 1.1 for ArcGIS (Rodgers et al. 2007), a software package designed for just this purpose. The Home Range Extension uses a standard bivariate normal probability density function as the “kernel” employed to estimate the intensity with which animals use each mapped area. A kernel is essentially a small 3-dimensional hill placed over the location of each telemetry observation. Where many observations are clustered together, these hills overlap and pile up, their total height indicates the probability of finding an animal at a given location. The width of the kernels, h_{ref}, is calculated as the square root of the mean variance in *x* (var *x*) and *y* (var *y*) co-ordinates divided by the sixth root of the number of points (Worton 1995):

$$href = n^{\frac{-1}{6}}\sqrt{\frac{\operatorname{var} x + \operatorname{var} y}{2}}$$

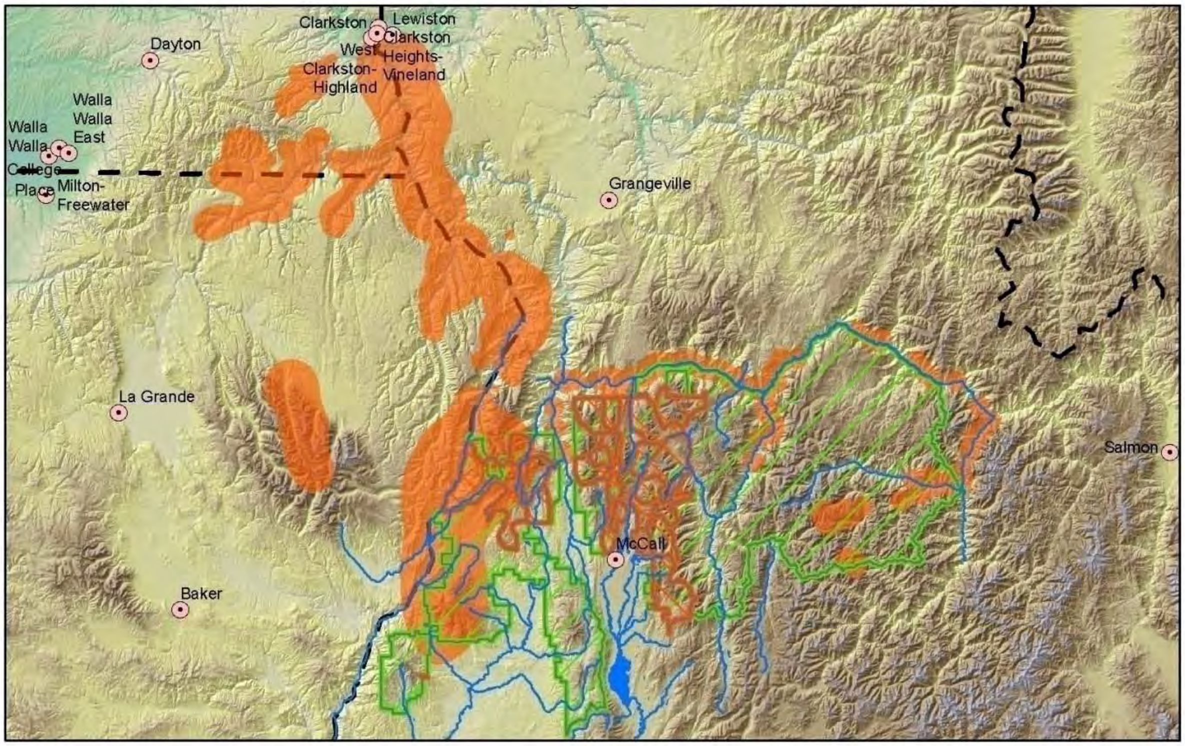
This method of selecting h_{ref} is widely used as a means of extrapolating from the dispersion of observed locations to the likely extent of the full home range (Figure W-0j).

This process of home range analysis was carried out for each identifiable individual within a herd for whom more than 20 telemetry points were available. All other telemetry and observation points for a herd that did not meet these criteria were excluded from the CHHR analysis but were used to verify the accuracy of the final CHHR volume contours. The results of these analyses were a collection of surface rasters, one for each animal, from which the volume contours were created.

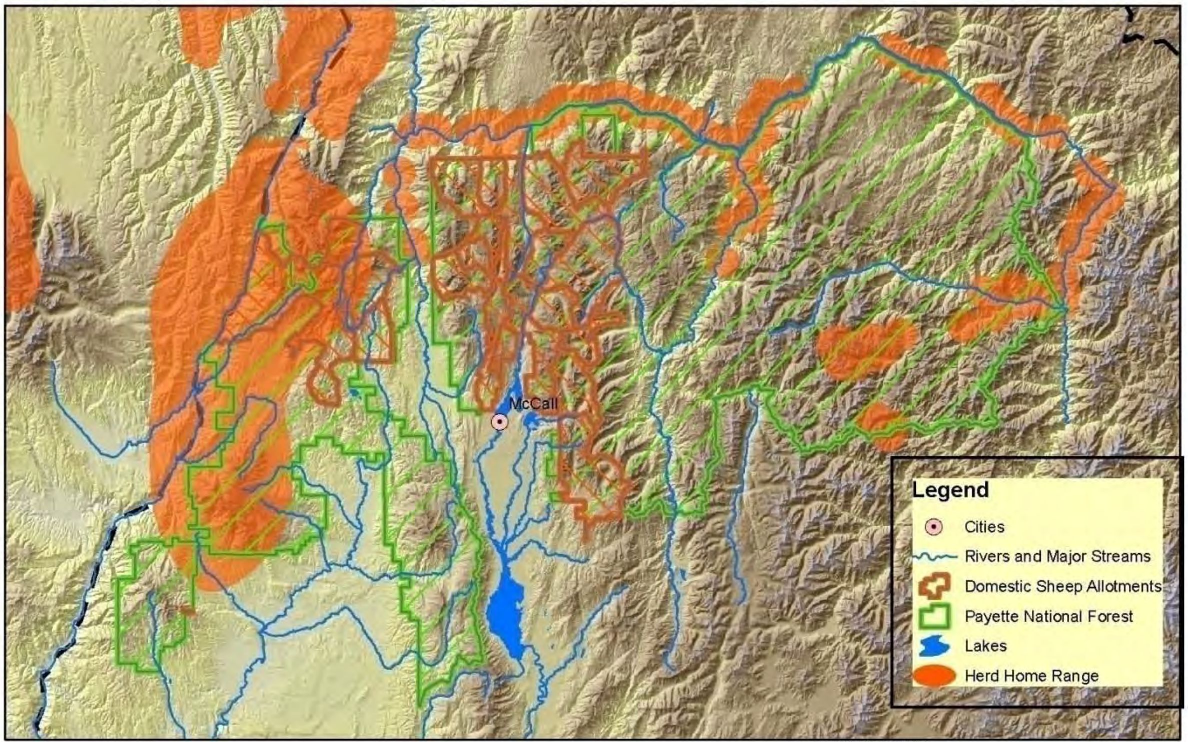
To create an overall CHHR, the raster surfaces from the individuals were added together. Then, volume contours, known as isopleths, were created from the merged herd surface using Hawth’s Analysis Tools version 3.27 Extension for ArcGIS (Beyer 2004). Isopleths are contours meant to enclose a given percentage of the telemetry observations; the 95th isopleth for example, is drawn to enclose an area in which 95 percent of the telemetry points are found. Volume contours were calculated for the 50th, 60th, 70th, 80th, 90th, and 95th isopleths, and are shown for each herd in the *Modeling and Analysis Technical Report* (Appendix L). The CHHR is defined as the area contained within the 95th isopleth. Points beyond the 95th isopleth were considered forays and analyzed separately (see Foray Analysis section below).

Figure W-0j. Combined Core Herd Home Ranges for the Entire Project Area and for the Payette National Forest

Herd Home Range with in Hells Canyon and The Salmon River Canyon



Herd Home Range on the Payette National Forest



Created by Chans O'Brien
June 16, 2010
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Foray Analysis

Similar to bighorn sheep elsewhere, Hells Canyon and Salmon River bighorn sheep—particularly rams—make occasional long-distance movements beyond their CHHR. Singer et al. (2001) called these movements forays and defined them as any short-term movement of an animal away from and back to its herd's CHHR. This life-history trait can put bighorn sheep at risk of contact with domestic sheep, particularly when suitable habitats are well connected and overlap with domestic sheep use areas (Singer et al. 2000c, Gross et al. 2000), even when domestic sheep use is outside of CHHR areas. The risk of contact between dispersing bighorn sheep and domestic sheep is related to the number of bighorn sheep in a herd, proximity of domestic sheep use areas (allotments) to a bighorn sheep CHHR, distribution of bighorn sheep source habitats across the landscape, and frequency and distance of bighorn sheep forays outside of the CHHR.

The foray model analyzed how often bighorn sheep leave the CHHR, whether they travel far enough to reach an allotment, and whether they then actually intersect an allotment (i.e., rather than intersecting a different area at the same distance from the CHHR). Movement behavior estimates were formed by analyzing the same large telemetry dataset of bighorn sheep movements in Hells Canyon that was used to determine each herd's CHHR. In the Salmon River system, only one and one-half years of telemetry data from 30 individuals in the Main Salmon/South Fork herd was available. Those data were useful in estimating the herd's CHHR, but not sufficient to characterize their foray behavior. As a result, modelers used the much more extensive data collected for the Hells Canyon herds to estimate the probable movement patterns of bighorn sheep in herds throughout the Payette National Forest.

The foray analysis most likely underestimates the true frequency of longer-distance forays. The reason for this underestimation is that the vast majority of the telemetry data are from standard VHF (very-high frequency) collars (rather than from GPS collars which collect and store or transmit data from everywhere an animal travels). With VHF collars, locations are determined by triangulation from a plane or boat travelling a route every few days or weeks through the areas in which the bighorn sheep of a herd are usually seen. The farther a bighorn sheep has travelled from its CHHR, the farther it is likely to be from the observers, and the less likely it is to be detected. There are in fact several cases in the telemetry data where rams last observed on a foray have "disappeared" for a couple of months before reappearing, likely from a journey that carried them beyond the range of detection of the survey.

For bighorn sheep moving through forested areas, detection may also be hampered by line-of-sight and signal bounce issues. Finally, even when an animal on foray is detected in every survey, the large interval between observations means that it is unlikely to be observed at the furthest extent of its foray. The extent to which these forms of sampling bias underestimate the frequency of long-distance movements in the foray analysis is unknown.

The path taken by a bighorn sheep traveling outside its CHHR might intersect any part of an allotment; therefore, the analysis began by calculating the probability of intersecting an allotment within each of 35 "rings" or annuli, each 1 km wide, located between 1 and 35 km from the CHHR boundary. That probability was broken into two parts:

(1) Probability of a foray movement
(2) Probability that a bighorn sheep on a foray will reach a ring and intersect an allotment within that ring.

Probability of a Foray Movement

Most bighorn sheep, especially ewes, never move beyond the CHHR in most years. Figure W-0k displays the maximum distance of ram forays outside of CHHR areas (95 percent isopleth) for the data set. Figure W-0l displays the proportion of rams with forays from 0 to 35 km from CHHR areas for the data set. Forays from all but one bighorn sheep were between 0 and 26 km; one ram had a documented foray that extended 35 km from its CHHR. Foray distances were stratified into 1-km concentric rings that emanated from CHHR areas and were used as a basis for calculating the probability of contact.

Figure W-0k. Maximum Distance of Ram Summer Forays beyond the Core Herd Home Range

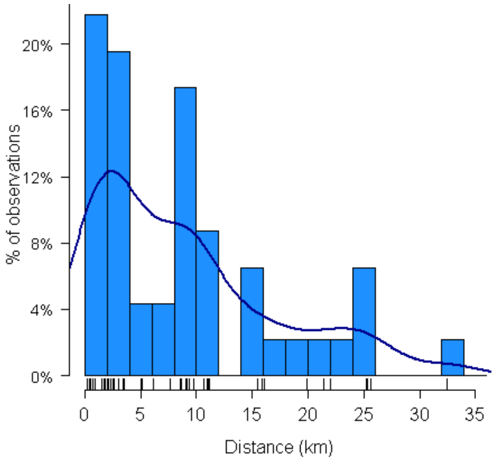
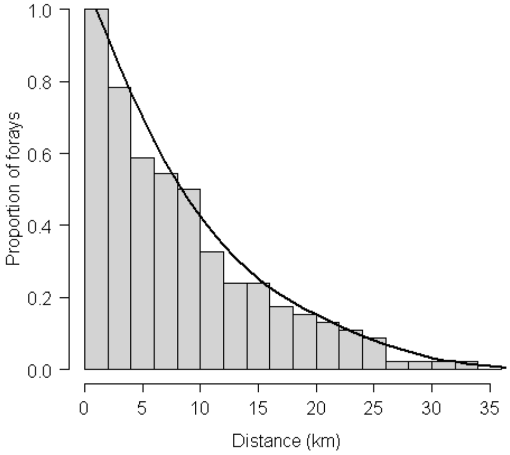


Figure W-0l. Proportion of Ram Summer Forays Reaching Each Ring



The frequency of foray movements by both rams and ewes in summer (May–October) and winter (November–April) are shown in Table W-3a. The probability of bighorn sheep–domestic sheep contact in summer and winter were calculated separately because characteristic movement patterns differ between seasons (e.g., the rut occurs in November/December and produces relatively frequent and long-distance exploratory forays by rams), and the allotments are only open to domestic sheep during the summer.

According to Table W-3a, 28.8 percent of radio-collared rams left the CHHR at least once (in summer) during the years they were observed. In any one summer, however, just 14.1 percent of rams left the CHHR. Accordingly, in the foray model, each ram was given a 14.1 percent probability per summer of making a foray outside of the CHHR. Similarly, ewes were given a 1.5 percent probability of leaving the CHHR each summer.

Table W-3a. Summary of Telemetry Observations Made Outside of the Core Herd Home Range

Summer (May–October)	Ewes		Rams	
	Percent of observations	Number out of total observations	Percent of observations	Number out of total observations
Animals leaving CHHR at least once	6.50%	14/215	28.80%	30/104
Animal-years with at least one foray	1.50%	15/985	14.10%	44/311
Telemetry points outside of CHHR	0.20%	29/17,258	4.40%	160/3,674
Winter (November–April)	**Ewes**		**Rams**	
Animals leaving CHHR at least once	12.9%	28/217	34.9%	38/109
Animal-years with at least one foray	5.6%	60/1,062	17.8%	68/380
Telemetry points outside of CHHR	0.8%	109/12,941	3.7%	156/4,200

Probability that a Bighorn Sheep will Intersect an Allotment

Many animals—particularly ewes—may not travel far, even if they are observed outside of the CHHR. The probability that a bighorn sheep on a foray will reach an allotment decreases as the travelling distance increases. To characterize that decreasing probability, the modelers first extracted from each foray, the maximum distance from the CHHR at which an animal was observed (Figure W-0k). In the dataset, the maximum distance was 35 km, so the model distribution extends to that distance.

It is known that an animal located 25 km from the CHHR has crossed each ring between itself and the CHHR. Also, 100 percent of the animals that make a foray intersect at least the first ring around the CHHR. More generally, the proportion of animals whose forays intersect each ring is equal to the proportion known to have reached it or one of the rings beyond it. That distribution is shown in Figure W-0l, along with a smooth curve fitted to it. Figure W-01 illustrates that half of the rams who leave the CHHR travel at least 10 km from the CHHR and almost a quarter of the rams travel 16 km. However, just one ram has been observed (in summer) to travel more than 26 km from the CHHR. This model uses the distribution in Figure W-0l to calculate the probability that an animal will reach any given ring surrounding its CHHR, $P(\text{Animal reaches ring}_k \mid \text{Foray})$.

Given that an animal has reached a ring, the probability that it will be in an allotment is proportional to the size of the allotment and to the quality of the habitat in the allotment relative to the size and quality of habitat in the ring as a whole. Calculating the size of the allotment is simple, but determining if a bighorn sheep will intersect an allotment first requires knowing bighorn sheep habitat preference.

Based on the source habitat model, all areas within 35 km of the CHHRs were assigned to one of three habitat classes—source habitat, connectivity area, and non-habitat. Source habitats are areas fitting the criteria described in the Source Habitat Model section above. Connectivity areas do not meet those criteria, but are located within 350 m of source habitat. Areas of non-habitat do not meet those criteria and are located more than 350 m from source habitat. Connectivity areas were distinguished from non-habitat because even when bighorn sheep are found outside of areas mapped as source habitat, they are usually not far from it. Of the 3,177 observations of bighorn sheep located outside of source habitat, all but 80 have been within 350 m of source habitat.

Next, the relative preference of bighorn sheep for these three classes of habitat was calculated using a resource selection function (Manley et al. 1993, Boyce et al. 2002). The habitat classes consisted of habitat, habitat connectivity, and non-habitat. The habitat class is the same as summer source habitat. Habitat connectivity was created by using a two-stage buffer on the summer source habitat. The first stage is a simple buffer around patches of habitat at 350 m, which was determined by measuring the distance of all telemetry data that fell outside habitat and finding one standard deviation of those distances. The second stage was a buffer of 1,050 m—three times the distance of the first stage—which is only applied to pieces of habitat connectivity that are within the 1,050 m distance. The second stage is designed to connect fragmented complexes of habitat. The third habitat class consists of the rest of the area that is not covered by the first two classes. The resource selection function was constructed using a use/availability approach that yields high values for habitat classes with many observations of bighorn sheep relative to their area. If the animals in a herd have equal areas of Habitat A and Habitat B available, but spend 90 percent of their time in Habitat A, their preference for Habitat A would be 9 times their preference for Habitat B.

While on forays, bighorn sheep in the Hells Canyon herds prefer source habitat to connectivity areas, and prefer both of those to non-habitat. Relative to a preference of 1.00 for source habitat, bighorn sheep showed a preference of 0.177 for connectivity areas and a preference of 0.029 for non-habitat. In other words, within the 35-km-wide ring surrounding a CHHR, bighorn sheep were 5.6 times more likely to be found in a given square-kilometer of source habitat than in a square-kilometer of connectivity area, and 35 times more likely to be found in source habitat than in non-habitat.

Finally, habitat preference and the distribution of habitat within each ring surrounding a CHHR was used to calculate the probability that a bighorn sheep that reaches a particular ring would cross the ring into an allotment. The map in Figure W-0m is a visualization of the estimated probabilities that bighorn sheep on a foray will reach each location within 35 km of the CHHR. Dark blues represent the highest probabilities, and light yellows the lowest. Moving outward from the CHHR, colors lighten as the probability of a foray reaching that distance drops. Within each ring, the darkest color (highest relative probability) marks areas of habitat, the lightest color (lowest relative probability) marks areas of non-habitat, and the intermediate color marks areas of connectivity habitat.

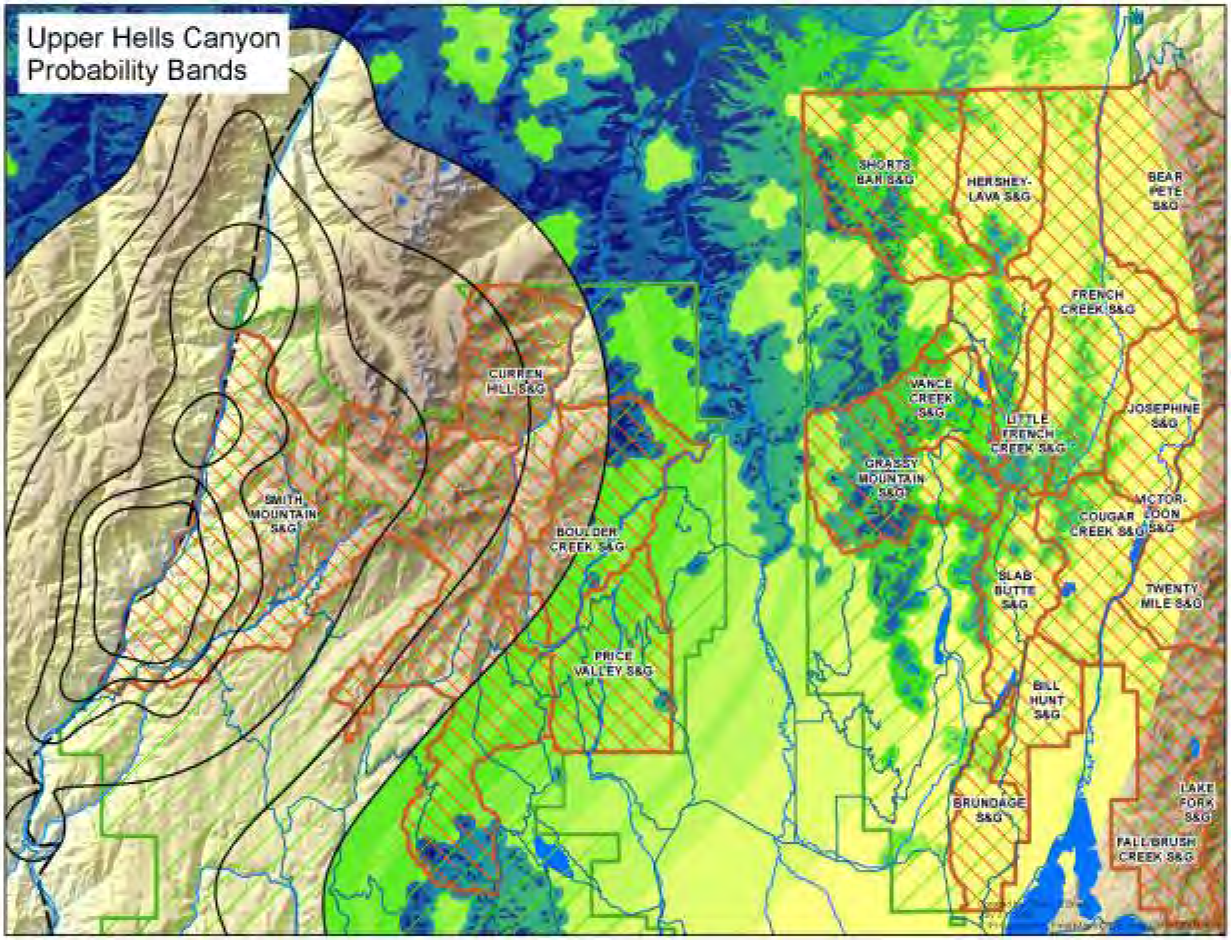
Foray Analysis results in the context of other published works

Both the frequency and distances of foray movements by Hells Canyon bighorn sheep were consistent with other reports in the literature. Singer et al. (2001) calculated annual foray rates of bighorn sheep in ten published studies. In those herds, the annual number of forays per radio-collared animal of either sex ranged from 0 to 0.23 (mean 0.10, standard deviation 0.09), comparable to 14% of rams and 1.5% of ewes making summer forays from herds in the Hells Canyon metapopulation.

In southwestern Alberta, Festa-Bianchet (1986) relocated rams as far as 48 km from the site of their capture. A recent 17 month study of three bighorn herds in Montana, (DeCesare and

Pletscher 2006) found relatively long (19- to 33-km) movements by four of five radio-collared males. Finally, Singer et al. (2000b) followed 31 translocated populations of bighorn, and documented numerous colonizations of nearby patches of habitat. In that study, the probability of colonization (75%) was highest for patches located 12.3 km from a bighorn sheep population indicating that such movements occur with relatively high frequency. This parallels our finding that nearly 25% of forays by Hells Canyon bighorn sheep reach a distance of at least 15 km from the CHHR.

Figure W-0m. Visualization of the Foray Probabilities for the Upper Hells Canyon Herd



Disease Model

Modeling population dynamics of large herbivores at the individual level requires estimating numerous parameters, from adult and juvenile survival rates to age at sexual maturity, fecundity, and lamb survival (Gaillard et al. 2000). In addition, the average values for each of those life-history parameters may be modified by interacting impacts of density dependence, weather, forage availability, and predation. Properly estimating these parameters would require extensive age- and class-specific population data, ideally from the populations being modeled.

Accurate individual-level modeling of the impacts of disease events is even more difficult, as the dynamics of respiratory disease in the wild are only partly known. An individual-based model would require understanding many factors, such as the incubation period and active infection durations, probability and rate of recovery from disease, rate of effective contact between individuals within the herd, and possible role of persistently infected individuals in harboring and spreading the disease. Variations in the resistance to disease of individual bighorn sheep and in the virulence of the disease-causing organisms themselves can also affect population dynamics.

Rather than attempting to create a complicated individual-based model that incorporated all of the parameters above, researchers built a population dynamics model using a “top-down” approach in which population size was the primary state variable. A simpler model may appear to have limited accuracy or realism but actually has several advantages for estimating the variables of greatest interest—projections of population size, volatility, and persistence. First, a simpler model requires estimating fewer and more easily estimated parameters. Population size is easier to estimate than individual mortality and fecundity rates that affect it. Likewise, the population-level impacts of respiratory disease outbreaks are better understood than the details of bacterial shedding within-herd effective contact rates and individual variation in disease susceptibility that determine the course of individual epidemics. A second important advantage of “top-down” models is that they have fewer moving and interacting parts and so are more interpretable, transparent, and accessible to scrutiny.

Model Organization

Researchers constructed a disease model with three components. The first component models the probability that an animal that is determined by the Foray Model to have reached an occupied allotment will subsequently contract respiratory disease and initiate an outbreak in its home herd. The second component models population growth in a healthy herd. Annual population growth in the disease model depends on the current disease status of the herd (disease-free or infected), current population size, and an estimate of the maximum sustainable herd size for each herd. In the absence of disease, herd numbers increase (unless they have fewer than 30 individuals). The third component models the magnitude and duration of impacts caused by an outbreak of respiratory disease in a bighorn herd. In the first year of a disease outbreak, herds suffer an all-age die-off, followed by a variable number of years of depressed lamb recruitment. Eventually, herds that survive are considered to be fully recovered from (although still susceptible to further outbreaks of) the disease outbreak.

Figures W-0n and W-0o provide an overview of the disease model structure. Figure W-0n illustrates the first step of the annual cycle in which the disease status of each herd is determined. Figure W-0o illustrates the consequences of current herd size and disease status on next year’s population size.

Figure W-0n. Disease Transmission and Recovery Sub-model

Does the herd harbor an ongoing infection?

YES → go to the Population Dynamics Sub-Model
NO → go to the next step

Does the herd contract respiratory disease this year? (Use the risk model to determine the probability of disease transmission into the herd from contact with either domestic sheep or infected bighorn sheep.)

YES → determine the number of years that the herd will suffer from depressed recruitment, and go to the Population Dynamics Sub-Model
NO → go to the Population Dynamics Sub-Model

Figure W-0o. Population Dynamics Sub-model

1) **Is the population size less than the minimum viable population size (30 animals)?**

YES → the population declines by 16 percent
NO → go to the next step

2) **Is the population free of respiratory disease?**

YES → the population grows by an amount determined by the logistic growth equation
NO → go to the next step

3) **Was the population just infected this year?**

YES → the population experiences an all-age die-off
NO → the population experiences increased mortality of juvenile bighorns.

Probability of Effective Contact and Subsequent Herd-level Die-off Given Co-habitation of Bighorn Sheep and Domestic Sheep within an Allotment

Although organisms that cause respiratory disease may be endemic in some bighorn sheep herds (Hobbs and Miller 1992), the current model is designed to assess the impact of disease transmitted from domestic sheep, so all outbreaks ultimately originate from contact with domestic sheep. The foray model estimates the probability that a bighorn sheep will reach an allotment occupied by domestic sheep (cohabitation), but it does not address the probability of the additional steps needed for an outbreak to occur. Once a bighorn sheep reaches an occupied allotment, the bighorn sheep must (1) come into contact with domestic sheep in the allotment and (2) contract the disease from the domestic sheep. Finally, for an outbreak to affect the animal’s home herd, the infected bighorn sheep must (3) make its way back to the CHHR and (4) transmit the disease to other members of the herd.

Assumptions governing the probability that a bighorn sheep that reaches an occupied allotment will contract disease from the domestic sheep are problematic. For a similar model applied to populations of endangered Sierra Nevada bighorn sheep (Clifford et al. 2009), researchers assumed that any cohabitation with domestic sheep was equivalent to contact between the two species, citing the attraction of bighorn sheep (particularly rams) to domestic sheep and past observations of stray domestic sheep associating with bighorn sheep. They estimated that the subsequent probability of disease transmission (effective contact) given such physical contact was between 50 and 100 percent, based on numerous pen studies that have shown that nearly 100 percent of bighorn sheep co-housed with apparently healthy domestic sheep develop respiratory disease (e.g., Onderka and Wishart 1988, Foreyt 1989, Foreyt 1990, Lawrence et al. Forthcoming). Less information is available about the probability that a diseased animal will return to its CHHR and initiate an outbreak.

Together, the four steps described above determine the overall probability of an outbreak happening given that an individual bighorn, whose movements were modeled by the Foray Model, reaches an open allotment. Because so much uncertainty surrounding this parameter exists, and essentially no research exists that would allow its estimation, the disease model was run with a range of probabilities of effective contact (a contact resulting in a disease transmission) and a subsequent herd-level outbreak, given cohabitation of a bighorn sheep and domestic sheep in an occupied allotment. Values used for probability of a disease outbreak given contact were 5 percent, 10 percent, 25 percent, 50 percent, 75 percent, and 100 percent.

Population growth in a healthy herd: density dependence and the logistic growth model

Bighorn sheep populations, like those of other large herbivores, are subject to density-dependent population growth regulation (Monello et al. 2001, Bonenfant et al. 2009). Even in the absence of disease, a population of bighorn sheep will not grow without bound; as the number of animals in an area increases, the rate of further growth eventually begins to slow. The dynamics by which that slowing occurs can be complicated and are not completely understood. Jorgenson et al. (1997) and Portier et al. (1998) analyzed a long-term mark–recapture study of two populations of Rocky Mountain bighorn sheep in Alberta, Canada, for evidence of density dependence. They found the main demographic response to large population size was a decrease in lamb survivorship. Yearling ewes also suffered some mortality increases when populations were high. Other researchers have also detected a decrease in the rate of recruitment with increasing density (with relatively little response in adult survival) (McCarty and Miller 1998), a pattern that is characteristic of many large ungulates (Gaillard et al. 1998, Bonenfant et al. 2009).

To incorporate density dependence into the disease model, researchers used the logistic equation, a common ecological model of population growth (Gotelli 2008). In the logistic growth model, the maximum per capita growth rate (*r*, with units of new individuals per individual per year) is only achieved when population size is quite small. As the population increases towards its maximum sustainable size (*K*), the number of surviving offspring per female steadily decreases and the rate of population growth slows. The logistic growth model is defined as follows:

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right)$$

Where:

dN/dt = yearly change in population size
N = current population size
r = maximum growth rate
K = maximum sustainable population.

K is usually known as the "carrying capacity;" in this model it is referred to as the "interim herd level" (IHL) to emphasize that it should not be interpreted as either a goal or a limit to the number of bighorn sheep that might be supported by any given herd.

The following three sections describe how modelers estimated the values of N, r, and K that were used by the disease model.

Estimating N—(Current Herd Size)

Population estimates for the 15 herds (Table W-3b) were taken from survey data collected by the IDFG, ODFG, Washington Department of Fish and Wildlife (WDFW), and SRBSP (administered by the Nez Perce Tribe). For each herd, we used data from the most recent survey available. Estimates of current herd sizes ranged from 10 to 210 and totaled 1,148 for all 15 herds.

The one area of concern, Little Salmon, was not treated as a fully independent population in our model. The Little Salmon has not been regularly surveyed for the presence of bighorn sheep, so a population estimate of 4 animals in the Little Salmon drainage was made on the basis of incidental observations of bighorn sheep within the last 3 years (Table W-3b).

Table W-3b. Population Estimates and Interim Herd Levels (IHLs) for 15 Herds and 2 Areas of Concern from Survey Data Collected by the Idaho Department of Fish and Game (IDFG), Oregon Department of Fish and Game (ODFG), Washington Department of Fish and Wildlife (WDFW), and Salmon River Bighorn Sheep Project (SRBSP)

Herd	Estimated Population (*N*)	Date of Estimate	Data Source	IHL (*K*)
Hells Canyon				
Asotin	84	2009	WDFW	201
Big Canyon	20	2008	IFG	112
Black Butte	47	2009	WDFW	538
Imnaha	135	2008	ODFW	475
Lostine	65	2008	ODFW	128
Mountain View	13	2009	WDFW	208
Muir Creek	30	2008	ODFW	100
Myers Creek	10	2008	IFG	40
Redbird	115	2008	IFG	376
Sheep Mountain	11	2008	ODFW	218
Upper Hells Canyon	45	2009	IFG	326
Wenaha	90	2008	ODFW	326
Salmon River				
Big Creek	186	2006	IFG	390
Main Salmon/South Fork	210	2009	SRBSP	336
Upper Salmon	87	2006–07	IFG	733
Areas of Concern				
Little Salmon	4	2007–09	Various	NA

Estimating r—Maximum Herd Growth Rate

Estimates of the maximum growth rate *r* (also known as the intrinsic or exponential growth rate) were taken from published literature. McCarty and Miller (1998) estimated *r* for 16 translocated populations of Rocky Mountain bighorn sheep in Colorado. They based their estimates on herd growth rates observed during the first few years after successful translocations, applying a correction to account for the skewed sex ratio of the translocated animals. Maximum growth rates for the 16 herds ranged between 0.051 and 0.26 (i.e., 5–26 percent annual increase in population size). In the disease model, a maximum growth rate for each herd was sampled from a normal distribution (mean = 0.136, standard deviation = 0.057) fitted to the estimates of McCarty and Miller (1998).

Estimating K—Interim Herd Level

Although historical reports indicate that bighorn sheep were once very abundant in Hells Canyon (Bailey 1936), we do not have accurate estimates of the current maximum potential population sizes of the herds found on or near the Payette National Forest. Even when studies are carried out to measure the actual carrying capacity of a population, directly measuring in the field can be difficult or even impossible (Coulson et al. 2008); in any case, such studies have not been conducted for bighorn sheep in our area.

However, some form of density dependence needs to be introduced to simulate likely future herd dynamics, which means some estimate of *K* needs to be included in the logistic growth model. Modelers named *K* the IHL to emphasize that the number should not be construed as a Forest Service management goal or a strong estimate of actual carrying capacity of the herd home ranges.

In the absence of better information, modelers estimated IHL on the past maximum number of animals observed for each herd. For the Salmon River herds, IHLs were estimated to be 175 percent of the highest population estimate from the past 30 years. For Hells Canyon herds, IHLs were estimated to be 175 percent of the highest population estimate from the past 40 years.

Nonviable Herd Numbers

The minimum population size, referred to as the nonviable herd number (NVN), is the threshold below which a population will not continue to grow at a disease-free rate and will, in fact, decline. The model used 30 individuals as the NVN for all herds except Big Canyon, Muir Creek, and Myers Creek—because these herds overlap, they were treated as a single herd with a combined NVN of 30.

Population Impacts of Disease

Disease-caused declines in bighorn populations typically consist of an initial all-age die-off event followed by several years of low lamb survival. Ewes that survive the initial die-off may give birth, but after a period of weeks to months, their lambs develop pneumonia and die. The disease model includes both of these impacts of disease outbreaks; in the first year, infected herds suffer an all-age die-off, followed by several years of slower decline due to elevated lamb mortality. The following sections describe how the population impacts of both types of disease-related mortality were modeled.

Initial All-age Die-off

Disease outbreak impact was measured as the product of the herd size and proportion of impact. This parameter was estimated using data from documented outbreaks in the Hells Canyon area. In 1983, an outbreak of pneumonia killed 60 percent of the animals in the Granite–Three Creeks area of Idaho (HCBSRC 1997). An outbreak of pneumonia in the Lostine herd in 1986–87 killed 66 percent of the herd (Coggins 1988). A 1995–96 outbreak affected several herds, with herd-level mortality amounting to 33, 50, 65, 69, and 75 percent (Cassirer et al. 1996). The lowest mortality rate (33 percent) occurred in the smallest herd (Upper Joseph Creek, with 30 animals); the highest mortality rate (75 percent) occurred in the largest herd (Black Butte, with 220 animals). In 1999, a disease outbreak resulted in the death of 59 percent of the McGraw herd and 53 percent of the Sheep Mountain herd in the first year, followed by subsequent declines in both herds and eventual extirpation of the McGraw herd. In the model, herd-level mortality during the first year of an outbreak was sampled from the distribution of values observed in the previous Hells Canyon outbreaks described above, with an equal probability of mortality of 33, 50, 53, 55, 65, 66, 69, and 75 percent.

Chronic Lamb Mortality

The significant impact of the all-age die-off that occurs during the first year of an epidemic is compounded by pneumonia and septicemia in young lambs that frequently suppresses recruitment for several additional years (Cassirer et al. 2001, Miller 2001, George et al. 2008). The duration of this chronic mortality of lambs is variable, but in almost all cases lasts for at least 2 years[3]. In some cases, poor lamb recruitment has continued for as long as 8 (Enk et al. 2001) or 9 years (George et al. 2008) post-outbreak. Several Hells Canyon herds have had poor lamb recruitment for 6 or more years (Wenaha, Muir Creek, Upper Hells Canyon, and Sheep Mountain); in the Sheep Mountain herd, lamb survival has still not recovered 10 years after a 1999 disease outbreak. In the disease model, herds affected by disease suffer poor lamb recruitment for between 2 and 10 years following the all-age die-off with the duration randomly selected.

The adult survival rate for healthy populations of bighorn sheep (i.e., the percentage of adults surviving from one year to the next) is around 90 percent (Jorgenson et al. 1997). Therefore, in the complete absence of recruitment, populations will decline an average of 10 percent per year. In herds with depressed recruitment, the percentage of ewes with surviving lambs ranges from 0 to 25 percent, which translates to an annual population change of between –10 percent and 2.5 percent. Therefore, for modeled herds suffering from disease-related lamb mortality, the annual population change was randomly selected from between –10 and 2.5 percent.

Extended Infectious Duration

When a simulated herd becomes infected, animals in the herd remain infectious for a variable length of time, generally more than 1 year. The duration of infectiousness ranges from 1 to 4 years and follows a uniform distribution.

Model Implementation

The disease model described above and in Figures W-0n and W-0o was implemented using @RISK, a commercially available Excel spreadsheet add-in (Palisade Corporation 2009). @RISK permits the model to include components of uncertainty and variability, thereby expanding it from a deterministic model to a stochastic (probabilistic) one. As such, multiple runs, or iterations, may be performed to evaluate the range of outcomes that may arise from selecting various actions.

Examples of the simulated individual herd populations for different outbreak results over 100 years are presented in Figure W-0p. Different outbreak results are presented to illustrate the stochastic nature of the model—each time the model is run, the results are different. These outputs were chosen because they show the range of possible outcomes that might result from a single management scenario.

The disease model was used to perform 1,000 simulations of each proposed alternative, with and without cumulative effects. Each simulation began with all bighorn sheep herds uninfected and at

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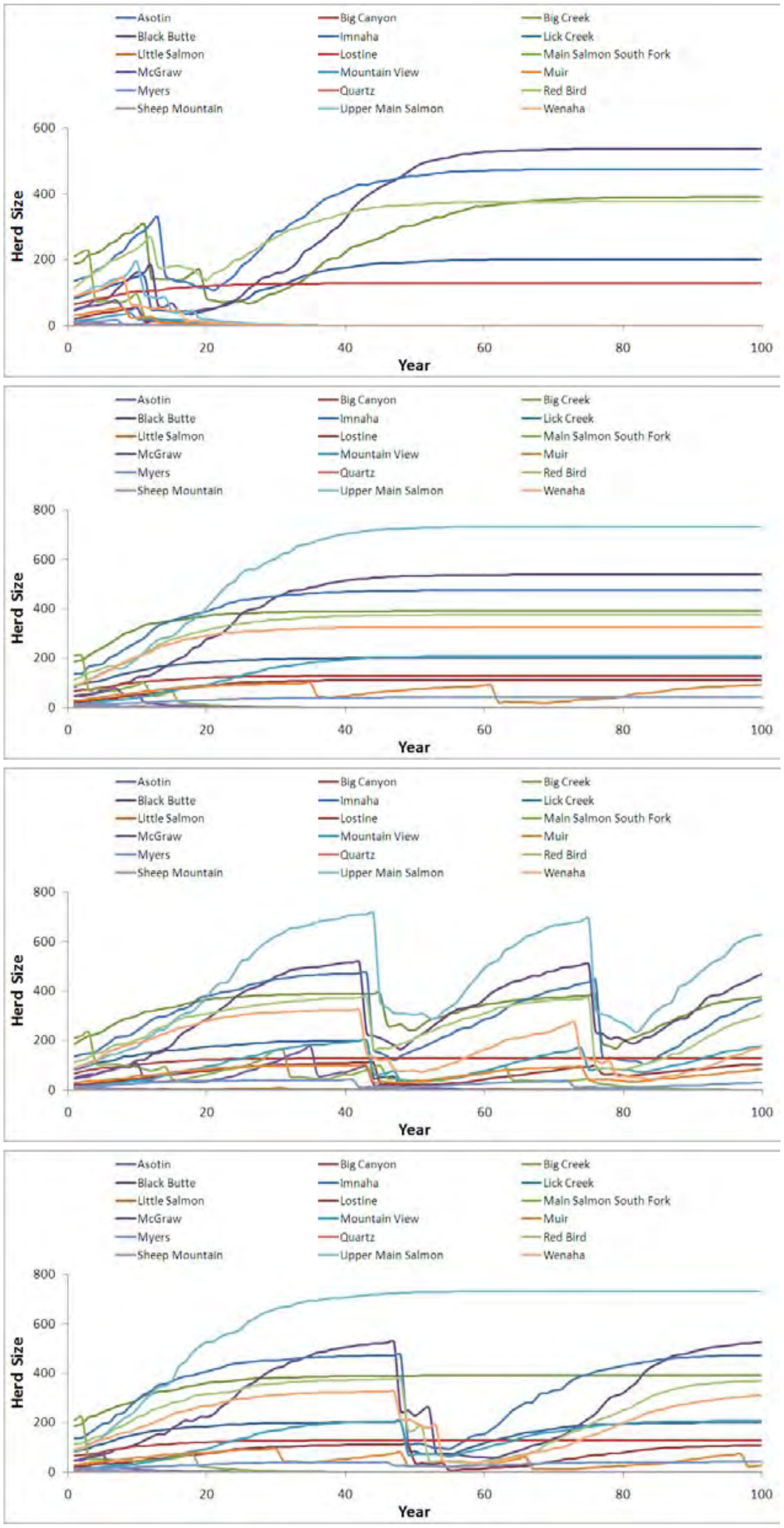
[3] Many studies reporting post-epidemic lamb mortality have been published in the second or third year after an outbreak, and in such cases, lamb recruitment was almost invariably still low at the time of the last reported observation (Onderka and Wishart 1984, Spraker et al. 1984, Schwantje 1986, Festa-Bianchet 1988, Foreyt 1990, Ryder et al. 1992, Aune et al. 1998).

their current population size and was run for 100 years. Results, including the number of herds suffering pseudo-extirpation in each simulation, were collected and summarized for use in the Environmental Consequences section.

Figure W-0p. Four Examples of the Outputs Possible from the Disease Model at an effective contact rate of 0.75 for a Single Management Scenario



Summary

Bighorn sheep currently occupy only an estimated 30 percent of historic habitats at population levels significantly diminished from pre-Euroamerican settlement (approximately 10 percent). Source environments and source habitats should be components used in addressing “suitable habitats to support viable populations,” but habitat alone does not equate to “population viability” for this species. Any viability assessment, and resulting management guidance for bighorn sheep, needs to address the potential for contact between domestic sheep and bighorn sheep and the implications for disease transmission between the species. Addressing the potential for contact requires understanding bighorn sheep life requisites, how bighorn sheep move through and utilize habitats, and domestic sheep management (i.e., timing, location, densities, season of use, and proximity of domestic sheep to bighorn sheep).

The aforementioned analyses offers a risk analysis approach that couples a significant telemetry database with habitat analyses to provide a reasonable basis for analyzing the likelihood of contact between bighorn sheep and domestic sheep. The results of these analyses allow modeling of the potential outcomes of interspecies contact on the persistence of bighorn sheep populations on and adjacent to the Payette National Forest.

Consistent with 36 CFR §219.20(a), the bighorn sheep discussion in the Direct and Indirect Effects by Alternative, Species of Special Interest section, page 3-316, of Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement will be deleted. The following pages will supplement the Direct and Indirect Effects by Alternative, Regional Forester Sensitive Species section, page 3-313, of the Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement.

ENVIRONMENTAL CONSEQUENCES

Direct and Indirect Effects by Alternative

Regional Forester Sensitive Species

Bighorn Sheep

Viability

This document was written in response to direction from the Forest Service Chief (Chief) to analyze bighorn sheep viability commensurate with the concerns and questions raised in the appeal decision related to the potential impacts of disease transmission from domestic sheep grazed on the Payette National Forest. However, the metapopulation structure of bighorn sheep is complicated by the fact that only portions of two different metapopulations occur within the Payette National Forest boundaries. Traditional population viability analyses are usually done within the context of isolated populations (Hanski 1998), and a viability analysis restricted to bighorn sheep on the Payette National Forest is meaningless unless the dynamics of the metapopulation are also considered. Therefore, viability discussions will need to extend beyond the borders of the Payette National Forest although the analysis of how domestic sheep use of the forest affects the two metapopulations is relevant.

Viability is generally expressed using two components—number of individuals and time—which can be used to describe population persistence over time. For example, Thompson (1991) describes population persistence as 99 percent of the population persisting for 1,000 years or 95 percent persisting over 100 years. Singer and Gudorf (1999) found no unequivocal minimum viable number for bighorn sheep, but suggest a minimum population size of 100 individuals if disease is not a factor and 300 individuals to buffer against the loss of genetic heterozygosity if severe or moderate epizootics are present. Singer et al. (2001) also found a strong correlation of population persistence with larger habitat patch sizes, greater distances from domestic sheep, higher population growth rates, greater home-range sizes, larger population sizes, and migratory movements. Larger populations (>250 animals) were more likely to recover following an epizootic, but habitat patch size was the primary correlate of both population performance and persistence (Singer et al. 2001).

Habitat Use

Current source habitat does not appear to be limiting for bighorn sheep as much of the apparently suitable bighorn habitat appears to be unoccupied (HCBSRC 1997). At scales below the Payette National Forest or watershed level, however, it is expected that the quality of habitat can have variances that cannot be detected at broader scales. The 2003 FEIS included successional modeling of both forested potential vegetation groups and sagebrush cover types. Comparable modeling was not completed for bighorn sheep habitat, since the information needed to model the change through time of grasslands, mountain mahogany, bitterbrush, and forest cover types with ≤10 percent canopy cover is sparse or unavailable.

The FEIS did, however, provide information on the trends of grassland vegetative response under each of the seven alternatives and ranked the alternatives (USDA Forest Service 2003b, pages 3-572 through 3-574). This discussion represented generalized grassland trends for the entire Ecogroup (Payette, Boise, and Sawtooth National Forests) and was not specific to the Payette National Forest although it did consider those management areas (i.e., Hells Canyon, Snake River, and Weiser River) that overlap the Hells Canyon bighorn sheep metapopulation and contain some of the higher risk domestic sheep allotments and trailing routes. Furthermore, these generalized trends represent more than bighorn sheep habitat but do not account for the escape terrain and other special habitat features important to bighorn sheep. Bighorn sheep habitat is a subset of these trends for grassland response.

The FEIS also discussed the generalized trends for deciduous riparian vegetation under the seven alternatives (USDA Forest Service 2003b, pages 3-575 through 3-576), which Wisdom et al. (2000) identified as a special habitat feature. Again, bighorn sheep habitat is a subset of deciduous riparian vegetation. Sagebrush cover types and their component grassland successional stages are discussed on pages 3-539 through 3-572 of the FEIS (USDA Forest Service 2003b).

Other factors that affect bighorn sheep habitat include patch dynamics of nonforest and forested habitats, and their juxtapositions to each other. For example, suppression of wildfires for several decades has resulted in a reduced fire return interval and larger wildfires in some vegetation types. One effect that has occurred to some extent on the community types used by bighorn sheep has been that the patch size of burned areas has increased relative to historical conditions. However, without specific information on the juxtaposition of needed patches on the landscape (size and arrangement) for this species, comparing trends further with the species' needs is difficult. Patch dynamics, which vary historically, may affect dispersal between source habitat patches for bighorn sheep. Although bighorn sheep can use a diverse array of terrestrial and aquatic systems to move across the landscape, altering historical vegetation dynamics can potentially affect migratory routes. Large patch sizes of burned areas can open up forested and dense shrub areas to bighorn sheep. In some fire regimes, these large patch sizes would have been historically present. However, their location on the landscape shifts over time as a burned area successes back to denser vegetation and new areas experience periodic disturbances. Livestock grazing practices can affect the balance between shrub and herbaceous vegetation and contribute to changes in the floristic composition of grass and shrub communities, both of which can result in altered fire regimes. These changes can also contribute to altering historical patch sizes.

In addition to patch dynamics, habitat quality is an important predictor of whether a species may be present. Habitat quality degradation through exotic weed invasions is a threat to habitat for this species. Depending on the type of exotic weed, food resources can be depleted and fire cycles disrupted, which can further alter species composition and structure. Livestock grazing can contribute to exotic weed invasions and damage to biological soil crusts, which can contribute to declines in source habitat quality.

Associated riparian areas within the ecosystem may also be affected by livestock grazing, with declines in habitat quality. Riparian systems can be particularly susceptible to livestock concentrations and grazing damage (Berry 1979). Defoliation, soil compaction, and floodplain water table subsidence due to channel widening or down-cutting have resulted in the loss of densely rooted graminoid and shrub species (Berry 1979, Kovalchik and Elmore 1992). Natural recovery of native riparian vegetation once occurring along the margins of the riparian area may be extremely slow, even with reductions in livestock grazing, because of deteriorating physical conditions of the stream during the last 150 years, dominance of exotic annuals within the riparian area, and loss of native seed sources (Clary et al. 1996). Livestock grazing can affect riparian vegetation by altering vegetation composition and seral stages. Excessive runoff from poor condition sagebrush and grasslands and direct damage to riparian vegetation and stream banks can result from livestock grazing and trampling, road construction, and recreational use (Blaisdell et al. 1982). Often, lowered water tables, resulting from heavy grazing pressure, have modified or destroyed normal riparian vegetation (Blaisdell et al. 1982), which has affected riparian ecosystem function. The ability of streams, associated vegetation, and wildlife populations to recover following reduced grazing stress appears to be situation specific and related to site characteristics, degree of degradation, and availability of native plant materials (Shaw 1992, Krueper 1993).

Human activities are also primary sources of potential habitat degradation for bighorn sheep. Roads can be a source of direct mortality through vehicle strikes, and their presence can increase disturbance to bighorn sheep during critical periods throughout the year. Road construction can exacerbate effects from other risk factors, such as the spread of exotic species. Another human factor that can accelerate risks associated with roads and weeds is the dramatic increase of off-highway vehicle use, which can facilitate the expansion of invasive species and adversely increase the potential for human disturbance and unlawful take. Roads and trails provide the primary access corridors for invasive plants, and some invasive species are able to out-compete native species, which can result in a substantial change in the overall biological diversity of the affected area and changes in historical fire regimes. The susceptibility of source habitat to weed establishment is important to investigate at finer scales in relation to ground-disturbing activities, such as prescribed fire, roads, livestock grazing, and energy development or exploration. Finally, winter recreation can disturb bighorn sheep.

The alternatives vary in the acres of suited rangelands available for domestic sheep grazing. The general effects listed above will also vary according to available rangelands, trailing routes, roads, and human disturbance associated with each alternative. This analysis can be an oversimplification as site-specific ecological conditions and livestock grazing practices will have different effects on more localized areas. Although habitat is not limiting at a Forest-wide scale on the Payette National Forest, these localized effects can limit habitat in some areas.

Evaluation Methods Used to Analyze Risk of Contact between Domestic and Bighorn Sheep and Implications for Disease Transmission

Outputs derived from the three models (source habitats, contact and disease transmission) were used to compare alternatives with respect to the risk of contact between domestic and bighorn sheep and to estimate implications for disease transmission between the species. Three factors are considered in assessing the potential impacts of disease on populations: (1) rate of contact between bighorn sheep and domestic sheep, (2) probability that contact will result in transmission of disease, and (3) effect of disease on the bighorn sheep population.

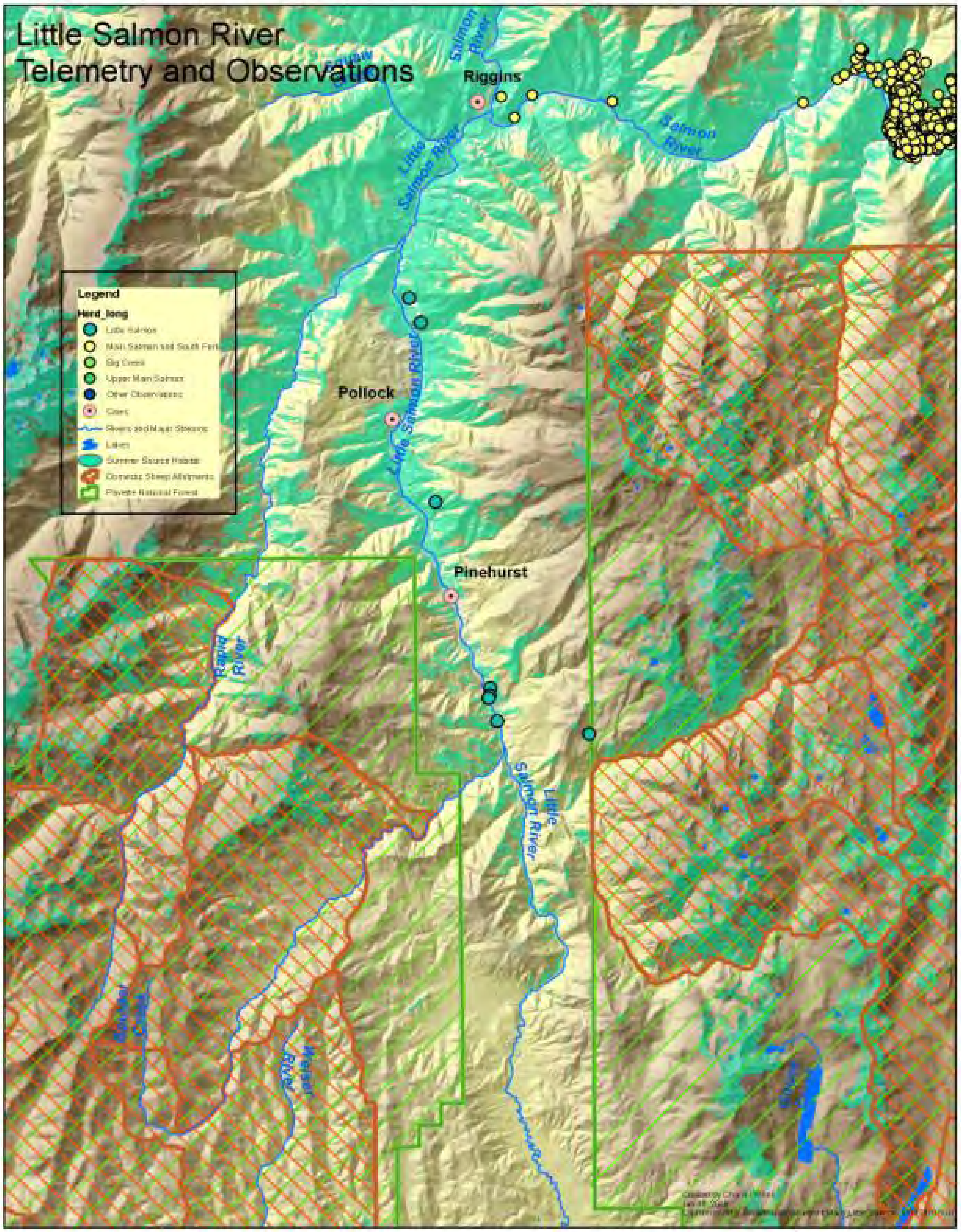
Modeling completed by Clifford et al. (2007) suggests that for some bighorn sheep populations, even a minimal level of contact can have severe persistence implications for bighorn sheep populations. For one Sierra Nevada bighorn sheep population that they modeled, they estimated a 2 percent annual risk of contact would result in a 50 percent probability of a catastrophic respiratory outbreak that would result in at least 40 percent mortality. In this analysis, the rate of contact was estimated using a large and robust telemetry data set to model CHHRs and bighorn sheep forays outside of CHHRs relative to the availability of source habitats. Outputs of the CHHR and foray analyses were used to determine the likely rate of bighorn sheep contact with domestic sheep allotments.

Comparison of Alternatives

Considerations in Evaluating Alternatives

Alternatives were evaluated on their merits for providing separation and minimizing likelihood of contact between bighorn sheep and domestic sheep on seven bighorn sheep populations on, and adjacent to, the Payette National Forest. These populations include Big Canyon, Little Salmon, Main Salmon/South Fork, Muir Creek, Myers Creek, Sheep Creek, and Upper Hells Canyon and have the highest likelihood for contact with domestic sheep allotments grazed on the Payette National Forest. Other populations were analyzed, but are not included in this section, such as Big Creek, Upper Salmon River, and Lostine. Little Salmon was included because recent incidental and telemetry observations suggest some animals already occupy the area and a new population has or will soon form in the area. The Little Salmon animals may comprise an important connectivity population between the two metapopulations (Figure W-9a).

Figure W-9a. Telemetry Data and Observations for the Little Salmon River



Source Habitat Model—Bighorn Sheep Summer Source Habitats

Although both summer (May–October) and winter (November–April) bighorn sheep source habitats were evaluated (see *Modeling and Analysis Technical Report* in Appendix L), modelers focused primarily on summer source habitats since domestic sheep are mostly present on the Payette National Forest and near bighorn sheep source habitats during this period. The source habitat model was used to estimate the amount of bighorn sheep summer source habitat receiving protection and the percentage of rangelands on the Payette National Forest identified as suited for domestic sheep grazing for each alternative. The juxtaposition and distances between bighorn sheep summer source habitats and suited rangelands for domestic sheep are important attributes and influence the probability of contact between the species. The alternatives exhibit substantial variation on both measures. The percentage of summer source habitat protected varies from 0 percent (Alternatives 1B, 2, 5, 7) to 100 percent (Alternative 7E). Similarly, the percentage of rangelands designated as suited for domestic sheep varies from 0 percent (Alternative 7E) to 100 percent (Alternatives 1B, 2, 5, 7) (Table W-10). Alternative maps spatially display these areas on and adjacent to the Payette National Forest (Figures W-9b through W-9i).

Table W-10. Comparison of Alternatives Displaying Protected Summer Source Habitats for Bighorn Sheep and Remaining Suited Habitats for Grazing in Summer Bighorn Sheep Habitat

Alternative	Protected Bighorn Sheep Summer Source Habitat (Acres)	Protected Bighorn Sheep Summer Source Habitat (%)	Suitable Range (Acres)	Suitable Range (%)
1B, 2, 5, 7	0	0.00	100,310	100.00
3, 4, 6	33,918	9.20	93,082	92.79
7E	368,641	100.00	0	0.00
7G	263,338	71.43	38,468	38.35
7L	315,715	85.64	64,311	64.11
7M	338,934	91.94	43,245	43.11
7N	337,532	91.56	38,392	38.27
7O	346,696	94.05	31,592	31.49
7P	332,372	90.16	46,106	45.96

Risk of Contact Model—Contact between Bighorn Sheep and Domestic Sheep

The risk of contact model (CHHR and foray analyses) is perhaps the most critical aspect of the analysis since the consequences of low levels of interspecies contact are potentially severe for bighorn sheep. Because the model is based on a large telemetry data set and corroborated with source habitats, it is considered a reliable proxy for how the Hells Canyon and Salmon River metapopulations utilize the landscapes and can be used to determine the likelihood that bighorn sheep will transect domestic sheep allotments (i.e., a contact is considered a bighorn sheep transecting a domestic sheep allotment boundary). Obviously, the lower the probability of contact, the more likely a bighorn sheep population will persist. At current population sizes, the number of contacts with allotments expected each year varies between alternatives, from 0 (Alternative 7E) to 1.33 (Alternatives 1B, 2, 5, 7) (Table W-11). For all alternatives, the

Main Salmon/South Fork and Upper Hells Canyon populations contributed the greatest number of contacts due to their combination of relatively large population sizes and closer proximity to domestic sheep allotments.

Table W-11. Contact between Bighorn Sheep and Domestic Sheep Allotments for Seven Bighorn Sheep Herds on the Payette National Forest

Herd Name	Population Estimate	Contacts per Year by Alternative								
		1B, 2, 5, 7	3, 4, 6	7E	7G	7L	7M	7N	7O	7P
Big Canyon	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Little Salmon	4	0.07	0.07	0.00	0.04	0.04	0.03	0.01	0.01	0.03
Main Salmon/South Fork	210	1.01	1.01	0.00	0.35	0.31	0.19	0.08	0.04	0.12
Upper Hells Canyon	45	0.15	0.15	0.00	0.09	0.13	0.05	0.03	0.03	0.05
Muir Creek	30	0.06	0.03	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Myers Creek	10	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sheep Mountain	11	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Contacts/Year		1.33	1.28	0.00	0.49	0.49	0.27	0.12	0.08	0.20

Disease Model—Bighorn Sheep Population Persistence

Lastly, the disease model displays the potential effects of contact on the persistence of bighorn sheep populations in these metapopulations. Contact rates for the seven bighorn sheep populations in the Hells Canyon and Salmon River metapopulations were used as disease model inputs. One important summary of the disease model output is the probability of herd extirpation over the next 100 years, given assumptions for probability of a disease outbreak given contact. The complexity of the model and number of variables whose estimation was necessary to run it (e.g., demographic characteristics of bighorn sheep herds, disease transmission rates resulting from contact between domestic sheep and bighorn sheep, disease transmission rates resulting from infected bighorn sheep contacting uninfected bighorn sheep, lethality of the diseases, time of recovery in infected bighorn sheep herds) imply a high degree of uncertainty of its results. Although the model does follow well-documented and logical processes, the results should be viewed as a means of comparing the relative impacts of alternatives, not as “hard and fast values.” Results of the model support our current understanding of these bighorn sheep populations, and outputs can be explained based on the understanding of contact and disease outcomes resulting from contact. Because of the high uncertainty surrounding the probability that contact of a bighorn sheep with an allotment will lead to infection of its herd with pneumonia, modelers ran the disease model with assumptions for a range of values, from 0.05 (1 in 20 contacts would result in a disease event) to 1.00 (every contact would result in a disease event). Extirpation probabilities were analyzed for seven populations (Table W-12 and W-13 through W-20). The timeframe used was 100 years for each herd.

Qualitative comparisons of alternatives are made on the basis of assumptions for the probability of a disease outbreak given contact (i.e. the probability that contact with an active allotment will lead to an outbreak). Probabilities of an outbreak given contact are considered low (0.05 or 1 in 20 contact leads to a disease outbreak), moderate (0.25 or 1 in 4 contacts lead to a disease outbreak), or high (1.00 or every contact results in a disease outbreak). Similarly, extirpation probability outcomes were estimated to be low (≤0.10), moderate (0.11–0.29), or high (≥0.30). In both cases, the terms low, moderate, and high are intended as relative terms.

Table W-12. Modeled Probability of Extirpation for Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact

Big Canyon						
	0.05	**0.1**	**0.25**	**0.5**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.236	0.300	0.443	0.561	0.645	0.720
Alternatives 3, 4, 6	0.174	0.213	0.331	0.439	0.497	0.570
Alternative 7G	0.065	0.109	0.153	0.185	0.218	0.242
Alternative 7L	0.072	0.120	0.175	0.226	0.260	0.300
Alternative 7M	0.044	0.081	0.166	0.195	0.234	0.257
Alternative 7N	0.026	0.057	0.123	0.191	0.201	0.222
Alternative 7O	0.018	0.045	0.102	0.165	0.190	0.208
Alternative 7P	0.039	0.073	0.151	0.206	0.226	0.268
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000
Little Salmon						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.374	0.605	0.898	0.982	0.999	1.00
Alternatives 3, 4, 6	0.309	0.535	0.884	0.981	0.999	1.00
Alternative 7G	0.092	0.184	0.406	0.726	0.864	0.935
Alternative 7L	0.088	0.168	0.39	0.664	0.83	0.925
Alternative 7M	0.062	0.103	0.269	0.466	0.656	0.769
Alternative 7N	0.034	0.061	0.149	0.280	0.354	0.463
Alternative 7O	0.018	0.042	0.100	0.179	0.209	0.285
Alternative 7P	0.047	0.084	0.205	0.369	0.494	0.617
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000
Main Salmon/South Fork						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.374	0.605	0.898	0.982	0.999	1.000
Alternatives 3, 4, 6	0.309	0.535	0.884	0.981	0.999	1.000
Alternative 7G	0.092	0.184	0.406	0.726	0.864	0.935
Alternative 7L	0.088	0.168	0.390	0.664	0.830	0.925
Alternative 7M	0.062	0.103	0.269	0.466	0.656	0.769
Alternative 7N	0.034	0.061	0.149	0.28	0.354	0.463
Alternative 7O	0.018	0.042	0.100	0.179	0.209	0.285
Alternative 7P	0.047	0.084	0.205	0.369	0.494	0.617
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000

Muir Creek						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.241	0.312	0.447	0.568	0.653	0.731
Alternatives 3, 4, 6	0.174	0.222	0.336	0.445	0.507	0.581
Alternative 7G	0.064	0.108	0.155	0.191	0.220	0.245
Alternative 7L	0.071	0.120	0.181	0.230	0.263	0.305
Alternative 7M	0.043	0.080	0.173	0.201	0.236	0.262
Alternative 7N	0.025	0.056	0.127	0.195	0.205	0.228
Alternative 7O	0.018	0.044	0.106	0.169	0.192	0.214
Alternative 7P	0.038	0.072	0.159	0.212	0.230	0.272
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000
Myers Creek						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.258	0.332	0.464	0.588	0.669	0.748
Alternatives 3, 4, 6	0.189	0.24	0.359	0.459	0.531	0.609
Alternative 7G	0.074	0.120	0.170	0.204	0.230	0.265
Alternative 7L	0.081	0.131	0.197	0.244	0.285	0.329
Alternative 7M	0.048	0.094	0.187	0.218	0.25	0.282
Alternative 7N	0.029	0.061	0.140	0.211	0.217	0.237
Alternative 7O	0.020	0.049	0.119	0.184	0.204	0.223
Alternative 7P	0.043	0.081	0.173	0.232	0.247	0.292
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000
Upper Hells Canyon						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	0.355	0.592	0.900	0.992	0.997	0.999
Alternatives 3, 4, 6	0.304	0.526	0.871	0.985	0.998	0.999
Alternative 7G	0.131	0.285	0.640	0.884	0.970	0.993
Alternative 7L	0.175	0.355	0.752	0.941	0.996	0.997
Alternative 7M	0.067	0.149	0.409	0.687	0.858	0.920
Alternative 7N	0.041	0.080	0.239	0.471	0.640	0.766
Alternative 7O	0.036	0.068	0.221	0.438	0.632	0.756
Alternative 7P	0.061	0.142	0.401	0.685	0.851	0.920
Alternative 7E	0.000	0.000	0.000	0.000	0.000	0.000

Sheep Mountain						
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Alternatives 1B, 2, 5, 7	1.000	1.000	1.000	1.000	1.000	1.000
Alternatives 3, 4, 6	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7G	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7L	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7M	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7N	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7O	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7P	1.000	1.000	1.000	1.000	1.000	1.000
Alternative 7E	1.000	1.000	1.000	1.000	1.000	1.000

Alternatives

The Sheep Mountain population has a 100 percent probability of extirpation due to frequent, recurrent disease events; small initial population size, and its proximity to domestic sheep allotments on the Payette National Forest. Hence under all alternatives, this population will likely be lost (Table W-12).

Alternatives 1B, 2, 5, 7

This alternative leaves all allotments open. No bighorn sheep summer source habitats are protected from domestic sheep grazing (Figure W-9b). This alternative results in the highest likelihood of contact between bighorn sheep and domestic sheep (1.33 contacts/year [Table W-11]) with most of the contacts occurring in the Main Salmon/South Fork (1.01 contacts/year) and Upper Hells Canyon populations (0.15 contacts/year) (Table W-11). Contact estimates for the remaining herds are <0.10.

The Little Salmon, Main Salmon/South Fork, and Upper Hells Canyon populations have a high probability of extirpation under this alternative, even when the probability of a disease outbreak given contact is assumed to be low (i.e., 1 in 20 or 0.05) (Table W-13) . All populations have a high likelihood of extirpation if the probability of a disease outbreak given contact is moderate (i.e., 0.25 or 1 in 4) (Table W-13).

Figure W-9b. Alternatives 1B, 2, 5, and 7—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

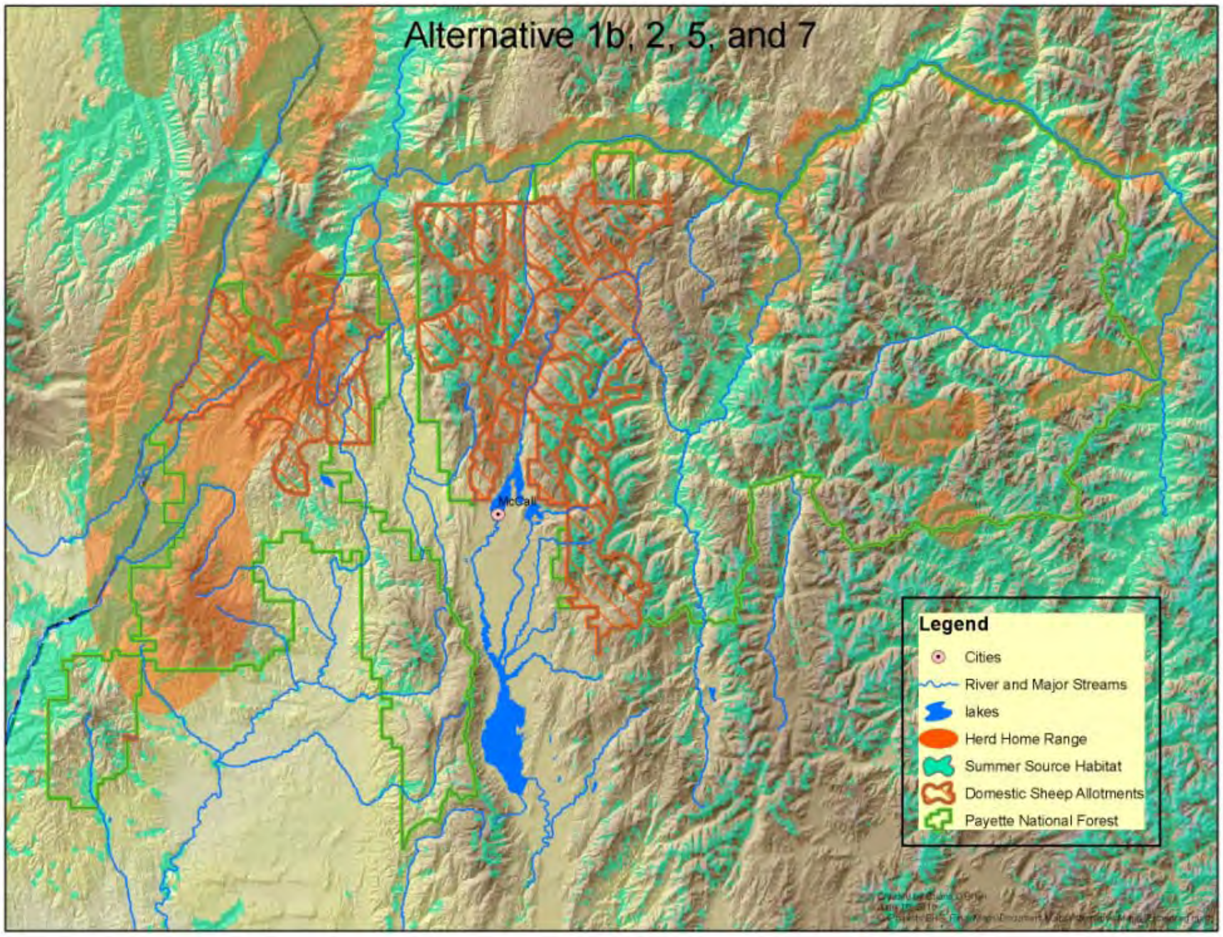


Table W-13. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 1B, 2, 5, and 7

Alternatives 1B, 2, 5, 7	P(Outbreak | Intersection with an allotment)					
	0.05	0.10	0.25	0.50	0.75	1.00
Big Canyon	0.236	0.300	0.443	0.561	0.645	0.720
Little Salmon	0.374	0.605	0.898	0.982	0.999	1.000
Main Salmon/South Fork	0.374	0.605	0.898	0.982	0.999	1.000
Muir Creek	0.241	0.312	0.447	0.568	0.653	0.731
Myers Creek	0.258	0.332	0.464	0.588	0.669	0.748
Upper Hells Canyon	0.355	0.592	0.900	0.992	0.997	0.999
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternatives 3, 4, 6

This alternative protects 9.2 percent of the summer bighorn sheep habitat on the Payette National Forest, and approximately 92.8 percent of the current suited rangelands for domestic sheep grazing are retained (Table W-10 and Figure W-9c). This alternative results in the second highest rate of contact between bighorn sheep and domestic sheep allotments (1.28 contacts/year [Table W-11]). As with the previous alternative, most of the contacts would occur in the Main Salmon/South Fork (1.01 contacts/year) and Upper Hells Canyon populations (0.15 contacts/year) (Table W-11), with low rates of contact (<0.10) expected in the other herds. As with Alternatives 1B, 2, 5, 7, there is a high likelihood of extirpation of the Upper Hells Canyon, Main Salmon/South Fork, and Little Salmon populations even when the probability of a disease outbreak given contact are assumed to be low (0.05) (Table W-14). When the probability of a disease outbreak given contact is increased to moderate (0.25), all populations would have a high probability of extirpation. Even though modeled outcomes are similar to Alternatives 1B, 2, 5, 7, the scenario under this alternative appears better for bighorn sheep populations than the previous alternative.

Figure W-9c. Alternative 3, 4, 6— Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

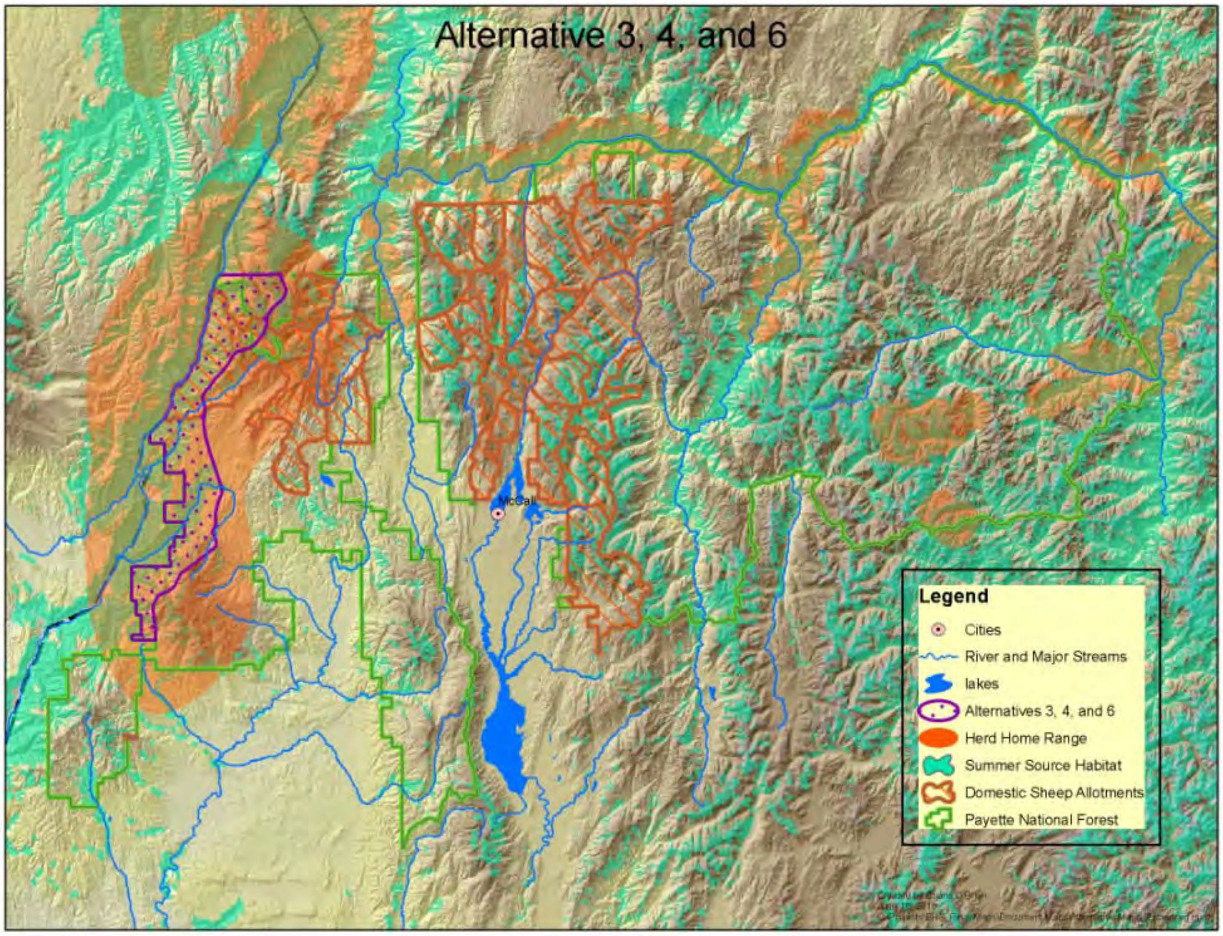


Table W-14. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternatives 3, 4, 6

Alternatives 3, 4, 6	P(Outbreak | Intersection with an allotment)					
	0.05	0.10	0.25	0.50	0.75	1.00
Big Canyon	0.174	0.213	0.331	0.439	0.497	0.570
Little Salmon	0.309	0.535	0.884	0.981	0.999	1.00
Main Salmon/South Fork	0.309	0.535	0.884	0.981	0.999	1.00
Muir Creek	0.174	0.222	0.336	0.445	0.507	0.581
Myers Creek	0.189	0.240	0.359	0.459	0.531	0.609
Upper Hells Canyon	0.304	0.526	0.871	0.985	0.998	0.999
Sheep Mountain	1.00	1.00	1.00	1.00	1.00	1.00

Alternative 7G

This alternative protects 71.4 percent of the summer bighorn sheep habitat on the Payette National Forest; approximately 38.4 percent of the suited rangelands where domestic sheep grazing is currently permitted are retained (Table W-10 and Figure W-9d). Implementing this alternative would result in 0.49 contacts/year (second highest of the action alternatives, and the same as Alternative 7L) (Table W-11). As with the previous alternatives, most of the contacts would occur in the Main Salmon/South Fork (0.35 contacts/year) and Upper Hells Canyon (0.09 contacts/year) populations (Table W-11). Low rates of contact are expected in the remaining herds. As with Alternatives 1B, 2, 5, 7 and 3, 4, 6, the Upper Hells Canyon, Main Salmon/South Fork, and Little Salmon populations would likely be extirpated, even when the probability of a disease outbreak given contact is assumed to be moderate (0.25) (Table W-15). However, the scenario under this alternative would be better for bighorn sheep populations in the Hells Canyon and Salmon River metapopulations than the previous two alternatives.

Figure W-9d. Alternative 7G— Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

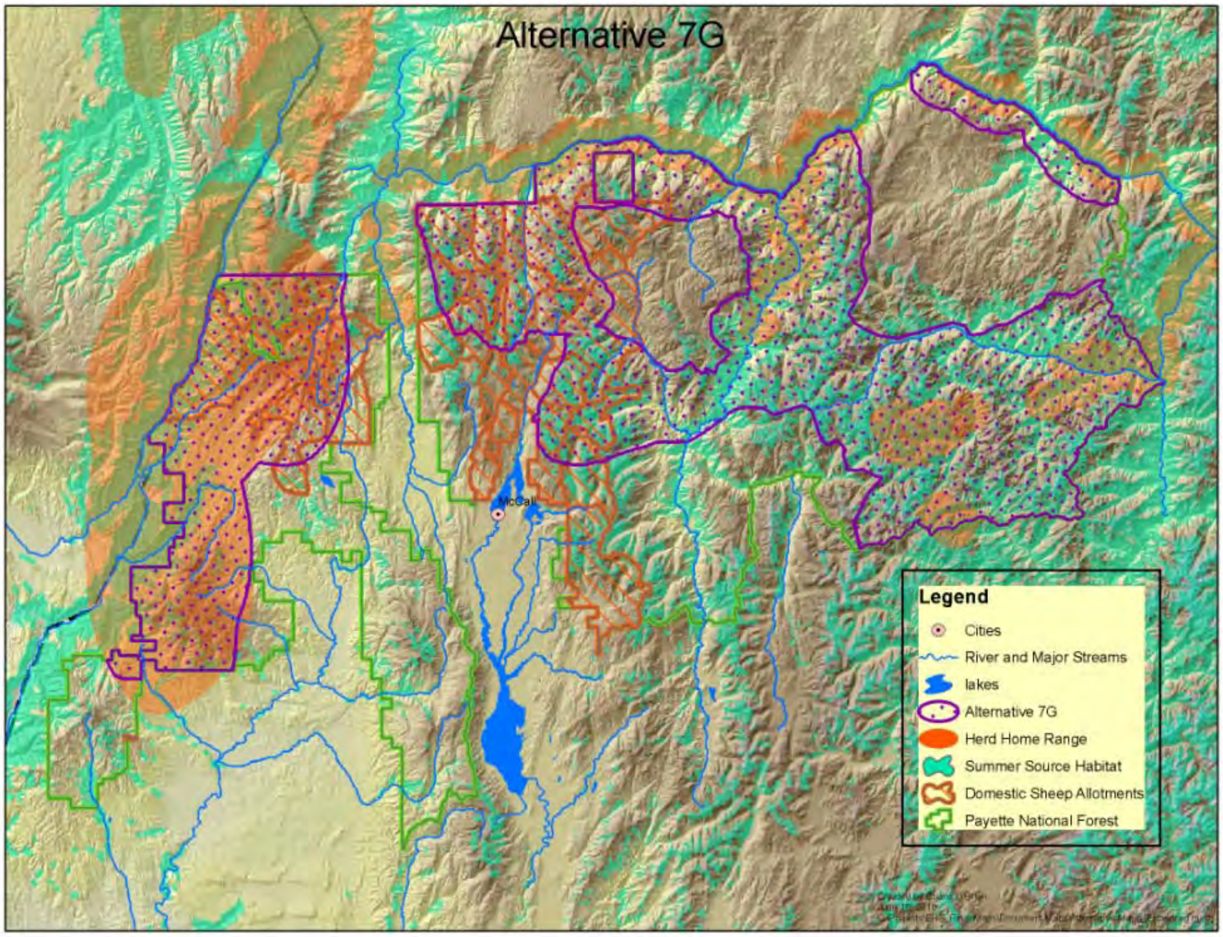


Table W-15. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7G

Alternative 7G	P(Outbreak | Intersection with an allotment)					
	0.05	0.10	0.25	0.50	0.75	1.00
Big Canyon	0.065	0.109	0.153	0.185	0.218	0.242
Little Salmon	0.092	0.184	0.406	0.726	0.864	0.935
Main Salmon/South Fork	0.092	0.184	0.406	0.726	0.864	0.935
Muir Creek	0.064	0.108	0.155	0.191	0.220	0.245
Myers Creek	0.074	0.120	0.170	0.204	0.230	0.265
Upper Hells Canyon	0.131	0.285	0.640	0.884	0.970	0.993
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternative 7L

Under Alternative 7L, 85.6 percent of bighorn sheep summer source habitat is protected; approximately 64.1 percent of rangelands suited for domestic sheep are retained (Table W-10 and Figure W-9e). Implementing this alternative would result in 0.49 contacts per year (second highest of the alternatives and the same as Alternative 7G) between bighorn sheep and domestic sheep allotments. The majority of contacts would occur in the Main Salmon/South Fork (0.31 contacts/year) and Upper Hells Canyon populations (0.13 contacts/year) (Table W-11). Expected contact rates in these populations would be similar to Alternative 7G. Although this alternative provides protection to additional bighorn sheep summer source habitats, it retains a higher percent of suited rangelands for domestic sheep grazing. As with Alternative 7G, extirpation rates for Little Salmon, Main Salmon/South Fork, and Upper Hells Canyon populations are high assuming moderate a probability of a disease outbreak given contact (0.25) (Table W-16).

Figure W-9e. Alternative 7L—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

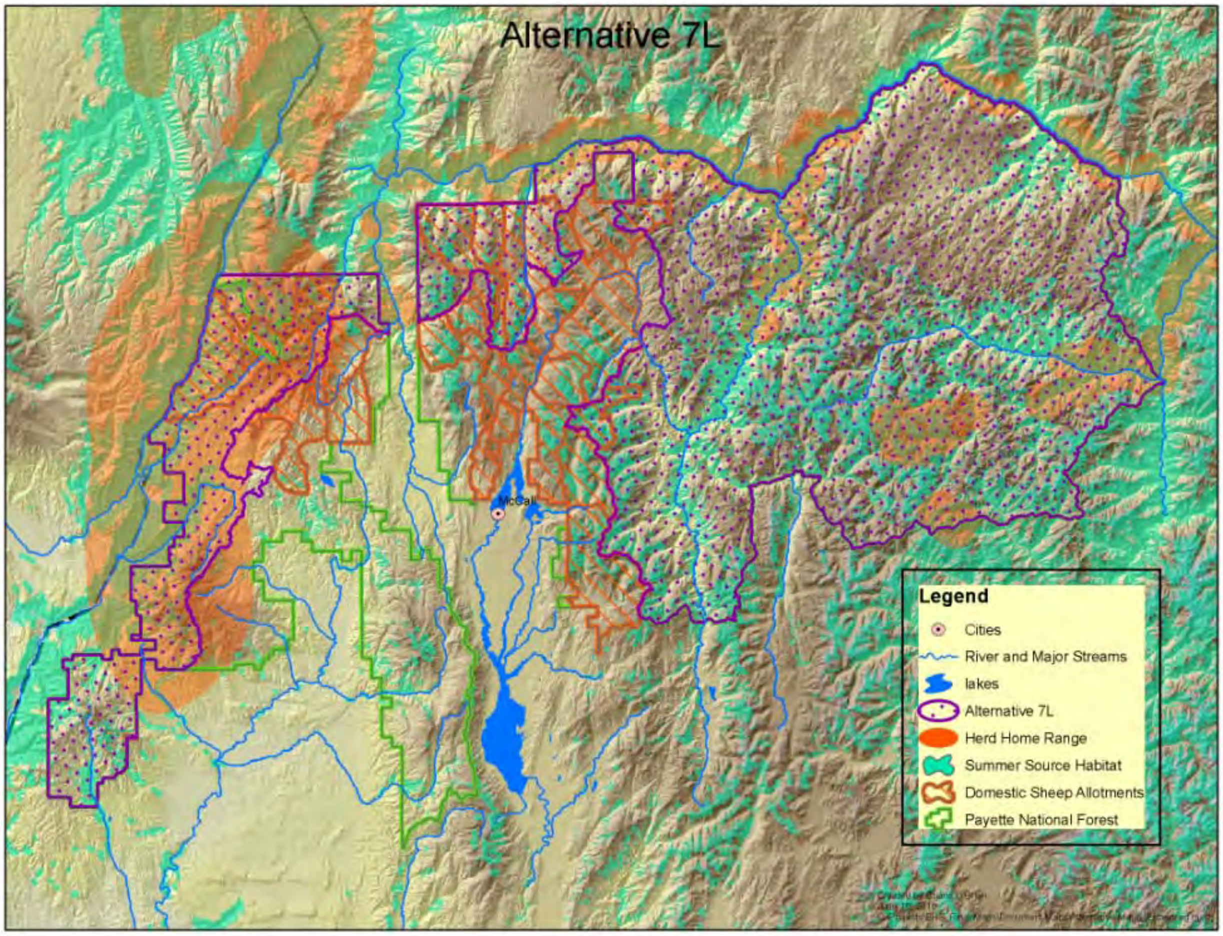


Table W-16. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7L

Alternative L	P(Outbreak | Intersection with an allotment)					
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Big Canyon	0.072	0.120	0.175	0.226	0.260	0.300
Little Salmon	0.088	0.168	0.390	0.664	0.830	0.925
Main Salmon/South Fork	0.088	0.168	0.390	0.664	0.830	0.925
Muir Creek	0.071	0.120	0.181	0.230	0.263	0.305
Myers Creek	0.081	0.131	0.197	0.244	0.285	0.329
Upper Hells Canyon	0.175	0.355	0.752	0.941	0.996	0.997
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternative 7M

Alternative 7M protects 91.9 percent of bighorn sheep summer source habitats and retains 43.1 percent of rangelands suited for domestic sheep (Table W-10 and Figure W-9f). The annual rate of contact for Alternative 7M would be 0.27 contacts/year (third highest of the action alternatives). Most of the contacts would occur in the Main Salmon/South Fork (0.19 contacts/year) and Upper Hells Canyon (.05 contacts/year) (Table W-11). Although the contact estimate is lower than for the previously discussed alternatives, there is a moderate likelihood of extirpation (0.27) for the Main Salmon/South Fork and Little Salmon populations and a high likelihood of extirpation (0.41) for the Upper Hells Canyon population (Table W-17), assuming a moderate probability (0.25) of a disease outbreak given contact. Big Canyon, Myers Creek, and possibly Muir Creek show low extirpation probabilities under this alternative, assuming moderate probabilities of a disease outbreak given contact (0.25) (Table W-17).

Figure W-9f. Alternative 7M—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

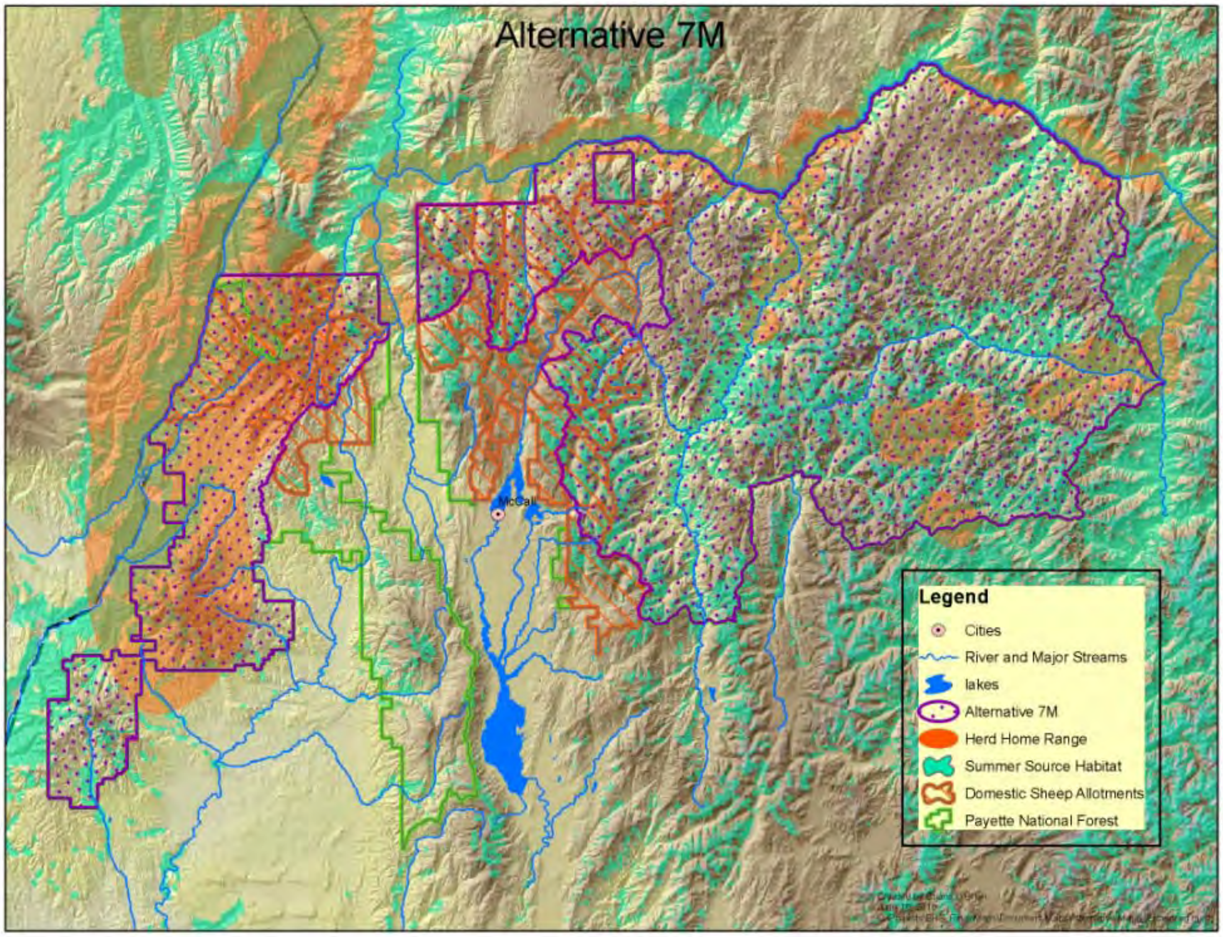


Table W-17. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7M

Alternative 7M	**P(Outbreak | Intersection with an allotment)**					
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Big Canyon	0.044	0.081	0.166	0.195	0.234	0.257
Little Salmon	0.062	0.103	0.269	0.466	0.656	0.769
Main Salmon/South Fork	0.062	0.103	0.269	0.466	0.656	0.769
Muir Creek	0.043	0.080	0.173	0.201	0.236	0.262
Myers Creek	0.048	0.094	0.187	0.218	0.250	0.282
Upper Hells Canyon	0.067	0.149	0.409	0.687	0.858	0.920
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternative 7P

Although this alternative is similar to 7M, it was analyzed separately because the outcomes appear more favorable for persistence of the Main Salmon/South Fork population. Alternative 7P would protect 90.1 percent of bighorn sheep summer source habitats and retains 45.9 percent of rangelands suited for domestic sheep (Table W-10 and Figure W-9g). The annual rate of contact for Alternative 7P would be 0.20, of which 0.12 would be for the Main Salmon/South Fork population and 0.05 is for the Upper Hells Canyon population (Table W-11). Although the contact estimate is lower than for the previously discussed alternatives, there is a moderate likelihood of extirpation (0.21) for the Main Salmon/South Fork and Little Salmon population, and a high likelihood of extirpation (0.40) for the Upper Hells Canyon population, even with a moderate (0.25) probability of a disease outbreak given contact (Table W-18).

Figure W-9g. Alternative 7P—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

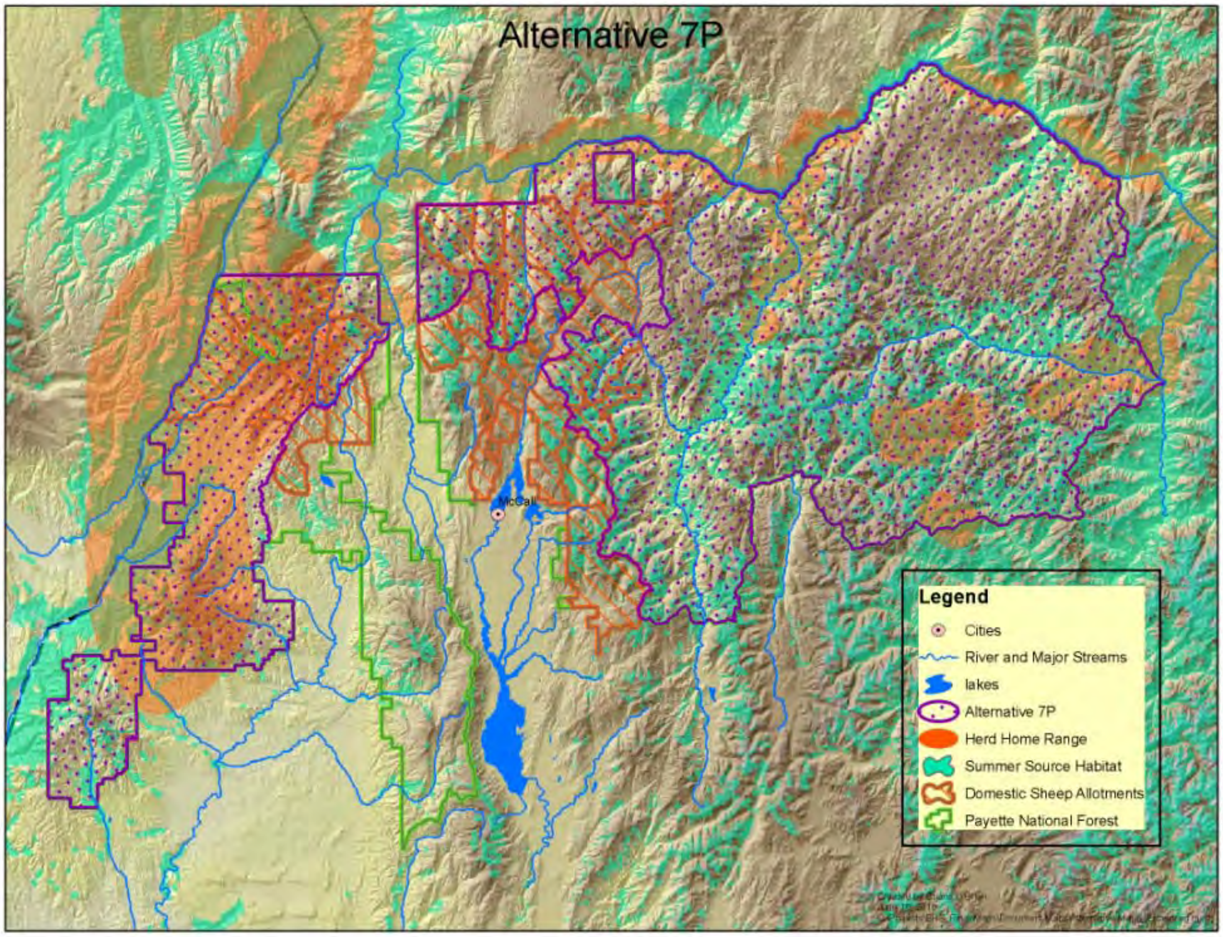


Table W-18. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7P

Alternative 7P	P(Outbreak | Intersection with an allotment)					
	0.05	0.10	0.25	0.50	0.75	1.00
Big Canyon	0.039	0.073	0.151	0.206	0.226	0.268
Little Salmon	0.047	0.084	0.205	0.369	0.494	0.617
Main Salmon/South Fork	0.047	0.084	0.205	0.369	0.494	0.617
Muir Creek	0.038	0.072	0.159	0.212	0.230	0.272
Myers Creek	0.043	0.081	0.173	0.232	0.247	0.292
Upper Hells Canyon	0.061	0.142	0.401	0.685	0.851	0.920
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternatives 7N and 7O

Comparisons of Alternatives 7N and 7O were combined because the outputs from implementing these alternatives have similar environmental consequences for these bighorn sheep herds. Alternatives 7N and 7O protect 91.5 percent and 94.1 percent, respectively, of summer bighorn sheep source habitats and retain 38.2 percent and 31.5 percent, respectively, of suited rangelands for domestic sheep (Table W-10 and Figures W-9h and W-9i). The annual rates of contact between bighorn sheep and domestic sheep allotments were calculated at 0.12 (7N) (1 contact every 7 years) and 0.08 (7O) (1 contact every 11 years). Of the action alternatives, Alternatives 7N and 7O would have the lowest probabilities of contact and the highest probabilities of herd persistence. Under Alternative 7N, with moderate probability of a disease outbreak given contact assumption (0.25), the probabilities of extirpation for the Main Salmon/South Fork and the Upper Hells Canyon populations are 0.15 and 0.24, respectively (Table W-19). Under Alternative 7O, the corresponding probabilities of extirpation for the Main Salmon/South Fork and the Upper Hells Canyon populations are 0.10 and 0.22, respectively (Table W-20). Even with contact rates this low, the disease model projects a low likelihood of extirpation when the probability of a disease outbreak given contact is assumed to be high (0.5). Similar to previous alternatives, the Little Salmon, Main Salmon/South Fork, and Upper Hells Canyon populations show the moderate risk for extirpation (Tables W-19 and W-20).

Figure W-9h. Alternative 7N—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

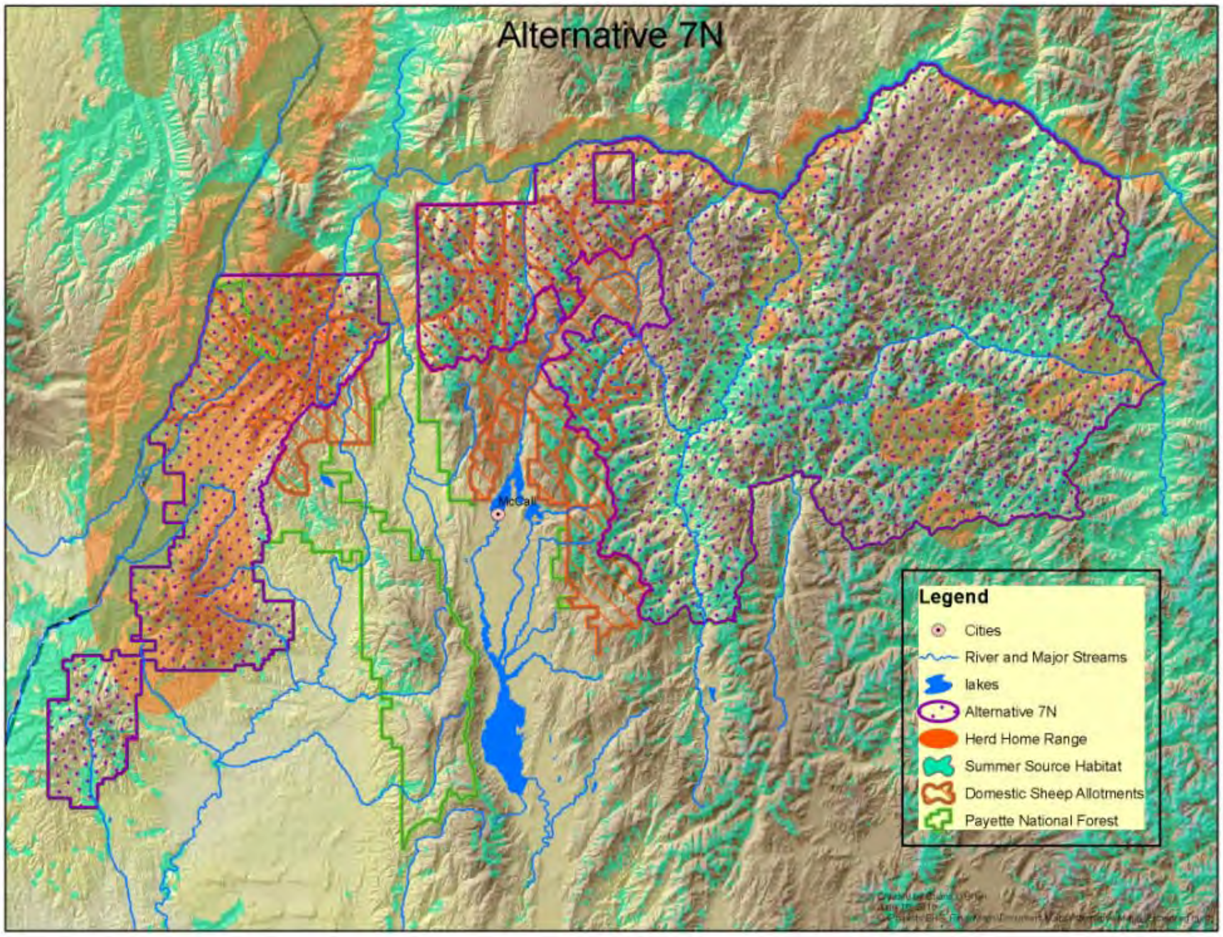


Figure W-9i. Alternative 7O— Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

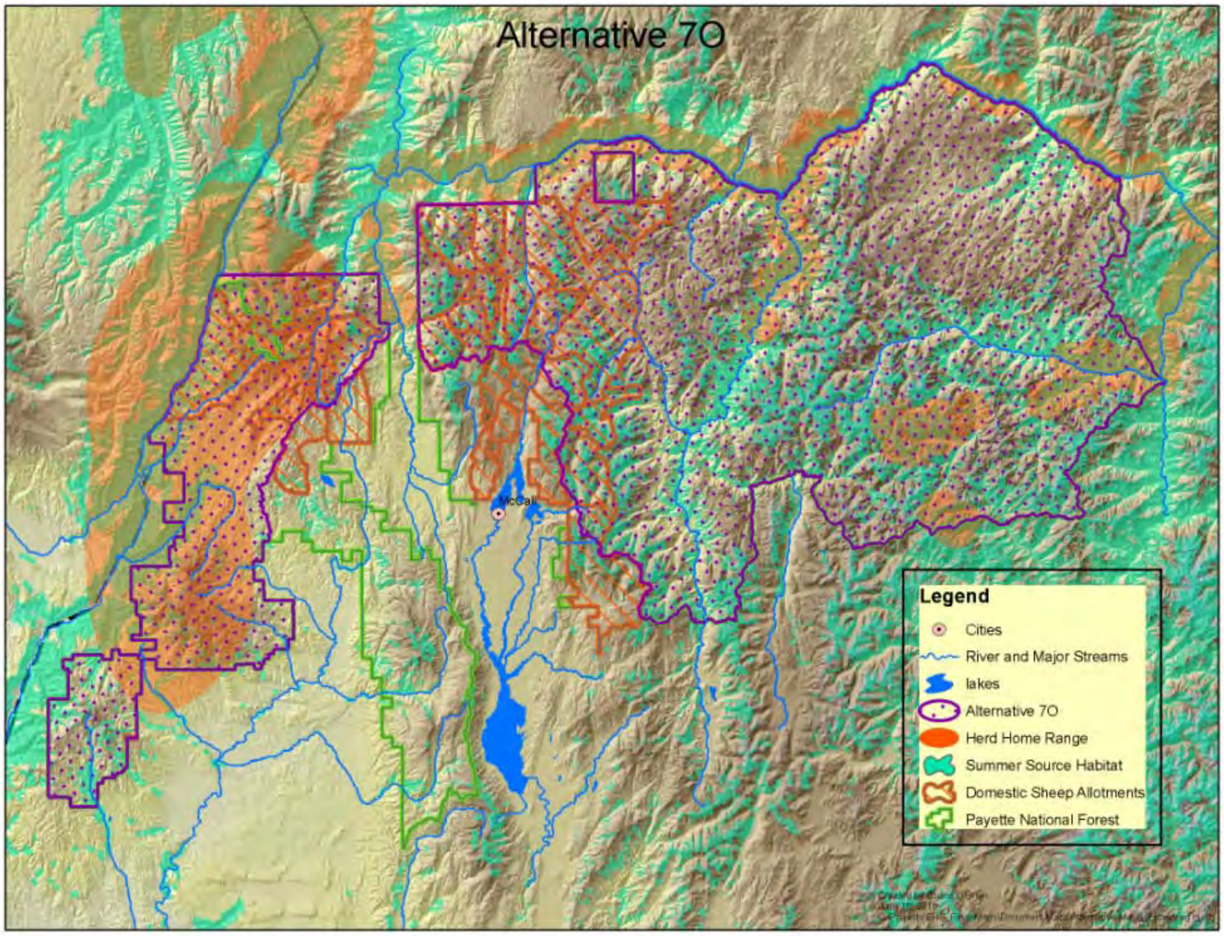


Table W-19. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7N

Alternative 7N	P(Outbreak | Intersection with an allotment)					
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Big Canyon	0.026	0.057	0.123	0.191	0.201	0.222
Little Salmon	0.034	0.061	0.149	0.280	0.354	0.463
Main Salmon/South Fork	0.034	0.061	0.149	0.280	0.354	0.463
Muir Creek	0.025	0.056	0.127	0.195	0.205	0.228
Myers Creek	0.029	0.061	0.14	0.211	0.217	0.237
Upper Hells Canyon	0.041	0.080	0.239	0.471	0.640	0.766
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Table W-20. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7O

Alternative 7O	P(Outbreak | Intersection with an allotment)					
	0.05	0.10	0.25	0.50	0.75	1.00
Big Canyon	0.018	0.045	0.102	0.165	0.190	0.208
Little Salmon	0.018	0.042	0.100	0.179	0.209	0.285
Main Salmon/South Fork	0.018	0.042	0.100	0.179	0.209	0.285
Muir Creek	0.018	0.044	0.106	0.169	0.192	0.214
Myers Creek	0.020	0.049	0.119	0.184	0.204	0.223
Upper Hells Canyon	0.036	0.068	0.221	0.438	0.632	0.756
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Alternative 7E

Alternative 7E removes domestic sheep grazing on all lands administered by the Payette National Forest. All bighorn sheep summer source habitats (368,641 acres) are protected (Table W-10 and Figure W-9j). No suited rangelands remain for domestic sheep. The risk of contact from domestic sheep on the Payette National Forest is 0 under this alternative (Table W-21). Hence, disease model results show no probability of bighorn sheep population extirpations for all populations except Sheep Mountain, for reasons previously given.

Figure W-9j. Alternative 7E—Bighorn Sheep Core Herd Home Range and Summer Source Habitat, and Domestic Sheep Allotments on the Payette National Forest

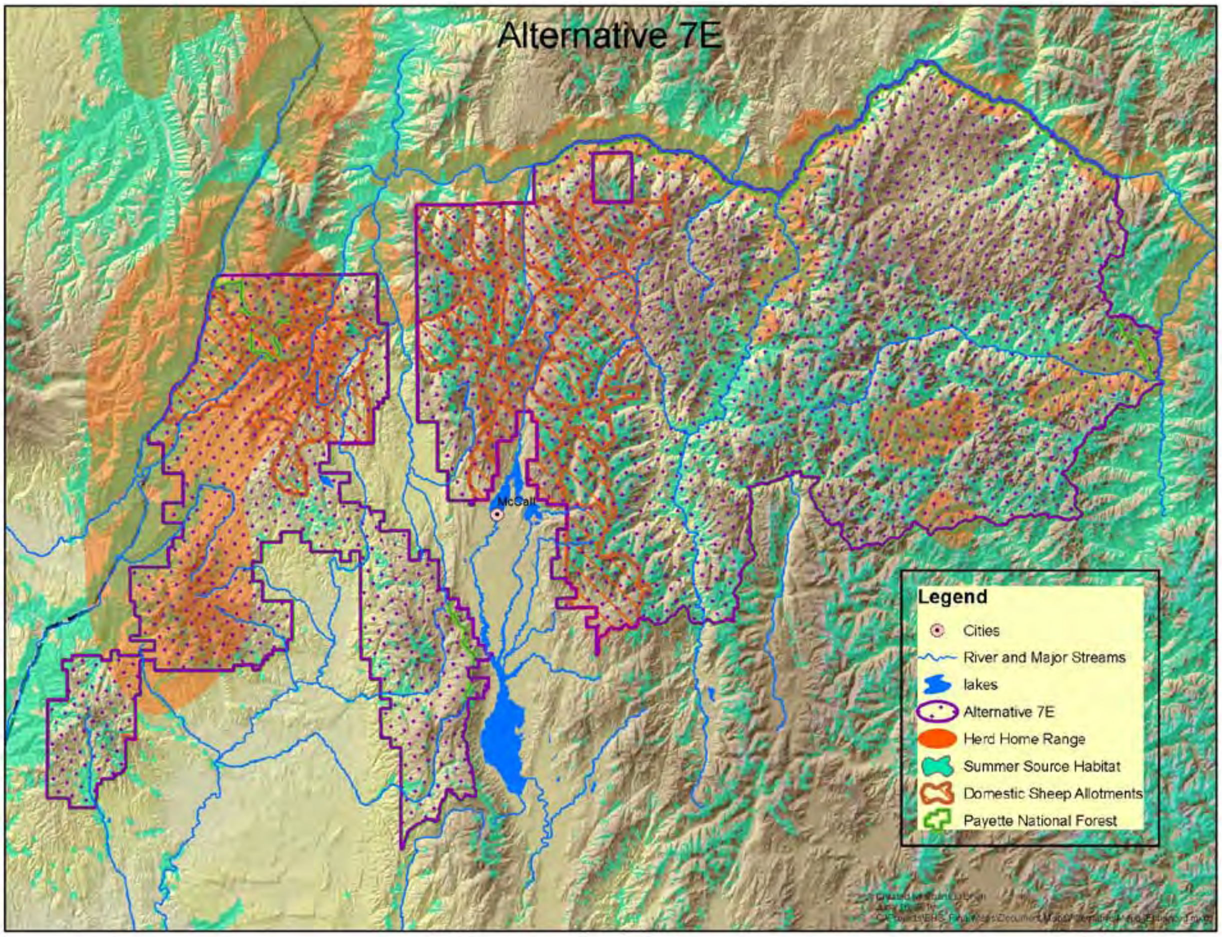


Table W-21. Modeled Probability of Extirpation of Seven Bighorn Sheep Populations under Varying Assumptions for Probability of Disease Outbreak Given Contact for Alternative 7E

Alternative 7E	P(Outbreak | Intersection with an allotment)					
	0.05	**0.10**	**0.25**	**0.50**	**0.75**	**1.00**
Big Canyon	0.000	0.000	0.000	0.000	0.000	0.000
Little Salmon	0.000	0.000	0.000	0.000	0.000	0.000
Main Salmon/South Fork	0.000	0.000	0.000	0.000	0.000	0.000
Muir Creek	0.000	0.000	0.000	0.000	0.000	0.000
Myers Creek	0.000	0.000	0.000	0.000	0.000	0.000
Upper Hells Canyon	0.000	0.000	0.000	0.000	0.000	0.000
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000

Evaluation of Alternatives

Previous discussion cites literature documenting the potential for severe impacts when even limited contact is made between these two species. For example, George et al. (2008) discuss the severe ramifications of contact that involved a single domestic sheep and resulted in a disease epidemic that affected three interconnected wintering populations of bighorn sheep in Colorado.

Both the Hells Canyon and Salmon River metapopulations include highly connected, interacting populations. Both of these metapopulations exhibit characteristics of repeated disease epizootics that have influenced both the distribution and abundance of bighorn sheep in Hells Canyon and the Salmon River drainages (IDFG 2004a, 2006; Cassirer and Sinclair 2007).

Although the alternatives vary widely in the amount of bighorn sheep summer source habitat protected from domestic sheep grazing, suited rangelands for domestic sheep, and interspecies contact probabilities, the disease model still infers relatively moderate-to-high extirpation risks when even modest assumptions are made for disease transmission leading to an epizootic. Although the model’s outcomes may seem severe, they are consistent with findings in the literature and hence are useful for comparing alternatives. Alternatives were compared on the basis of three analyses: source habitats, contact probability, and disease model results.

Source Habitats Analysis

Generally, alternatives that protect the highest number of acres (and percentage) of bighorn sheep summer source habitat with the fewest acres remaining as suited rangelands for domestic sheep offer the greatest likelihood of conserving habitats that contribute to bighorn sheep viability. The configuration of source habitats, bighorn sheep use of these habitats, and the geographical proximity of bighorn sheep to domestic sheep allotments are significant factors in evaluating the potential for contact and disease transmission. Hence, we infer that overlap between bighorn sheep CHHRs and domestic sheep allotments will result in repeated contacts that will result in a disease outbreak.

Table W-22 displays the percentage of bighorn sheep CHHRs that overlap with domestic sheep allotments. This table suggests that Alternatives 1B, 2, 5, 7 and 3, 4, 6 pose significant threats to the Muir Creek and Upper Hells Canyon bighorn sheep populations. Further, Alternatives 7G and 7L pose threats to the Upper Hells Canyon population.

Table W-22. Percent of Bighorn Sheep Core Home Ranges that overlap with Domestic Sheep Allotments by Alternative

Herd Home Range	Total (Acres)	1B, 2, 5, 7 (%)	3, 4, 6 (%)	7E (%)	7G (%)	7L (%)	7M, 7N, 7O, 7P (%)
Big Canyon	45,688	0.00	0.00	0.00	0.00	0.00	0.00
Little Salmon	26,199	0.00	0.00	0.00	0.00	0.00	0.00
Main Salmon/South Fork	187,380	0.00	0.00	0.00	0.00	0.00	0.00
Muir Creek	285,539	5.97	0.68	0.00	0.00	0.00	0.00
Myers Creek	154,961	0.00	0.00	0.00	0.00	0.00	0.00
Upper Hells Canyon	592,005	15.83	10.84	0.00	0.02	3.13	0.00
Sheep Mountain	21,459	0.00	0.00	0.00	0.00	0.00	0.00
Big Creek	113,975	0.00	0.00	0.00	0.00	0.00	0.00

We further evaluated distances from bighorn sheep CHHRs to domestic sheep allotments, the inference being greater distances between the species offer the greatest probability for persistence of bighorn sheep herds (Table W-23). These data suggest Little Salmon, Main Salmon/South Fork, Upper Hells Canyon, and Muir Creek are potentially at risk in all alternative scenarios except 7E. This result may explain why contact scenarios and the resulting disease modeling indicate moderate-to-high risk extirpation probabilities for these bighorn sheep populations under most alternatives, even when probabilities of outbreak per contact with an occupied allotment are assumed to be low.

Table W-23. Distance (km) from Bighorn Sheep Core Home Ranges to Domestic Sheep Allotments

Core Herd Home Range	1B, 2, 5, 7	3, 4, 6	7E	7G	7L	7M	7N	7O	7P
Big Canyon	35	35	No allotments	42	42	43	51	51	43
Little Salmon	1	1	No allotments	1	1	1	8	8	1
Main Salmon/South Fork.	0	0	No allotments	5	3	11	12	22	12
Upper Hells Canyon	0[a]	0[a]	No allotments	0[a]	0[a]	0	0	0	0
Muir Creek	0[a]	0[a]	No allotments	15	7	13	13	13	13
Myers Creek	6	6	No allotments	21	20	20	30	30	20
Sheep Mountain	12	16	No allotments	20	20	20	20	20	20
Big Creek	38	38	No allotments	39	39	40	40	43	39

[a] Core herd home range overlaps a domestic sheep allotment

Table W-24 summarizes the alternative outcomes and ranks the alternatives based on their ability to provide separation between bighorn sheep summer source habitats potentially occupied by the two species (1 providing the greatest separation and 9 providing the least separation). Obviously, those alternatives where no overlap occurs between CHHRs and domestic sheep allotments are considered better for bighorn sheep than those where overlap occurs.

Table W-24. Relative Ranking of Alternatives Based on Protection of Bighorn Sheep Summer Source Habitats and Separation between Allotments and Bighorn Sheep Core Herd Home Ranges

Source Habitat Implications on CHHR	Alternatives								
	1B, 2, 5, and 7	3, 4, and 6	7G	7L	7M	7N	7O	7P	7E
Summer Source Habitat Protected (%)	0.0	9.2	71.4	85.6	91.9	91.6	94.0	90.2	100.0
Suited Rangeland Habitat for Domestic Sheep (%)	100.0	92.8	38.4	64.1	43.1	38.3	31.5	46.0	0.0
Sheep Allotments within a Core Herd Home Range	Yes	Yes	Yes	Yes	Yes	No	No	No	No
Distance from Main Salmon/South Fork to Nearest Allotment (km)	0	0	5	3	11	12	22	12	NA
Distance from Little Salmon Herd to Nearest Allotment (km)	1	1	1	1	1	8	8	1	NA
Distance from Upper Hells Canyon Herd to Nearest Allotment (km)	0*	0*	0*	0*	0	0	0	0	NA
Relative Ranking of Alternatives For Providing Separation Between Domestic and Bighorn Sheep	9	8	6/7	6/7	5	3	2	4	1

*Inside Core Herd Home Range (CHHR)

Contact Risk Analysis—Core Home Range and Foray Analyses

Alternatives were ranked based on the frequency of interspecies contact modeled through the core home range and foray analyses (Table W-25). Logically, if the likelihood of contact is greater, the potential for disease transmission and resulting disease outbreaks are also greater.

Table W-25. Relative Ranking of Alternatives Based on Modeled Contact between Bighorn Sheep and Domestic Sheep Allotments

Herd Name	Alternatives								
	1B, 2, 5, and 7	3, 4, and 6	7E	7G	7L	7M	7N	7O	7P
Big Canyon	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Little Salmon	0.07	0.07	0.00	0.04	0.04	0.03	0.01	0.01	0.03
Main Salmon/South Fork	1.01	1.01	0.00	0.35	0.31	0.19	0.08	0.04	0.12
Upper Hells Canyon	0.15	0.15	0.00	0.09	0.13	0.05	0.03	0.03	0.05
Muir Creek	0.06	0.03	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Myers Creek	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sheep Mountain	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Contacts per Year	1.33	1.28	0.00	0.49	0.49	0.27	0.12	0.08	0.20
Relative Ranking of Alternatives For Minimizing Contact	8/9	8/9	1	6/7	6/7	5	2/3	2/3	4

Alternative 7E is the only alternative that prevents direct interspecies contact from permitted grazing on the Payette National Forest. Some level of contact is expected for all bighorn sheep populations, except for Big Canyon, in the other alternatives. Alternatives 7N and 70 reveal low contact rates (0.12 and 0.08, respectively). Although these are the lowest contact rates, the potential for contact still exists between the species for the two populations that contribute to the largest populations on, or adjacent to, the Payette National Forest (Main Salmon/South Fork and Upper Hells Canyon). Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; and 7L have moderate-to-high contact rates that involve four to seven of the populations. Alternatives 7M and 7P have moderate contact rates that affect the Main Salmon/South Fork, Little Salmon, and Upper Hells Canyon populations, with the greatest contact risk to the Main Salmon/South Fork (highest current population).

Disease Model Analysis

Alternatives were compared using low (0.05), moderate (0.25), and high (1.0) probabilities of a disease outbreak given contact. As discussed earlier, under all alternatives, the Sheep Creek population has a high probability of extirpation due to recurrent disease outbreaks that have reduced this population to 11 individuals, all ewes in older age classes. For Alternative 7E, the probability of a disease outbreak for all herds is 0. Action alternatives were ranked from 1 to 8, with 1 having the highest likelihood of population persistence.

When the probability of a disease outbreak given contact is assumed to be low (i.e, 0.05), all herds have a high probability of persistence under Alternatives 7M, 7N, 7O and 7P (Table W-26). Under Alternatives 1B, 2, 5, 7 and 3, 4, 6, the Little Salmon, Main Salmon/South Fork, and Upper Hells Canyon populations have high extirpation probabilities (Table W-26). Under Alternatives 7G and 7L, the Upper Hells Canyon population has a moderate extirpation probability.

Table W-26. Relative Ranking of the Alternatives Based on the Probability of Extirpation when using Low Inference for Probability of Disease Outbreak Given Contact (0.05)

Herd Name	1B, 2, 5, 7	3, 4, 6	7G	7L	7M	7N	7O	7P
Big Canyon	0.236	0.174	0.065	0.072	0.044	0.026	0.018	0.039
Little Salmon	0.374	0.309	0.092	0.088	0.062	0.034	0.018	0.047
Main Salmon/South Fork	0.374	0.309	0.092	0.088	0.062	0.034	0.018	0.047
Muir Creek	0.241	0.174	0.064	0.071	0.043	0.025	0.018	0.038
Myers Creek	0.258	0.189	0.074	0.081	0.048	0.029	0.020	0.043
Upper Hells Canyon	0.355	0.304	0.131	0.175	0.067	0.041	0.036	0.061
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Relative Ranking of Alternatives	7/8	7/8	5/6	5/6	3/4	1/2	1/2	3/4

Under moderate (0.25) assumptions for the probability of a disease outbreak given contact, the Upper Hells Canyon population has a high extirpation probability under all alternatives except 7N and 7O. The Little Salmon and Main Salmon/South Fork have high extirpation probabilities under Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; and 7L (Table W-27). Alternatives 7N, 7O, and possibly 7P have the highest persistence levels for maintaining the Main Salmon/South Fork and Little Salmon populations (Table W-27), or a low to moderate probability of extirpation.

Table W-27. Relative Ranking of Alternatives Based on Probability of Extirpation when using Moderate Inference for Probability of Disease Outbreak Given Contact (0.25)

	1B, 2, 5, 7	3, 4, 6	7G	7L	7M	7N	7O	7P
Big Canyon	0.443	0.331	0.153	0.175	0.166	0.123	0.102	0.151
Little Salmon	0.898	0.884	0.406	0.390	0.269	0.149	0.100	0.205
Main Salmon/South Fork	0.898	0.884	0.406	0.390	0.269	0.149	0.100	0.205
Muir Creek	0.447	0.336	0.155	0.181	0.173	0.127	0.106	0.159
Myers Creek	0.464	0.359	0.170	0.197	0.187	0.140	0.119	0.173
Upper Hells Canyon	0.900	0.871	0.64	0.752	0.409	0.239	0.221	0.401
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Relative Ranking of Alternatives	8	7	5/6	5/6	4	2	1	3

Under a high (1.0) probability of a disease outbreak given contact, nearly all populations show a high probability of extirpation under Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; and 7L. The Big Canyon, Muir Creek, and Myers Creek populations may persist under Alternatives 7M, 7N, 7O, and 7P. The Upper Hells Canyon population has a high extirpation probability under all alternatives (Table W-28). Main Salmon/South Fork and Little Salmon populations show high probabilities of extirpation under all alternatives except 7O, for which modeled probability of extirpation is moderate.

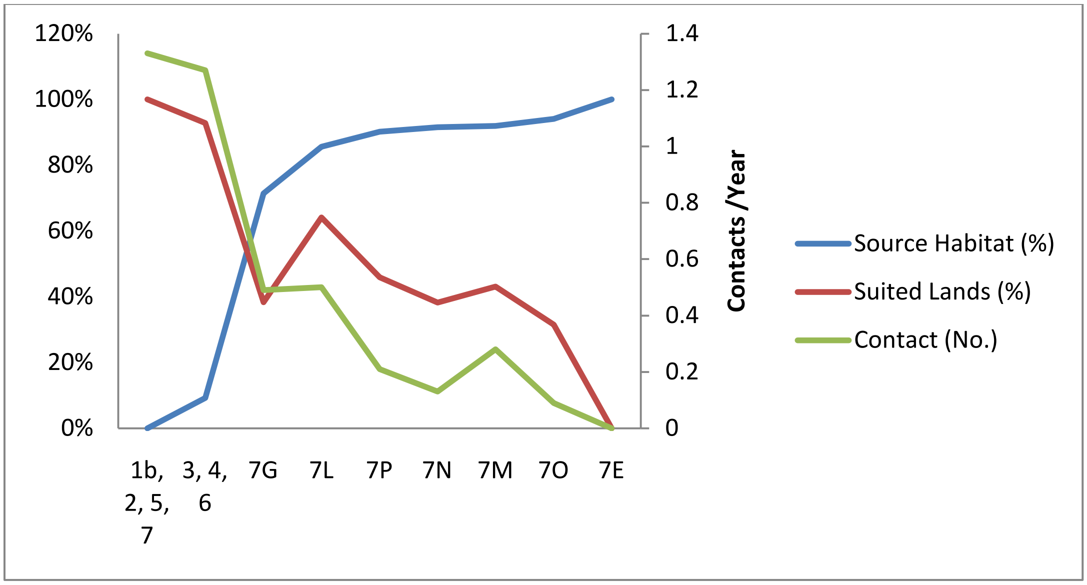
Table W-28. Relative Ranking of Alternatives Based of Probability of Extirpation when using High Inference (1.0) for Probability of Disease Outbreak Given Contact

	1B, 2, 5, 7	3, 4, 6	7G	7L	7M	7N	7O	7P
Big Canyon	0.720	0.570	0.242	0.300	0.257	0.222	0.208	0.268
Little Salmon	1.000	1.000	0.935	0.925	0.769	0.463	0.285	0.617
Main Salmon/South Fork	1.000	1.000	0.935	0.925	0.769	0.463	0.285	0.617
Muir Creek	0.731	0.581	0.245	0.305	0.262	0.228	0.214	0.272
Myers Creek	0.748	0.609	0.265	0.329	0.282	0.237	0.223	0.292
Upper Hells Canyon	0.999	0.999	0.993	0.997	0.92	0.766	0.756	0.920
Sheep Mountain	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Relative Ranking of Alternatives	8	7	5	6	4	2	1	3

Summary/Conclusion

The Payette National Forest compared alternatives by source habitats, areas remaining in suited rangelands for domestic sheep, and interspecies contact results (Figure W-9k). Although a noticeable relationship between the percent of source habitats protected from domestic sheep grazing and interspecies contact exists (i.e., more protected habitats infers lower contact likelihood), an even a stronger correlation between the percentage of suited rangelands for domestic sheep and interspecies contact is seen. The inference is that even relatively small amounts of suited rangelands remaining result in a high likelihood of contact, which ultimately can be translated to increased disease transmission opportunities and disease outbreaks. These findings are consistent with the previously discussed literature.

Figure W-9k. Comparison of Percentage protected Summer Source Habitat, Percentage Suited Rangelands for Domestic Sheep, and Estimated Number of Contacts/Year by Alternative



Results from the three separate models—source habitat, risk of contact, disease—result in a similar ranking of the alternatives. The order of ranking of the alternatives was consistent with each other for all analyses. The outcome severity from the disease model depends largely on assumptions for the probability of a contact resulting in a disease outbreak. Even though the severity of these assumptions varies, the alternative rankings from the models are largely unchanged.

Alternative 7E provides the greatest protection to bighorn sheep habitats, the least likelihood of contact, and the highest probabilities of persistence for all bighorn sheep populations.

Alternatives 7N and 7O protect the most source habitat, retain the least suited rangeland for domestic sheep and have the lowest contacts per year (0.12 and 0.08, respectively) (Table W-25). At moderate inferences for the probability of a disease outbreak given contact (0.25), several herds show moderate-to-high probabilities for persistence (Table W-27). The Upper Hells Canyon population has a low probability of persistence under all alternatives, except 7E, at moderate inferences of contact (Table W-27).

Alternatives 7M and 7P are viewed as middle-ground alternatives and have similar outputs from the three models. The main difference between the alternatives is that 7M has CHHRs that overlap domestic sheep allotment boundaries (Table W-24). The risk of contact falls between Alternatives 7N and 7O, and the remaining alternatives (0.27 and 0.20 contacts per year for 7M and 7P, respectively) (Table W-25). Assuming a moderate probability of a disease outbreak given contact, under both Alternatives 7M and 7P, the disease model suggests that the Little Salmon and Main Salmon/South Fork populations could persist (moderate probability), whereas the Upper Hells Canyon populations would likely not persist under these two scenarios (Table W-17 and W-18). Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; and 7L would have the highest risks of contact and protect the least amount of source habitats (Tables W-10 and W-11). These alternatives would likely not ensure bighorn sheep populations on, and adjacent to, the Payette National Forest.

In alternative 7P the rates of contact and extirpation probabilities for the Upper Hells Canyon herd are higher than for 7N or 7O even though the alternatives are identical on the westside of the Payette National Forest. The reason for this is that the Vance Creek and Grassy Mountain allotments on the eastside of the Payette National Forest are left open in alternative 7P. It is highly improbable that bighorn sheep would make a straight line foray from the Upper Hells Canyon CHHR to the Vance Creek and Grassy Mountain allotment, However it is plausible that bighorn sheep may follow the habitat corridor down Rapid River into the Little Salmon River drainage and then onto those allotments. The origin of the bighorn sheep sighted in the Little Salmon River drainage is unknown. It is not known if this is a midpoint of a migration, the end point of a foray, or if there is an undocumented population that is resident in the Little Salmon River drainage. The possible migration corridor down Rapid River makes the contact rates and extirpation probabilities are higher for alternative 7P.

Based on the contact rates and probabilities of a disease outbreak given contact, modelers calculated mean outbreak return intervals for these populations for the alternatives (Table W-29). Assuming a moderate probability of a disease outbreak given contact (0.25), most alternatives show outbreaks every few years, which would mean that these populations are consistently exposed to ongoing disease transmission and resultant outbreaks. Alternatives 7N and 7O show the longest intervals (31 and 46 years respectively), followed by Alternative 7P (19 years) (Table W-29). The return intervals for all other alternatives indicate that these populations would likely be extirpated as a result of consistent exposure to interspecies contact.

Table W-29. Estimated Mean Outbreak Intervals (in Years) for the Action Alternatives Based on Modeled Contact Probabilities

	Alternatives							
Probability[1]	1B, 2, 5, and 7	3, 4, and 6	7G	7L	7M	7N	7O	7P
1.00	1.4	1.4	2.6	2.6	4.1	8.2	12	5.2
0.75	1.6	1.6	3.2	3.2	5.3	11	16	6.7
0.50	2.1	2.1	4.6	4.6	7.7	16	23	9.9
0.25	3.5	3.7	8.6	8.6	15	31	46	19
0.10	8	8.4	21	21	37	77	110	47
0.05	16	16	41	41	73	150	230	94

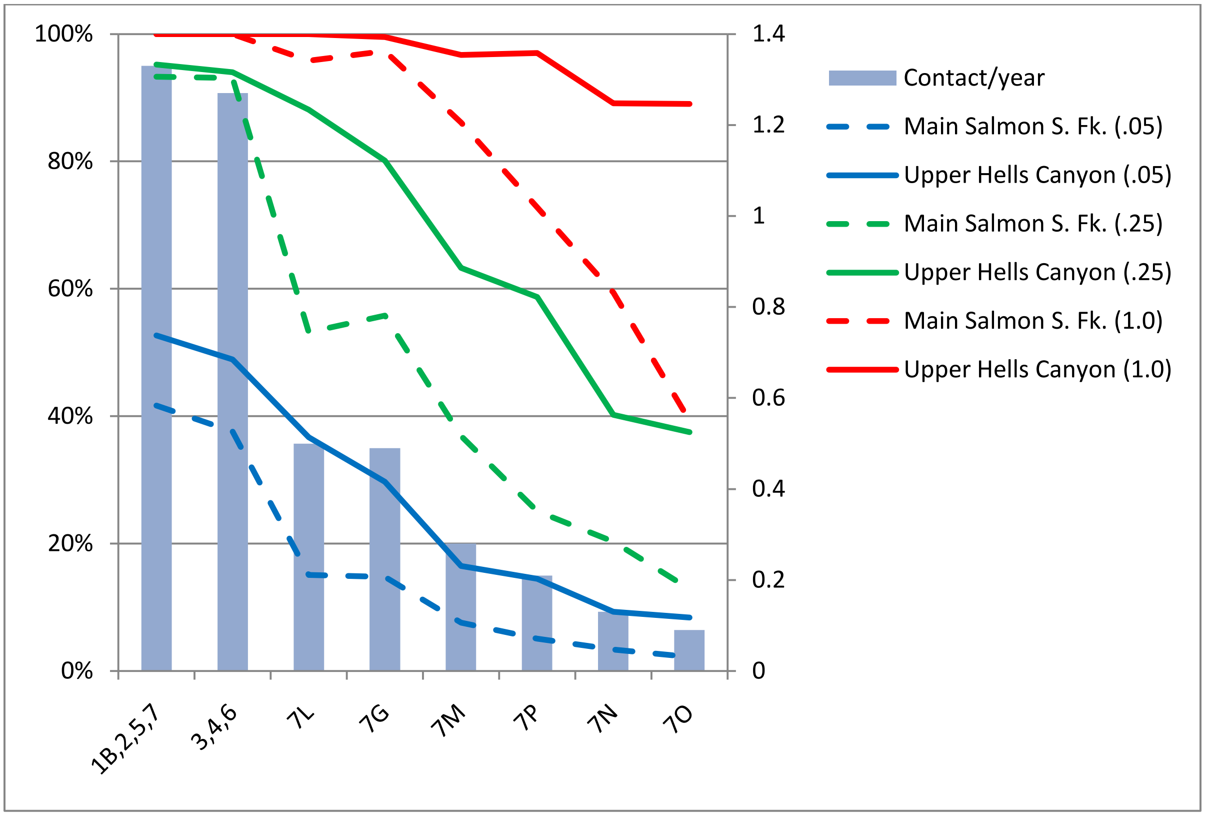
[1] Probability of a disease outbreak given contact

Alternatives are thus ranked as follows from the highest to lowest probability for bighorn sheep persistence: 7E–7N/7O–7P–7M–7G/7L–1B, 2, 5, 7/3, 4, 6. Under a moderate probability of outbreak given contact (0.25), extirpation of all populations is considered likely under Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; 7L; and 7M (Table W-27). The Main Salmon/South Fork population may persist under Alternatives 7N, 7O, and possibly 7P. Alternative 7E has the greatest likelihood for persistence for all bighorn sheep populations. The sensitive species determinations for these alternatives are as follows:

- **Alternative 7E—**This alternative would have a **Beneficial Impact** on bighorn sheep
- **Alternatives 7N, 7O, 7P--**These alternatives **May Impact Individuals or Habitat, But Will Not Likely Contribute to a Trend Towards Federal Listing or Loss of Viability to the Population or Species**
- **Alternatives 1B, 2, 5, 7; 3, 4, 6; 7G; 7L, 7M—**These alternatives **Will Impact Individuals or Habitat with a Consequence that the Action May Contribute to a Trend Towards Federal Listing or Cause a Loss of Viability to the Population or Species**

Assumptions made for the probability of a disease outbreak given contact have huge implications on the modeled persistence of these bighorn sheep populations on, and adjacent to, the Payette National Forest. Figure W-9k displays outcomes of these assumptions on the modeled extirpation potential under each of the alternatives for the two largest bighorn sheep populations analyzed. For all of scenarios, the relative rankings of the action alternatives are similar, with Alternatives 7N and 7O offering the greatest persistence probabilities for all populations. Alternatives 1B, 2, 5, 7 and 3, 4, 6 consistently had the highest extirpation probabilities. The remaining alternatives fell in between 1B, 2, 5, 7,and 7O, with Alternatives 7M and 7P generally contributing to higher population persistence than Alternatives 7G and 7L (Figure W-9l).

Figure W-9l. Inferences for Contacts Per Year and Modeled Extirpation Probabilities for the Two Largest Bighorn Sheep Populations (Main Salmon/South Fork and Upper Hells Canyon) on and Adjacent to the Payette National Forest for all alternatives except 7E and Assumptions for Contact/Outbreaks at Three Different Levels, 0.05, 0.25, and 1.0.



Consistent with 36 CFR §219.20(a), the bighorn sheep discussion in the Cumulative Effects, Species of Special Interest section, page 3-328, of Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement will be deleted. These pages will supplement the Cumulative Effects, Sensitive Species section, page 3-326, of the Chapter 3 Terrestrial Wildlife Habitat and Species section of the 2003 Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement.

ENVIRONMENTAL CONSEQUENCES

Cumulative Effects

Sensitive Species

Bighorn Sheep

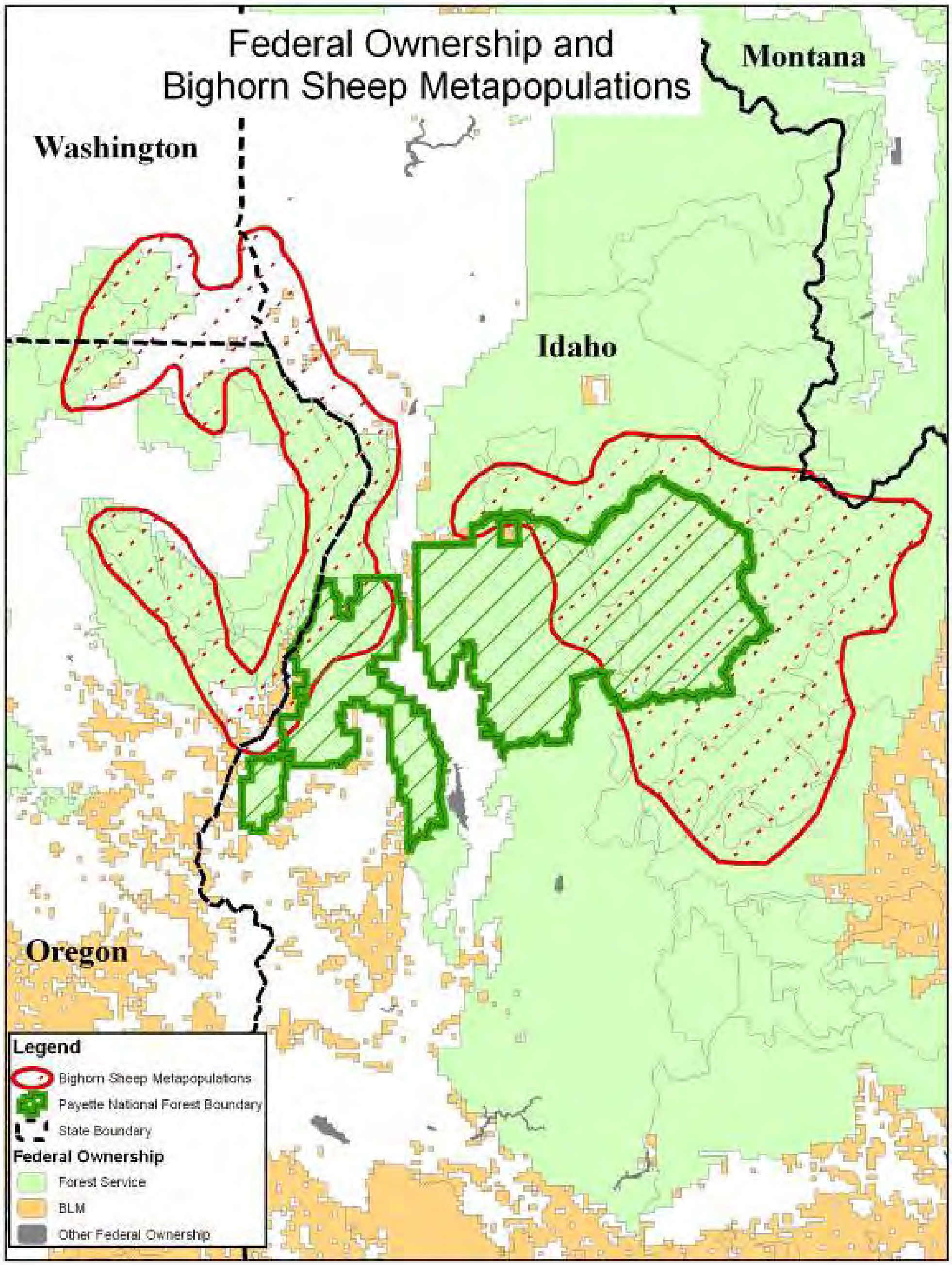
Activities and disturbances that take place on National Forest System lands can affect larger-scale ecosystem processes and functions beyond National Forest borders, and conversely, the management of lands outside of the National Forest may influence National Forest ecosystems. Management on other adjacent ownerships, including private, State, and other Federal lands, may or may not consider the broad needs of ecosystem integrity or the more specific components, including wildlife populations. Therefore, National Forest System lands must provide attributes that contribute to functioning ecosystems and viable populations regardless of how other ownerships are managed. Adjacent lands under varied ownerships and interspersed ownerships may have different management objectives regarding wildlife populations than the National Forests. Therefore, any Forest Service management activities affecting the specific components, particularly those components that are scarce outside of National Forest System lands, would potentially affect the overall ecology and habitat properties that these components provide for the entire region. How the Payette National Forest manages habitat can have far-reaching impacts on other ownerships and throughout the region, such as the dispersal of wildlife, and in this specific case, the impacts of disease. National Forest System lands can also be influenced in similar ways by the habitat management on other ownerships. Understanding the interactions that generate processes in wildlife populations and how they change with management actions through space and time is crucial to providing for well-distributed habitat across the Planning Unit.

Each one of the alternatives discussed above would have effects on and off of National Forest System lands. Those alternatives that eliminate all or most of the potential risk of contact between domestic and bighorn sheep on the Payette National Forest (e.g., Alternatives 7E, 7N, and 7O) are hoped to also benefit the broader metapopulations by reducing the probability of disease transmission between the species and subsequent spread across the metapopulation. Alternatives that reduce the risk of contact on summer source bighorn sheep habitats and also reduce the area of lands considered suited for domestic sheep grazing should reduce the probability of contact and disease in the metapopulations. Similarly, reducing the potential for contact by foraying bighorn sheep would reduce the potential of transferring disease to adjacent bighorn sheep populations off of the Payette National Forest. Hence, those areas of moderate and even high risk contribute to the potential for disease transference well beyond the boundaries Payette National Forest. Alternatives with higher potential risks for contact are expected to result in disease effects that extend well beyond the boundaries of the Payette National Forest to the larger metapopulations.

Other ownerships can also be affected by changes in National Forest domestic sheep allotments. Other Federal and State agencies that issue domestic sheep permits can see changes in their capacity to issue permits if some of the biological and physical infrastructure needed to continue domestic sheep grazing is lost on the Payette National Forest. A similar trend could also extend to private lands. While reducing infrastructure could affect the economics associated with domestic sheep grazing, it could also reduce additional risks to bighorn sheep by reducing potential risks of contact from other ownerships.

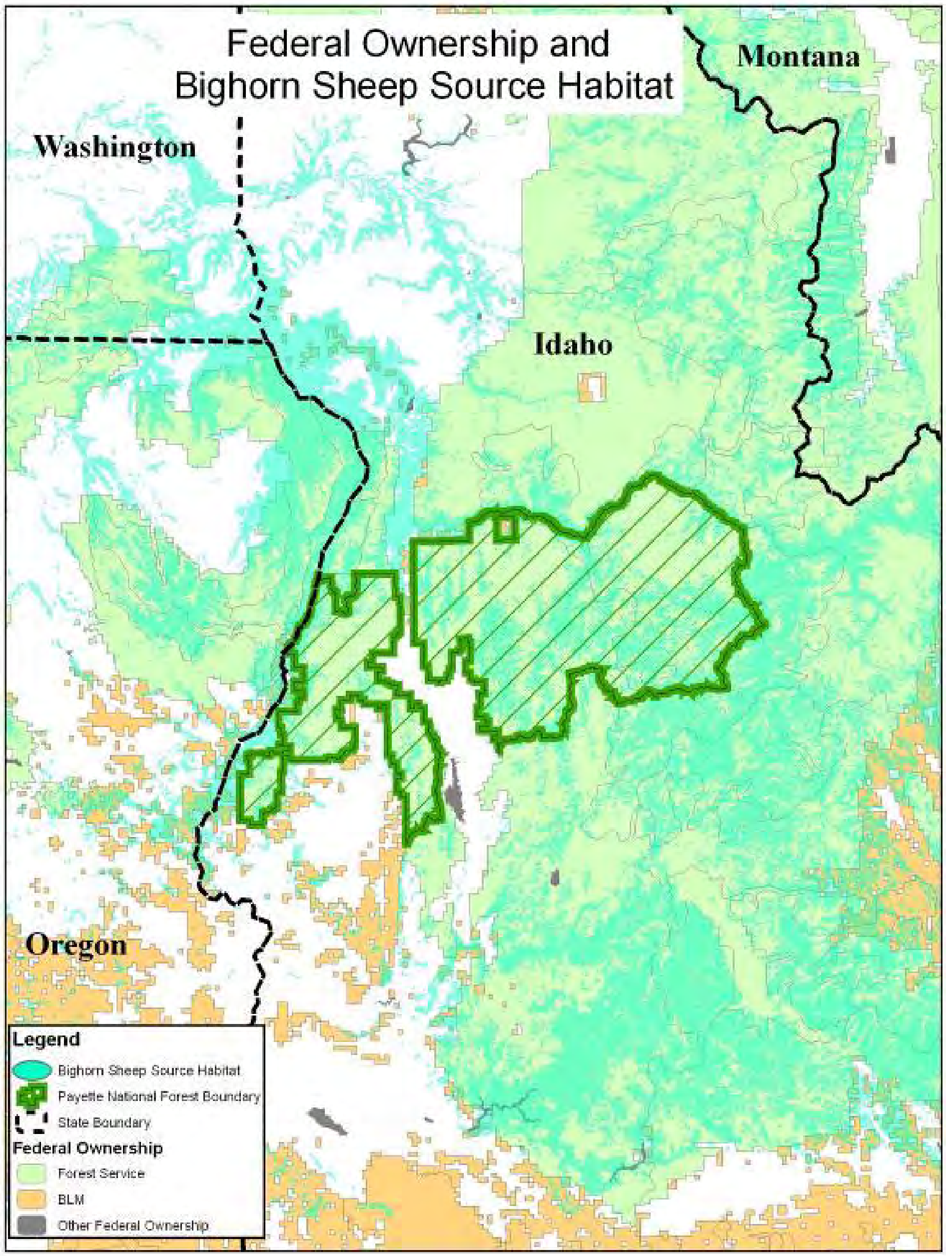
Ownerships that can affect the potential risk of contact to bighorn sheep on the Payette National Forest are shown in Figure W-11. Even if the Payette National Forest eliminated all domestic sheep grazing (Alternative 7E), a potential risk of contact still exists from the adjoining ownerships that graze domestic sheep, particularly given the overlap of the CHHRs, potential foray movements, and metapopulations located on adjacent ownerships. Domestic sheep are currently grazed on adjacent National Forests, the BLM, and private farms. Therefore, disease could still be a factor for bighorn sheep populations on the Payette National Forest, regardless of how much domestic sheep grazing remains within the Payette National Forest. The effects to the two metapopulations are unknown, since the potential risk of contact from lands other than the Payette National Forest is not completely known.

Figure W-11. Regional Metapopulations and Landownerships



Given the continuous bighorn sheep source habitat that exists in the region (Figure W-12), across state boundaries, and throughout Idaho, the effects of the potential risk of contact from the Payette National Forest can extend beyond the boundaries of the known metapopulations. How many bighorn sheep intermingle between populations is unknown, although given their metapopulation structure, intermingling throughout the region can be assumed. Radiotelemetry data from the Hells Canyon metapopulation indicates that subpopulations are interconnected, which increases the risk of disease transmission moving throughout the metapopulations as demonstrated by the disease model. Conversely, other ownerships that graze domestic sheep can be a potential source of disease to populations of bighorn sheep on the Payette National Forest, regardless of the alternative implemented by the Payette National Forest Service.

Figure W-12. Source Habitats for Bighorn Sheep Displaying the Continuity of these Habitats at Large Spatial Scales



Cumulative Effects Analyses

The risk of contact model was run under two potential cumulative effects scenarios: (1) the assumption that domestic sheep management on BLM, Nez Perce National Forest, State, and private lands would be managed as they are currently (C0) (Figure W-13) and (2) the assumption that domestic sheep grazing on all adjacent Federal lands would be curtailed (i.e., analogous to Alternative 7E in this analysis), while existing domestic sheep grazing would continue on State and private lands (C1) (Figure W-14). Table W-30 displays estimated contacts per year in addition to those modeled under the alternatives previously analyzed.

Figure W-13. Cumulative Addition of Federal (Bureau of Land Management and National Forest), State, and Private Lands that Allow Domestic Sheep Grazing Adjacent to the Payette National Forest

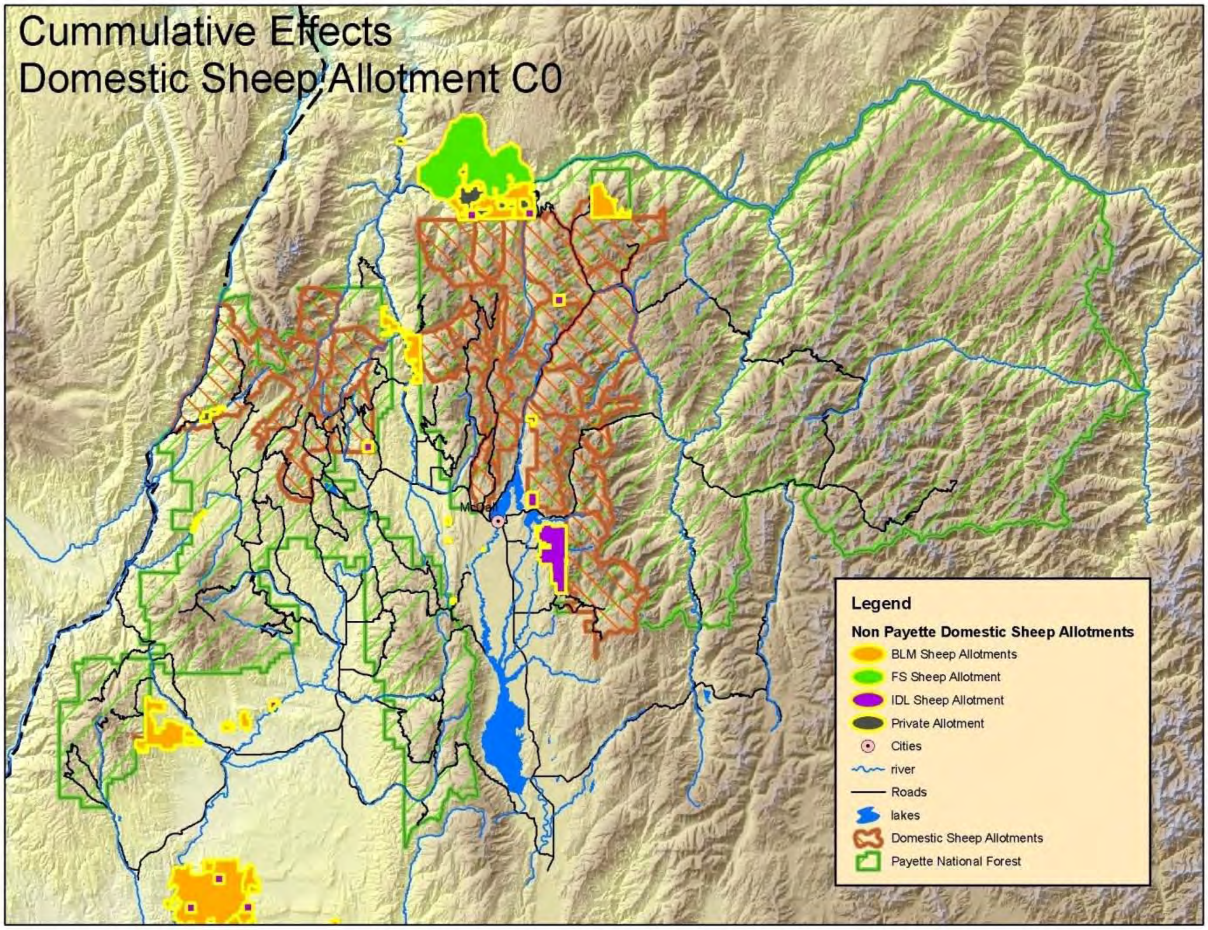


Figure W-14. Cumulative Addition of Only State and Private Lands that Allow Domestic Sheep Grazing Adjacent to the Payette National Forest

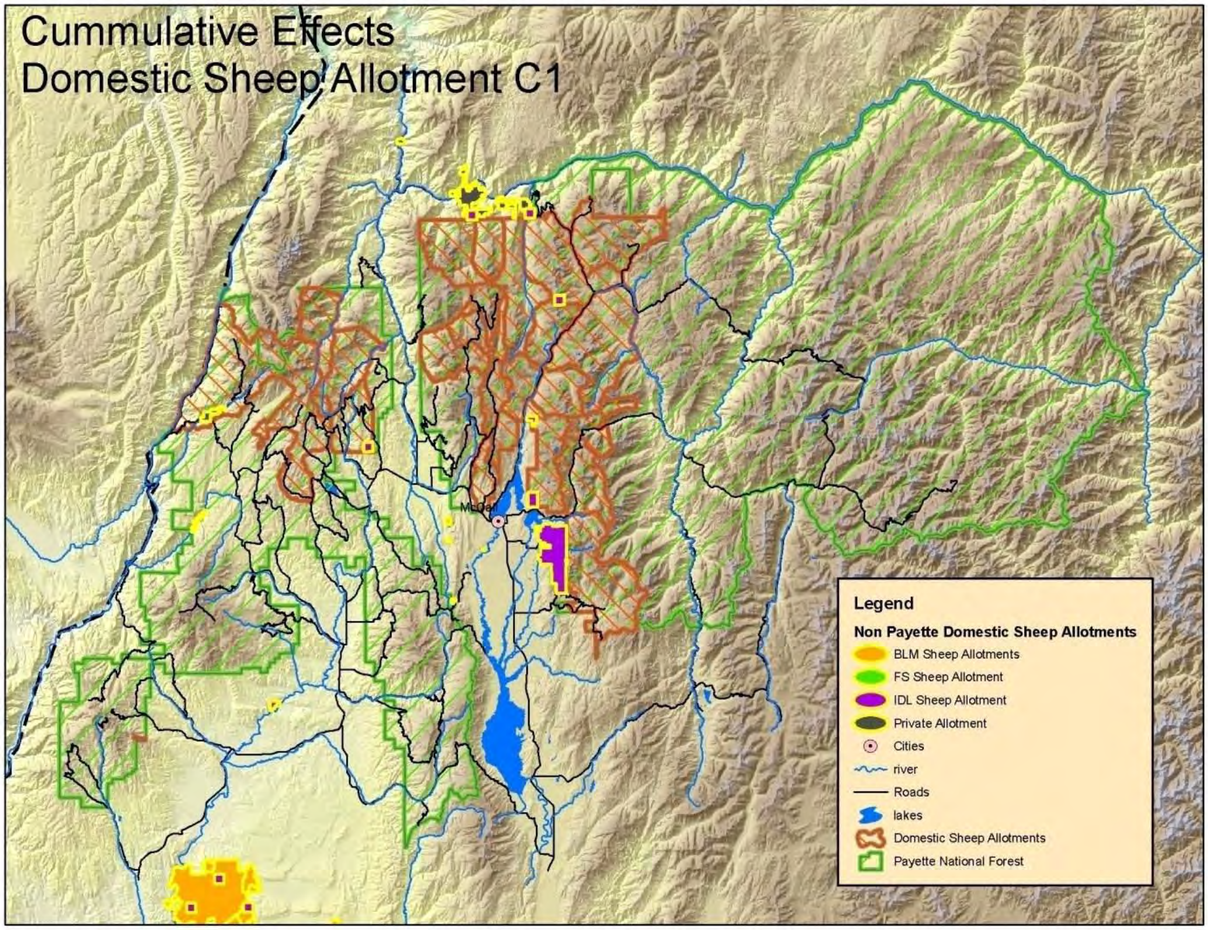


Table W-30. Contact Rates Between Bighorn Sheep and Domestic Sheep Allotments for Seven Bighorn Sheep Herds on the Payette National Forest and Additional Cumulative Effects from land ownerships adjacent to the Payette National Forest

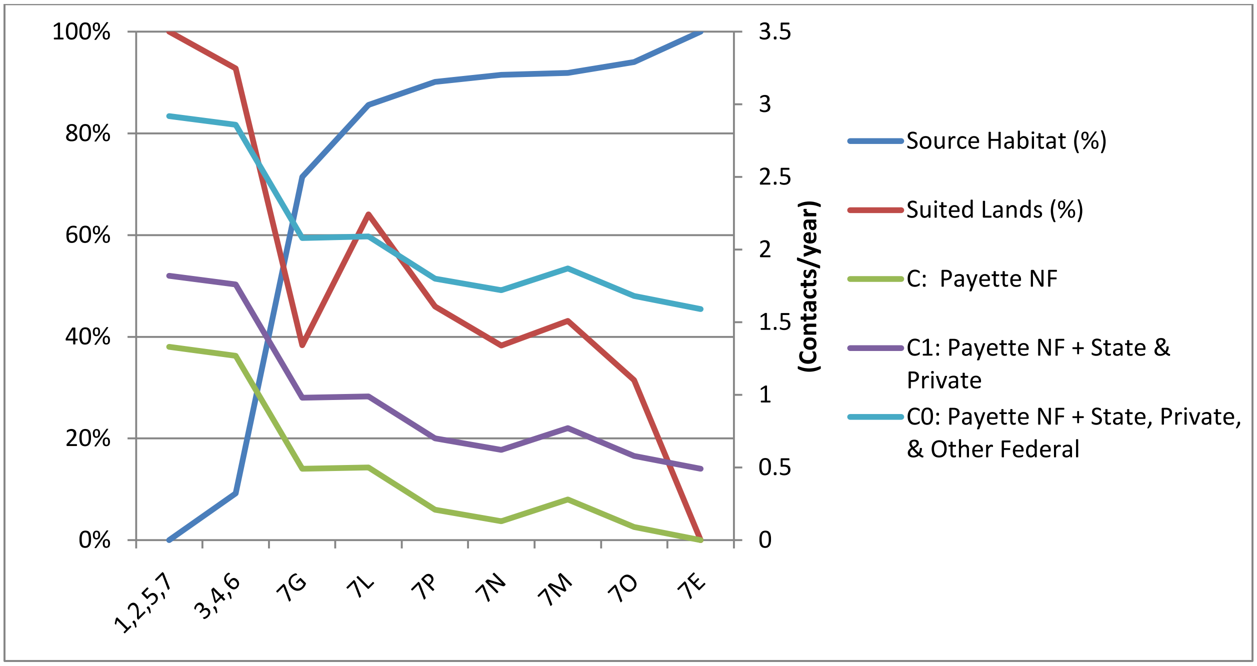
Herd	1B, 2, 5, 7	3, 4, 6	7G	7L	7M	7N	7O	7P	C0	C1
Big Canyon	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Little Salmon	0.07	0.07	0.04	0.04	0.03	0.01	0.01	0.03	0.02	0.01
Main Salmon/South Fork	1.01	1.01	0.35	0.31	0.19	0.08	0.04	0.12	1.49	0.45
Upper Hells Canyon	0.15	0.15	0.09	0.13	0.05	0.03	0.03	0.05	0.02	0.01
Muir Creek	0.06	0.03	0.01	0.01	0.00	0.00	0.00	0.00	0.02	0.01
Myers Creek	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Sheep Mountain	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Contacts/year	1.33	1.28	0.49	0.49	0.27	0.12	0.08	0.20	1.59	0.50
Cumulative contacts/year—C0	2.92	2.86	2.08	2.09	1.87	1.72	1.68	1.80	—	—
Cumulative contacts/year—C1	1.82	1.76	0.98	0.99	0.77	0.62	0.58	0.70	—	—

The risk of contact model suggests an additional 1.59 contacts per year for C0. The majority of the additional contacts are from Federal lands along the Main Fork of the Salmon River. If domestic sheep grazing is curtailed on Federal lands, State and private lands adjacent to the Payette National Forest contribute an additional 0.50 contacts per year. Hence, under Alternative 7E, which removes domestic sheep grazing on the Payette National Forest, the estimated mean return interval for an outbreak, assuming 0.25 probability of a disease outbreak given contact would be 1.59 and 0.50 for C0 and C1, respectively, under a cumulative effects scenario.

The implications of these additional contacts, particularly from adjacent Federal lands, are substantial and contribute more to contact risk between the species than any of the alternatives. Modeled contacts per year increase from 0.09–1.33 to 1.68–2.92 for the alternatives. Although the disease model was not run for the cumulative effects analysis, they would dramatically increase the extinction probabilities for all scenarios.

Even 0.50 (C1 - private land) additional contacts per year pose a substantial increase in contact risk. Modeled contacts per year increase from 0.09–1.33 to 0.58–1.82. The largest bighorn sheep populations (Main Salmon/South Fork and Upper Hells Canyon), even under the most favorable alternatives (7N and 7O), would likely not persist under this cumulative effects scenario. The relative ranking of the alternatives (7E–7N/7O–7P–7M–7G/7L–1B, 2, 5, and 7/3, 4, and 6 from best to worst scenario) remain the same, but the probabilities of contact are higher by 0.50 for each alternative. Figure W-15 displays source habitats, suited rangelands remaining open for domestic sheep grazing, and the probabilities of contact for each of the alternatives including the cumulative effects scenarios.

Figure W-15. Source Habitats, Suited Rangelands Remaining Open for Domestic Sheep Grazing, and the Probabilities of Contact for each of the Alternatives, Including the Cumulative Effects Scenarios.



Trailing Routes

Trailing routes are the stock trails that producers use to move domestic sheep onto and off of the Payette National Forest. Trailing routes are treated as linear features in the model and rated separately, depending on their relationship to CHHRs, bighorn sheep foray routes, and current domestic sheep allotments (where domestic sheep are likely to exist). Trailing routes that intersect bighorn sheep CHHRs have a high probability of contributing to interspecies contact. Trailing routes that intersect bighorn sheep source habitats and domestic sheep allotments also have implications for contact and disease transmission.

Implications for trailing sheep can also result in stray domestic sheep that utilize habitats occupied by bighorn sheep outside of the grazing season (i.e., potential contact on winter source habitats). Some trailing routes are near bighorn sheep core ranges (e.g., Sheep Mountain). Strays from trailing domestic sheep may contact these sheep for prolonged periods, thus threatening herd persistence.

Trailing routes on rangelands unsuited for domestic sheep would be closed. Thus, under Alternative 7E no trailing routes would remain open and the remaining alternatives would leave varying percentages of trailing routes for domestic sheep open between 31 percent (Alternative 7O) and 100 percent (Alternatives 1B, 2, 5, 7). A contact analysis was completed that displayed the risk of contact with a trailing route area, which was mapped as a polygon the length of trail segment remaining open, buffered by 1.0 km (500 m on each side of the trail). However, since domestic sheep only use these areas for a short time, the results were not considered instructive.

Compliance with the Hells Canyon National Recreation Area Act

The *Payette National Forest Land and Resource Management Plan* (Forest Plan) (USDA Forest Service 2003a) had an appeal issue related to the consistency between language in the HCNRA Act and its implementing regulations (36 CFR §292.48), and maintaining domestic sheep grazing because of the risk of disease transmission.

The following determinations were made regarding compatibility with the HCNRA Act and the HCNRA Comprehensive Management Plan (CMP) for the alternatives analyzed for this Draft Supplemental Environmental Impact Statement (DSEIS) (Letter from Steven Ellis to Suzanne Rainville dated January 6, 2010).

Alternatives 7M, 7N, 7O, and 7P

Alternatives 7M, 7N, 7O, and 7P would eliminate domestic sheep grazing from the Payette National Forest within the boundary of the HCNRA and within modeled bighorn sheep CHHR. The contact model results indicate a 4 percent or less risk rating for each of the alternatives, indicating mixing of the two species once every 25 years or less, which is considered a low risk of disease transmission. Eliminating domestic sheep grazing in the HCNRA and surrounding area is compatible with the HCNRA Act and its implementing regulations by providing for the protection, restoration, and maintenance of bighorn sheep and their habitat. All four alternatives would be in compliance with the HCNRA CMP by maintaining separation between bighorn and domestic sheep at current population levels. In all four alternatives, grazing would continue within 2 miles of the modeled bighorn sheep CHHR. If that grazing continues near the CHHR, some effective monitoring both inside and outside of the CHHRs is recommended to help detect bighorn sheep before contact is made.

Alternative 7G

Alternative 7G would eliminate domestic sheep grazing from the Payette National Forest within the boundary of the HCNRA. It would also eliminate domestic sheep grazing at least 6 air miles from the boundary of the HCNRA. Only a small sliver of the CHHR would be within suitable area for domestic sheep grazing.

Eliminating domestic sheep grazing in the HCNRA and surrounding area is compatible with the HCNRA Act and its implementing regulations by providing for the protection, restoration, and maintenance of bighorn sheep and their habitat. Alternative 7G would be in compliance with the HCNRA CMP by maintaining separation between bighorn and domestic sheep at the current population levels. If the population levels of bighorn sheep increase, the likelihood of contact may increase and this evaluation may need to be revisited. Monitoring should be conducted to assess future locations of bighorn sheep and ensure no contact occurs with domestic sheep on permitted allotments.

Alternatives 1B, 2, 5, 7; 3, 4, 6; and 7L

Alternatives 1B, 2, 5, 7; 3, 4, 6; and 7L would allow domestic sheep grazing on the Payette National Forest within the boundary of the HCNRA or within modeled bighorn sheep CHHR outside the HCNRA boundary. Adequate separation between the two species is needed to maintain bighorn sheep on the HCNRA (Schommer and Woolever 2001). Probabilities of contact between bighorn sheep herds and domestic sheep allotments have been calculated for bighorn sheep herds on the Payette National Forest utilizing a quantitative risk for contact analysis. Allotments lying within the CHHR have a 100 percent probability of a bighorn sheep contacting that allotment (Table W-24). The Smith Mountain and Curren Hill Allotments are within and adjacent to the HCNRA. The majority of these allotments are within CHHR, which represents a high risk of disease transmission to bighorn sheep. The risk will increase if, and when, the bighorn sheep population increases. None of the alternatives would be in compliance with the compatibility requirements of the HCNRA Act.

Alternative 7E

Alternative 7E would eliminate domestic sheep grazing from the Payette National Forest within the boundary of the HCNRA and within the modeled bighorn sheep CHHR. It would also determine all of the Payette National Forest as unsuited for domestic sheep grazing. Eliminating domestic sheep grazing in the HCNRA and surrounding area would be compatible with the HCNRA Act and its implementing regulations by providing for the protection, restoration, and maintenance of bighorn sheep and their habitat. Alternative 7E would be in compliance with the HCNRA CMP by maintaining no potential for contact between bighorn and domestic sheep and may allow the population to recover and expand.

Conclusion

The extent of connectivity between the Hells Canyon metapopulation and the Salmon River metapopulation is unknown because both populations are at depressed population levels. The connectivity corridors, which are the routes bighorn sheep use to move between areas, are also unknown.

The high connectivity of source habitats indicates that historically these metapopulations would have been more interconnected. They may have even been one larger metapopulation. A disease outbreak affecting one metapopulation may readily spread to another given the continuous source habitat, potential for individuals of separate adjacent populations to contact each other, and telemetry data that indicate movement between the Hells Canyon and Salmon River habitats. Shared summer ranges may also contribute to disease spread; therefore, if one population is at a higher risk of contracting disease, it increases the risk to other populations within the metapopulation above and beyond just the immediate risk of proximity to domestic sheep. The cumulative effects analyses do infer that habitat and population connectivity risks between the Payette National Forest and other ownerships do occur. This SEIS only considers risks from the Payette National Forest commercial livestock grazing allotments. Pack animals, other classes of livestock, and other potential disease sources are not considered and could also occur across other land ownerships.

Models have shown that reducing the impact of disease on bighorn sheep has greater effects to population persistence than increasing areas of suitable habitat and/or corridors (Gross et al. 2000). Empirical data found that persistence of bighorn sheep populations was negatively correlated with the presence of domestic sheep, and that larger patch size, larger home-range size, greater migratory tendency, and the absence of domestic sheep are the most critical factors for population persistence in bighorn sheep (Singer et al. 2001). Habitat is not currently limiting for bighorn sheep on the Payette National Forest, but the successful establishment of bighorn sheep in those habitats is limited, and even detrimental, when domestic sheep are present. Competition for the same habitat and the species' inherent attraction to each other increases the risk of contact whenever the species are in close proximity. Given the wide-ranging behavior of bighorn sheep, close proximity can encompass fairly large areas. Modeling by Gross et al. (2000) found that mild disease events tended to have more persistent effects on population growth than severe infections, due to the dispersal ability of bighorn sheep from populations with mild disease. More severe events resulting in rapid, large die-offs tend to prevent dispersal. If the social structure is destroyed at the time of the event, regardless of the disease severity, population dispersal and dynamics can be affected (V. L. Coggins, ODFG, pers. comm., 2008). Larger population sizes with higher rates of dispersal had higher rates of persistence in the absence of disease; increased rates of movement facilitated disease transmission but also buffered the effects of disease by contributing to a spatially structured population and overall larger population size (Gross et al. 2000). Genetic exchange between populations is crucial for healthy metapopulations to function (Bleich et al. 1996). Careful attention to substructuring within and between populations is critical to management plans (Bleich et al. 1996). Furthermore, small populations and small patches of suitable habitat should not be undervalued, as these can be critical in a larger colonization process (Krausman and Leopold 1986). Unoccupied habitat patches represent an important aspect of bighorn sheep metapopulation dynamics because these areas may be the sites of future populations and critical for long-term persistence (Nunney and Campbell 1993, Hanski 1998).

The bighorn sheep is a species that needs large areas to create the spatially structured populations required for their persistence. Small, isolated populations are not optimal for this species. Therefore, the need to minimize contact with domestic sheep within the large areas needed by bighorn sheep is crucial for strong, healthy populations of bighorn sheep. Keeping an adequate spatial buffer between bighorn sheep and domestic sheep is the most reliable method of preventing contact between these species (Desert Bighorn Council Technical Staff 1990, Schommer and Woolever 2001, Singer et al. 2001), but spatial buffers are not always adequate given the distances bighorn sheep rams will travel. Clifford et al. (2009) recommended that if eliminating the risk of interspecies contact (thereby eliminating the probability of respiratory disease transmission to bighorn sheep from domestic sheep) is a management goal, at a minimum, domestic sheep grazing should not occur within the known population utility distribution of the bighorn sheep. Husbandry practices such as removing domestic sheep well before the onset of rut, following vigilant herd management to reduce strays, and responding to wandering bighorn sheep are other methods to separate the species and reduce risk, but extensive monitoring efforts are required and are not always effective (DSEIS IDT and Cooperators 2007, 2008).

In large portions of habitat found in Alaska and Canada where domestic sheep are not grazed, the distribution of native sheep remains essentially unchanged from historical distribution (Valdez and Krausman 1999). Singer and Gudorf (1999) and Monello et al. (2001) also reported that bighorn sheep were more successful if they were located further from domestic sheep. Similar effects have also been observed in Hells Canyon.

As bighorn sheep numbers increase and populations expand their geographic range, probabilities of domestic sheep contact could increase (Clifford et al. 2009). The models and literature used in this analysis are based on current population levels and documented movements of bighorn sheep using telemetry-based home range and foray analyses; future movement of bighorn sheep can change during population growth or exploration by rams seeking mates (Clifford et al. 2009). Habitat is based on current habitat conditions, which may also change due to succession, disturbance, and management. Changes in habitat could alter quantity and/or location on the landscape. Continued monitoring and advances in science are essential to understanding the management implications of bighorn sheep movement, population growth, changing habitat, and changes in livestock grazing practices. Adjustments to the selected alternative may be needed, based on this monitoring.

Appendix K: Payette FSEIS, Technical Appendix

This appendix contains "Appendix L. Modeling and Analysis Technical Report" from the Payette National Forest's 2010 Final Supplemental Environmental Impact Statement, the document in which they reported the results of their bighorn sheep risk of contact analysis (USDA-FS, 2010). It is included here because, along with O'Brien et al. (2014), it provides a detailed description of the model implemented by the current Risk of Contact Tool.

The Modeling and Analysis Technical Report fully describes the computations used to estimate a core herd home range boundary and the risk of contact from a CHHR to an occupied sheep allotment. In addition, it describes the data and analyses used to produce the default parameter values (herd sex ratios, ewe and ram foray frequencies, and ewe and ram foray distance distributions) made available on the Tool's **Input herd demographics** and **Input foray behavior** tabs (Sections 4.5.4 and 4.5.5). Finally, it explains the steps used to construct the habitat preference layer used in the analysis and included alongside the current Risk of Contact Tool in the "raster" subdirectory of the "Sample Data" folder.

Appendix L

Modeling and Analysis Technical Report

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LIST OF TABLES

LIST OF FIGURES

LIST OF EQUATIONS

Consistent with 36 CFR §219.20(a), this section will be added to Appendix F of the 2003 Payette National Forest Land and Resource Management Plan.

1.0 INTRODUCTION

In response to a *Payette National Forest Land and Resource Management Plan* (Forest Plan) (USDA Forest Service 2003a) appeal remand by the Washington Office of the U.S. Forest Service in 2005, the Payette National Forest completed a Draft Supplemental Environmental Impact Statement (DSEIS).

In 2003, the Payette National Forest completed the *Southwest Idaho Ecogroup Land and Resource Management Plans Final Environmental Impact Statement* (FEIS) (USDA Forest Service 2003b) to implement the Forest Plan. The Intermountain Region Forester received five appeals of the decision to implement Alternative 7 as described in the Record of Decision, with appellants contending that the Regional Forester violated the National Forest Management Act and the Hells Canyon National Recreation Area Act on the Payette National Forest by allowing grazing of domestic sheep within or near the range of bighorn sheep (*Ovis canadensis*), thus threatening the viability of bighorn sheep through disease transmission.

On March 9, 2005, the Chief of the Forest Service concurred that the effects analyses and discussion of cumulative effects pertaining to bighorn sheep presented in the FEIS did not adequately address viability and reversed the Intermountain Regional Forester's 2003 decision to approve revised management direction for the Hells Canyon Management Area as it pertains to bighorn sheep and its habitat. The Regional Forester was instructed analyze bighorn sheep viability in the Payette National Forest commensurate with the concerns and questions discussed in the appeal review and amend the Forest Plan accordingly to ensure bighorn sheep viability. The analysis was to be thorough enough to determine compliance with applicable law and regulation, specifically the Hells Canyon National Recreation Area Act.

In April 2007, the Payette National Forest convened an Interdisciplinary Team (IDT) to develop a supplemental environmental impact statement to the 2003 FEIS and to supplement the Forest Plan. In August 2007, the Payette National Forest received requests from the State of Idaho, State of Oregon, State of Washington, Nez Perce Tribe, Shoshone-Bannock Tribe, Shoshone-Paiute Tribe, and Confederated Tribes of the Umatilla Indian Reservation to be involved in the DSEIS process. The process was revised to include their cooperators, and the DSEIS was published in 2008 (USDA Forest Service 2008).

Since the DSEIS was published, the Payette National Forest has developed a new method for analyzing the effects of the alternatives. Some of those differences between the analysis used for the DSEIS and the Final SEIS (FSEIS) are the result of improvements and/or adjustments to the techniques used in the DSEIS or better and more appropriate uses of models, while others are completely new methods or models developed specifically for the FSEIS. These improvements were based on field reviews conducted by the IDT, monitoring of bighorn sheep populations, discussions with scientists, and feedback on the DSEIS.

These changes are as follows:

1. An improved source habitat model and an accurate spatial depiction of bighorn sheep
2. A more useful population model of individual bighorn sheep in the Hells Canyon and Salmon River Mountain areas
3. A scientifically relevant analysis of telemetry points and temporal variability information
4. A new quantitative risk analysis model that utilizes the bighorn sheep database to determine the contact risk between bighorn sheep and domestic sheep (this new quantitative model replaces the DSEIS risk model)
5. A disease model to assist with cumulative effects analyses and determine bighorn sheep population persistence
6. An improved economic analysis explaining the benefits that a bighorn sheep population on the Payette National Forest has on the affected communities

This document details each of the models used in the analysis for the FSEIS.

2.0 SOURCE HABITAT MODEL

The source habitat model for bighorn sheep used in the FSEIS was originally designed by the Hells Canyon Initiative (HCI) (Table L-1). The HCI is managed by the Hells Canyon Bighorn Sheep Restoration Committee, a State, Federal, and private partnership to restore Rocky Mountain bighorn sheep in the Hells Canyon of Oregon, Idaho, and Washington. Source habitat is defined as those characteristics of macrovegetation that contribute to stationary or positive population growth, which is distinguished from habitats associated with species occurrence since such habitats may or may not contribute to long-term population persistence (Wisdom et al. 2000). The original suitable habitat model was primarily a two-component model that consisted of escape terrain and horizontal visibility. The water sources component was not used in the Payette National Forest version of this model because the criteria used in the HCI model (>3.2 kilometers [km] from a water source) encompassed every portion of the Payette National Forest. The Payette National Forest model also did not include the lambing range.

Table L-1. Hells Canyon Initiative bighorn sheep habitat model

Habitat Component	Criteria	Source
Escape terrain		
Slope	31° ≤slope ≤85°	Gudorf et al. 1996; Smith et al. 1991
Buffer	300 meters (m) or land areas ≤1,000 m wide bounded on ≥2 sides by escape terrain (500 m)	Smith et al. 1991; Gudorf and Sweanor 1996
Minimum area	1.6 hectares (ha)	Gudorf and Sweanor 1996
Horizontal visibility	Grassland, rock, open shrub, or forest cover <40%, from satellite imagery	Schirokauer 1996
Water sources	≤3.2 km	Smith et al. 1991; Gudorf and Sweanor 1996
Summer range	Suitable habitat within 300 m of escape terrain	Smith et al. 1991; Gudorf and Sweanor 1996; Schirokauer 1996
Winter range	Suitable habitat all aspects below 1,463 m; aspect 135°–225°above 1,463 m	Smith et al. 1991; Gudorf and Sweanor 1996; Coggins pers. comm.
Lambing range	Escape terrain 45°–315° ≤1 km from water ≥2contiguous ha	Gudorf and Sweanor 1996

Source: Hells Canyon Bighorn Sheep Restoration Committee (1997)

The source habitat model used for the DSEIS needed several modifications for the FSEIS. First, the geographic range of the model only covered the Hells Canyon and not the entire Payette National Forest. The second issue concerned the vegetation layer used in the horizontal visibility component of the original model. The HCI model utilized vegetation supervised classification of Thematic Mapper satellite imagery, which was too broad and contained no canopy cover information, resulting in an insufficient level of detail for the vegetation data. To solve the problems of scale and detail, Payette National Forest modelers used a different vegetation dataset for horizontal visibility and included low canopy cover forested cover types. Using forested types is supported by the HCI's cited literature but was not used by the HCI because of limitations of the supervised classification of TM satellite imagery.

The escape terrain component was found to overmap in areas that met the steepness criterion but lacked the ruggedness to make the area source habitat. To correct this problem, Payette National Forest modelers used a ruggedness ArcGIS script (Sappington et al. 2007) to create a ruggedness surface that was then overlaid with the telemetry and observation data. From this overlay, modelers created a histogram of ruggedness to determine the ruggedness cutoff point for source habitat, which was 310 or less out of a range of 0 to 3455. Adding this new criterion changed the overall amount of mapped source habitat by 2% and reduced the correlation between the source habitat and telemetry data from 92% to 90%.

The winter version of the source habitat model was also modified for the FSEIS. The original HCI model and the version used in the DSEIS restricted the habitat to southern aspects above 4,800 feet or 1,463 m, which grossly overmapped the amount of winter source habitat. However, field reviewers found that most of the areas above 1,463 m are covered by snow and therefore not suitable habitat. To overcome this problem, Payette National Forest modelers used persistent snow data (Copeland et al. 2010) and removed from winter source habitat areas above 1,463 m that were snow covered 2 or more years out of the last 7. This change in mapping dropped the amount of mapped winter source habitat by 18%; however, it only dropped the correlation between winter source habitat and winter telemetry points from 82% to 80%.

The horizontal visibility component used the vegetation dataset from the LANDFIRE project (The National Map LANDFIRE 2006), an interagency effort to map vegetation and fuels data in a consistent fashion and at a scale useful at an incident level nationally. The nonforest vegetation cover types from the HCI model were crosswalked into the LANDFIRE nonforested cover types by Payette National Forest staff. Documentation created by the HCI stated that forested cover types of less than 40% canopy cover can be used in the model; however, they were not used in the actual model because canopy cover was not included in the original supervised classification of TM satellite imagery. Forested cover types for canopy cover≤30% were added to the FSEIS model using LANDFIRE. The ≤30% canopy cover for forest cover type was chosen based on review by Payette National Forest staff using the 2004 National Agricultural Imagery Program (NAIP) 1-m full-color photographs. The LANDFIRE data at ≤40% canopy cover in forested types tended to map canopy covers that appeared denser than 40% cover, particularly on the east zone of the Payette National Forest. This discrepancy would have overestimated the amount of source habitat available to bighorn sheep on the eastern portion of the Payette National Forest and may have contributed to some undermapping of source habitat on the western side where the canopy covers better matched photograph images. However, underestimating the habitat in the western side of the Payette National Forest appeared to be less of an error compared to the amount that would have been overmapped in the east. This choice of using a ≤30% canopy cover was also confirmed during a season of field reviews of the habitat data.

Modelers also decided to filter the habitat model to a minimum mapping size of 2.0 hectares. The original HCI model only filtered the escape terrain component to approximately 1.6 hectares. The overall 2.0 hectare minimum mapping area filter was a more appropriate filter because of the nature of the LANDFIRE vegetation data. The final product and the forest cover type/canopy cover choices were verified with NAIP photography and on-the-ground field reviews at several locations throughout a field season.

The source habitat model used for the FSEIS was compared with over 54,000 telemetry and observation points, mainly from Hells Canyon and the Salmon River canyon; 90% of all known bighorn sheep telemetry points fell within the modeled summer source habitat and 80% fell within the winter source habitat. A final review of all source habitat model components and outcomes was completed by the IDT and accepted as adequate to fulfill the needs of this analysis. In one area, the output of the source habitat model was manually edited. In the Lost Valley area, the model was determined to be overmapping the presence of source habitat, leading to an overestimate in the risk of contact analysis. This manual change was also accepted by the IDT. Detailed information on each input and function for bighorn sheep summer source habitat in the Hells Canyon and the Payette National Forest is found in Table L-2. Table L-3 shows winter source habitat for bighorn sheep in Hells Canyon and the Payette National Forest. Table L-4 describes the LANDFIRE cover types.

Table L-2. Summer habitat model

Name	Explanation[a]
CON selection of nonforest cover types	This command creates the nonforested input for the horizontal visibility portion of the Bighorn Sheep Summer Source Habitat model. The input data is Existing Vegetation Type downloaded from LANDFIRE on May 2, 2007. The map algebra command is "con (F:\Bighorn\Landfire\33677953\33677953 in {12, 31, 2001, 2006, 2079, 2080, 2081, 2106, 2123, 2124, 2125, 2126, 2127, 2134, 2135, 2139, 2140, 2142, 2143, 2144, 2145, 2153, 2169, 2181, 2182, 2183, 2220, 2062, 2065, 2144, 2070, 2017, 2115, 2165},1)".
CON selection of forest cover types and canopy covers	This command creates the forested input for the horizontal visibility portion of the Bighorn Sheep Summer Source Habitat model. The input data are Existing Vegetation Type and Existing Vegetation Cover downloaded from LANDFIRE on May 2, 2007. The map algebra command is "con ((F:\Bighorn\Landfire\33677953\33677953 in {2008, 2009, 2011, 2012, 2016, 2018, 2019, 2020, 2035, 2036, 2037, 2038, 2039, 2041, 2042, 2045, 2046, 2047, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2060, 2061, 2063, 2154, 2156, 2157, 2158, 2161, 2166, 2167, 2173, 2174, 2178, 2200, 2203, 2205, 2206, 2208, 2227, 2228, 2232} and F:\Bighorn\Landfire\30745420\30745420 in {101, 102}), 1)". The canopy covers from LANDFIRE are as follows: 101, Tree Cover ≥10 and <20%; 102, Tree Cover ≥20 and <30%.
MERGE of forested and nonforest selections	This command merges the forested and nonforest components of the horizontal visibility component of the Bighorn Sheep Summer Source Habitat model. The map algebra for this command is "merge (nonforest, forest)".
Project Raster from Albers to Universal Transverse Mercator (UTM)	This command changes the projection of the combined forested and nonforested vegetation components. The LANDFIRE projection was Albers NAD83, which was projected to the local projection of UTM Zone 11 NAD83.
Region Group for minimum mapping size	This Region Group command is the first step in filtering for a minimum mapping unit. This command takes the input and groups the cells based on if they touch and then gives all the touching cells the total count for that group.
CON selection of minimum mapping size of 5 acres	This command selects from the grouped input groups of cell 5 acres or larger. The map algebra for this command is "con (F:\Bighorn\Landfire\hor_vis_rg.count ≥23,1)".
"Slope ≥31 and ≤85 degrees" CON	This CON function selects slopes from the slope grid derived from the National Elevation Dataset elevation grid. The slopes selected are equal to or greater than 31° and less than or equal to 85° and roughness index of ≤310. This selection is as follows "C:\Projects\BHS_Final\Data\Elevations\deg_slp ≥31 AND C:\Projects\BHS_Final\Data\Elevations\deg_slp ≤85" and C:\Projects\BHS_Final\Data\Elevations\ruf_10000 ≤310.
Region Group	This command takes the input and groups the cells based on if they touch and then gives all the touching cells the total count for that group.
CON & ZONALAREA (Single Output Map Algebra)	This command selects from the grouped input groups of cell 16000 or larger. The map algebra for this command is "con (zonalarea (slpgp) ≥16000, 1)".
CON & EUCDISTANCE LE 300 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells ≤300 m. The map algebra for this command is "con (eucdistance (escslp) ≤300, 1)".
CON & EUCDISTANCE GT 500 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells greater than 500 m. The map algebra for this command is "con (eucdistance (escslp) > 500, 1)".
CON & EUCDISTANCE GE 500 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells ≥500 m. The map algebra for this command is "con (eucdistance (gt500) ≥500, 1)".
CON & ISNULL (Single Output Map Algebra)	This CON function erases the "buff300" from "wi500" to create the final output for the escape terrain component. The map algebra for this function is "con (isnull (buff300), con (wi500 == 1, 1), 1)".
CON combines the two model components	This CON command combines the two model components so that on the cell and overlap from the two inputs appear in the final output.

[a] See Table L-4 for descriptions of the LANDFIRE cover types

Table L-3. Winter habitat model

Name	Explanation[a]
CON selection of nonforest cover types	This command creates the nonforested input for the horizontal visibility portion of the Bighorn Sheep Winter Source Habitat model. The input data is Existing Vegetation Type downloaded from LANDFIRE on May 2, 2007. The map algebra command is "con (F:\Bighorn\Landfire\33677953\33677953 in {12, 31, 2001, 2006, 2079, 2080, 2081, 2106, 2123, 2124, 2125, 2126, 2127, 2134, 2135, 2139, 2140, 2142, 2143, 2144, 2145, 2153, 2169, 2181, 2182, 2183, 2220, 2062, 2065, 2144, 2070, 2017, 2115, 2165},1)".
CON selection of forest cover types and canopy covers	This command creates the forested input for the horizontal visibility portion of the Bighorn Sheep Winter Source Habitat model. The input data are Existing Vegetation Type and Existing Vegetation Cover downloaded from LANDFIRE on May 2, 2007. The map algebra command is "con ((F:\Bighorn\Landfire\33677953\33677953 in {2008, 2009, 2011, 2012, 2016, 2018, 2019, 2020, 2035, 2036, 2037, 2038, 2039, 2041, 2042, 2045, 2046, 2047, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2060, 2061, 2063, 2154, 2156, 2157, 2158, 2161, 2166, 2167, 2173, 2174, 2178, 2200, 2203, 2205, 2206, 2208, 2227, 2228, 2232} and F:\Bighorn\Landfire\30745420\30745420 in {101, 102}), 1)". The canopy covers from LANDFIRE are as follows: 101, Tree Cover ≥10 and <20%; 102, Tree Cover ≥20 and <30%.
MERGE of forested and nonforest selections	This command merges the forested and nonforest components of the horizontal visibility component of the Bighorn Sheep Winter Source Habitat model. The map algebra for this command is "merge (nonforest, forest)".
Project Raster from Albers to Universal Transverse Mercator (UTM)	This command changes the projection of the combined forested and nonforested vegetation components. The LANDFIRE projection was Albers NAD83, which was projected to the local projection of UTM Zone 11 NAD83.
Region Group for minimum mapping size	This Region Group command is the first step in filtering for a minimum mapping unit. This command takes the input and groups the cells based on if they touch and then gives all the touching cells the total count for that group.
CON selection of minimum mapping size of 5 acres	This command selects from the grouped input groups of cell 5 acres or larger. The map algebra for this command is "con (F:\Bighorn\Landfire\hor_vis_rg.count ≥23,1)".
"Slope ≥31 and ≤85 degrees" CON	This CON function selects slopes from the slope grid derived from the National Elevation Dataset elevation grid. The slopes selected are equal to or greater than 31° and ≤85° and roughness index of ≤310. This selection is as follows "C:\Projects\BHS_Final\Data\Elevations\deg_slp ≥31 AND C:\Projects\BHS_Final\Data\Elevations\deg_slp ≤85" and C:\Projects\BHS_Final\Data\Elevations\ruf_10000 ≤310.
Region Group	This command takes the input and groups the cells based on if they touch and then gives all the touching cells the total count for that group.
CON & ZONALAREA (Single Output Map Algebra)	This command selects from the grouped input groups of cell 16000 or larger. The map algebra for this command is "con (zonalarea (slpgp) ≥16000, 1)".
CON & EUCDISTANCE LE 300 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells ≤300 m. The map algebra for this command is "con (eucdistance (escslp) ≤300, 1)".
CON & EUCDISTANCE GT 500 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells greater than 500 m. The map algebra for this command is "con (eucdistance (escslp) > 500, 1)".
CON & EUCDISTANCE GE 500 (Single Output Map Algebra)	This CON function calculates the straight line distance from the input then selects all cells ≥500 m. The map algebra for this command is "con (eucdistance (gt500) ≥500, 1)".
CON & ISNULL (Single Output Map Algebra)	This CON function erases the "buff300" from "wi500" to create the final output for the escape terrain component. The map algebra for this function is "con (isnull (buff300), con (wi500 == 1, 1), 1)".
CON combines the two model components	This CON command combines the two model components so that on the cell and overlap from the two inputs appear in the final output.
Southern Aspects above 4,800 feet excluded	The Map Algebra expression creates a grid that masks out area above 4,800 feet that are not on southern aspect. "con ((c:\Projects\BHS_Final\Data\Elevation\large_elev le 1463.04) OR ((c:\Projects\BHS_Final\Data\Elevation\large_elev gt 1463.04) and (c:\Projects\BHS_Final\Data\Elevation\large_asp ge 135 and c:\Projects\BHS_Final\Data\Elevation\large_asp le 225)), 1)"

Name	Explanation[a]
Perennial Snow Areas excluded	The Map Algebra expression masks out, of the southern aspect mask, areas that are covered by persistent snow. “con((win_area1 eq 1) and (pere_snow le 1),1)”
Merge winter exclusions with the escape terrain and horizontal visibility	This CON command combines the winter exclusions with the escape terrain and horizontal visibility components so that only the areas that overlap between components are the only areas in the final output.

a See Table L-4 for descriptions of the LANDFIRE cover types

Table L-4. LANDFIRE cover types

No.	Type of Vegetation
12	Snow/Ice
31	Barren
2001	Inter-Mountain Basins Sparsely Vegetated Systems
2006	Rocky Mountain Alpine/Montane Sparsely Vegetated Systems
2008	North Pacific Oak Woodland
2009	Northwestern Great Plains Aspen Forest and Parkland
2011	Rocky Mountain Aspen Forest and Woodland
2012	Rocky Mountain Bigtooth Maple Ravine Woodland
2016	Colorado Plateau Pinyon-Juniper Woodland
2017	Columbia Plateau Western Juniper Woodland and Savanna
2018	East Cascades Mesic Montane Mixed-Conifer Forest and Woodland
2019	Great Basin Pinyon-Juniper Woodland
2020	Inter-Mountain Basins Subalpine Limber-Bristlecone Pine Woodland
2035	North Pacific Dry Douglas-fir Forest and Woodland
2036	North Pacific Hypermaritime Sitka Spruce Forest
2037	North Pacific Maritime Dry-Mesic Douglas-fir-Western Hemlock Forest
2038	North Pacific Maritime Mesic Subalpine Parkland
2039	North Pacific Maritime Mesic-Wet Douglas-fir-Western Hemlock Forest
2041	North Pacific Mountain Hemlock Forest
2042	North Pacific Mesic Western Hemlock-Silver Fir Forest
2045	Northern Rocky Mountain Dry-Mesic Montane Mixed Conifer Forest
2046	Northern Rocky Mountain Subalpine Woodland and Parkland
2047	Northern Rocky Mountain Mesic Montane Mixed Conifer Forest
2049	Rocky Mountain Foothill Limber Pine-Juniper Woodland
2050	Rocky Mountain Lodgepole Pine Forest
2051	Southern Rocky Mountain Dry-Mesic Montane Mixed Conifer Forest and Wood
2052	Southern Rocky Mountain Mesic Montane Mixed Conifer Forest and Woodland
2053	Northern Rocky Mountain Ponderosa Pine Woodland and Savanna
2054	Southern Rocky Mountain Ponderosa Pine Woodland
2055	Rocky Mountain Subalpine Dry-Mesic Spruce-Fir Forest and Woodland
2056	Rocky Mountain Subalpine Wet-Mesic Spruce-Fir Forest and Woodland
2057	Rocky Mountain Subalpine-Montane Limber-Bristlecone Pine Woodland
2060	East Cascades Oak-Ponderosa Pine Forest and Woodland
2061	Inter-Mountain Basins Aspen-Mixed Conifer Forest and Woodland
2062	Inter-Mountain Basins Mountain Mahogany Woodland and Shrubland
2063	North Pacific Broadleaf Landslide Forest and Shrubland
2065	Columbia Plateau Scabland Shrubland
2070	Rocky Mountain Alpine Dwarf-Shrubland
2079	Great Basin Xeric Mixed Sagebrush Shrubland
2080	Inter-Mountain Basins Big Sagebrush Shrubland
2081	Inter-Mountain Basins Mixed Salt Desert Scrub

No.	Type of Vegetation
2106	Northern Rocky Mountain Montane-Foothill Deciduous Shrubland
2115	Inter-Mountain Basins Juniper Savanna
2123	Columbia Plateau Steppe and Grassland
2124	Columbia Plateau Low Sagebrush Steppe
2125	Inter-Mountain Basins Big Sagebrush Steppe
2126	Inter-Mountain Basins Montane Sagebrush Steppe
2127	Inter-Mountain Basins Semi-Desert Shrub-Steppe
2134	Columbia Basin Foothill and Canyon Dry Grassland
2135	Inter-Mountain Basins Semi-Desert Grassland
2139	Northern Rocky Mountain Lower Montane-Foothill-Valley Grassland
2140	Northern Rocky Mountain Subalpine-Upper Montane Grassland
2142	Columbia Basin Palouse Prairie
2143	Rocky Mountain Alpine Fell-Field
2144	Rocky Mountain Dry Turf
2145	Rocky Mountain Subalpine-Montane Mesic Meadow
2153	Inter-Mountain Basins Greasewood Flat
2154	Inter-Mountain Basins Montane Riparian Systems
2156	North Pacific Lowland Riparian Forest and Shrubland
2157	North Pacific Swamp Systems
2158	North Pacific Montane Riparian Woodland and Shrubland
2161	Northern Rocky Mountain Conifer Swamp
2165	Northern Rocky Mountain Foothill Conifer Wooded Steppe
2166	Middle Rocky Mountain Montane Douglas-fir Forest and Woodland
2167	Rocky Mountain Poor-Site Lodgepole Pine Forest
2169	Northern Rocky Mountain Subalpine Deciduous Shrubland
2173	North Pacific Wooded Lava Volcanic Flowage
2174	North Pacific Dry-Mesic Silver Fir-Western Hemlock-Douglas-fir Forest
2178	North Pacific Hypermaritime Western Red-cedar-Western Hemlock Forest
2181	Introduced Upland Vegetation—Annual Grassland
2182	Introduced Upland Vegetation—Perennial Grassland and Forbland
2183	Introduced Upland Vegetation—Annual and Biennial Forbland
2200	Pseudotsuga menziesii-Quercus garryana Woodland Alliance
2203	Juniperus occidentalis Woodland Alliance
2205	Tsuga mertensiana-Abies amabilis Woodland Alliance
2206	Pseudotsuga menziesii Giant Forest Alliance
2208	Abies concolor Forest Alliance
2220	Artemisia tridentata ssp. vaseyana Shrubland Alliance
2227	Pseudotsuga menziesii Forest Alliance
2228	Larix occidentalis Forest Alliance
2232	Abies grandis Forest Alliance

3.0 RISK OF CONTACT MODEL

The sequence of events by which a disease outbreak could result from contact between a bighorn sheep and a domestic sheep in an active allotment located outside of bighorn sheep core herd home range (CHHR) can be broken down into a number of steps. First, to reach an occupied allotment, a bighorn sheep must (1) leave the CHHR; (2) travel far enough to reach the allotment; and (3) intersect the allotment (i.e., rather than some other area at the same distance from the CHHR). For disease transmission to occur, the bighorn sheep must (4) come into contact with domestic sheep in the allotment and (5) contract the disease from the domestic sheep. Finally, for an outbreak to affect the animal’s home herd, the infected bighorn sheep must (6) return to the CHHR and (7) transmit the disease to other members of the herd.

The contact model described in this section aims to determine the probability that a bighorn sheep will reach an occupied allotment, steps 1–3 above. Steps 4–7, which are also necessary for an outbreak to results from such a movement, are discussed below as part of disease model.

The contact model is based on an analysis of 12 years of bighorn sheep telemetry data from the Hells Canyon and Salmon River populations, and its construction involved two distinct analyses. First, the CHHR analysis was used to delineate areas where most animals in each herd spend most of their time. Then, the analysis examined the characteristics of bighorn sheep movements or “forays” outside of the CHHR. This foray analysis examined how frequently and at what season foray movements occur, as well as how far beyond the CHHR animals are likely to travel. Together, the habitat, CHHR and foray analyses were used to estimate the probability that a ewe or a ram in any of the herds would reach any of the open allotments in a given year.

3.1 Risk of Contact Model

3.1.1 Bighorn Sheep Core Herd Home Range Analysis

CHHR analysis was conducted as part of the major bighorn sheep herd analysis for the Hells Canyon and the Main and South Fork Salmon Rivers. The CHHR analysis made analyzing the impacts of domestic sheep grazing on the Payette National Forest to the broader bighorn sheep metapopulations possible. The analysis showed the extent of overlap between the different herds throughout the Hells Canyon and the Main and South Fork Salmon Rivers. This type of modeling also allowed the IDT to determine the core areas of bighorn sheep habitat usage.

The tools and processes used to complete this analysis are common to home range analyses used for many species. The analysis consisted of a fixed kernel home range model created with observations and telemetry data collected by the HCI from 1997 through 2008. Francis Cassirer (Idaho Department of Fish and Game [IDFG]), who is the HCI project leader responsible for the telemetry database management, used the telemetry data to divide the bighorn sheep population into herds.

The herd assignments were based on transplant locations and breeding groups of ewes that shared the same range. A population is based on the entirety of the breeding individuals independent of shared range. Identified herds in the Hells Canyon metapopulation are the Asotin, Big Canyon, Black Butte, Imnaha, Lostine, Upper Hells Canyon[1], Mountain View, Muir Creek, Myers Creek, Redbird, Sheep Mountain, and Wenaha herds (Figures L-1 through L-12). Herds in the Salmon River metapopulation are the Main Salmon/South Fork, Big Creek, and Upper Main Salmon herds (Figures L-13 through L-15). Several small herds had too few points to accurately create a CHHR or telemetry from transplants that failed to form a herd, so no home range modeling was conducted on them. These small herds are called 05IMREL, Lower Hells Canyon, Saddle Creek, Quartz Creek, Minam, and Sheep Creek.

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[1] The McGraw Herd that was modeled in the draft has been renamed the Upper Hells Canyon Herd. The Upper Hells Canyon Herd has an estimated population of 45 individuals, with insufficient telemetry or observational data. Telemetry data are available from animals of the now extirpated McGraw Herd, which occupied the same part of Hells Canyon. The IDT decided to used the CHHR of the McGraw Herd and attach the current population from the Upper Hells Canyon Herd.

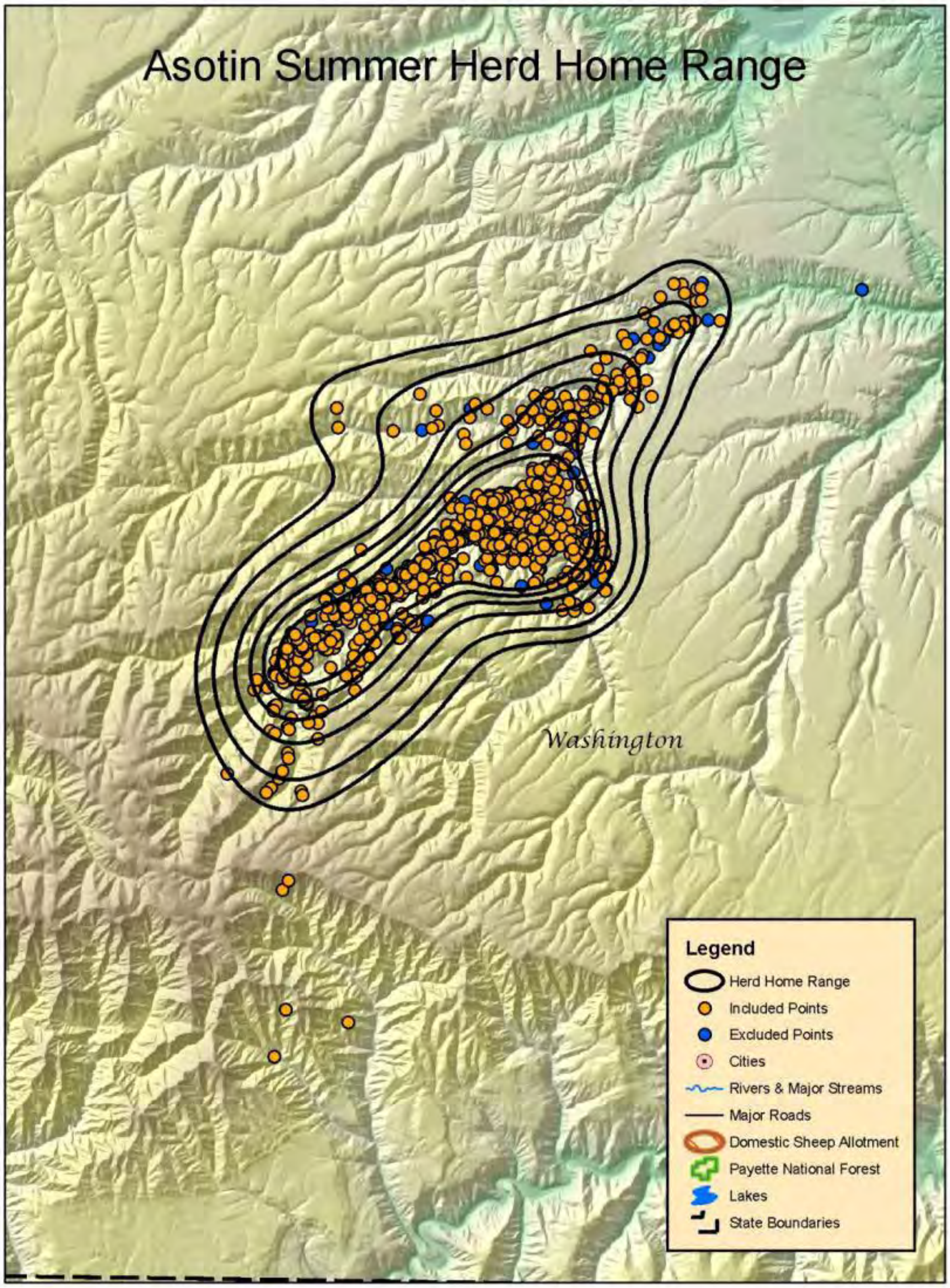


Figure L-1. Asotin core herd home range

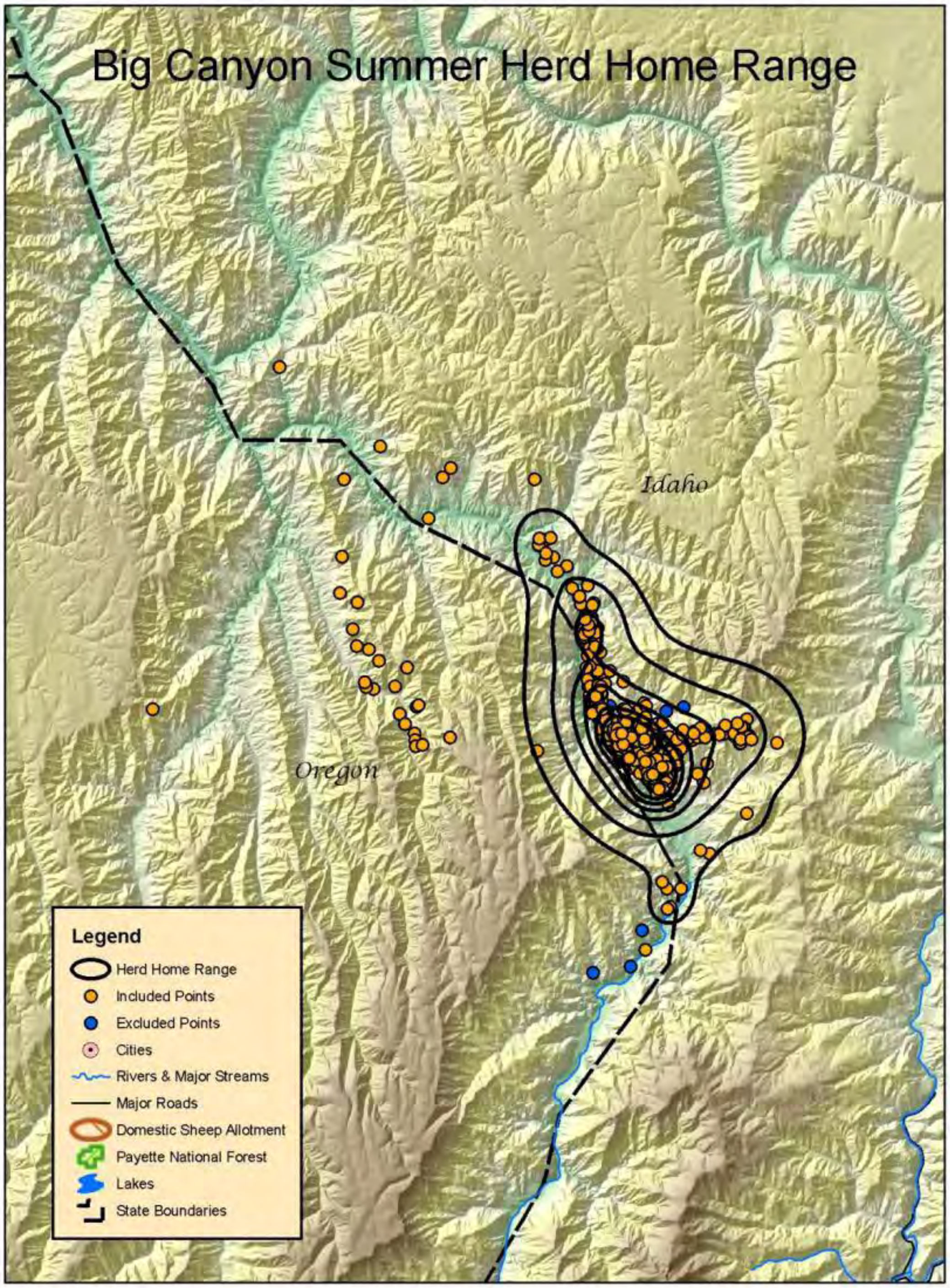


Figure L-2. Big Canyon core herd home ranges

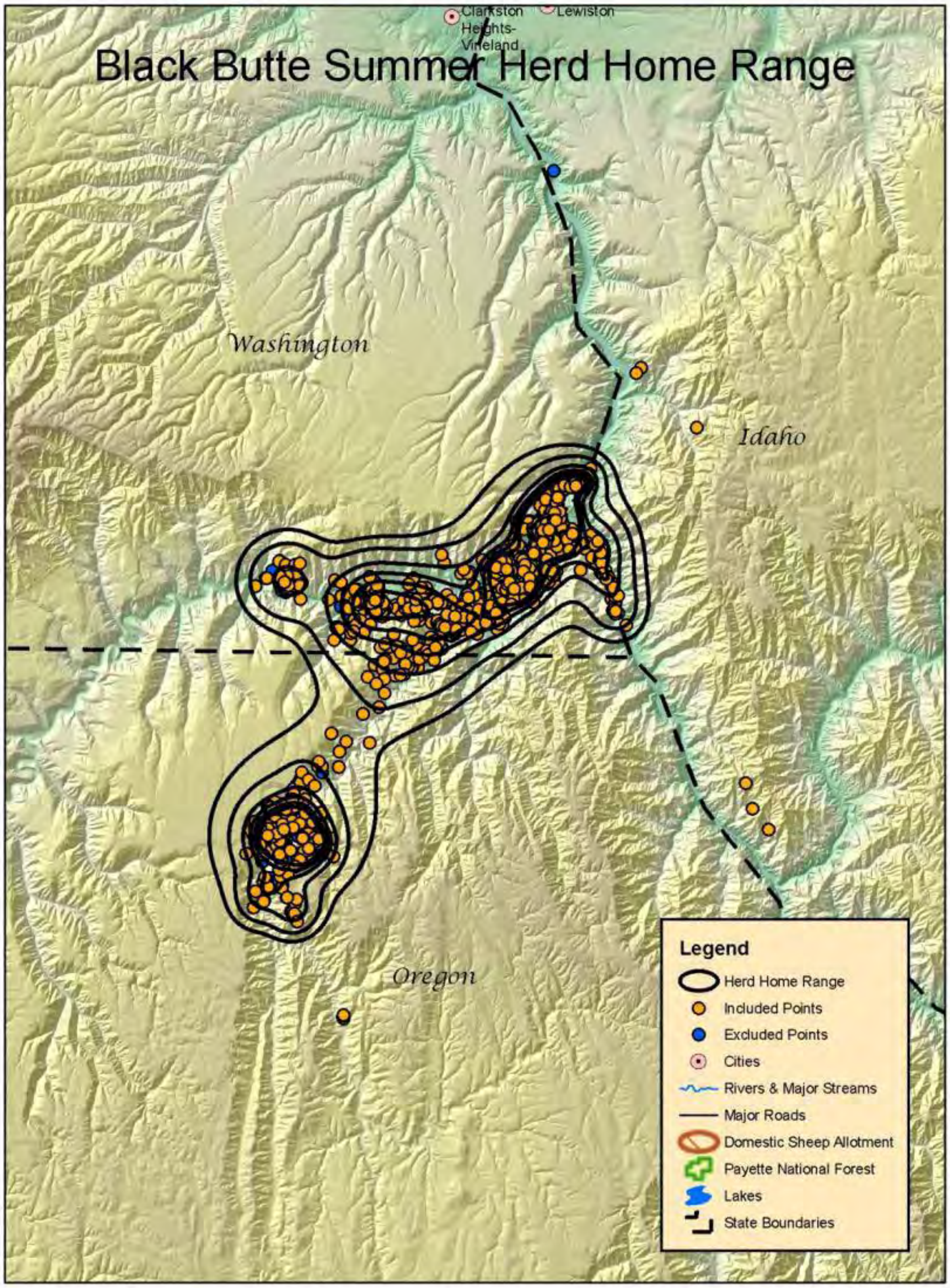


Figure L-3. Black Butte core herd home range

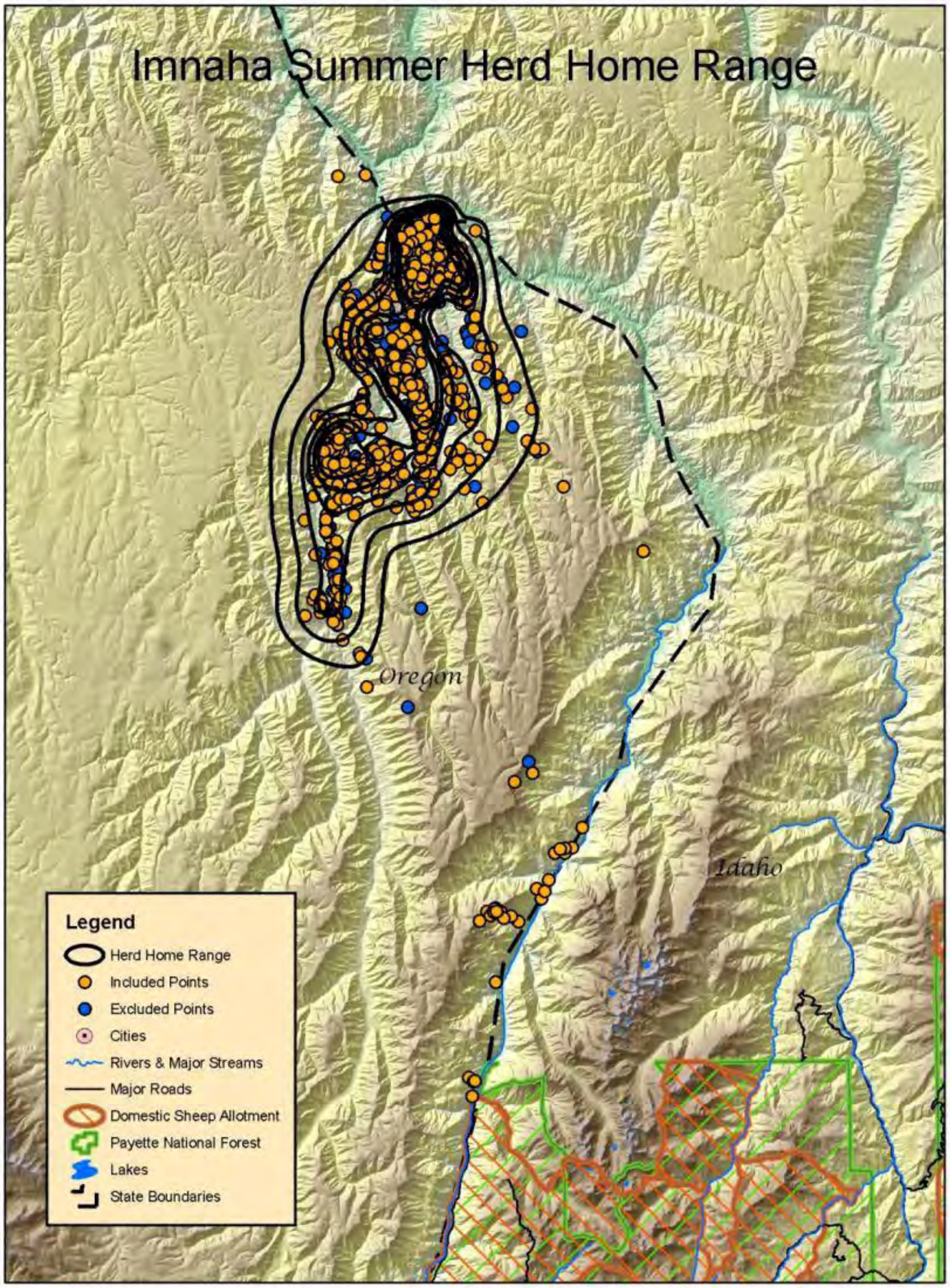


Figure L-4. Imnaha core herd home range

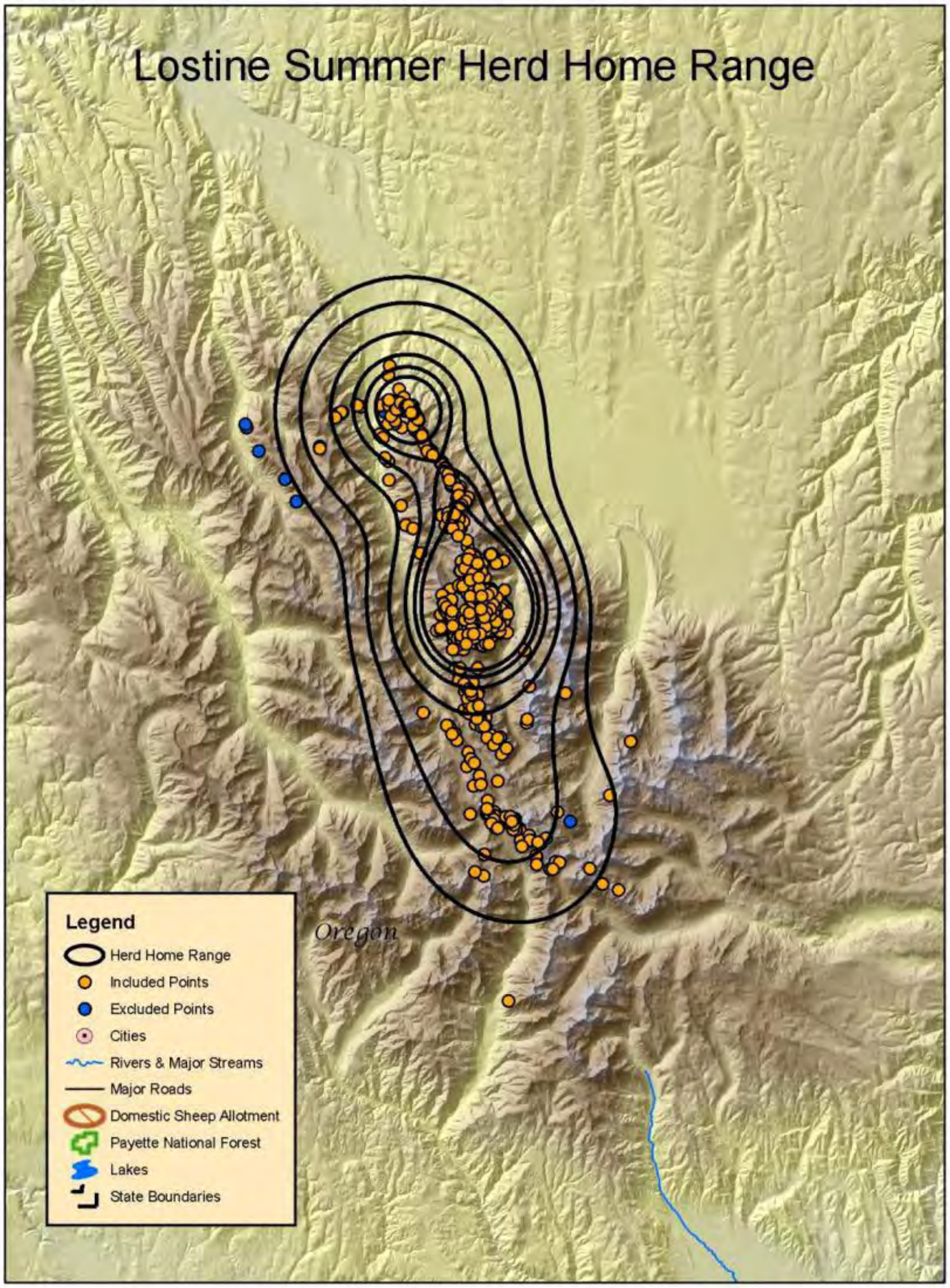


Figure L-5. Lostine core herd home range

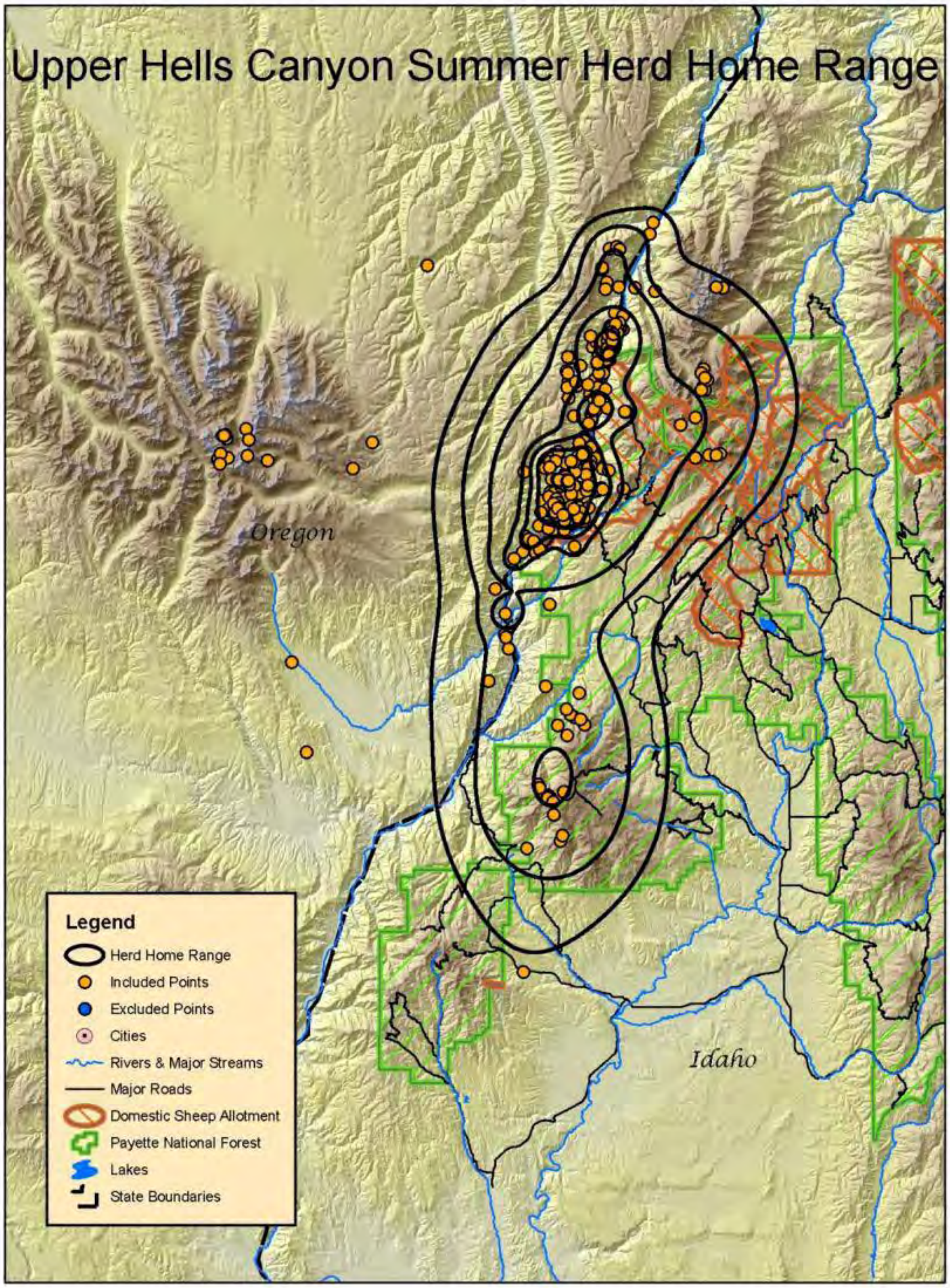


Figure L-6. Upper Hells Canyon core herd home range

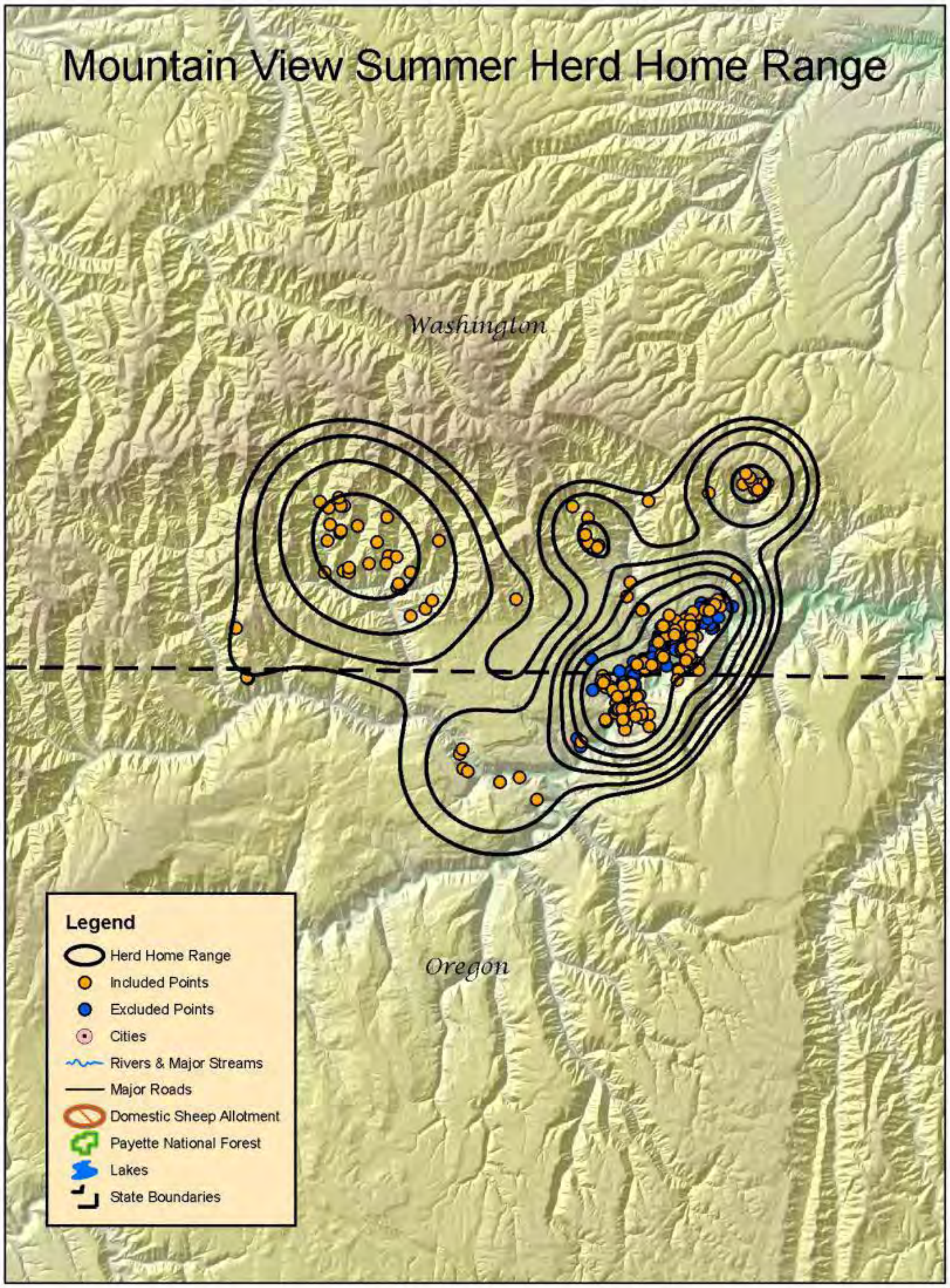


Figure L-7. Mountain View core herd home range

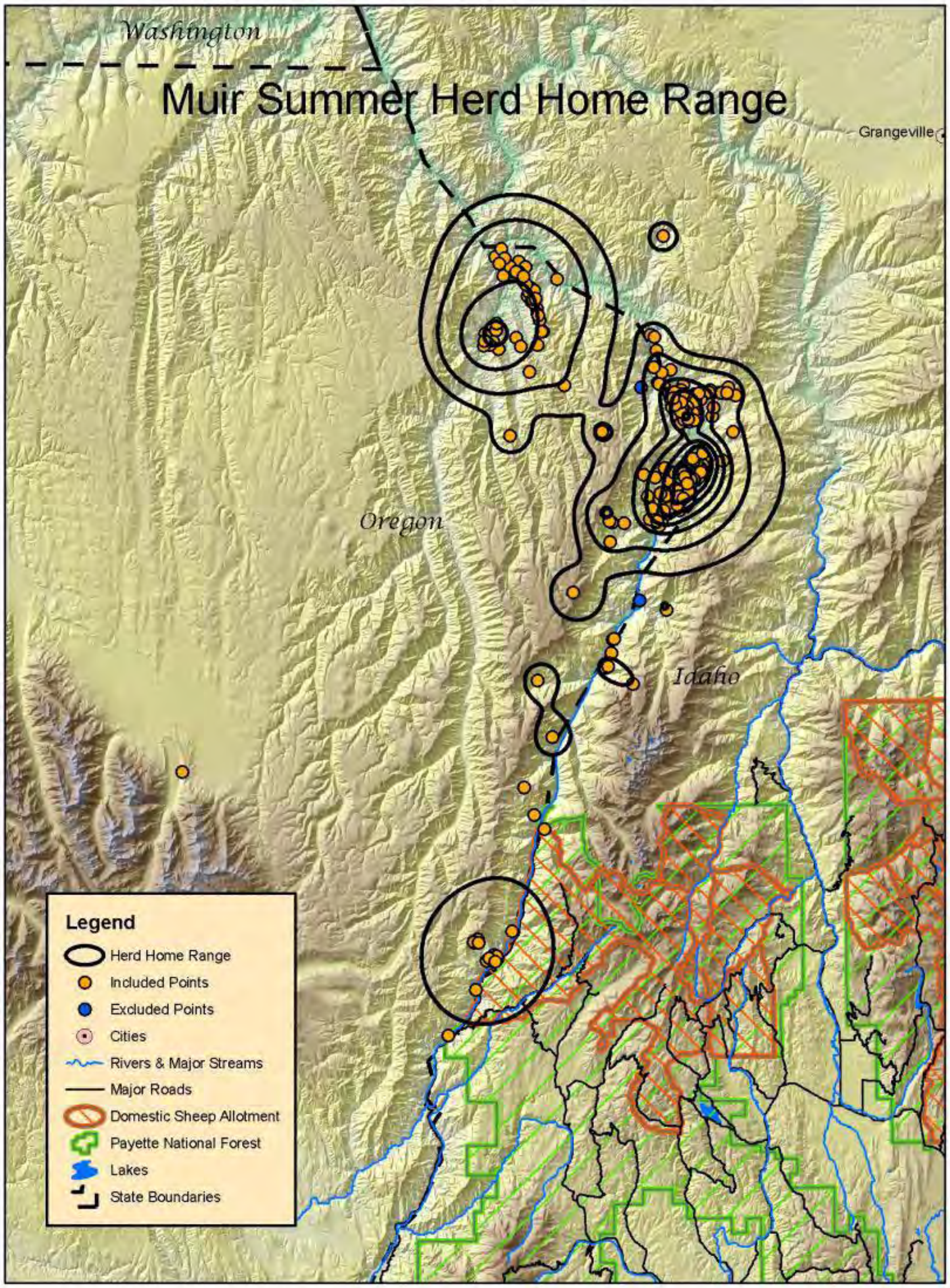


Figure L-8. Muir Creek core herd home range

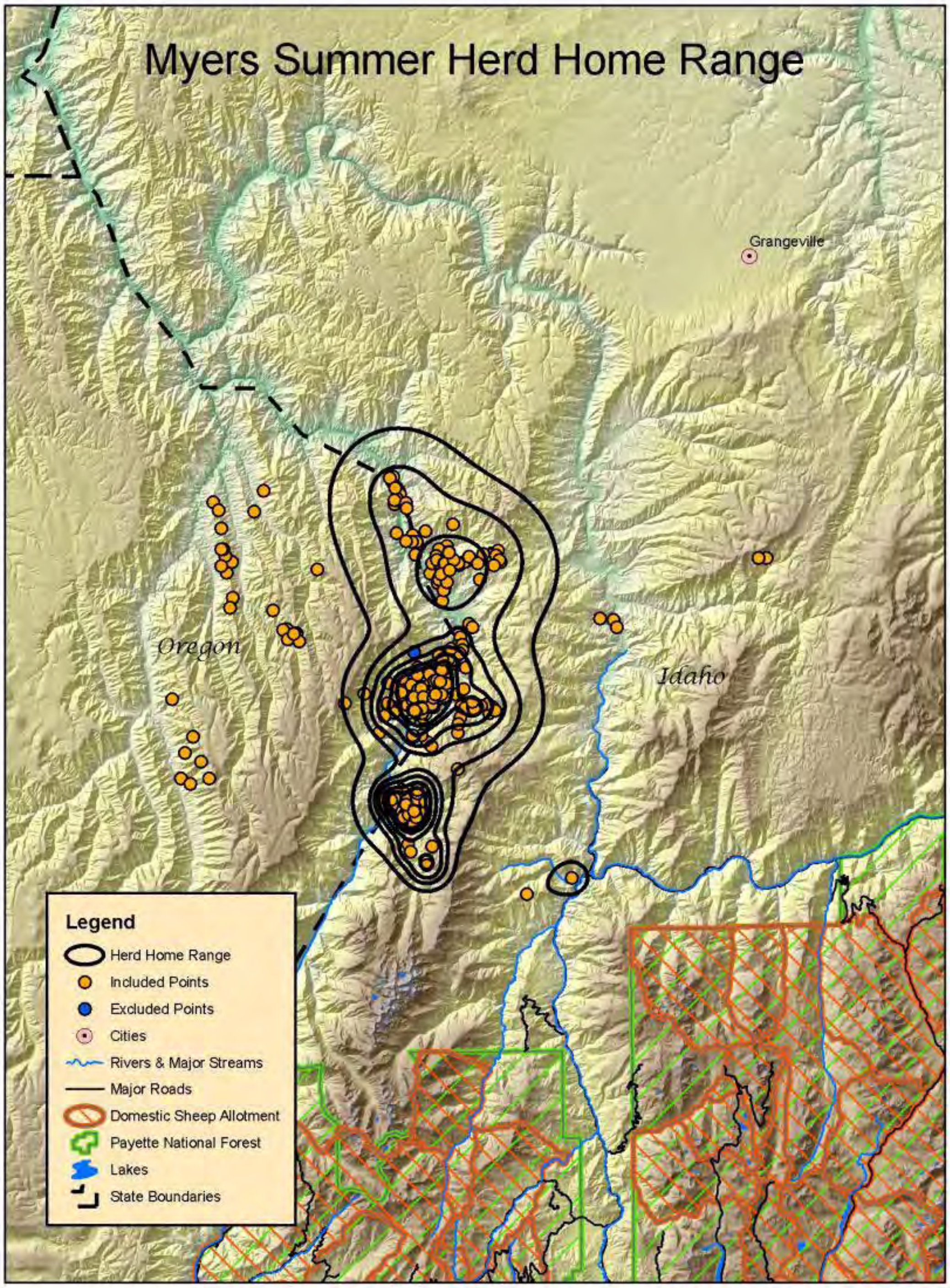


Figure L-9. Myers Creek core herd home range

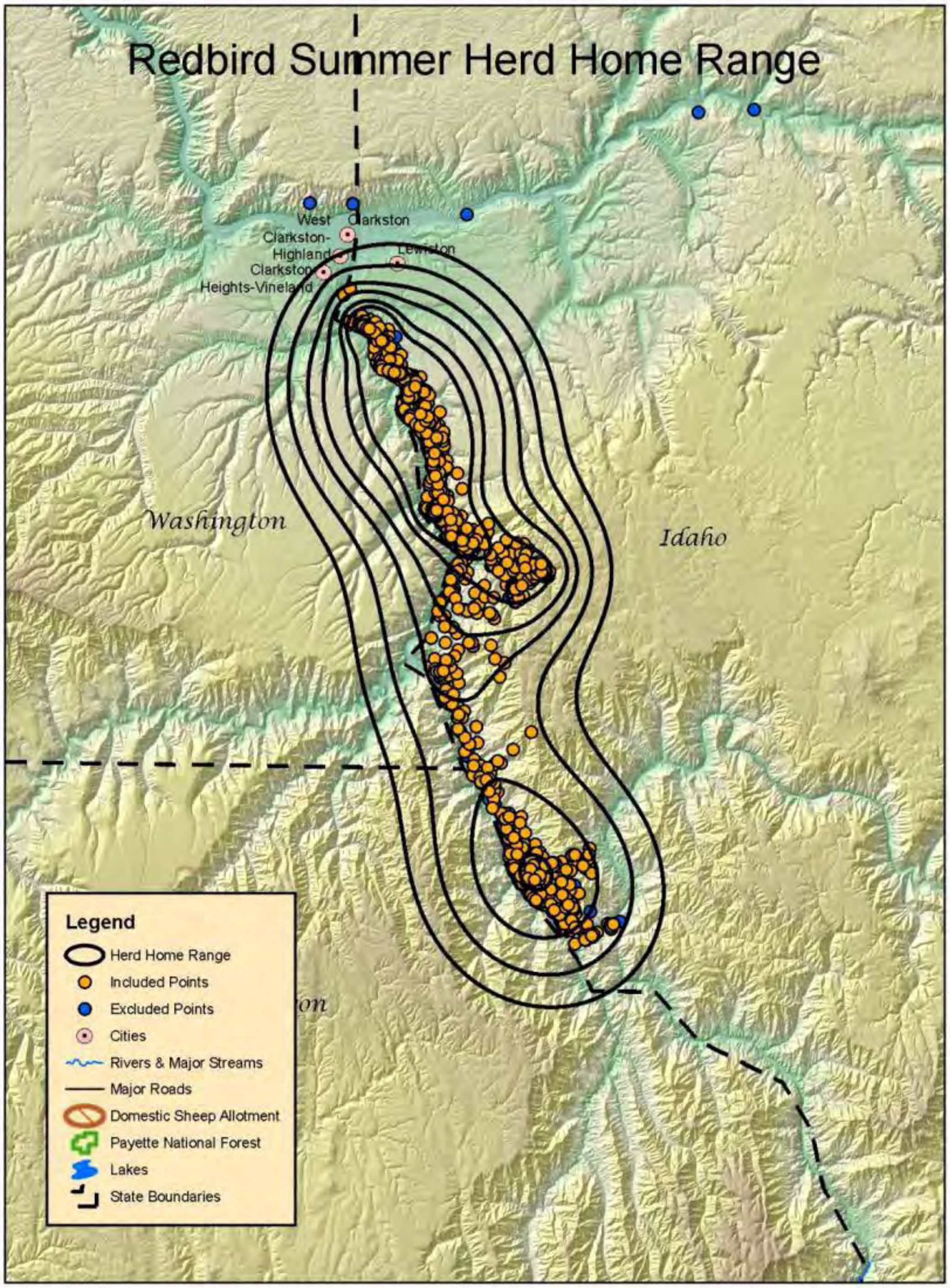


Figure L-10. Redbird core herd home range

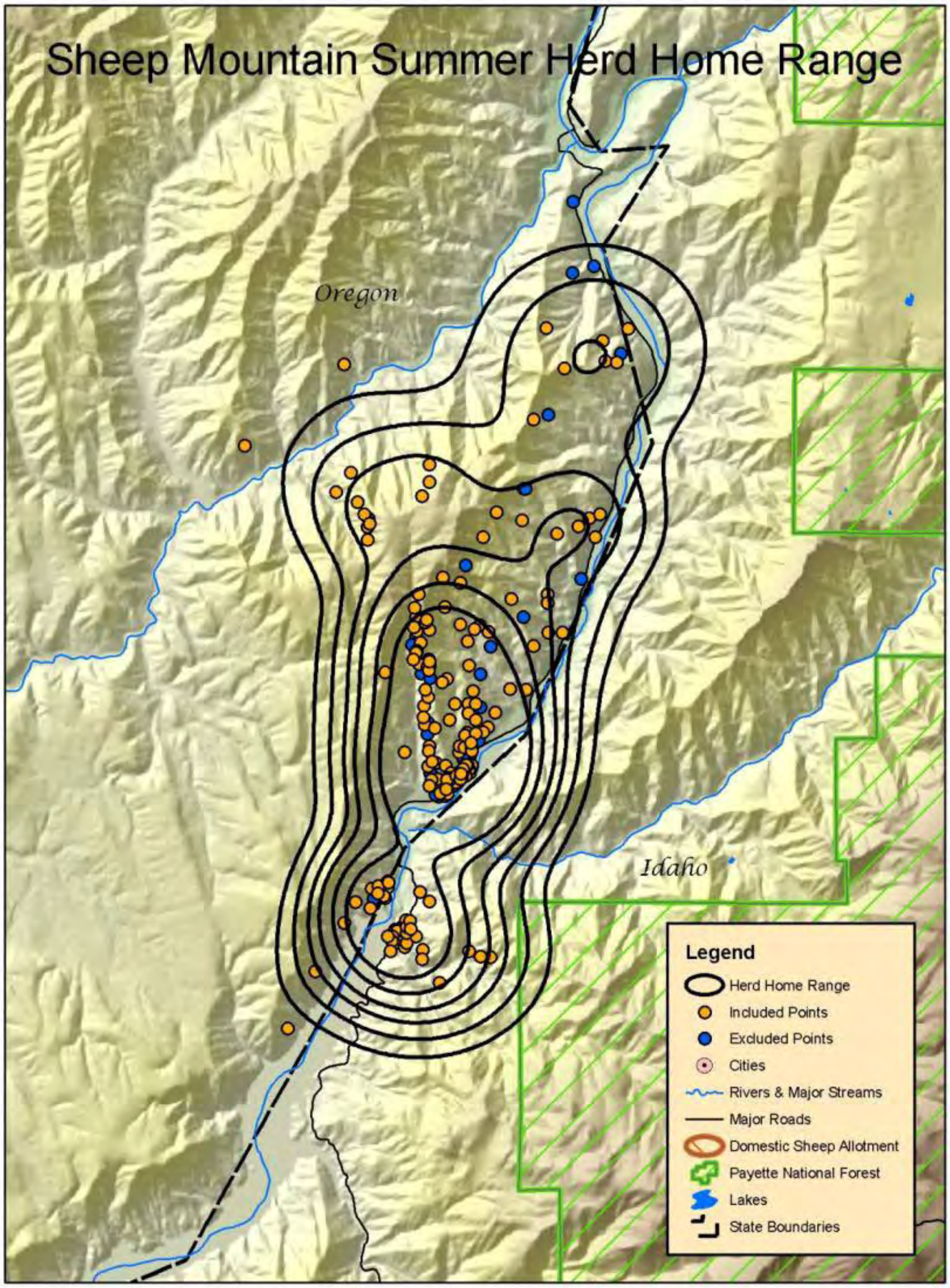


Figure L-11. Sheep Mountain core herd home range

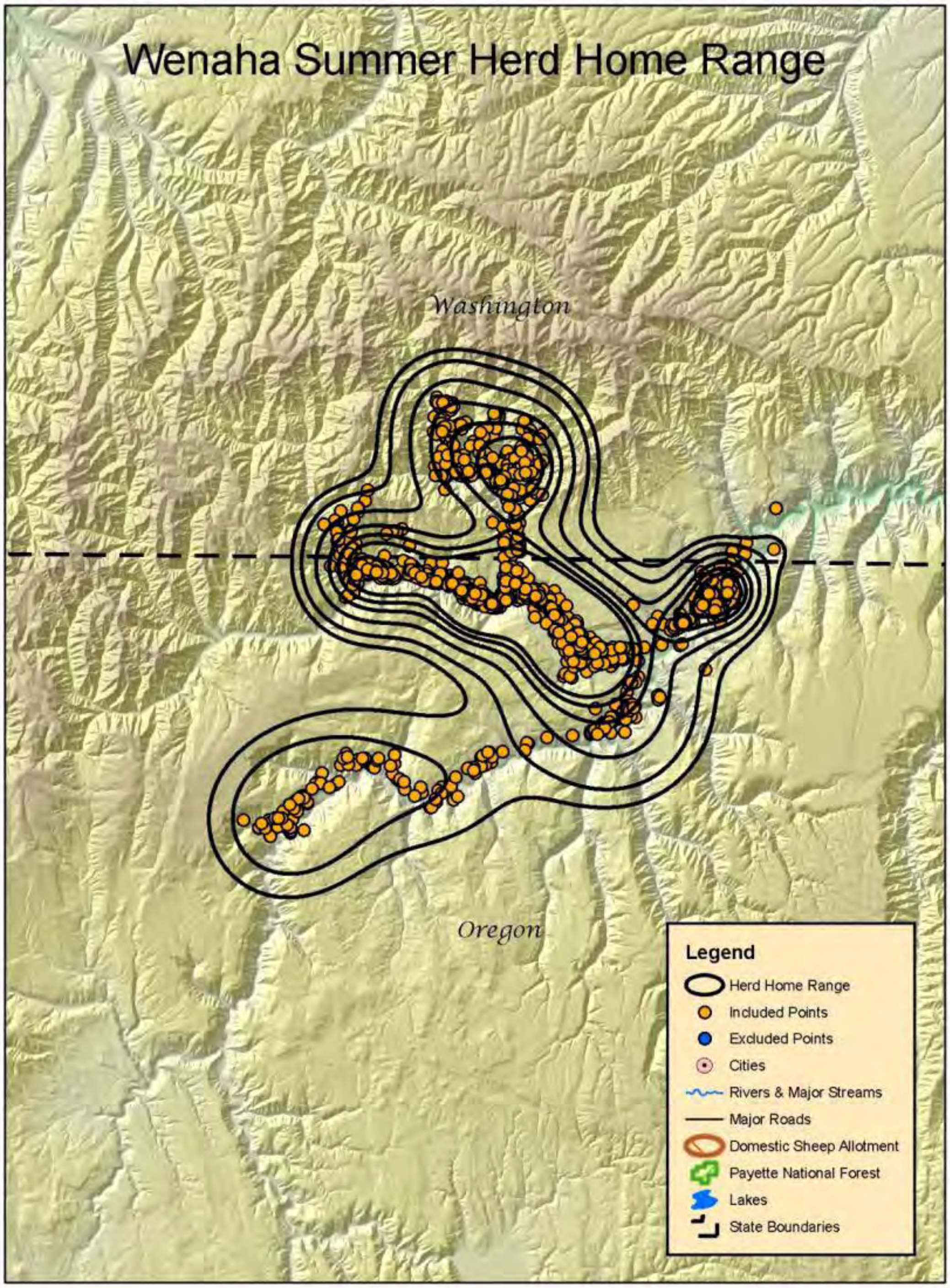


Figure L-12. Wenaha core herd home range

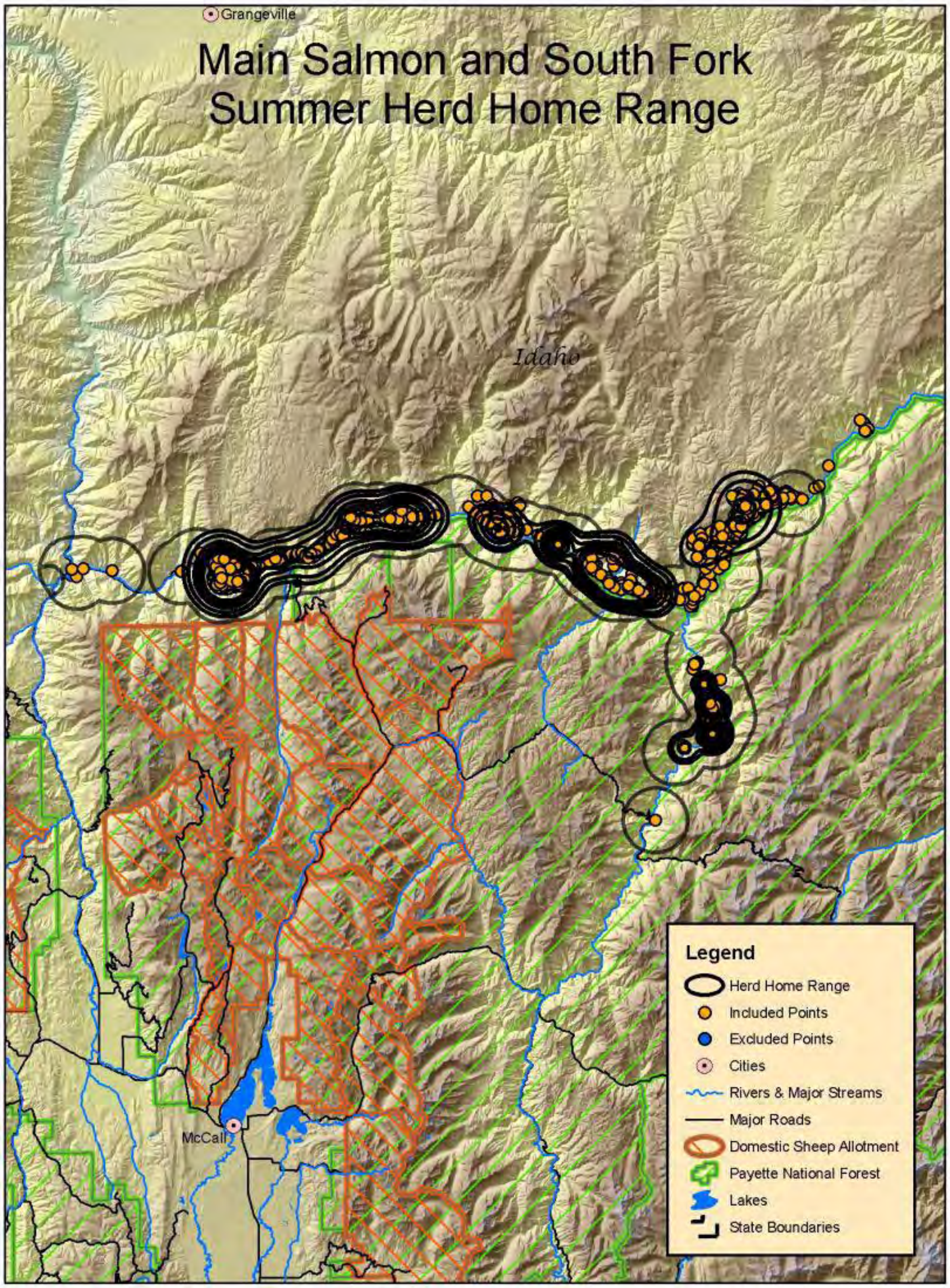


Figure L-13. Main Salmon/South Fork core herd home range

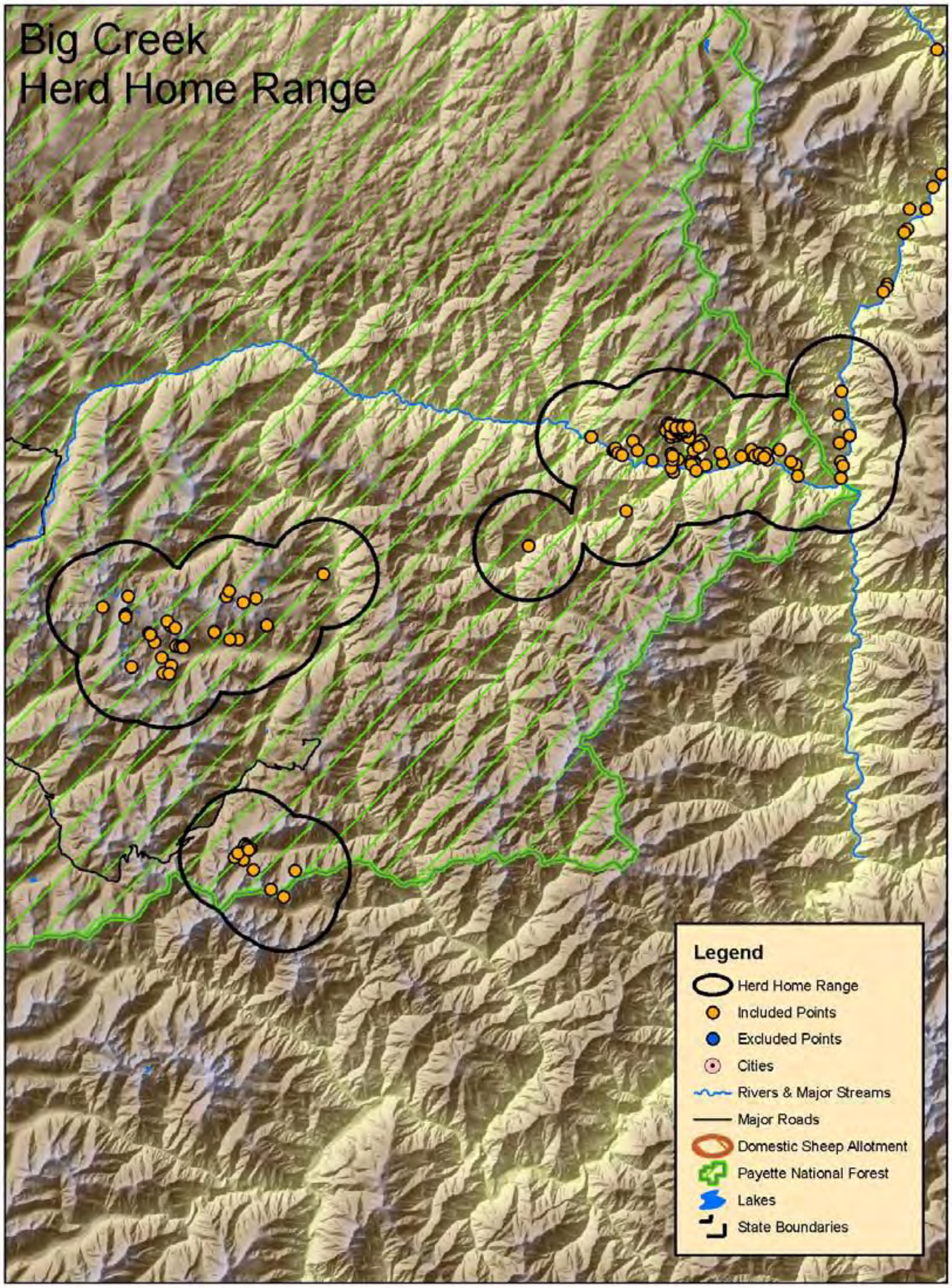


Figure L-14. Big Creek core herd home range

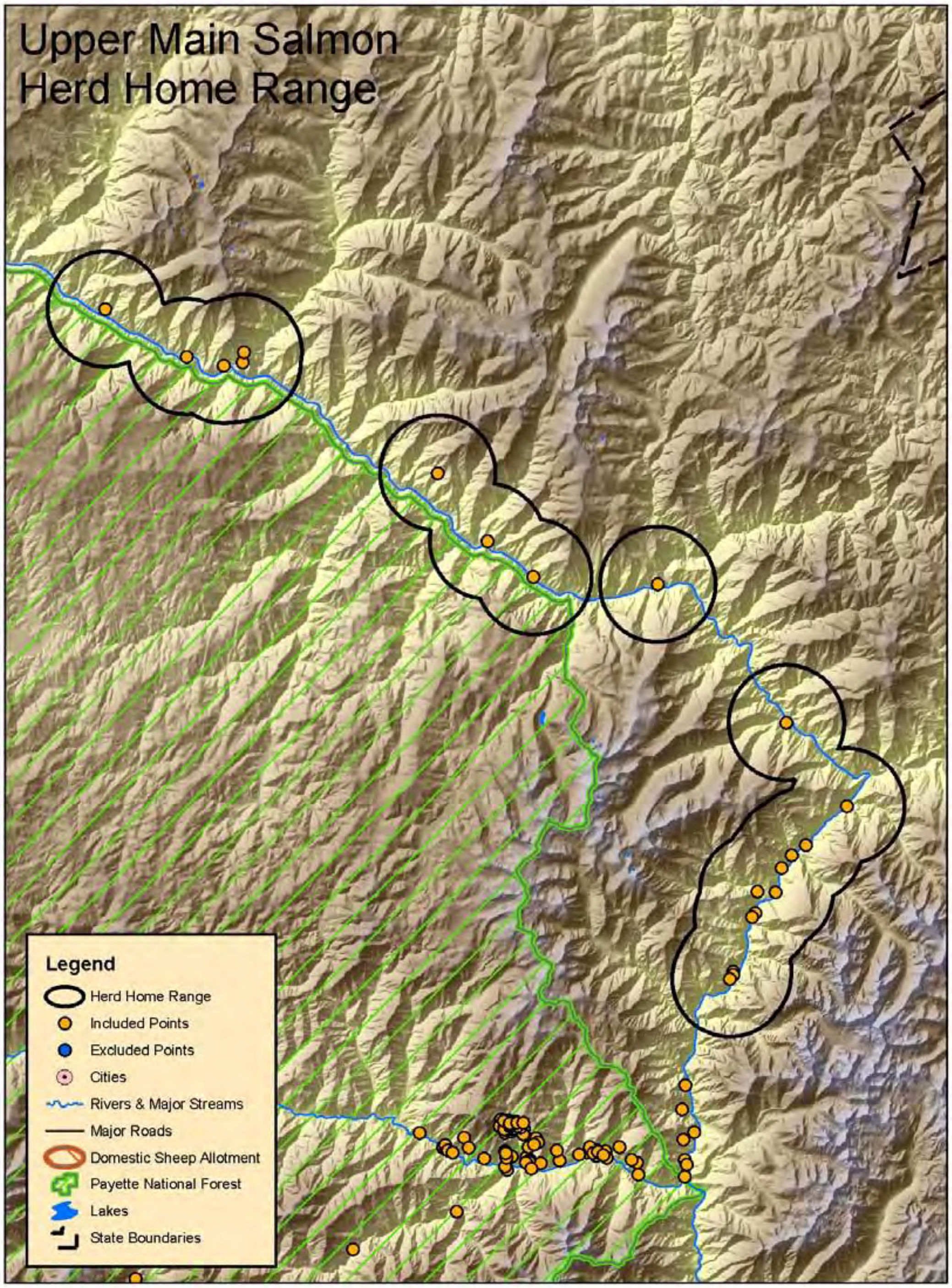


Figure L-15. Upper Main Salmon core herd home range

Home range modeling for the Main Salmon/South Fork Herd and for herds in the Hells Canyon metapopulation was completed with Home Range Extension version 1.1 for ArcGIS (Rodgers et al. 2007), a software package designed for just this purpose. The Home Range Extension uses a standard bivariate normal probability density function as the "kernel" employed to estimate the intensity with which animals use each mapped area. A kernel is essentially a small 3-dimensional hill placed over the location of each telemetry observation. Where many observations are clustered together, these hills overlap and pile up, their total height indicates the probability of finding an animal at a given location. The width of the kernels, *href*, is calculated in Equation L-1 as the square root of the mean variance in *x* (var *x*) and *y* (var *y*) co-ordinates divided by the sixth root of the number of points (Worton 1995):

$$href = n^{\frac{-1}{6}}\sqrt{\frac{\operatorname{var} x + \operatorname{var} y}{2}}$$

Equation L-1. Calculation for band width of the kernels (href)

This method of selecting *href* is widely used as a means of extrapolating from the dispersion of observed locations to the likely extent of the full home range

This process of home range analysis was done for each identifiable individual within a herd that had more than 20 telemetry points. All other telemetry and observation points for a herd that did not meet these criteria were excluded from the home range analysis and used to verify the accuracy of the final CHHR volume contours. One of the byproducts of the process is a surface raster from which the volume contours were created.

To create an overall CHHR, the raster surfaces from the individuals were added together. Then, volume contours, known as isopleths, were created from the merged herd surface using Hawth's Analysis Tools version 3.27 Extension for ArcGIS (Beyer 2004). Isopleths are contours meant to enclose a given percentage of the telemetry observations; the 95th isopleth for example, is drawn to enclose an area in which 95% of the telemetry points are found. Volume contours were calculated for the 50th, 60th, 70th, 80th, 90th, and 95th isopleths, and are shown for each herd in Figures L-1 through L-15. The CHHR is defined as the area contained within the 95th isopleth. Points beyond the 95th isopleth were considered forays and analyzed separately (see Foray Analysis section below). For several reasons, this analysis differs from the procedure used by Clifford et al. (2007) that was referenced (and used as a template) in the DSEIS analysis. The draft analysis used the 100% volume contour calculated by the Home Range Extension (HRE) to estimate the extent of the area used by the whole population. For the Gaussian kernel used by the HRE, however, the actual 100% volume contour is ill defined, extending to infinity in all directions. Accordingly, when a user asks for the 100% contour, the software actually calculates a contour containing close to 100% of the probability density, such as 99.9999%. The actual volume contour calculated when a user requests the 100% contour is undocumented, and has changed between versions of the HRE. The HRE version used in the DSEIS was 0.99, and it had a different internal limit than version 1.1, which was used for the analysis in the FSEIS. A second problem with the approach used in the draft is that home range analyses are not designed to model the distribution of relatively infrequent excursions from the CHHR. With Gaussian kernels in particular, the modeled probability of utilization falls off extremely rapidly with distance from the CHHR, drastically underestimating the probabilities of the occasional long distance forays that are characteristic of bighorn sheep.

Because of these problems, the analysis of bighorn sheep utilization of the landscape was split into two parts. The first part used herd home range analysis to define a core area of habitat usage inside of the 95th volume contour, referred to here as the CHHR. (The analysis for the DSEIS used the 50% to 90% volume contours to define this area of core habitat usage.) The second part was an analysis for the foray behaviors that bighorn sheep exhibit, especially young rams. The probabilities of movements to different distances from the CHHR were empirically derived, rather than being inappropriately extrapolated from the tails of Gaussian kernels used to define the CHHR. The analysis for the DSEIS used the 90–100% volume contour areas to analyze these foray behaviors. The approach used in the current analysis is more appropriate because movements within herd home ranges and foray movements beyond home ranges are two very different types of habitat usage behaviors that need to be handled by two different analyses. While this process differs from the analysis in Clifford et al. (2007), it does allow calculation of the annual rates of contact between bighorn sheep populations and domestic sheep allotments.

While recent telemetry data were available from most Hells Canyon herds and from the Main Salmon/South Fork Herd, telemetry data were not available for the two other herds and the two areas of concern in the Salmon River metapopulation. As a result, modelers used a different method to estimate the extent of CHHRs in the Upper Main Salmon and Big Creek herds, and the Lick Creek and Little Salmon areas of concern.

The CHHR of the Main Salmon/South Fork herd (Figure L-13) shows that most animal movements in the herd are confined to areas near the river at the bottom of the canyon. Because the river canyons of the Salmon River drainage are more similar to one another than to the areas occupied by herds in the Hells Canyon metapopulation, the distribution of the Main Salmon/South Fork Herd's CHHR was taken to be most likely representative of the distribution of the other herds in the Salmon River metapopulation. Accordingly, its average cross-canyon width was measured and determined to be 6.5 km. Next, each observation recorded in those four areas was surrounded by a circular buffer with a diameter of 6.5 km, and the area within these buffers was taken to be the best estimate of the herd's CHHR. Due to a lack of telemetry or other observational data in much of the Salmon River drainage, it is possible that some areas currently occupied by bighorn sheep are not mapped as CHHR by this method.

3.1.2 Foray Analysis

Like bighorn sheep elsewhere, Hells Canyon and Salmon River bighorn sheep—particularly rams—make occasional long-distance movements beyond their CHHRs. Singer et al. (2001) called these movements "forays" and defined them as any short-term movement of a radio-collared animal away from and back to its herd's home range. This life history trait can put bighorn sheep at risk of contact with domestic sheep, particularly when suitable habitats are well connected and overlap with domestic sheep use areas (Gross et al. 2000; Singer et al. 2000a), even when domestic sheep use is outside of the CHHR. The risk of contact between dispersing bighorn sheep and domestic sheep is related to the number of bighorn sheep in a herd, the proximity of domestic sheep use areas (allotments) to the bighorn sheep CHHR, the distribution of bighorn sheep source habitats across the landscape, and the frequency and distance of bighorn sheep forays outside of the CHHR.

The foray analysis covers the first three steps in the sequence of events needed for contact with an active allotment and a subsequent disease outbreak to occur, described at the beginning of the Risk of Contact Model section. To reiterate, those steps involved a bighorn sheep (1) leaving the

CHHR, (2) traveling far enough to reach the allotment, and (3) intersecting the allotment (i.e., rather than some other area at the same distance from the CHHR). The foray analysis was used to estimate the per-season (summer or winter) probability that an individual ram or ewe would go on a foray that intersected a given allotment. Separate analyses were carried out for rams and ewes due to the distinct movement patterns exhibited by the two sexes.

All estimates of movement behavior were formed by analyzing the same large telemetry dataset on bighorn sheep movements in Hells Canyon that was used to determine the CHHR of each herd. The dataset consisted of approximately 52,000 point locations from more than 400 animals in 13 herds collected between 1997 and 2008. In the Salmon River system, only 1.5 years of telemetry data for 30 individuals in one herd exist—the Main Salmon/South Fork herd. These data are useful for estimating the herd's CHHR, but are not sufficient to characterize the foray behavior of animals in that herd. As a result, modelers used the much more extensive data collected for the Hells Canyon herds to estimate the likely movement patterns of bighorn sheep in herds throughout the Payette National Forest.

The path taken by a bighorn sheep traveling outside its CHHR might intersect any part of an allotment. Therefore, the analysis began by calculating the probability of intersection in each of 35 "rings" or annuli of 1-km width located between 1 and 35 km from the CHHR boundary. That probability was broken down into three parts, as follows in Equation L-2:

$$\begin{aligned} P(\text{Intersect allotment}_{\text{Ring\_k}}) = {} & P(\text{Foray}) \times \\ & P(\text{Animal reaches ring}_{\text{k}} \mid \text{Foray}) \times \\ & P(\text{Intersect allotment} \mid \text{Animal reaches ring}_{\text{k}}) \end{aligned}$$

Where:

ring_k = the ring located k kilometers from the CHHR
P(Foray) = probability of a bighorn sheep leaving the core herd home range
P(Animal reaches ringk | Foray) = probability of a bighorn sheep traveling far enough to reach an allotment
P(Intersect allotment | Animal reaches ringk) = probability of a bighron sheep intersecting an allotment

Equation L-2. Propability of a bighorn sheep interescting each of the 1-kilometer annuli located between 1 and 35 kilometers from the core herd home range

The following three sections describe how the probabilities in steps 1–3 were estimated from telemetry data collected from the Hells Canyon herds.

3.1.2.1 Probability of a Foray Movement—P(Foray)

Most bighorn sheep, in most years, never move beyond the CHHR. Table L-5 summarizes the frequency of foray movements by rams and ewes in summer (May–October) and winter (November–April). Modelers calculated the probability of bighorn sheep–domestic sheep contact in summer and winter separately because characteristic movement patterns differ between the seasons (e.g., the rut occurs in November/December and produces relatively frequent and long distance exploratory forays by rams) and the allotments are only permitted to domestic sheep during spring and summer.

For the foray analysis, the key values in Table L-5 are the proportion of animal-years with at least one foray. (Animal-years refer to observations with a unique combination of both animal identification and year: If a single ram was observed in 4 different years and left the CHHR during 1 of those years, it would be said to have made a foray in 1 of 4 animal-years.) In any one summer, 14.1% of rams and 1.5% of ewes typically leave the CHHR at least once. Alternatively, a given ram has a 14.1% probability and a ewe has a 1.5% probability of making a foray. This percentage is the per-season probability of a foray, termed *P*(Foray) and used above in Equation L-2.

Table L-5. Summary of telemetry observations made outside of the core herd home ranges

	Ewes		**Rams**	
Summer—May to October	**Percent of observations (%)**	**Number out of total observations**	**Percent of observations (%)**	**Number out of total observations**
Animals located beyond CHHR at least once during period of observation	**6.50**	14/215	**28.80**	30/104
Animal-years with at least one foray	**1.50**	15/985	**14.10**	44/311
Telemetry points outside of CHHR	**0.20**	29/17,258	**4.40**	160/3,674
Winter—November to April				
Animals located beyond CHHR at least once during period of observation	**12.9**	28/217	**34.9**	38/109
Animal-years with at least one foray	**5.6**	60/1,062	**17.8**	68/380
Telemetry points outside of CHHR	**0.8**	109/12,941	**3.7**	156/4,200

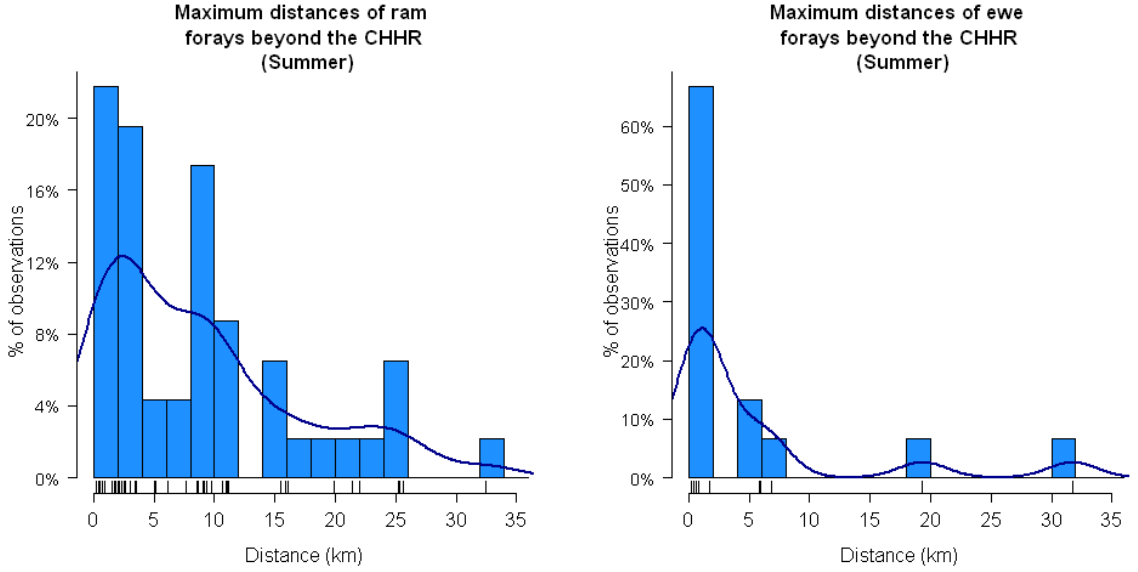
In some of the Hells Canyon herds (Big Canyon, McGraw, Muir, Myers, and Quartz Creek), telemetry data were collected the first year after the initial release. One concern in extrapolating from data collected in Hells Canyon herds to foray behavior in the Salmon River herds is that recently translocated animals may have a higher propensity to move outside of their mapped CHHR. If so, their behavior may be inappropriate as a model for movements made by animals in the endemic populations of the Salmon River metapopulation. Rams from the Big Canyon and McGraw herds did show relatively high numbers of foray movements (with forays occurring in 12 of 24, and 5 of 11 animal years, respectively), while the Myers and Quartz Creek herds had lower rates of foray movements (2 of 14, and 1 of 13 animals). Among "resident herds" (i.e., herds that had been resident in Hells Canyon for a decade or more before telemetry observation began), the rate of forays ranged from 1 out of 46 animal-years (Redbird Herd) to 12 of 49 animal years (Wenaha Herd). Four of the seven resident herds (Imnaha, Mountain View, Sheep Mountain, and Wenaha herds) exhibited a rate of foray movements greater than the value of 14.1% that was used in the foray analysis, which does not appear to be a gross overestimate of the actual value. On balance, a decision was made to include telemetry data from all of the herds.

3.1.2.2 Distance from Core Herd Home Range Travelled on Typical Forays—*P*(Animal reaches ring$_k$ | Foray)

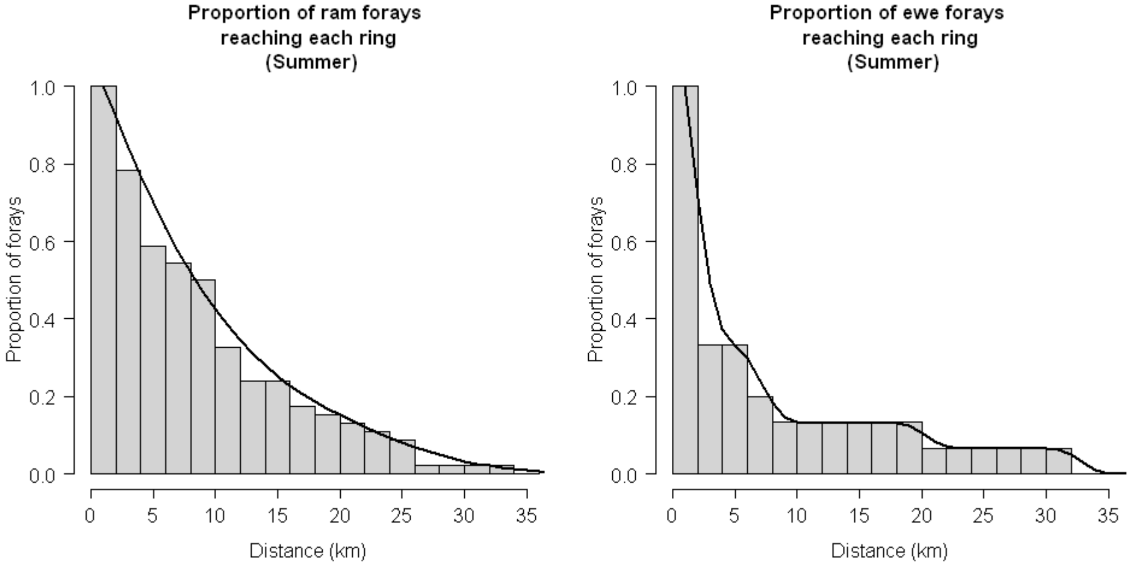
Many animals—particularly ewes—may not travel far, even if they are observed outside of the CHHR. The probability that a bighorn sheep on a foray will reach an allotment decreases as distance increases. To characterize that decreasing probability, modelers first extracted from each foray the maximum distance from the CHHR at which a ram or ewe was observed (Figures L-16a and L-16b). One bighorn sheep (a ram) was observed during the summer nearly 35 km from its CHHR, so the distributions extend out to that distance.

An animal located 25 km from the CHHR has crossed each ring between itself and the CHHR. Likewise, 100% of the animals that make a foray intersect at least the first ring around the CHHR. More generally, the proportion of animals whose forays intersect each ring is equal to the proportion known to have reached it or one of the rings beyond it. That distribution is shown in Figure L-17a, along with a smooth curve fitted to it. The figure shows that fully half of the rams who leave the CHHR travel at least 10 km from it; nearly a quarter get to 16 km, but just one ram has been observed (in summer) more than 26 km away. Modelers used the distributions in Figures L-17a and L-17b to calculate the probability that a ram or ewe on a foray will reach any given ring surrounding its CHHR, *P*(Animal reaches ring$_k$ | Foray) in Equation L-2.

Figures L-16a and L-16b display the observed maximum distances of ram and ewe forays outside of CHHRs (95% isopleth) and Figures L-17a and L-17b display the proportion of rams and ewes with forays reaching each of the rings between 0 and 35 km from CHHR areas.



Figures L-16a and L-16b. Maximum distances of ram and ewe summer forays beyond the core herd home range.



Figures L-17a and L-17b. Proportion of ram and ewe summer forays that reach each ring

The foray analysis most likely underestimates the true frequency of longer-distance forays because the vast majority of the telemetry data is from standard VHF (very-high frequency) collars rather than from GPS collars, which collect and store or transmit data from everywhere an animal travels. With VHF collars, locations are determined by triangulation from a plane or boat travelling a route every few days or weeks through the areas in which the bighorn sheep of a herd are usually seen. The farther a bighorn sheep has travelled from its CHHR, the farther it is likely to be from the observers, and the less likely it is to be detected. There are in fact several examples of telemetry data where rams last observed on a foray have “disappeared” for a couple of months before reappearing, likely from a journey that carried them beyond the range of detection of the survey.

For bighorn sheep moving through forested areas, detection may also be hampered by line-of-sight and signal bounce issues. Finally, even when an animal on foray is detected in every survey, the large interval between observations means that it is unlikely to be observed at the furthest extent of its foray. The extent to which these forms of sampling bias underestimate the frequency of long-distance movements in the foray analysis is unknown.

Despite these biases, both the observed frequency and distances of foray movements by Hells Canyon bighorn sheep are consistent with other reports in literature. Singer et al. (2001) calculated annual foray rates of bighorn sheep in 10 published studies. In those herds, the annual number of forays per radio-collared animal of either sex ranged from 0 to 0.23 (mean 0.10, standard deviation 0.09), comparable to 14% of rams and 1.5% of ewes making summer forays from herds in the Hells Canyon metapopulation.

In southwestern Alberta, Festa-Bianchet (1986) relocated rams as far as 48 km from the site of their capture. A recent 17-month study of three bighorn herds in Montana, (DeCesare et al. 2006) found relatively long (19- to 33-km) movements by four of five radiocollared males. Finally, Singer et al. (2000b) followed 31 translocated populations of bighorn, and documented numerous colonizations of nearby patches of habitat. In that study, the probability of colonization (75%)

was highest for patches located 12.3 km from a bighorn sheep population, indicating that such movements occur with relatively high frequency. This parallels our finding that nearly 25% of forays by Hells Canyon bighorn sheep reach a distance of at least 15 km from the CHHR.

3.1.2.3 Habitat Selection within a Ring—*P*(Intersect allotment | Animal reaches ring$_k$)

Given that an animal has reached a ring, the probability that an animal will be in an allotment is proportional to the size of the allotment relative to the ring and the quality of the habitat in the allotment relative to that in the ring. Calculating the size of the allotment relative to the ring is simple, but determining the quality of the habitat in the allotment relative to that in the ring requires knowing the habitat preference of bighorn sheep. Modelers represented that preference by calculating a resource selection function, defined as a function that is proportional to the probability of its use by an organism (Manley et al. 1993; Boyce et al. 2002).

Based on the source habitat model, all areas within 35 km of the CHHRs were assigned to one of three habitat classes—source habitat, connectivity area, and non-habitat. Source habitats are areas fitting the criteria described in the Source Habitat Model section above. Connectivity areas do not meet those criteria, but are either located within 350 m of source habitat or between two mapped patches of source habitat that are separated by 1,050 m or less. Areas of non-habitat do not meet those criteria and are located more than 350 m from source habitat. Connectivity areas were distinguished from non-habitat because even when bighorn sheep are found outside of areas mapped as source habitat, they are usually not far from it. Of the 3,177 observations of bighorn sheep located outside of source habitat, all but 80 have been within 350 m of source habitat.

Next, the relative preference of bighorn sheep for these three classes of habitat was calculated using a resource selection function (Manley et al. 1993, Boyce et al. 2002).Modelers constructed the resource selection function using a use/availability approach and expressed the relative preference for connectivity areas and non-habitat relative to the preference for source habitat using Equation L-3:

$$\mathrm{Pref}_{\mathrm{h}} = \frac{\mathrm{Use}_{\mathrm{h}} / \mathrm{Area}_{\mathrm{h}}}{\mathrm{Use}_{\mathrm{source\_hab}} / \mathrm{Area}_{\mathrm{source\_hab}}}$$

Where:

Use_h = the number of telemetry points found in habitat type h;
$Area_h$ = the area of habitat type h available to the bighorn sheep; and
h = one of source habitat, connective area, or non-habitat.

Equation L-3. Relative preference for connectivity areas and non-habitat relative to the preference for source habitat

The resource selection function yields high values for habitat classes with many observations of bighorn sheep relative to their area. If the animals in a herd have equal areas of Habitat A and Habitat B available, but spend 90% of their time in Habitat A, their preference for Habitat A would be 9 times their preference for Habitat B.

To investigate whether habitat preferences differ between animals within the CHHR and those on forays outside of it, modelers calculated habitat preferences exhibited in three different areas:

within the CHHR, in the rings between 1 and 10 km from the CHHR, and in the rings between 11 and 35 km from the CHHR (Figure L-18). The results indicate that while on forays (i.e., in rings 1–35) bighorn sheep are more likely to spend time outside of mapped source habitat than they are while within the CHHR.

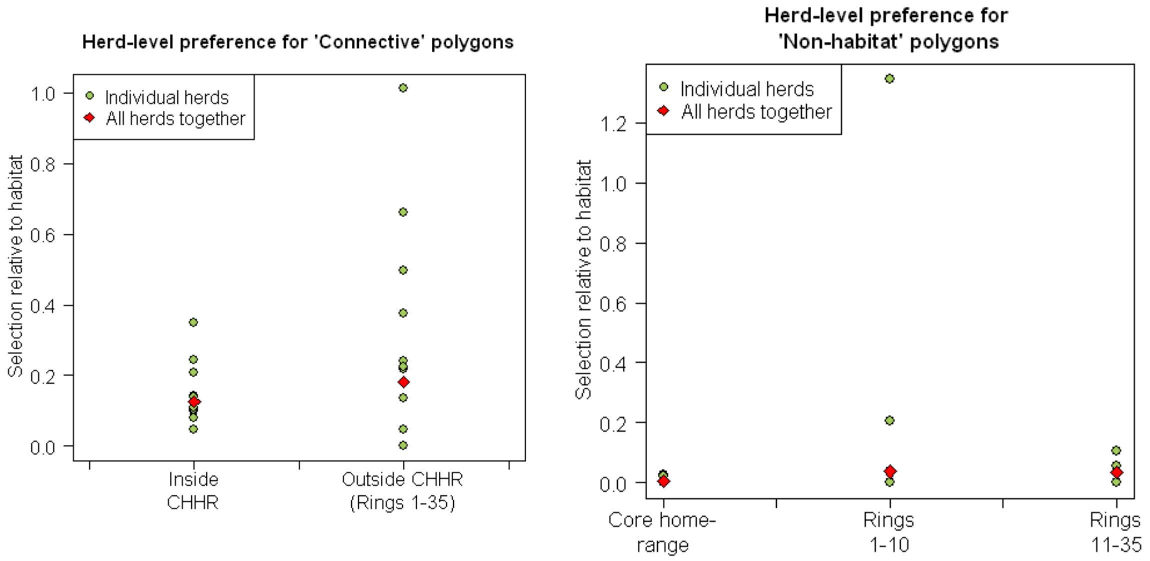


Figure L-18. Observed herd-level preferences for connectivity area and non-habitat, relative to source habitat.

Based on the findings, modelers used the habitat selection preferences observed for animals in rings 1–35 to model the behavior of bighorn sheep in the foray analysis. While on forays, bighorn sheep in the Hells Canyon herds prefer source habitat to connectivity areas and prefer both source habitat and connectivity areas to non-habitat. Relative to a preference of 1.00 for source habitat, bighorn sheep showed a preference of 0.177 for connectivity areas and a preference of 0.029 for non-habitat. In other words, within the 35-km-wide ring surrounding a CHHR, bighorn sheep were 5.6 times more likely to be found in a given square-kilometer of source habitat than in a square-kilometer of connectivity area, and 35 times more likely to be found in source habitat than in non-habitat.

Next, modelers used the preferences and distribution of habitat within each ring surrounding a CHHR to calculate the probability that a bighorn sheep that reaches a ring would intersect the ring in an allotment using Equation L-4:

$$P(\text{Intersect allotment}_{\text{Ring\_k}} \mid \text{Animal reaches ring k}) = \frac{\sum_{h} (\text{Area}_{h} \text{ in allotments w/in ring k}) \times (\text{Pref}_{h})}{\sum_{h} (\text{Area}_{h} \text{ in ring k}) \times (\text{Pref}_{h})}$$

Where:

Ring_k = the ring k kilometers from the CHHR
Area_h = the area of habitat type_h in that ring

Equation L-4. Probability that a bighorn sheep that reaches a ring will intersect an allotment in that ring.

Equation L-4 implies that in a ring of homogeneous habitat, the probability of intersecting an allotment is simply proportional to the allotment's size. If, on the other hand, the habitat composition of the allotment is less (or more) favorable to bighorns than the composition of the ring as a whole, bighorns will be correspondingly less (or more) likely to intersect the allotment.

Finally, modelers used Equation L-4 to complete the calculation of Equation L-2 for each of the 35 rings surrounding the CHHR. Equation L-2 expresses the annual probability that a bighorn sheep will go on a foray, reach a ring at a given distance from the CHHR, and intersect that ring within an active allotment.

Going from the probability of intersecting with individual rings to the overall probability of intersection is complicated by the fact that ring-level probabilities are not independent (i.e., a bighorn whose foray intersects a large allotment in ring 17 is also likely to have intersected parts of the allotment lying in rings 16 or 15 on the same foray). As a result, the ring level probabilities cannot simply be added together to determine the overall risk. Although the approach is somewhat conservative (underestimating the probability of intersection), the modelers took the overall probability of intersection with an allotment to be the maximum value found for any one of the rings as shown in Equation L-5:

$$P(\mathrm{Intersect\ allotment}) = \max_{\mathrm{k}} P(\mathrm{Intersect\ allotment}_{\mathrm{Ring\_k}})$$

Equation L-5. Probability of a bighorn sheep on a foray intersecting an allotment

A sample foray probability map is shown in Figure L-19.

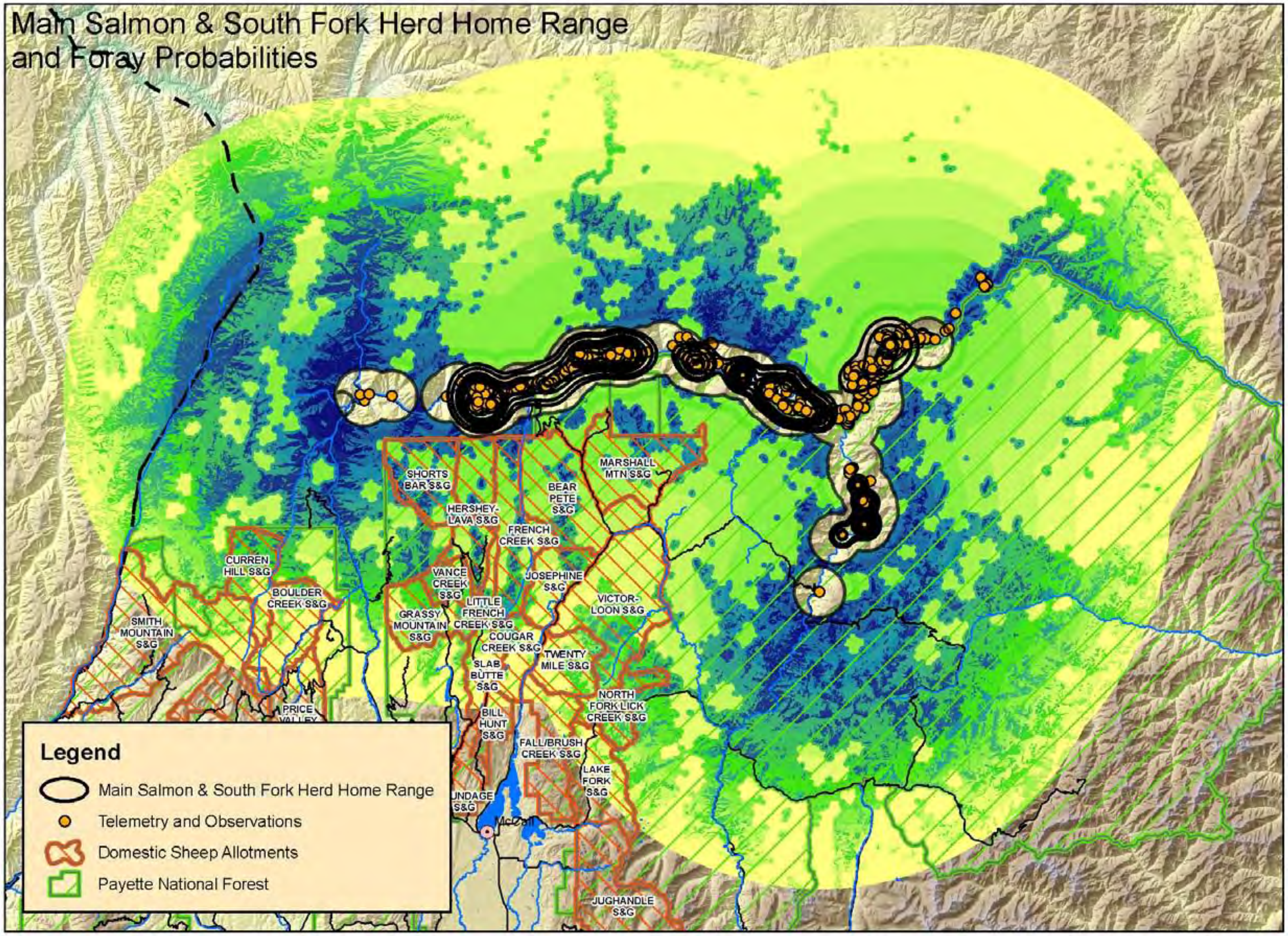


Figure L-19. Map foray probability for the Main Salmon/South Fork Herd

3.1.3 Probability of Contact with another Bighorn Herd

Following infection of one herd in a metapopulation of bighorn sheep, respiratory disease has often been observed to spread between herds (Onderka and Wishart 1984; Cassirer et al. 1996; George et al. 2008). In the disease model, the probability of disease transmission from contact with infected bighorn sheep herds was calculated in much the same way as the probability of disease transmission from domestic sheep. For pairs of herds with overlapping home ranges, the probability of cohabitation was set at 100%; for all other herd pairs, the annual probability of cohabitation was given by the probability of a foray occurring from one herd to the other as described above. Given that cohabitation occurred, the probability of disease transmission and a subsequent outbreak of disease was set at 75%.

4.0 DISEASE MODEL

Modeling population dynamics of large herbivores at the individual level requires estimating numerous parameters, from adult and juvenile survival rates to age at sexual maturity, fecundity, and lamb survival (Gaillard et al. 2000). In addition, the average values for each of those life-history parameters may be modified by interacting impacts of density dependence, weather, forage availability, and predation. Properly estimating these parameters would require extensive age- and class-specific population data, ideally from the populations being modeled.

Accurate individual-level modeling of the impacts of disease events is even more difficult since the dynamics of respiratory disease in the wild are only partly known. An individual-based model would require understanding many factors, such as the incubation period and active infection durations, probability and rate of recovery from disease, rate of effective contact between individuals within the herd, and possible role of persistently infected individuals in harboring and spreading the disease. Variations in the resistance to disease of individual bighorn sheep and in the virulence of the disease-causing organisms themselves can also affect population dynamics.

Rather than attempting to create a complicated individual-based model that incorporated all of the parameters above, researchers built a population dynamics model using a “top-down” approach in which population size was the primary state variable. A simpler model may appear to have limited accuracy or realism but actually has several advantages for estimating the variables of greatest interest—projections of population size, volatility, and persistence. First, a simpler model requires estimating fewer and more easily estimated parameters. Population size is easier to estimate than individual mortality and fecundity rates that affect it. Likewise, the population-level impacts of respiratory disease outbreaks are better understood than the details of bacterial shedding, within-herd effective contact rates, and individual variation in disease susceptibility that determine the course of individual epidemics. A second important advantage of “top-down” models is that they have fewer moving and interacting parts and so are more interpretable, transparent, and accessible to scrutiny.

4.1 Model Organization

Researchers constructed a disease model with three components. The first component modeled the probability that an animal that was determined by the foray analysis to have reached an occupied allotment would subsequently contract respiratory disease and initiate an outbreak in its home herd. The second component modeled population growth in a healthy herd. Annual population growth in the disease model depends on the current disease status of the herd (disease-free or infected), current population size, and an estimate of the maximum sustainable herd size for each herd. In the absence of disease, herd numbers increase (unless they have fewer than 30 individuals). The third component modeled the magnitude and duration of impacts caused by an outbreak of respiratory disease in a bighorn herd. In the first year of a disease outbreak, herds suffer an all-age die-off, followed by a variable number of years of depressed lamb recruitment. Eventually, herds that survive are considered to be fully recovered from (although still susceptible to further outbreaks of) the disease outbreak.

Figures al-20 and L-21 provide an overview of the disease model structure. Figure L-30 illustrates the first step of the annual cycle in which the disease status of each herd is determined. Figure L-21 illustrates the consequences of current herd size and disease status on next year's population size.

Figure L-20. Disease transmission and recovery sub-model

1) Does the herd harbor an ongoing infection?

- **YES →** go to the Population Dynamics Sub-Model
- **NO →** go to the next step

2) Does the herd contract respiratory disease this year? (Use the risk model to determine the probability of disease transmission into the herd from contact with either domestic sheep or infected bighorn sheep.)

- **YES →** determine the number of years that the herd will suffer from depressed recruitment, and go to the Population Dynamics Sub-model
- **NO →** go to the Population Dynamics Sub-model

Figure L-21. Population dynamics sub-model

1) Is the population size less than the minimum viable population size (30 animals)?

- **YES →** the population declines by 16 percent
- **NO →** go to the next step

2) Is the population free of respiratory disease?

- **YES →** the population grows by an amount determined by the logistic growth equation
- **NO →** go to the next step

3) Was the population just infected this year?

- **YES →** the population experiences an all-age die-off
- **NO →** the population experiences increased mortality of juvenile bighorns

4.1.1 Probability of Effective Contact and Subsequent Herd-level Die-off Given Co-habitation of Bighorn Sheep and Domestic Sheep in an Allotment

Although organisms that cause respiratory disease may be endemic in some bighorn sheep herds (Hobbs and Miller 1992), the current model is designed to assess the impact of disease transmitted from domestic sheep, so all outbreaks ultimately originate from contact with domestic sheep. The foray analysis estimates the probability that a bighorn sheep will reach an allotment occupied by domestic sheep (cohabitation), but it does not address the probability of the additional steps needed for an outbreak to occur. Once a bighorn sheep reaches an occupied allotment, the bighorn sheep must (4) come into contact with domestic sheep in the allotment and (5) contract the disease from the domestic sheep. Finally, for an outbreak to affect the animal's home herd, the infected bighorn sheep must (6) make its way back to the CHHR and (7) transmit the disease to other members of the herd (steps 4 through 7 from the Risk of Contact section).

Assumptions governing the probability that a bighorn sheep that reaches an occupied allotment will contract disease from the domestic sheep are problematic. For a similar model applied to populations of endangered Sierra Nevada bighorn sheep (Clifford et al. 2009), researchers assumed that any cohabitation with domestic sheep was equivalent to contact between the two species, citing the attraction of bighorn sheep (particularly rams) to domestic sheep and past observations of stray domestic sheep associating with bighorn sheep. They estimated that the subsequent probability of disease transmission (effective contact) given such physical contact was between 50% and 100%, based on numerous pen studies that have shown that nearly 100% of bighorn sheep co-housed with apparently healthy domestic sheep develop respiratory disease (e.g., Onderka and Wishart 1988, Foreyt 1989, Foreyt 1990, Lawrence et al. Forthcoming). Less information is available about the probability that a diseased animal will return to its CHHR and initiate an outbreak.

Together, the four steps described above determine the overall probability of an outbreak happening given that an individual bighorn sheep, whose movements were modeled by the foray analysis, reaches an open allotment. Because so much uncertainty surrounding this parameter exists, and essentially no research exists that would allow its estimation, the disease model was run with a range of probabilities of effective contact (a contact resulting in a disease transmission) and a subsequent herd-level outbreak, given cohabitation of a bighorn sheep and domestic sheep in an open allotment. The values used were 5%, 10%, 25%, 50%, 75%, and 100%.

Each individual in a herd has the potential to make a foray that will bring disease back from a contact with domestic sheep. The annual probability that any individual animal will make a foray that results in disease transmission is the product of steps 1–3 (given in Equation L-5) and the probabilities of steps 4–7 (described above). Expressed as an equation (Equation L-6), the composite probability is as follows:

$$P(\text{Outbreak})_{\text{individual}} = P(\text{Outbreak} \mid \text{Intersect allotment}) \bullet P(\text{Intersect allotment})$$

Equation L-6. Probability that a bighorn sheep on a foray will lead to an outbreak of disease in its herd

Equation L-6 is used to calculate two individual-level probabilities for each herd—one for ewes ($P(\text{Outbreak})_{\text{ewe}}$) and one for rams ($P(\text{Outbreak})_{\text{ram}}$). The annual probability that a herd will experience a die-off due to contact by one of its members with sheep in an active allotment depends on these two probabilities and also on the number of ewes and rams in the herd. The herd-level probability of contact is given by Equation L-7:

$$P(\text{Outbreak})_{\text{herd}} = 1 - \left(1 - P(\text{Outbreak})_{\text{ewe}})^{\#\text{ewes}}\right) \bullet \left(1 - P(\text{Outbreak})_{\text{ram}})^{\#\text{rams}}\right)$$

Equation L-7. The annual probability that a herd will experience an outbreak due to contact with and allotment

4.1.2 Population Growth in a Healthy Herd: Density Dependence and the Logistic Growth Model

Bighorn sheep populations, like those of other large herbivores, are subject to density-dependent population growth regulation (Monello et al. 2001; Bonenfant et al. 2009). Even in the absence of disease, a population of bighorn sheep will not grow without bound; as the number of animals in an area increases, the rate of further growth eventually begins to slow. The dynamics by which that slowing occurs can be complicated and are not completely understood. Jorgenson et al. (1997) and Portier et al. (1998) analyzed a long-term mark–recapture study of two populations of Rocky Mountain bighorn sheep in Alberta, Canada, for evidence of density dependence. They found the main demographic response to large population size was a decrease in lamb survivorship. Yearling ewes also suffered some mortality increases when populations were high. Other researchers have also detected a decrease in the rate of recruitment with increasing density (with relatively little response in adult survival) (McCarty and Miller 1998), a pattern that is characteristic of many large ungulates (Gaillard et al. 1998, Bonenfant et al. 2009).

To incorporate density dependence into the disease model, researchers used the logistic equation, a common ecological model of population growth (Gotelli 2008). In the logistic growth model, the maximum per capita growth rate (*r*, with units of new individuals per individual per year) is only achieved when the population size is quite small. As the population increases toward its maximum sustainable size (*K*), the number of surviving offspring per female steadily decreases and the rate of population growth slows. The logistic growth model is defined in Equation L-8:

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right)$$

Where:

dN/dt = yearly change in population size
N = current herd size
r = maximum herd growth rate
K = maximum sustainable population.

Equation L-8. Logistic growth model for the rate of population increase in a healthy herd

K is usually known as the "carrying capacity;" in this model it is referred to as the "interim herd level" (IHL) to emphasize that it should not be interpreted as either a goal or a limit to the number of bighorn sheep that might be supported by any given herd.

The following three sections describe how modelers estimated the values of *N*, *r*, and *K* that were used by the disease model.

4.1.2.1 Estimating *N*—Current Herd Size

Population estimates for the 15 herds (Table L-6) were taken from survey data collected by the IDFG, ODFG, Washington Department of Fish and Wildlife (WDFW), and SRBSP (administered by the Nez Perce Tribe) (Table L-6). For each herd, we used data from the most recent survey available. Estimates of current herd sizes ranged from 10 to 210 and totaled 1,148 for all 15 herds.

One "area of concern," Little Salmon, was not treated as a fully independent population in our model. The Little Salmon has not been regularly surveyed for the presence of bighorn sheep, so a population estimate of four animals in the Little Salmon drainage was made on the basis of incidental observations of bighorn sheep within the last 3 years (Figure L-22 and Table L-6). In the disease model, the Little Salmon area of concern is linked to and effectively treated as a satellite population of the Main Salmon/South Fork Herd. Its CHHR extends 3.25 km around each known observation, and like any other bighorn sheep in the model, each animal in the Little Salmon has a fixed probability of making a foray in any given year. If an outbreak occurs in the Little Salmon, it is spread to the Main Salmon/South Fork Herd, and vice versa. Finally, in the model, the population size of the Little Salmon is tied to that of the Main Salmon/South Fork Herd, with the number in the Little Salmon staying in a constant proportion to the number in the Main Salmon/South Fork Herd. One consequence of this is that when the population of the Main Salmon/South Fork Herd is extirpated in the model, so are the animals in the Little Salmon area of concern.

The proportion of rams and ewes in each herd was determined by analyzing demographic data collected by the Oregon Department of Fish and Wildlife and the Washington Department of Fish and Wildlife. In 200 herd-years of data collected from six herds in Oregon (Muir, Sheep Mountain, Wenaha, Fox Creek, Imnaha, and Lostine), an average of 35.4% of adults were rams. In 141 herd-years of data collected from five herds in Washington (Asotin, Black Butte, Mountain View, Tucannon, and Wenaha), an average of 35.2% of adult animals were rams. In both states, the ram-to-ewe ratio varied from year to year, but the average ratios were consistent among herds. The values calculated here are consistent with those reported by in the Hells Canyon Bighorn Sheep Restoration Plan (Hells Canyon Initiative, 1997), which found an average ram:ewe ratio of 52:100 (i.e. 34% rams) in twelve herds. Accordingly, in both the disease and foray models, the percentage of rams among adult animals was set at 35%.

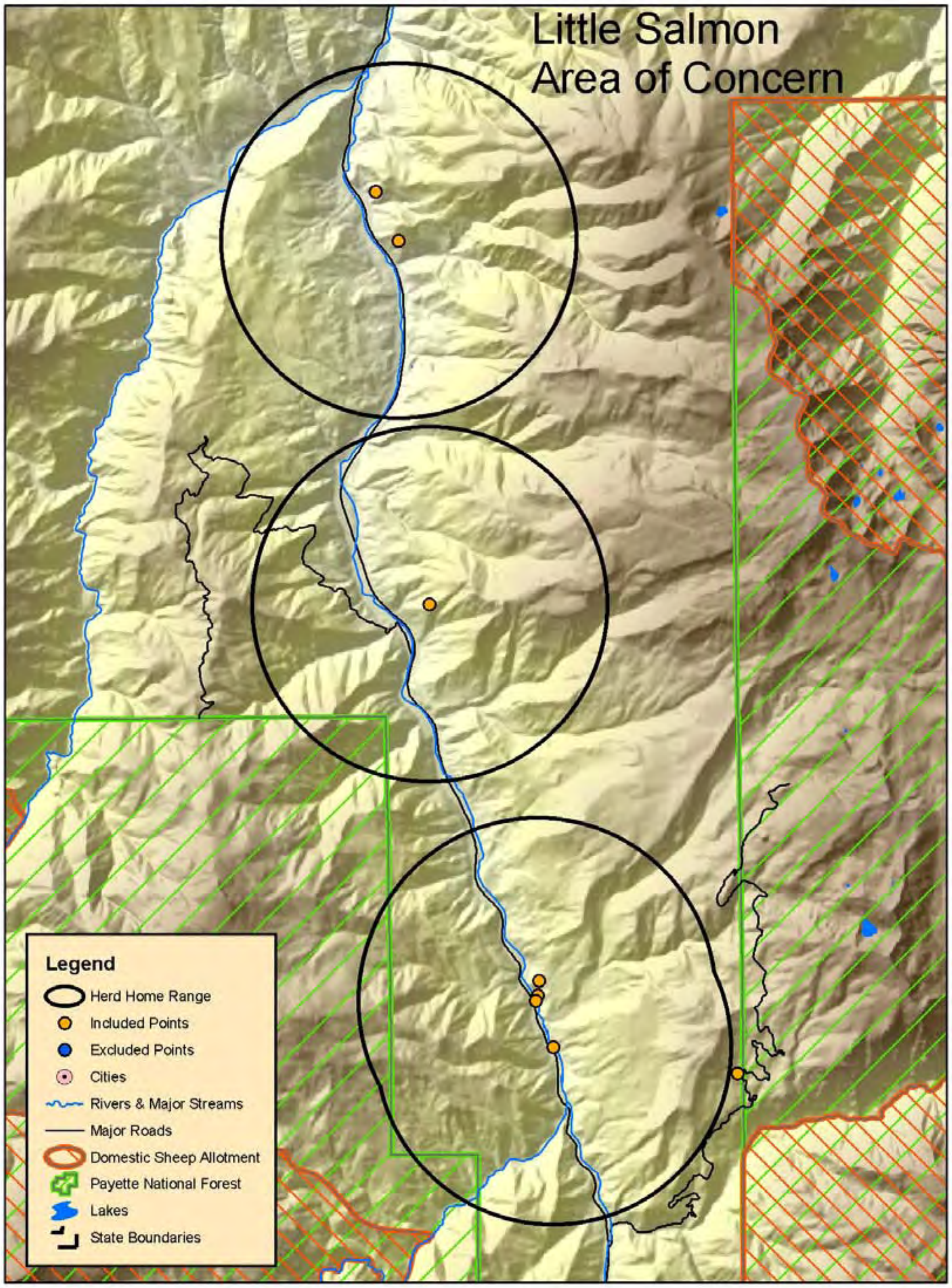


Figure L-22. Little Salmon Area of Concern

Table L-6. Population estimates and interim herd levels (IHLs) for 15 Herds and 1 area of concern from survey data collected by the Idaho Department of Fish and Game (IDFG), Oregon Department of Fish and Game (ODFG), Washington Department of Fish and Wildlife (WDFW), and Salmon River Bighorn Sheep Project (SRBSP)

Herd	Estimated Population (*N*)	Date of Estimate	Data Source	IHL (*K*)
Hells Canyon				
Asotin	84	2009	WDFW	172
Big Canyon	20	2008	IDFG	96
Black Butte	47	2009	WDFW	461
Imnaha	135	2008	ODFW	407
Lostine	65	2008	ODFW	110
Mountain View	13	2009	WDFW	178
Muir Creek	30	2008	ODFW	86
Myers Creek	10	2008	IDFG	34
Redbird	115	2008	IDFG	322
Sheep Mountain	11	2008	ODFW	187
Upper Hells Canyon	45	2009	IDFG	279
Wenaha	90	2008	ODFW	279
Salmon River				
Big Creek	186	2006	IDFG	479
Main Salmon/South Fork	210	2009	SRBSP	413
Upper Salmon	87	2006–07	IDFG	975
Area of Concern				
Little Salmon	4	2007–09	Various	NA

4.1.2.2 Estimating *r*—Maximum Herd Growth Rate

Estimates of the maximum growth rate *r* (also known as the intrinsic or exponential growth rate) were taken from published literature. McCarty and Miller (1998) estimated *r* for 16 translocated populations of Rocky Mountain bighorn sheep in Colorado. They based their estimates on herd growth rates observed during the first few years after successful translocations, applying a correction to account for the skewed sex ratio of the translocated animals. Maximum growth rates for the 16 herds ranged between 0.051 and 0.26 (i.e., 5–26% annual increase in population size). In the disease model, a maximum growth rate for each herd was sampled from a normal distribution (mean = 0.136, standard deviation = 0.057) fitted to the estimates of McCarty and Miller (1998).

4.1.2.3 Estimating *K*—Interim Herd Level

Although historical reports indicate that bighorn sheep were once very abundant in Hells Canyon (Bailey 1936), we do not have accurate estimates of the current maximum potential population sizes of the herds found on or near the Payette National Forest. Even when studies are carried out to measure the actual carrying capacity of a population, directly measuring it in the field can be difficult or even impossible (Coulson et al. 2008); in any case, such studies have not been conducted for bighorn sheep in our area.

However, some form of density dependence needs to be introduced to simulate likely future herd dynamics, which means some estimate of *K* needed to be included in the logistic growth model. Modelers named *K* the IHL to emphasize that the number should not be construed as a Forest Service management goal or a strong estimate of actual carrying capacity of the herd home ranges.

In the absence of better information, modelers estimated IHL on the past maximum number of animals observed for each herd. For the Salmon River herds, IHLs were estimated to be 175% of the highest population estimate from the past 30 years. For Hells Canyon herds, IHLs were estimated to be 175% of the highest population estimate from the past 40 years.

4.1.2.4 Nonviable herd numbers

The minimum population size, referred to as the nonviable herd number (NVN), is the threshold below which a population will not continue to grow at a disease-free rate and will, in fact, decline. The model used 30 individuals as the NVN for all herds except Big Canyon, Muir Creek, and Myers Creek—because these herds overlap, they were treated as a single herd with a combined NVN of 30.

Theory and observation have shown that extinction becomes more likely for populations that fall below some threshold of small size (Traill et al. 2010). Small populations become increasingly vulnerable to fluctuations driven by environmental and demographic stochasticity (Melbourne and Hastings 2008), single catastrophic events, and the deleterious effects of inbreeding (O'Grady et al. 2006). In bighorn sheep there is also some evidence that individuals in small groups (less than 10 individuals) need to spend more time on the look-out for predators, and as a consequence may forage less efficiently (Risenhoover and Bailey 1985; Berger and Cunningham 1988) than larger groups.

The existence of clear thresholds or minimum viable population sizes in bighorn sheep has been a matter of contention. Berger (Berger 1990) analyzed 122 bighorn sheep populations in California, Colorado, Nevada, and New Mexico and found that 100% of populations that fell below 50 animals went extinct within 50 years. Subsequently, other biologists (Krausman et al. 1993, Wehausen 1999) analyzed additional populations and noted that extinction of herds dropping below 50 animals, while quite likely, is not inevitable. Berger (Berger 1999) and (McCarty and Miller 1998) argued that, thanks to modern management recommendations and practices (including separation of bighorn and domestic sheep), small populations are now more likely to survive than they were in the past.

Singer et al. (2000a) examined 100 translocations of bighorn sheep and found only one population that fell below 30 animals ever later grew above that number. Based on that finding, Singer et al. (2001) defined quasi-extirpation as a decline of a bighorn sheep population below 30 animals, a size from which they deemed population recovery unlikely.

Other researchers have proposed different minimum sizes necessary for persistence. Based on genetic considerations, Singer and Gudorf (1999) recommended against attempting reintroduction to sites capable of supporting fewer than 100–125 animals, for which they argued that the probability of persistence was low. In their population model, Clifford et al. (2009) defined quasi-extinction as ensuing when the number of ewes in a population dropped below five. They cited the high likelihood that such small populations would be driven to extinction by a single stochastic event, as well as evidence mentioned above, that small groups forage less efficiently (Berger 1978).

While there is no single threshold below which extinction of a herd is absolutely inevitable, it seems clear that as populations of bighorn sheep decline below 50 animals, they become increasingly vulnerable to extinction. In the present disease model, following Singer et al. (2001), a minimum population size, referred to as the NVN was set at 30 animals. The NVN is the threshold below which a population will not continue to grow at a disease-free rate and will, in fact, decline to eventual extinction. Because, in reality, extinction of herds with fewer than 30 animals is only likely, rather than certain, herds in the model that drop below 30 animals are referred to in this document as having suffered "quasi-extirpation" or "quasi-extinction". The NVN of 30 individuals applied to all herds except Big Canyon, Muir Creek, and Myers Creek—because these herds overlap, they were treated as a single herd with a combined NVN of 30.

4.1.2.5 Population impacts of disease

Disease-caused declines in bighorn sheep populations typically consist of an initial all-age die-off event followed by several years of low lamb survival. Ewes that survive the initial die-off may give birth, but after a period of weeks to months, their lambs develop pneumonia and die. The disease model includes both of these impacts of disease outbreaks; in the first year, infected herds suffer an all-age die-off followed by several years of slower decline due to elevated lamb mortality. The following sections describe how the population impacts of both types of disease-related mortality were modeled.

4.1.2.6 Initial All-age Die-off

Disease outbreak impact was measured as the product of the herd size and proportion of impact. This parameter was estimated using data from documented outbreaks in the Hells Canyon area. In 1983, an outbreak of pneumonia killed 60% of the animals in the Granite–Three Creeks area of Idaho (HCBSRC 1997). An outbreak of pneumonia in the Lostine Herd in 1986–87 killed 66% of the herd (Coggins 1988). A 1995–96 outbreak affected several herds, with herd-level mortality amounting to 33%, 50%, 65%, 69%, and 75% (Cassirer et al. 1996). The lowest mortality rate (33%) occurred in the smallest herd (Upper Joseph Creek, with 30 animals); the highest mortality rate (75%) occurred in the largest herd (Black Butte, with 220 animals). In 1999, a disease outbreak resulted in the death of 59% of the McGraw Herd and 53% of the Sheep Mountain Herd in the first year, followed by subsequent declines in both herds and eventual extirpation of the McGraw Herd. In the model, herd-level mortality during the first year of an outbreak was sampled from the distribution of values observed in the previous Hells Canyon outbreaks described above, with an equal probability of mortality of 33%, 50%, 53%, 55%, 65%, 66%, 69%, and 75%.

4.1.2.7 Chronic Lamb Mortality

The significant impact of the all-age die-off that occurs during the first year of an epidemic is compounded by pneumonia and septicemia in young lambs that frequently suppresses recruitment for several additional years (Cassirer et al. 2001, Miller 2001, George et al. 2008). The duration of this chronic mortality of lambs is variable, but in almost all cases lasts for at least 2 years[2]. In some cases, poor lamb recruitment has continued for as long as 8 years (Enk et al. 2001) or 9 years (George et al. 2008) post-outbreak. Several Hells Canyon herds have had poor lamb recruitment for 6 or more years (Wenaha, Muir Creek, Upper Hells Canyon, and Sheep Mountain); in the Sheep Mountain Herd, lamb survival has still not recovered 10 years after a 1999 disease outbreak. In the disease model, herds affected by disease suffer poor lamb recruitment for between 2 and 10 years following the all-age die-off with the duration randomly selected.

The adult survival rate for healthy populations of bighorn sheep (i.e., the percentage of adults surviving from one year to the next) is around 90% (Jorgenson et al. 1997). Therefore, in the complete absence of recruitment, populations will decline an average of 10% per year. In herds with depressed recruitment, the percentage of ewes with surviving lambs ranges from 0% to 25%, which translates to an annual population change of between –10% and 2.5%. Therefore, for modeled herds suffering from disease-related lamb mortality, the annual population change was randomly selected from between –10% and 2.5%.

4.1.2.8 Extended Infectious Duration

When a simulated herd becomes infected, animals in the herd remain infectious for a variable length of time, generally more than 1 year. The duration of infectiousness ranges from 1 to 4 years and follows a uniform distribution.

4.1.3 Model Implementation

The disease model described above and in Figures L-20 and L-21 was implemented using @RISK, a commercially available Excel spreadsheet add-in (Palisade Corporation 2009). The @RISK add-in permits the model to include components of uncertainty and variability, thereby expanding it from a deterministic model to a stochastic (probabilistic) one. As such, multiple runs, or iterations, may be performed to evaluate the range of outcomes that may arise from selecting various actions.

Examples of the simulated individual herd populations for different outbreak results over 100 years are presented in Figure L-23. Different outbreak results are presented to illustrate the stochastic nature of the model—each time the model is run, the results are different. These outputs were chosen because they show the range of possible outcomes that might result from a single management scenario.

The disease model was used to perform 1,000 simulations of each proposed alternative, with and without cumulative effects. Each simulation began with all bighorn sheep herds uninfected and at their current population size and was run for 100 years. Results, including the number of herds suffering pseudoextirpation in each simulation, were collected and summarized for use in the Environmental Consequences section of the FSEIS (USDA Forest Service 2010).

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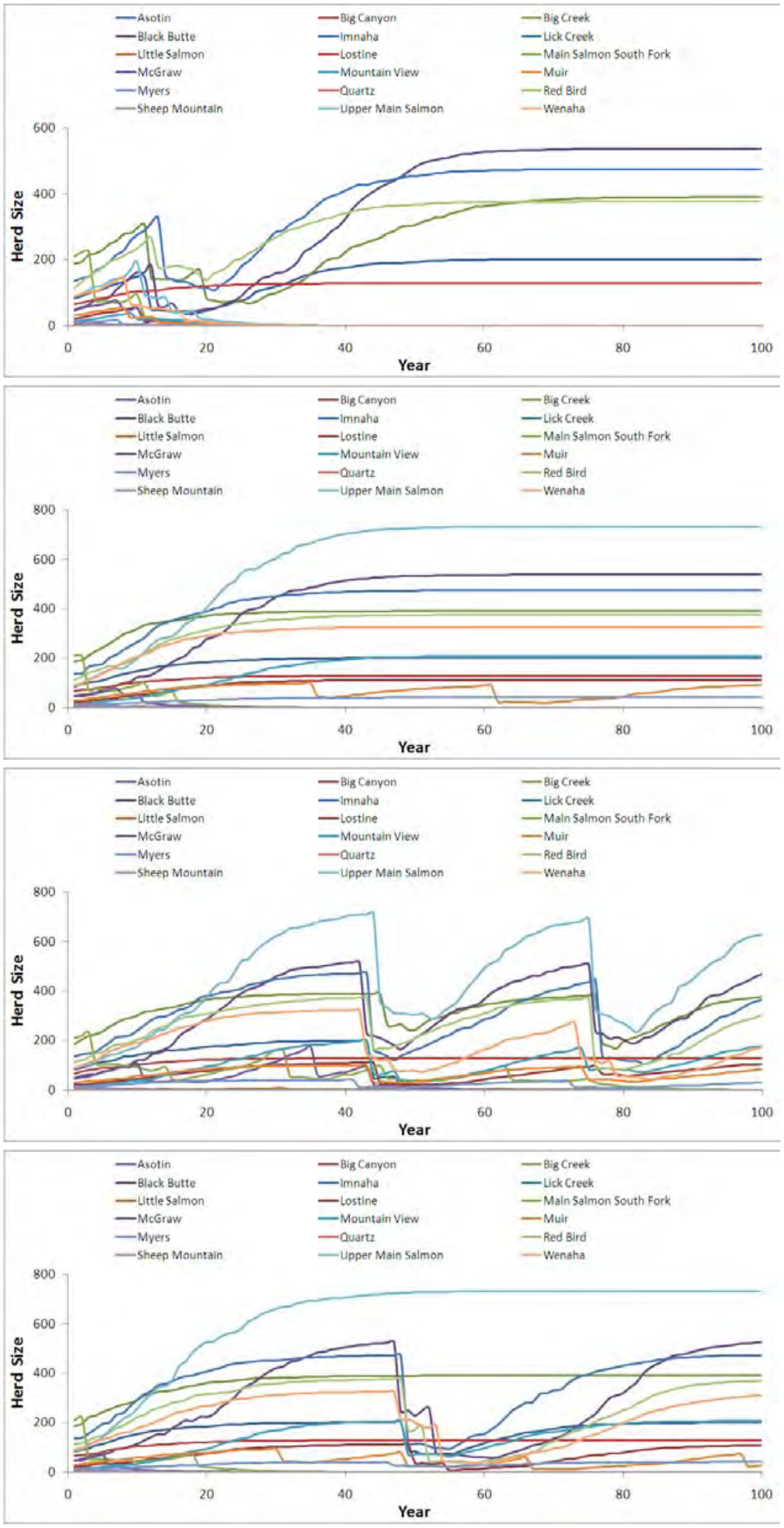
[2] Many studies reporting post-epidemic lamb mortality have been published in the second or third year after an outbreak, and in such cases, lamb recruitment was almost invariably still low at the time of the last reported observation (Onderka and Wishart 1984; Spraker et al. 1984; Schwantje 1986; Festa-Bianchet 1988; Foreyt 1990; Ryder et al. 1992; Aune et al. 1998).

Figure L-23. Four Examples of the Outputs Possible from the Disease Model for a Single Management Scenario



5.0 REFERENCES

Aune, K., N. Anderson, D. Worley, L. Stackhouse, J. Henderson, and J. Daniel. 1998. A comparison of population and health histories among seven Montana bighorn sheep populations. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 11, ed. F. Moore, 46–69.

Bailey, V. 1936. The mammals and life zones of Oregon. North American fauna no. 55. Washington, D.C. U.S. Department of Agriculture, Bureau of Biological Survey.

Berger, J. 1978. Group-size, foraging, and antipredator ploys - analysis of bighorn sheep decisions. *Behavioral Ecology and Sociobiology* 4:91–99.

Berger, J. 1990. Persistence of different-sized populations—an empirical-assessment of rapid extinctions in bighorn sheep. *Conservation Biology* 4:91–98.

Berger, J. 1999. Intervention and persistence in small populations of bighorn sheep. *Conservation Biology* 13:432-435.

Berger, J. and C. Cunningham. 1988. Size-related effects on search times in North-American grassland female ungulates. *Ecology* 69:177-183.

Beyer, H. L. 2004. Hawth's analysis tools for ArcGIS. Available at: http://www.spatialecology.com/htools.

Bonenfant, C., J. M. Gaillard, T. Coulson, M. Festa-Bianchet, A. Loison, M. Garel, L. E. Loe, P. Blanchard, N. Pettorelli, N. Owen-Smith, J. Du Toit, and P. Duncan. 2009. Empirical evidence of density-dependence in populations of large herbivores. In: Advances in ecological research, vol. 41, ed. H. Caswell, 313–357.

Boyce, M. S., P. R. Vernier, S. E. Nielsen, and F. K. A. Schmiegelow. 2002. Evaluating resource selection functions. *Ecological Modeling* 157:281–300.

Cassirer, E. F., L. E. Oldenburg, V. L. Coggins, P. Fowler, K. Rudolph, D. L. Hunter, and W. J. Foreyt. 1996. Overview and preliminary analysis of a bighorn sheep die-off, Hells Canyon 1995–96. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 10, eds. K. Hurley, D. Reed, and N. Wild, 78–86.

Cassirer, E. F., K. M. Rudolph, P. Fowler, V. L. Coggins, D. L. Hunter, and M. W. Miller. 2001. Evaluation of ewe vaccination as a tool for increasing bighorn lamb survival following pasteurellosis epizootics. *Journal of Wildlife Diseases* 37:49–57.

Clifford, D. L., B. A. Schumaker, T. R. Stephenson, V. C. Bleich, M. Leonard-Cahn, B. J. Gonzalez, W. M. Boyce, and J. A. K. Mazet. 2007. Modeling risks of disease transmission from domestic sheep to bighorn sheep: Implications for the persistence and restoration of an endangered endemic ungulate. Final report. Davis, CA: U.C. Davis Wildlife Health Center, Department of Fish and Game Resource Assessment Program.

Clifford, D. L., B. A. Schumaker, T. R. Stephenson, V. C. Bleich, M. L. Cahn, B. J. Gonzales, W. M. Boyce, and J. A. K. Mazet. 2009. Assessing disease risk at the wildlife-livestock interface: a study of Sierra Nevada bighorn sheep. *Biological Conservation* 142:2559–2568.

Coggins, V. L. 1988. The Lostine Rocky Mountain bighorn sheep die off and domestic sheep. Biennial Symposium of the Northern Wild Sheep and Goat Council 6:57–64.

Copeland, J. P., K. S. McKelvey, K. B. Aubry, A. Landa, J. Persson, R. M. Inman, J. Krebs, E. Lofroth, H. Golden, J. R. Squires, A. Magoun, M. K. Schwartz, J. Wilmot, C. L. Copeland, R. E. Yates, I. Kojola, and R. May. 2010. The bioclimatic envelope of the wolverine (*Gulo gulo*): do climatic constraints limit its geographic distribution? Canadian Journal of Zoology-Revue Canadienne De Zoologie 88:233-246.

Coulson, T., T. H. G. Ezard, F. Pelletier, G. Tavecchia, N. C. Stenseth, D. Z. Childs, J. G. Pilkington, J. M. Pemberton, L. E. B. Kruuk, T. H. Clutton-Brock, and M. J. Crawley. 2008. Estimating the functional form for the density dependence from life history data. *Ecology* 89:1661–1674.

DeCesare, N. J., and D. H. Pletscher. 2006. Movements, connectivity, and resource selection of Rocky Mountain bighorn sheep. *Journal of Mammalogy* 87:531–538.

Enk, T. A., H. D. Picton, and J. S. Williams. 2001. Factors limiting a bighorn sheep population in Montana following a dieoff. *Northwest Science* 75:280–291.

Festa-Bianchet, M. 1986. Site fidelity and seasonal range use by bighorn rams. *Canadian Journal of Zoology* 64:2126–2132.

Festa-Bianchet, M. 1988. A pneumonia epizootic in bighorn sheep, with comments on preventive management. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 6, 66–76.

Foreyt, W. J. 1989. Fatal Pasteurella haemolytica pneumonia in bighorn sheep after direct contact with clinically normal domestic sheep. *American Journal of Veterinary Research* 50:341–344.

Foreyt, W. J. 1990. Pneumonia in bighorn sheep: Effects of Pasteurella haemolytica from domestic sheep and effects on survival and long-term reproduction. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 7, 92–101.

Gaillard, J. M., M. Festa-Bianchet, and N. G. Yoccoz. 1998. Population dynamics of large herbivores: variable recruitment with constant adult survival. *Trends in Ecology and Evolution* 13:58–63.

Gaillard, J.-M., M. Festa-Bianchet, N. G. Yoccoz, A. Loison, and C. Toïgo. 2000. Temporal variation in fitness components and population dynamics of large herbivores. *Annual Review of Ecology and Systematics* 31:367-393.

George, J. L., D. L. Martin, P. M. Lukacs, and M. W. Miller. 2008. Epidemic Pasteurellosis in a bighorn sheep population coinciding with the appearance of a domestic sheep. *Journal of Wildlife Diseases* 44:388–403.

Gotelli, N. J. 2008. A Primer of Ecology, 4th edition. Sunderland, MA: Sinauer Associates, Inc.

Gross, J. E., F. J. Singer, and M. E. Moses. 2000. Effects of disease, dispersal, and area on bighorn sheep restoration. *Restoration Ecology* 8:25–37.

Gudorf, M., Sweanor, P., and F. Singer. 1996. Bighorn sheep habitat assessment of the greater bighorn canyon national recreation area. U.S. Department of Interior, National Biological Services, National Park Service.

Hells Canyon Bighorn Sheep Restoration Committee (HCBSRC). 1997. Restoration of bighorn sheep to Hells Canyon: The Hells Canyon Initiative. Unpublished manuscript. Lewiston, ID: Idaho Department of Fish and Game. 59 pp.

Hobbs, N. T., and M. W. Miller. 1992. Interactions between pathogens and hosts: Simulation of pasteurellosis epizootics in bighorn sheep populations. In: Wildlife 2001: populations. D. R. McCullough and R. H. Barrett, editors. London: Elsevier Science Publishers, Ltd. p. 997–1007

Jorgenson, J. T., M. Festa-Bianchet, J. M. Gaillard, and W. D. Wishart. 1997. Effects of age, sex, disease, and density on survival of bighorn sheep. *Ecology* 78:1019–1032.

Krausman, P. R., R. C. Etchberger, and R. M. Lee. 1993. Persistence of mountain sheep. *Conservation Biology* 7:219-219.

Lawrence, P.K., .S. Shanthalingam, R. P. Dassanayake, R. Subramaniam, C. N. Herndon, D. P. Knowles, F. R. Rurangirwa, W. J. Foreyt, G. Wayman, A. M. Marciel, S. K. Highlander, and S. Srikumaran. Forthcoming. Transmission of Mannheimia haemolytica from domestic sheep (*Ovis aries*) to bighorn sheep (*Ovis canadensis*): 8 unequivocal demonstration with green fluorescent 9 protein-tagged organisms. *Journal of Wildlife Diseases*.

Manly, B. F., L. McDonald, and D. L. Thomas. 1993. Resource selection by animals: Statistical design and analysis of field studies. London: Chapman & Hall. p. 177.

Melbourne, B. A. and A. Hastings. 2008. Extinction risk depends strongly on factors contributing to stochasticity. *Nature* 454:100-103.

McCarty, C. W., and M. W. Miller. 1998. Modeling the population dynamics of bighorn sheep: A synthesis of literature. Denver, CO: Colorado Division of Wildlife.

Miller, M. W. 2001. Pasteurellosis. In: Infectious diseases of wild mammals, eds. E. S. Williams and I. K. Barker, 330–337. Ames, IA: Iowa State University Press.

Monello, R. J., D. L. Murray, and E. F. Cassirer. 2001. Ecological correlates of pneumonia epizootics in bighorn sheep herds. *Canadian Journal of Zoology-Revue Canadienne De Zoologie* 79:1423–1432.

O'Grady, J. J., B. W. Brook, D. H. Reed, J. D. Ballou, D. W. Tonkyn, and R. Frankham. 2006. Realistic levels of inbreeding depression strongly affect extinction risk in wild populations. *Biological Conservation* 133:42–51.

Onderka, D. K., and W. D. Wishart. 1984. A major bighorn sheep die-off from pneumonia in southern Alberta. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 4, 356–363.

Onderka, D. K., and W. D. Wishart. 1988. Experimental contact transmission of *Pasteurella haemolytica* from clinically normal domestic sheep cuasing pneumonia in Rocky Mountain bighorn sheep. *Journal of Wildlife Diseases* 24(4):663–667.

Palisade Corporation. 2009. @Risk. 5.5. Ithaca, NY: Palisade Academic Software.

Portier, C., M. Festa-Bianchet, J.-M. Gaillard, J. T. Jorgenson, and N. G. Yoccoz. 1998. Effects of density and weather on survival of bighorn sheep lambs (Ovis canadensis). *Journal of Zoology* 245:271–278.

Risenhoover, K. L. and J. A. Bailey. 1985. Foraging ecology of mountain sheep - implications for habitat management. *Journal of Wildlife Management* 49:797–804.

Rodgers, A. R., A. P. Carr, H. L. Beyer, L. Smith, and J. G. Kie. 2007. HRT: Home range tools for ArcGIS. Ontario, Canada: Ontario Ministry of Natural Resources, Centre for Northern Forest Ecosystem Research, Thunder Bay.

Ryder, R. J., E. S. Williams, K. W. Mills, K. H. Bowles, and E. T. Thorne. 1992. Effect of pneumonia on population size and lamb recruitment in Whiskey Mountain bighorn sheep. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 8,136–146.

Sappington, J. M., K. M. Longshore, and D. B. Thomson. 2007. Quantifying landscape ruggedness for animal habitat analysis: A case study using bighorn sheep in the Mojave Desert. *Journal of Wildlife Management* 71(5): 1419–1426.

Schirokauer, D. 1996. The effects of 55 years of vegetative change on bighorn sheep habitat in the Sun River area of Montana. M.S. thesis. Missoula, MT: University of Montana.

Schwantje, H. M. 1986. A comparative study of bighorn sheep herds in southeastern British Columbia. In: Proceedings of the biennial symposium of the Northern Wild Sheep and Goat Council, vol. 5, 231–252.

Singer, F. J., E. Williams, M. W. Miller, and L. C. Zeigenfuss. 2000a. Population growth, fecundity, and survivorship in recovering populations of bighorn sheep. *Restoration Ecology* 8:75–84.

Singer, F. J., M. E. Moses, S. Bellew, and W. Sloan. 2000b. Correlates to colonizations of new patches by translocated populations of bighorn sheep. *Restoration Ecology* 8:66–74.

Singer, F. J., and M. A. Gudorf. 1999. Restoration of bighorn sheep metapopulations in and near 15 national parks: Conservation of a severely fragmented species. Fort Collins, CO: Midcontinent Ecological Science Center. U.S. Geological Survey Open File Report 99-102.

Singer, F. J., L. C. Zeigenfuss, and L. Spicer. 2001. Role of patch size, disease, and movement in rapid extinction of bighorn sheep. *Conservation Biology* 15:1347–1354.

Smith, T. S., J. T. Flinders, and D. S. Winn. 1991. A habitat evaluation procedure for Rocky Mountain bighorn sheep in the intermountain west. *Great Basin Naturalist* 51:205–225.

Spraker, T. R., C. P. Hibler, G. G. Schoonveld, and W. S. Adney. 1984. Pathologic changes and microorganisms found in bighorn sheep during a stress-related die-off. *Journal of Wildlife Diseases* 20:319–327.

Traill, L. W., B. W. Brook, R. R. Frankham, and C. J. A. Bradshaw. 2010. Pragmatic population viability targets in a rapidly changing world. *Biological Conservation* 143:28–34.

LANDFIRE 2006. The national map LANDFIRE: LANDFIRE national existing vegetation type layer. Washington, D.C.: U.S. Department of Interior, Geological Survey. Available at: http://gisdata.usgs.net/website/landfire/ (accessed February 8, 2007).

USDA Forest Service. 2003a. Payette National Forest land and resource management plans final environmental impact statement. Ogden, UT: USDA Forest Service, Intermountain Region.

USDA Forest Service. 2003b. Payette National Forest land and resource management plan. Odgen, UT: USDA Forest Service, Intermountain Region.

USDA Forest Service. 2008. Southwest Idaho Ecogroup land and resource management plans: draft supplemental environmental impact statement. Ogden, UT: USDA Forest Service, Intermountain Region, Payette National Forest.

USDA Forest Service. 2010. Southwest Idaho Ecogroup land and resource management plans: final supplemental environmental impact statement. Ogden, UT: USDA Forest Service, Intermountain Region, Payette National Forest.

Wehausen, J. D. 1999. Rapid extinction of mountain sheep populations revisited. *Conservation Biology* 13:378-384.

Wisdom, M. J., R. S. Holthausen, B. C. Wales, C. D. Hargis, V. A. Saab, D. C. Lee, W. J. Hann, T. D. Rich, M. M. Rowland, W. J. Murphy, and M. R. Eames. 2000. Source habitats for terrestrial vertebrates of focus in the Interior Columbia Basin: Broad-scale trends and management implications. Portland, OR: USDA Forest Service, Pacific Northwest Research Station. General Technical Report PNW-GTR-485.

Worton, B. J. 1995 Using Monte Carlo simulation to evaluate kernel-based home range estimators. *J. Wildl. Manage*. 59, 794–800.