United States Department of Interior Bureau of Land Management

# Bighorn Sheep Risk of Contact Tool

**User Guide** 



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Clinton McCarthy, former USFS Region 4 Regional Wildlife Ecologist, contributed substantially to the FAQ section in Appendix G.

The BLM Wildlife Habitat Spatial Analysis Lab (Karla Mayne, Shannon Glazer, Ken Lambert, Brent Newman, and Bryan Franey) thoroughly tested version 14 of the Risk of Contact Tool (RoCT-GUI-v14-R-3.6.3-win.exe) and revised and updated the associated version of this User Guide.



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## 1. Introduction

In response to bighorn sheep population viability concerns, the Payette National Forest constructed a model for estimating the probability and rates of contact between bighorn sheep and active domestic sheep allotments. Subsequently, in 2011, the Forest Service and Bureau of Land Management (BLM) initiated a process to develop a geospatial platform that would support similar risk of contact analyses on other National Forests and BLM Field Offices/Districts. The resulting Risk of Contact Tool provides a user-friendly geospatial desktop application for use by field unit wildlife biologists and resource managers. Methods implemented by the decision support tool provide critical information needed for addressing the potential of contact and pathogen transmission for use in large scale and project level planning and developing bighorn sheep conservation measures on public lands.

The objective of this user guide is to provide instruction on the installation and use of the Bighorn Sheep Risk of Contact Tool (hereafter referred to as the RoCT or Tool). The Tool uses several inputs, including telemetry point data, a core herd home range (CHHR) polygon, a habitat raster model, and a set of active domestic sheep allotments to estimate the probability and rate of contact between bighorn sheep and occupied domestic sheep allotments. The CHHR is either generated by the Tool from user-supplied telemetry or observation points, or directly provided as a user-delineated polygon based on local expert knowledge. Draft summer habitat raster models for the western states have been developed by the Forest Service and are used in calculating habitat suitability and connectivity for purposes of bighorn sheep movements across landscapes. Forest Service, BLM and the states are collaborating on the review and refinement of these models to fit local biophysical settings. Winter habitat raster models for the western states are also in development. A local active domestic sheep allotment polygon layer is used in the last part of the analysis to calculate the probability and rates of contact between bighorn sheep and each allotment.

This user guide consists of four sections: 1) *Introduction*, 2) *Background*, 3) *Software and Data Requirements*, and 4) *Conduct a Risk of Contact Assessment*. The Background section briefly describes the history of the model and its applicability to Forest Service and BLM units west-wide. The Software and Data Requirements section lists the software and geospatial data layers needed to conduct a risk of contact assessment. The Conduct a Risk of Contact Assessment section details the workings of the Tool itself, describing the steps and decisions involved in an assessment.

Instructions for installing the required software are contained in Appendix A: Tool Installation Guide. Appendix B includes an example of a ram foray distance probability distribution file, derived from telemetry data collected from Hells Canyon bighorn sheep (in 12 herds along the borders of Oregon, Idaho, and Washington) and used as the default by the Tool. Appendix C describes how to easily discover where on a computer the version of R that runs the Tool has been installed. Appendices D and E describe the contents of the optional CHHR and RoCT "archive" subdirectories, which store all data and parameters used in their respective analyses. Appendix F describes the contents of the "Sample Data" folder that is distributed alongside the Risk of Contact Tool. Appendix G supplies a glossary of specialized terms used in the manual. Appendix H contains a list of Frequently Asked Questions, the answers to which provide extensive guidance in the use of the Tool and the interpretation in practice of its outputs. Appendix I lists all documents referenced in the User Manual and its Appendices. Finally, Appendices J and K excerpt portions of the Payette National Forest's 2010 Final Supplemental Environmental Impact Statement (USDA-FS, 2010). Appendix J is the FSEIS's discussion of risk of contact between bighorn sheep and active domestic sheep allotments under a variety of alternative management scenarios. Appendix K is the FSEIS's technical appendix, describing in detail the computations underlying core herd home range estimation and risk of contact estimation in the Risk of Contact Tool.



## 2. Background

In 2005, the Chief of the Forest Service remanded the Payette National Forest's Forest Plan because of bighorn sheep viability concerns, largely due to the potential for contact and pathogen transmission between domestic sheep and bighorn sheep in the Forest. In response, in 2010 the Forest published the Bighorn Sheep Viability Analysis and Forest Plan Amendment, which establishes Forest guidance for the management of domestic sheep in proximity to bighorn sheep populations. As part of the analysis process, the Forest worked with scientists from the University of California, Davis' Center for Animal Disease Modeling and Surveillance to develop a set of models to estimate the probability and rates of contact between free-ranging bighorn sheep and active domestic sheep allotments. This set of models was also intended to simulate the potential impacts of disease outbreaks on bighorn sheep populations on and adjacent to the Forest.

Three models were used to assess the potential for pathogen transmission between domestic sheep and bighorn sheep. These models were: (1) a bighorn sheep summer habitat model; (2) a risk of contact model; and (3) a disease model. The summer habitat model used remote sensing derived data (vegetation, topography, etc.) to map suitable summer bighorn sheep habitat and to develop a habitat preference map. The risk of contact model used bighorn sheep locations, movement data, and habitat preference to model the probability and rate of contact between bighorn sheep and active domestic sheep allotments (O'Brien et al., 2014). This model used telemetry or observation data to construct a core herd home range (CHHR). Based on foray rates and habitat preferences, the model then estimated the probability that bighorn sheep (rams and ewes) that foray outside of the CHHR will contact domestic sheep allotments, and calculated a rate of contact with those domestic sheep allotments. The disease model used the calculated rate of contact and demographic characteristics of bighorn sheep (given disease perturbations) to assess the extirpation probabilities of bighorn sheep herds.

Extensive scientific literature supports the relationship between disease in bighorn sheep populations and contact with domestic sheep. Field observations have associated bighorn sheep respiratory disease events subsequent to being observed near domestic sheep, which has led to numerous independent research efforts. Research results provide strong evidence that bighorn sheep have a high probability of contracting fatal pneumonia following contact with domestic sheep, either through direct contact or via aerosol droplets (Besser et al., 2012). Consequently, many Federal land management agencies and State wildlife managers recommend eliminating shared use of ranges by bighorn and domestic sheep. In 2010 alone, 11 bighorn sheep die-offs occurred in the western states. Some of these occurred in close proximity to National Forests and BLM-managed lands.

Hence, pathogen transmission between domestic and bighorn sheep remains an issue for many National Forest and BLM units in the western United States. In August 2011, a four-step approach to viability analysis and standardized risk assessment was outlined and mandated by the Deputy Chief of Forest Service to minimize the potential for pathogen transmission through interaction between bighorn and domestic sheep. Forests require a strategy and consistent analysis tools to assess the potential association between Forest Service active domestic sheep allotments and bighorn sheep disease events.

The Tool described in this manual is meant to support public land management agencies that are attempting to minimize the risk of contact of domestic sheep and goats with bighorn sheep, by enabling them to estimate the risk of contact under various possible management scenarios. It replaces several earlier ArcGIS-based versions of the Risk of Contact Tool, which were each broken in one way or another by changes between ArcGIS versions. This version is coded entirely in R, a free open-source programming language that is widely used by biologists, among others. By freeing the Risk of Contact Tool from any dependencies on ArcGIS or other proprietary software, it is expected that this version will remain stable and freely available for the foreseeable future.



# 3. Software and Data Requirements

## 3.1. Required Software

Previous versions of the Risk of Contact Tool were distributed as ArcGIS Add-ins and required a working installation of ArcGIS equipped with the ArcGIS Spatial Analyst extension. This version, by contrast, is entirely implemented in the free, open source programming language **R**. It does not depend on ArcGIS.

The Tool can be installed on any machine running a 64-bit version of Windows, using the customized installer described in Appendix A. That installer places a version of **R** and all the **R** packages needed to run the Tool on the user's computer, along with desktop and Start menu shortcuts that can be used to launch the Tool. The only additional software requirement is that the computer should be equipped with a web browser (preferably Chrome, Firefox, Microsoft Edge), which the Tool uses to display its user interface.

## 3.2. Required Data

Every risk of contact assessment requires three spatial feature layers and two .csv files as inputs:

- 1. Bighorn Sheep Telemetry/Observation Points or CHHR Polygon Feature Layer: A Risk of Contact analysis requires a core herd home range (CHHR) polygon. This polygon may be supplied directly by the user as a polygon feature whose boundaries have been drawn based on local expertise. Alternatively, the user may supply a point feature class or shapefile consisting of bighorn sheep telemetry or observation locations, which includes a fully-populated ID field differentiating animals, which the Tool will then use to compute a CHHR polygon.
- 2. Active Domestic Sheep Allotment Polygon Feature Layer: This polygon feature should contain the boundaries of active domestic sheep or goat allotments, with an ID field giving the name of each allotment.
- 3. **Bighorn Sheep Habitat Class or Habitat Preference Raster Layer:** A layer representing bighorn sheep habitat preference for different parts of the landscape may be supplied as either a "habitat class raster" or a "habitat preference raster". In a habitat class raster, each cell's value indicates its habitat class (e.g. habitat, non-habitat, etc.). If a habitat class raster is supplied, the user will be prompted to enter the relative habitat preference value associated with each habitat class. In a habitat preference raster, each cell's value directly represents its relative habitat preference, so no additional user input is required.

User-supplied vector layers may be supplied as Esri shapefiles or file geodatabases. Raster layers need to be supplied as GeoTIFF files with extension "tif" or "tiff".

**NOTE:** The Tool expects that the user-supplied habitat preference raster will be in a Cartesian coordinate system such as the UTM coordinate system, that uses meters as the unit of distance. The Tool projects vector layers to the coordinate system used by the raster layer.

In addition to the three spatial feature layers, a Risk of Contact analysis requires two "foray distance distribution files", one for rams and one for ewes. These .csv files give the probabilities that individual ram or ewe forays will reach each of the 1-kilometer-wide concentric rings surrounding the CHHR boundary. The format of the files must match the example shown in Appendix C, with a "Distance" column containing distances in kilometers, and a "ForayProb" column containing the probabilities that a foray will extend at least that far from the CHHR.

Foray distance distribution .csv files for rams and ewes, derived from 12 years of Hells Canyon area telemetry data, are located in the "Sample Data" folder distributed alongside the Risk of Contact Tool and are also installed with the RoCT for use in analyses. The foray distance distributions exhibited by the Hells Canyon area bighorn sheep were consistent with published observations of bighorn sheep movements from several other areas in western North America. These default data should be used

unless other well-supported, scientifically derived estimates of foray distance distributions are available for the area under consideration.

## 3.2.1. Telemetry/Observation Points or CHHR Polygon Feature Layer

The telemetry/observation point feature layer consists of bighorn sheep location data stored in a vector format and must include a fully-populated animal ID field that distinguishes points derived from different animals. Careful consideration should be given to the telemetry or observation points (or the combination thereof) used for the home range analyses. These data should represent a *current* population with discrete geographical boundaries, season of use dates, and other potentially relevant factors germane to addressing the risk of contact between bighorn sheep and occupied domestic sheep allotments. Also, the total number of points in a telemetry/observation dataset is only one measure of its quality; equally important is how representative of whole-year (or whole-season) use patterns those points are. In general, it's better to have a small number of records well distributed throughout the year rather than many "non-independent" points collected over a short time interval.

A telemetry/observation point layer is not required if a core herd home range polygon (or multipart polygon) is otherwise available. The CHHR polygon may be delineated by a knowledgeable wildlife biologist (or computed during a previous contact assessment). In that case, the Tool's "Estimate CHHR" tab can be skipped and the polygon layer can be input directly in the "Estimate Risk of Contact" component described below.

## 3.2.2. Active Domestic Sheep Allotment Polygon Layer

The active domestic sheep allotment layer consists of allotment boundaries in a vector polygon format. This allotment layer must include an ID field that differentiates each unique allotment either by number or name.

#### 3.2.3. Habitat Class or Habitat Preference Raster Layer

The habitat layer consists of data in raster format. The values of the raster's cells may represent either habitat classes or habitat preferences.

In most cases, users will supply a "habitat class raster", in which each cell value is an integer that indicates the habitat class to which the cell belongs. In the habitat class raster included in the "Sample Data" folder, for example, the cells all have values of 1, 2, or 5, indicating areas of "habitat" (1), "connectivity area" (2), and "non-habitat" (5), respectively. If a habitat class layer is supplied, the Tool will prompt the user to provide a relative habitat preference value for each class. The preference for each class should be provided by the wildlife biologist or the raster layer's creator.

It is also possible to supply a "habitat preference raster", a raster whose cell values directly represent relative habitat preferences. This option will be especially useful in areas for which a more complex and or nuanced model of bighorn sheep habitat preference is available and each cell may have its own unique value.



## 4. Conduct a Risk of Contact Assessment

This section describes the Risk of Contact Tool, its three main components, and how they may be used to carry out a Risk of Contact assessment. Section 4.1 provides an overview of the Tool's three main tabs and their roles in a Risk of Contact assessment. Sections 4.2 and 4.3 describe how to launch the Tool and how to use it to upload spatial data from the user's computer. Finally, Sections 4.4 and 4.5 give more detailed documentation of the main tabs and how to use them.

## 4.1. Tool Interface Overview

A Risk of Contact assessment proceeds in several distinct stages, shown schematically in FIGURE 4.1. In the first stage (proceeding from left to right in the workflow schematic), a core herd home range (CHHR) boundary is identified, either by estimating it from animal location data (from radio- or GPS-collared animals or field observations) or based on a biologist's site-specific knowledge of a bighorn herd's use of the landscape. In the next stage, two "foray probability rasters" are generated, representing the estimated probabilities that a single foraying ram or ewe will reach each point on the landscape outside of the CHHR. In the third and final stage, the resulting bighorn ram and ewe foray probability layers are combined with occupied domestic sheep allotment boundary polygons to calculate estimated individual- and herd-level allotment contact probabilities and rates. The RoC Tool collects these rates into an estimated contact rates table and writes them to a file named RoC-results.csv. Stages two and three are combined in the workflow schematic in the box labeled "Risk of Contact Estimation"

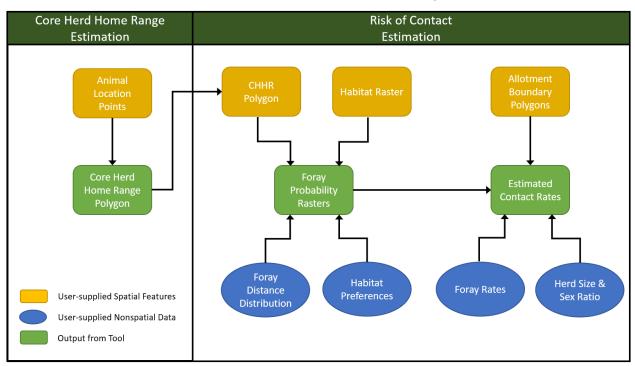


FIGURE 4.1. RISK OF CONTACT ASSESSMENT WORKFLOW

The Risk of Contact Tool (FIGURE 4.2) has three main tabs. The **Estimate CHHR** tab (the main tab currently selected in FIGURE 4.2) implements the "CHHR Estimation" portion of the workflow above. The **Estimate Risk of Contact** tab (FIGURE 4.3) implements the "Risk of Contact Estimation" portion of the analysis. Finally, the **Map** tab (FIGURE 4.4) displays spatial inputs and spatial model outputs as they are uploaded or computed while using either of the other two tabs.

Selecting either of the first two main tabs brings up a sidebar menu of numbered sidebar tabs, as shown in FIGURE 4.2 and FIGURE 4.3. To estimate a CHHR or a Risk of Contact table, work in order through each of the sidebar tabs.



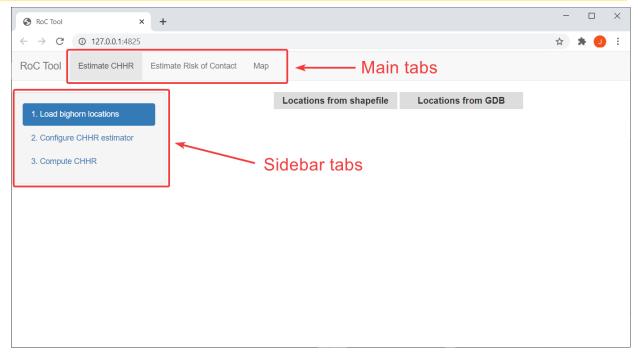


FIGURE 4.2. RISK OF CONTACT TOOL: "ESTIMATE CHHR" TAB

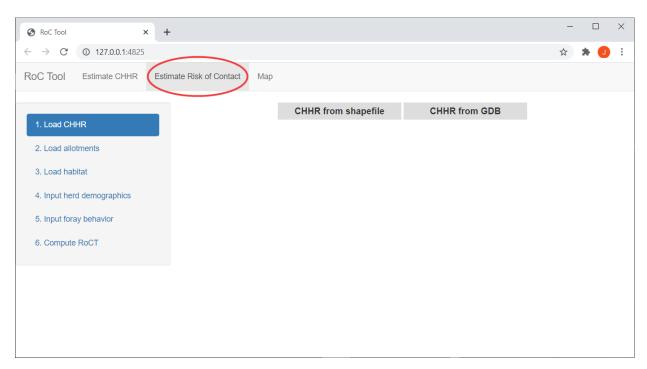


FIGURE 4.3. RISK OF CONTACT TOOL: "ESTIMATE RISK OF CONTACT" TAB



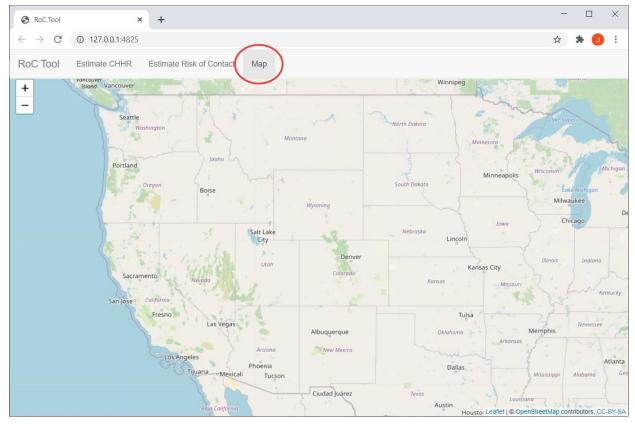


FIGURE 4.4. RISK OF CONTACT TOOL: "MAP" TAB

# 4.2. Launching the Tool

Successfully installing the Tool (as described in Appendix A) places shortcuts to the Tool on the computer's desktop and in its Start menu. To launch the Tool, simply double-click on the desktop shortcut (FIGURE 4.5) or click on the Start menu shortcut (FIGURE 4.6). To select the Start menu shortcut, click **Start** (at the screen's bottom left) to open a search bar, type "BHS-RoCT", and then click on the BHS-RoCT icon.



FIGURE 4.5. DESKTOP TOOL SHORTCUT





FIGURE 4.6. START MENU TOOL SHORTCUT

As the Tool launches, it first opens a Windows command prompt, the black command screen shown in FIGURE 4.7. The command prompt reports on the progress of the R process that launches and runs the Tool. Within a few seconds, the Tool itself will open in a web browser tab, displaying the **Estimate CHHR** tab shown in FIGURE 4.2. The command prompt stays open as long as the Tool is running; it may be minimized, but if you close it, the Tool will also halt.

```
BHS-RoCT
                                                                                                                X
Loading required package: shiny
oading required package: shinyjs
Attaching package: 'shinyjs'
The following object is masked from 'package:shiny':
   runExample
The following objects are masked from 'package:methods':
   removeClass, show
Loading required package: shinyalert
Attaching package: 'shinyalert'
The following object is masked from 'package:shinyjs':
   runExample
The following object is masked from 'package:shiny':
   runExample
Loading required package: shinybusy
Loading required package: shinyBS
Loading required package: leaflet
Loading required package: sf
Linking to GEOS 3.8.0, GDAL 3.0.4, PROJ 6.3.1
```

FIGURE 4.7. COMMAND PROMPT LAUNCHED ON TOOL STARTUP

The Tool uses a computer's default web browser to display its user interface. It has been tested in Chrome, Firefox, and Microsoft Edge. If you need to change your default browser to one of those: (1) Click on the **Start** icon; (2) type and then select **Settings**; (3) type and then select **Default apps**; (4) click on the current default browser under "Web browser"; and then (5) select the desired new default browser from the list.



## 4.3. Uploading Spatial Data to the Tool

As noted in Section 4.1, both of the Tool's estimation tabs require that the user upload spatial data – a points feature layer with animal locations for the **Estimate CHHR** tab, and two polygon features (containing a CHHR and allotment polygons) plus a habitat raster for the **Estimate Risk of Contact** tab. This section describes the spatial file formats expected by the Tool and the interface it uses to upload them.

The Tool expects that each of the vector features that it uploads will be stored as either an Esri shapefile or in a file geodatabase. Each of the Tool's vector data upload tabs (namely, the **Load bighorn locations**, **Load CHHR**, and **Load allotments** sidebar tabs) presents a nearly identical user interface which supports both types of spatial file inputs.

To illustrate that interface, we take as an example the **Load bighorn locations** sidebar tab that is the first step of the **Estimate CHHR** analysis. The user is presented with two buttons, used to select the type of spatial file to be uploaded, as highlighted in FIGURE 4.8.

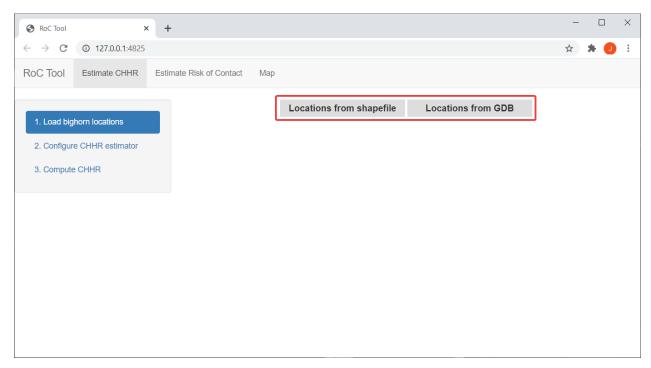
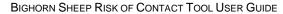


FIGURE 4.8. VECTOR FILE TYPE SELECTION BUTTONS

## 4.3.1. Uploading Vector Data from a Shapefile

Selecting **Locations from shapefile** brings up the Upload BHS locations shapefile button (FIGURE 4.9) The grey dash to the right of the **Upload BHS locations shapefile** button indicates that this is a required input. Clicking that button launches a file explorer (FIGURE 4.10) that can be used to navigate to the shapefile that you would like to upload.

**NOTE:** The file explorer will sometimes open up behind the web browser that is displaying the Tool or other open windows. If you click on a button that should launch a file explorer and nothing seems to happen, **be sure to look behind the browser and other open windows**; as that is almost certainly where the file explorer will be found.





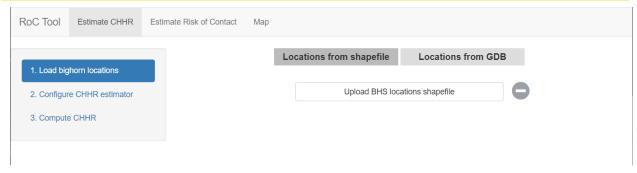


FIGURE 4.9. SHAPEFILE UPLOAD DIALOG

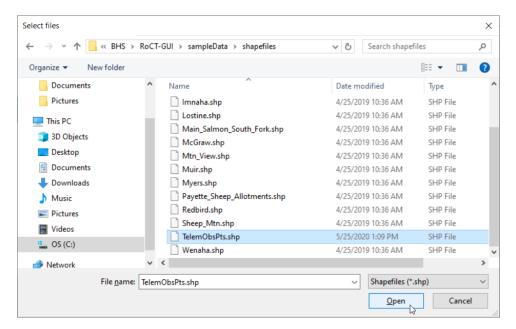


FIGURE 4.10. SHAPEFILE FILE EXPLORER

Once you have selected a shapefile, the grey dash will be replaced by a green check mark, indicating that the shapefile has been successfully uploaded. In addition, the Tool adds a text box summarizing attributes of the selected feature layer and requires users to select the feature attribute corresponding to animal ID (FIGURE 4.11). The grey check mark next to this field again indicates that this is a required input.



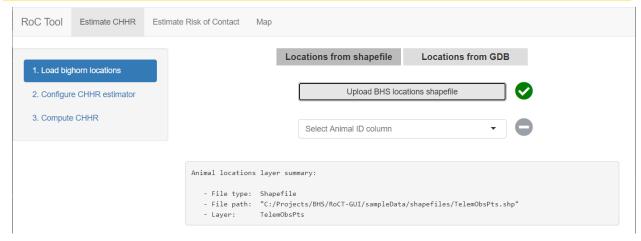


FIGURE 4.11. "LOCATIONS FROM SHAPEFILE" DIALOG AFTER SUCCESSFUL SHAPEFILE UPLOAD

Clicking on the **Select Animal ID column** box in FIGURE 4.11 opens a pulldown menu like the one shown in FIGURE 4.12. Scroll through it and select the data field that contains animal ID.

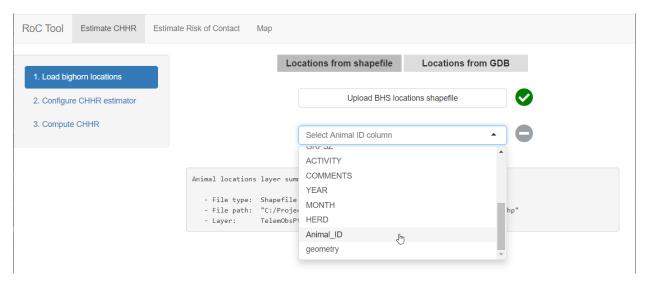


FIGURE 4.12. ANIMAL ID PULLDOWN MENU

Once you have selected an animal ID field, the tab will update, replacing the grey dash with a second green check mark. When no grey check marks remain, the tab is complete and you may proceed to the next sidebar tab (FIGURE 4.13).





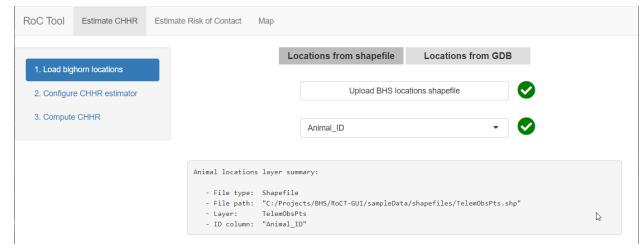


FIGURE 4.13 COMPLETED SHAPEFILE UPLOAD DIALOG

## 4.3.2. Uploading Vector Data from a File Geodatabase

Uploading vector data from a file geodatabase is similar to uploading them from a shapefile (Section 4.3.1) with two important differences. First, a file geodatabase is a directory, not a file, so the user needs to select a directory rather than a file. Second, after selecting a file geodatabase, there is an additional step in which the user must select *which* feature class within the geodatabase is to be uploaded.

After selecting the Locations from GDB button, the user is presented with the dialog in FIGURE 4.14.

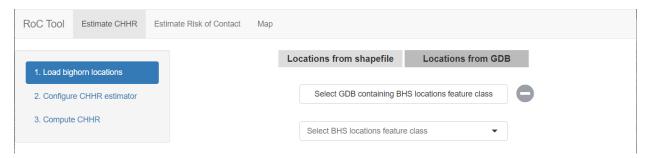


FIGURE 4.14. GEODATABASE UPLOAD DIALOG

Next, click on the button labeled **Select GDB containing BHS locations feature class** as indicated by the grey dash next to it. This will open a directory explorer like the one in FIGURE 4.15. Use the explorer to navigate to and then select the geodatabase, which will appear as a folder whose name ends with the extension ". gdb".

**NOTE:** Like the file explorer, the directory explorer will sometimes open behind the web browser or other open windows. If you click on a button that should launch a directory explorer and nothing seems to happen, **be sure to look behind the browser or other open windows**; as that is almost certainly where the directory explorer will be found.



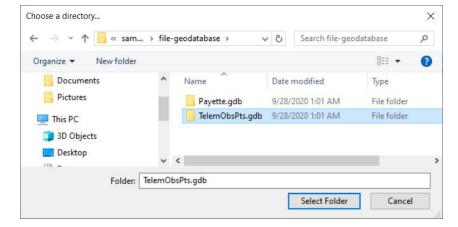


FIGURE 4.15. GEODATABASE DIRECTORY EXPLORER

Once a geodatabase has been selected, the pulldown menu labeled **Select BHS locations feature class** will be populated with the available feature classes in the geodatabase, as shown in FIGURE 4.16. Click on the small triangle on the box's right-hand side to view and then select one of the features from the pulldown menu.

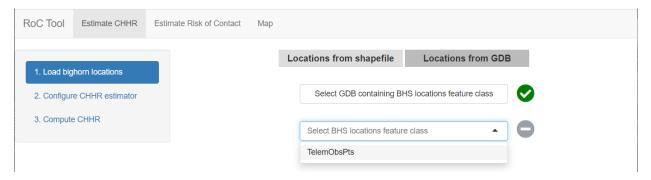


FIGURE 4.16. GEODATABASE FEATURE SELECTION

Once you have selected a feature class, you must select the animal ID field, as described in Section 4.3.1. When no grey check marks remain (FIGURE 4.17), the tab is complete, and you may proceed to the next sidebar tab.



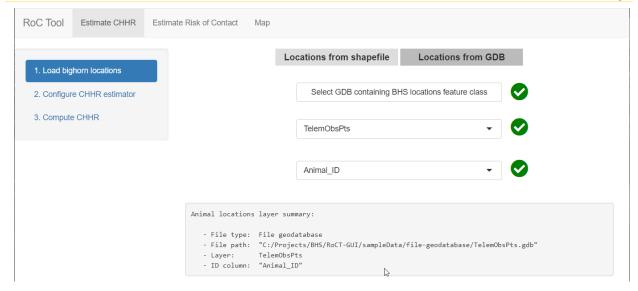


FIGURE 4.17. COMPLETED FILE GEODATABASE UPLOAD DIALOG

## 4.4. Estimating a Core Herd Home Range

For herds from which sufficient telemetry or other animal location data are available, a Core Herd Home Range (CHHR) may be estimated using the **Estimate CHHR** tab. This section describes the data and parameters required to estimate a CHHR and walks, in order, through the three numbered sidebar tabs used to carry out such an analysis.

The **Estimate CHHR** tab may be skipped if an estimated CHHR polygon that has been delineated by knowledgeable wildlife biologists is available. In that case, skip ahead to Section 4.5.1, which includes a description of how to directly upload a CHHR polygon.

## 4.4.1. Tab 1: "Load bighorn locations"

The first step in estimating a CHHR is to upload a points file containing telemetry or other observations of bighorn sheep locations. Starting with the two options available in FIGURE 4.18, follow the instructions in Section 4.3 to upload the point locations feature.

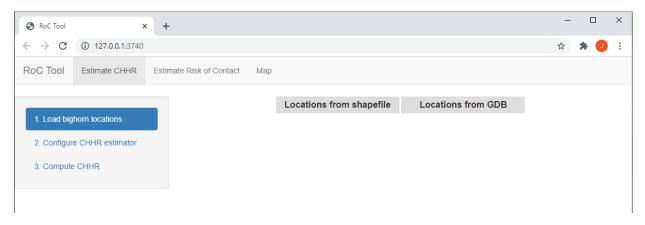


FIGURE 4.18. "LOAD BIGHORN LOCATIONS" TAB



FIGURE 4.19 shows a completed **Load bighorn locations** tab. The first two completed inputs (annotated with the numerals 1 and 2) give the path to a file geodatabase and the name of the point location feature stored in it that will be used to estimate the CHHR. The third input contains the name of the animal ID field that will be used to identify the individual animals whose home ranges will be calculated and then combined to form the CHHR.

**NOTE:** Location data uploaded by this tab must be in a projection whose units are expressed in meters. In particular, the points' spatial coordinates may not be expressed in degrees of latitude and longitude.

**NOTE:** For some herds, observational location data are available but the identities of individual animals are not known. In others, the identities of individual animals are known, but the number of points per animal is too low to reasonably estimate individual animals' contributions to the CHHR. In these cases, users may want to pool all the point data to directly estimate the CHHR. Past versions of the Tool supported this approach by providing an option to "**treat all animals as one**". To compute a CHHR that pools data from all animals with this version of the Tool, simply select as the animal ID field an attribute (such as the herd name) that is the same for all of the points.

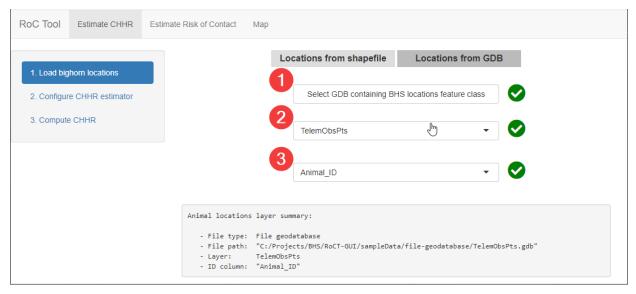


FIGURE 4.19. COMPLETED "LOAD BIGHORN LOCATIONS" TAB

As points are uploaded, they are immediately added to the Map tab (FIGURE 4.20). It is good practice to check the map to ensure that the desired points have been selected and that they have been plotted to the correct location. The currently uploaded points location layer can, at any point, be replaced with another using the interface described above



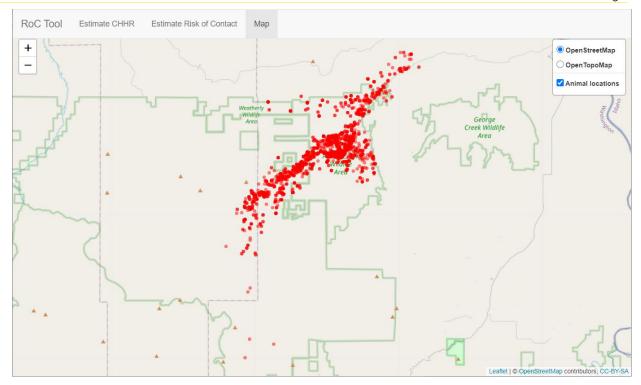


FIGURE 4.20. MAPPED BIGHORN LOCATIONS

Once the desired points have been uploaded and only green checkmarks (no grey dashes) are displayed on the **Load bighorn locations** tab, one may move on to the second sidebar tab.

## 4.4.2. Tab 2: "Configure CHHR estimator"

The **Configure CHHR estimator** sidebar tab allows users to set several parameters of the kernel density estimator that the Tool uses to estimate a CHHR (FIGURE 4.21). Each of the parameters is initially set to a default value, matching that used in the Payette NF risk of contact analysis that is reported in O'Brien et al. (2014).

**NOTE:** In the absence of site or region-specific data, it is recommended to keep the validated default values visible when first opening the Home Range dialog box, which are derived from 12 years of telemetry points collected from 444 radio collared animals in 12 Hells Canyon area herds. Altering these values without some empirical basis will change outcomes and reduce defensibility of the final results.



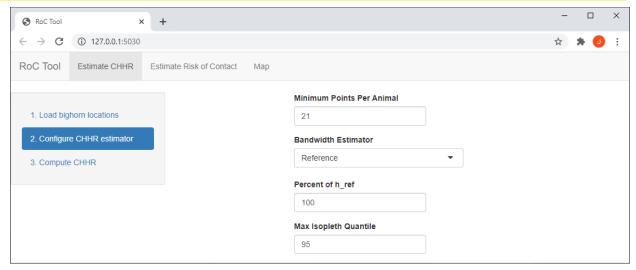


FIGURE 4.21. "CONFIGURE CHHR ESTIMATOR" TAB

The parameters are defined as:

1. **Minimum Points Per Animal:** Sets the minimum number of observations required for data from an animal to be included in the home range calculations. This filter excludes points from animals having fewer than the minimum number of observations specified by the user in the Minimum Points per Animal field. This cutoff is necessary because individual-level home range estimates based on too few points are less likely to be reliable or accurate. Keep in mind that each included animal's home range is weighted equally in determining the CHHR.

**NOTE**: Although the Tool allows inclusion of animals with as few as two observations, the cutoff should never be set that low. Several past analyses have only included points from animals with 21 or more distinct telemetry observations.

- 2. **Bandwidth Estimator:** Sets the type of kernel smoother used to estimate individual animals' utilization distributions, an intermediate step in CHHR estimation. Two bandwidth estimators are currently available:
  - Reference: Implements the "reference" bandwidth estimator described in Fieberg (2007). Produces a rounder, larger home range. This is the default and recommended method as the foray frequency and foray distance distributions supplied with the Tool were computed relative to CHHRs, which were produced using the Reference bandwidth estimator.
  - Plug-in: Implements "plug-in" bandwidth estimator of Sheather and Jones (1991).
    Tends to produce a longer, narrower home range. This option is not
    recommended in most cases because the default foray frequency and foray
    distance distributions for the CHHRs were not calculated using the plug-in
    bandwidth estimator. If this option is used, the rationale for this decision should
    be thoroughly documented.
- 3. **Percent of h\_ref:** A factor (expressed as a percentage) by which the estimated bandwidth should be multiplied. The default value (100 percent) leaves the automatically selected bandwidth unchanged. Values smaller than 100 result in smaller estimated CHHRs, while values greater than 100 result in relatively larger estimated CHHRs.
- 4. **Max Isopleth Quantile**: Enter a value between 0 and 99. (A 100 percent isopleth cannot be specified, as it is undefined for the home range estimators implemented in this Tool). The value entered here determines which "isopleth" or contour will be taken as the boundary of the CHHR polygon; the isopleth that is returned surrounds the smallest region within which the animals in a herd are expected to be found X% of the time. Entering 95 (the default value) results in a CHHR polygon expected to contain 95% of bighorn movements. Increasing the max isopleth quantile will lead to a larger estimated CHHR.



The 95% contour is commonly used in the home-range literature as a delimiter describing population boundaries and is the default value for this model. The estimated foray frequency and foray distance distributions used as the Tool's defaults were both computed relative to CHHRs defined by the 95th isopleth, and as a result it is inappropriate to use any other value for Max Isopleth Quantile. The rationale for any change to this value (95%) should be documented. Additional changes to other portions of the model will be required to account for any changes to the isopleth quantile size relative to foraying bighorn sheep distances.

## 4.4.3. Tab 3: "Compute CHHR"

Once a points feature has been uploaded and parameters have been set, the Tool's **Compute CHHR** tab (FIGURE 4.22) is ready to estimate a CHHR. First, though, you must specify how and where you would like to store the results of the CHHR estimation. FIGURE 4.23 shows a completed Compute CHHR tab, with the tab's several inputs annotated with red numbered circles.

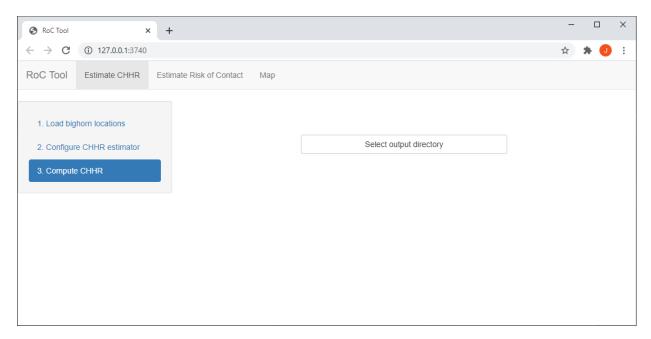


FIGURE 4.22. "COMPUTE CHHR" TAB

Step 1 is to select the output directory into which a shapefile containing the to-be-estimated CHHR will be saved. (Keep in mind that the Tool may open up the directory explorer *behind* the web browser, so look for it there if it doesn't immediately appear.) Step 2 is to name the CHHR. The default name is "CHHR", which directs the tool to save a shapefile named CHHR. shp to the output directory. Step 3 is to indicate, using the **Archive inputs** checkbox, whether an "archive" of all inputs used to estimate the CHHR is to be saved to the output directory. For a detailed description of the archive's contents and how it may be used to reproduce a CHHR estimate, see Appendix D. When ready to compute an estimated CHHR, click the **Compute CHHR** button.



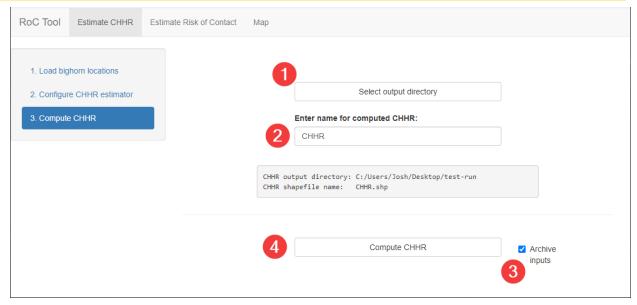


FIGURE 4.23. COMPLETED "COMPUTE CHHR" TAB

After clicking the **Compute CHHR** button, the Tool pops up a "busy indicator" (FIGURE 4.24) to inform users that CHHR estimation is in progress.

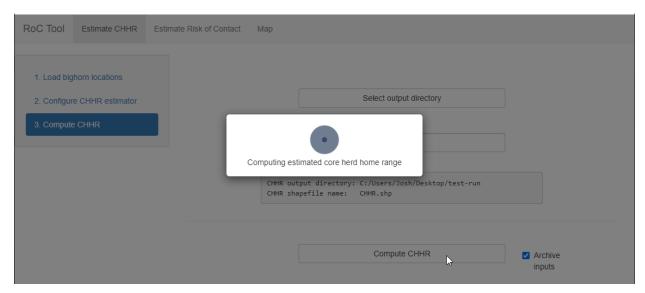


FIGURE 4.24. CHHR COMPUTATION BUSY INDICATOR

The busy indicator will be replaced by an alert (FIGURE 4.25) announcing that the CHHR estimation is complete. The just-computed CHHR is automatically added to the Map tab (FIGURE 4.26) and to the **Load CHHR** sidebar tab of the "Estimate RoCT" tab (FIGURE 4.27). Section 4.5 describes the Risk of Contact estimation steps.



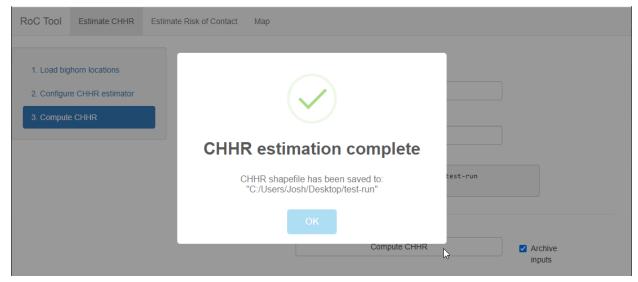


FIGURE 4.25. CHHR COMPUTATION COMPLETE

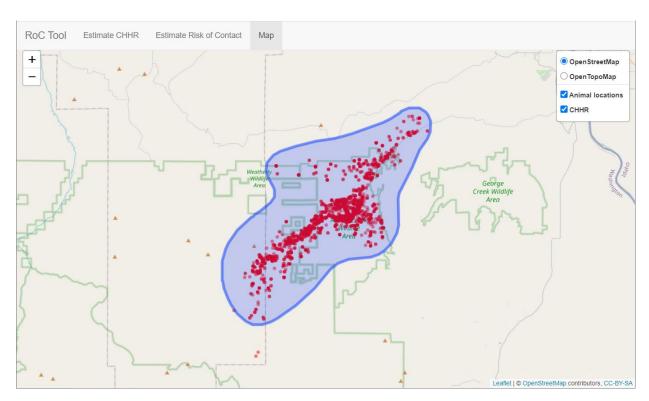


FIGURE 4.26. NEWLY ESTIMATED CHHR ADDED TO MAP



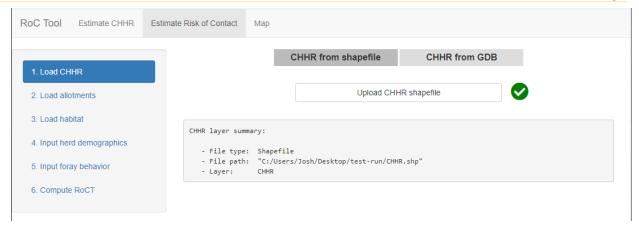


FIGURE 4.27. NEWLY ESTIMATED CHHR ADDED TO "ESTIMATE RoCT" TAB

## 4.5. Estimating Risk of Contact

The **Estimate Risk of Contact** tab calculates annual or seasonal probabilities that individual bighorn rams and ewes will leave their CHHR and come into contact with an active domestic sheep allotment boundary. The results are collected in a single Risk of Contact (RoC) table that summarizes individual-level probabilities and herd level rates of contact with each allotment.

This section describes the data and parameters required to estimate a RoC table and walks, in order, through the six numbered sidebar tabs used to carry out such an analysis.

#### 4.5.1. Tab 1: "Load CHHR"

If the **Estimate CHHR** tab was used to compute a core herd home range during the current session, the **Load CHHR** tab will already have been automatically populated with the just-computed polygon (FIGURE 4.28). Otherwise, use this tab to upload a core herd home range polygon feature from a shapefile or file geodatabase by following spatial data upload instructions in Section 4.3.

A green check mark icon (FIGURE 4.1) indicates that a CHHR has been successfully uploaded. To confirm that the correct polygon feature has been uploaded, have a look at the **Map** tab (FIGURE 4.29). Then proceed to the next sidebar tab.



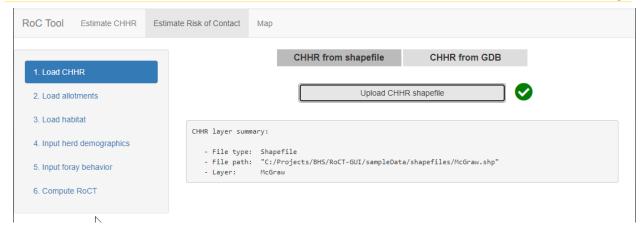


FIGURE 4.28. COMPLETED "LOAD CHHR" TAB

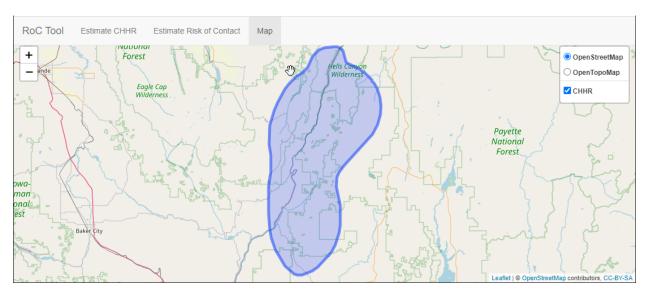


FIGURE 4.29. MAP OF CHHR

#### 4.5.2. Tab 2: "Load allotments"

To upload an allotments polygon feature from a shapefile or file geodatabase, follow the spatial data upload instructions in Section 4.3. The polygon feature should contain the boundaries of each allotment to be evaluated for risk of contact.

Once an allotment feature has been uploaded, the user is prompted to select an attribute that gives the name or unique ID of each allotment. Click on the triangle at the right-hand side of the **Select allotments ID column** box to open a pulldown menu, then scroll through it to select the data field that contains the allotment ID (FIGURE 4.30).



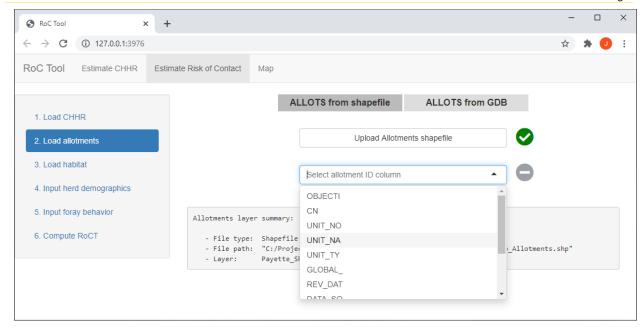


FIGURE 4.30. ALLOTMENT ID PULLDOWN MENU

Once an allotment ID attribute has been selected, the tab is complete, as indicated by the green check marks next to both required data fields (FIGURE 4.31).

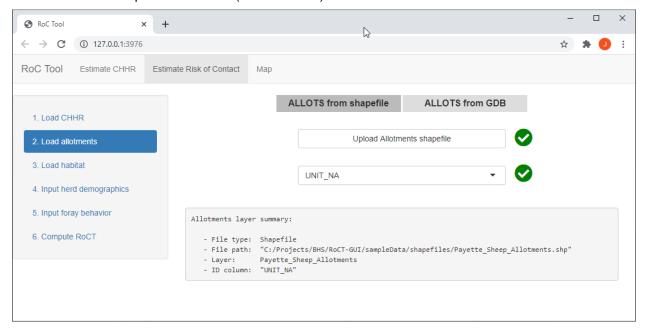


FIGURE 4.31. COMPLETED "LOAD ALLOTMENTS" TAB

To confirm that the correct polygon feature has been uploaded, look at the **Map** tab (FIGURE 4.32). Then proceed to the next sidebar tab.



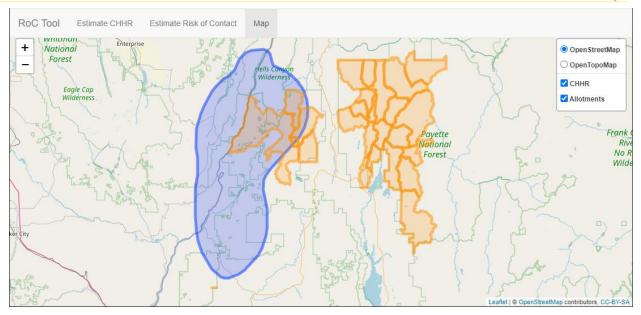


FIGURE 4.32. MAP OF ALLOTMENTS AND CHHR

#### 4.5.3. Tab 3: "Load habitat"

The **Load habitat** sidebar tab (FIGURE 4.33) is used to load a habitat preference raster. As discussed in Section 3.2, the values of the raster's cells may represent either habitat classes or habitat preferences. In either case, the raster file that is uploaded to the Tool needs to be stored as a GeoTIFF file with extension "tif" or "tiff".

To upload a habitat preference raster, click on the **Upload habitat raster GeoTiff** button.

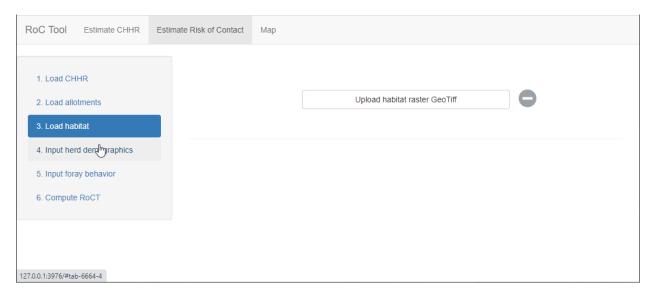
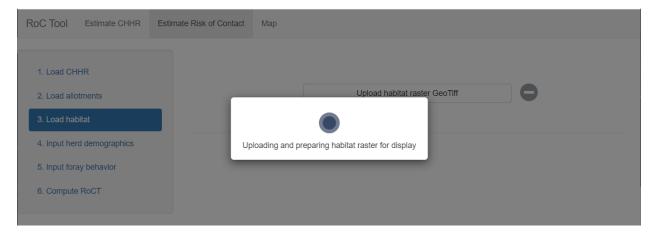


FIGURE 4.33. "LOAD HABITAT" TAB

After clicking the **Upload habitat raster GeoTiff** button, use the resulting file explorer to navigate to and then select the habitat raster file. The Tool will then pop up a "busy indicator" (FIGURE 4.34) to inform the user that the raster is being uploaded and prepared for display on the **Map** 





#### FIGURE 4.34. HABITAT RASTER UPLOAD BUSY INDICATOR

Once raster upload is complete (it should take only a few seconds), the Tool opens an interface that can be used to specify the type of habitat raster that has been supplied. (FIGURE 4.35). The interface consists of three radio buttons, one of which must be selected for a RoC analysis to proceed.

In most cases, the user will have supplied a habitat class raster, each of whose cell values is an integer that indicates the habitat class to which the cell belongs. In this case, select one of the first two radio buttons, which provide two alternative methods of supplying the relative habitat preference values associated with each habitat class.

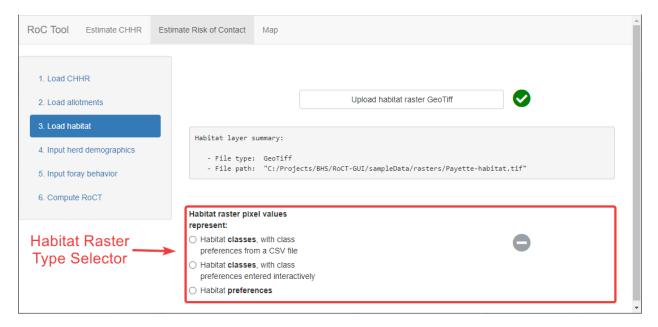


FIGURE 4.35. HABITAT RASTER TYPE SELECTOR

**Selecting the first radio button** presents the user with an upload button (FIGURE 4.36) that can be used to provide a "csv" file containing the habitat preferences associated with each class.



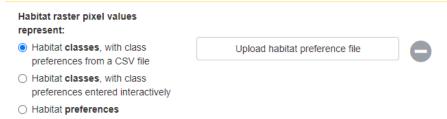


FIGURE 4.36. RASTER TYPE SELECTOR OPTION 1, FILE UPLOAD BUTTON

Clicking the **Upload habitat preference file** button will then open a file explorer that can be used to navigate to a "csv" file that associates habitat preferences with each habitat class. That file should consist of two columns labeled "ID" and "VAL". The "ID" column must include an entry for every unique cell value (class) in the raster while the "VAL" column contains the relative habitat values associated with each of the classes. FIGURE 4.37 displays an example, the Payette-habitat-prefs.csv file that is included in the "raster" directory of the "Sample Data" folder distributed alongside the Risk of Contact Tool.

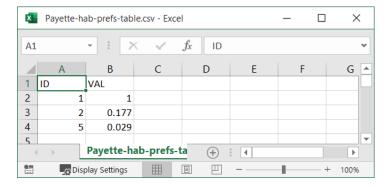


FIGURE 4.37. RASTER TYPE SELECTOR OPTION 1, EXAMPLE CSV FILE

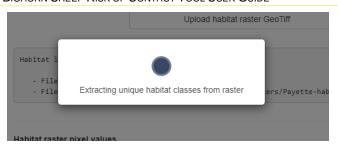
Success in uploading the habitat preference file is displayed with a green check mark, as shown in FIGURE 4.38.



FIGURE 4.38. RASTER TYPE SELECTOR OPTION 1, COMPLETED

**Selecting the second radio button** allows the user to supply the habitat preference values associated with each habitat class by typing them into a table in the Tool. To build that table, the Tool first needs to extract all unique values from the habitat class raster. While the Tool is extracting the unique class values, it displays the "busy indicator" shown in FIGURE 4.39.





#### FIGURE 4.39. RASTER TYPE SELECTOR OPTION 2, HABITAT TYPE EXTRACTION BUSY INDICATOR

Once it is finished, the Tool presents the user with a table into which the habitat preference values can be typed (FIGURE 4.40).



#### FIGURE 4.40. RASTER TYPE SELECTOR OPTION 2, HABITAT PREFERENCE INPUT TABLE

Once habitat preference values have been entered in all "VAL" column elements, a green check mark indicates that the table is complete (FIGURE 4.41). The values entered here (1.00, 0.177, and 0.029) corresponding to habitat classes 1, 2, and 5 ("habitat", "connectivity area", and "non-habitat" in the habitat raster layer included in the "Sample Data" directory) are the relative habitat preferences assigned to those habitat classes in the Payette NF's 2010 risk of contact analysis.



FIGURE 4.41. RASTER TYPE SELECTOR OPTION 2. COMPLETED HABITAT PREFERENCE INPUT TABLE

**Selecting the third radio button** tells the Tool that the habitat raster is a "habitat preference raster", in which the raster's cell values are themselves relative habitat preferences. If your habitat raster is a habitat preference raster, no additional user input is needed (FIGURE 4.42).



FIGURE 4.42. RASTER TYPE SELECTOR OPTION 3

Before moving on to the next step, it's advisable to look at the **Map** tab, to be sure the uploaded raster layer covers the area that includes the CHHR and allotment polygons (FIGURE 4.43).



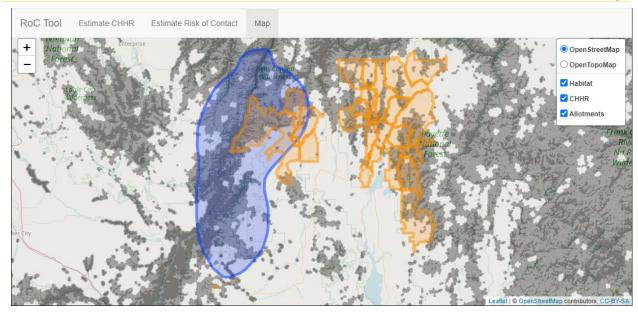


FIGURE 4.43. MAP OF HABITAT, ALLOTMENTS AND CHHR

## 4.5.4. Tab 4: "Input herd demographics"

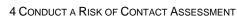
The **Input herd demographics** tab (FIGURE 4.44) presents a straightforward interface for entering information about the size and sex ratio of the bighorn sheep herd being analyzed. The two radio buttons on its left (the top one of which is initially selected) support two methods of setting these demographic parameters.

When the top radio button is selected, one may directly enter the herd size in the **Herd Size** field, and set **Ram** % and **Ewe** % to the desired values (FIGURE 4.45). The inactivated **Ram** # and **Ewe** # fields will update accordingly. This option can be useful if you know or can estimate the number of animals in the herd, but do not know the number of rams and ewes. The default ratio of 35:65 is based on observations of Hells Canyon area herds and should be changed if better information regarding the sex composition of local herds is available.

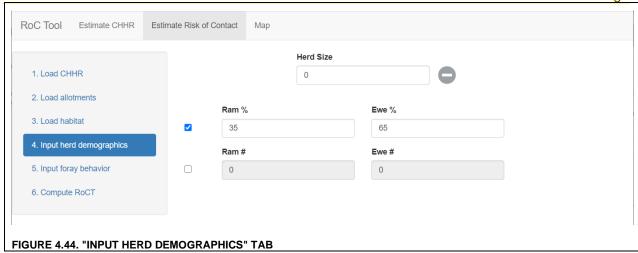
When the bottom radio button is selected, the Ram # and Ewe # fields may be directly updated.

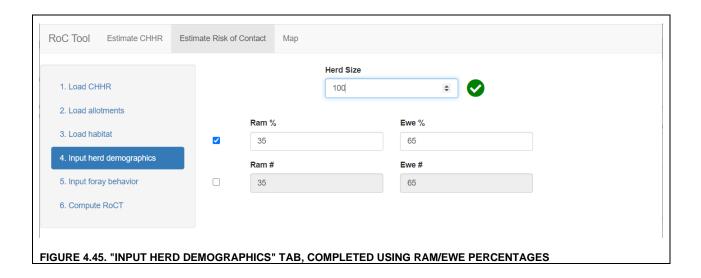
In either case, if the **Herd Size** is non-zero, a green check mark will indicate that the values are acceptable to the Tool.

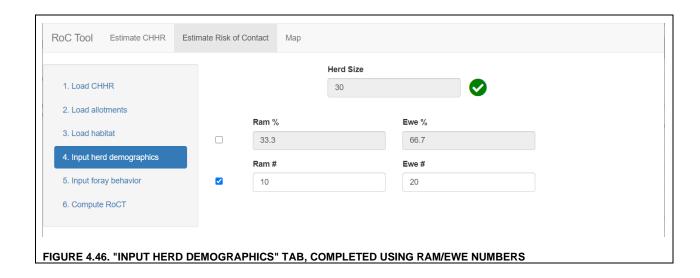














## 4.5.5. Tab 5: "Input foray behavior"

The **Input foray behavior** tab collects information about the annual (or seasonal) probability that a ram or ewe will leave their core herd home range on a foray, and the maximum distance from the CHHR to which they are likely to travel on such forays. It has four required input fields, marked with red numbers in FIGURE 4.47.

The Ram foray frequency and Ewe foray frequency fields take as inputs the probabilities that an individual ram or ewe will foray out of the CHHR during the grazing season being analyzed. Enter the value as a decimal rather than a percentage (i.e., 0.15 rather than 15%). To use the default values of 0.141 (14.1%) for rams and 0.015 (1.5%) for ewes, simply click on the checkbox labeled "Use default foray frequencies".

**NOTE:** The default values of 0.141 for rams and 0.015 for ewes are derived from 29,800 summer-season (May–October) observations of bighorn sheep in 13 Hells Canyon area herds, collected over a 12-year period. The values represent the proportion of radio-collared individuals that were observed outside their CHHR during the summer grazing season. Changing these values will directly affect estimated probabilities and rates of contact. If different values are used, the rationale for the changes and the observational basis for the estimated rates should be documented.

The **Upload Ram Foray Distance File** and **Upload Ewe Foray Distance File** buttons each launch a file explorer that can be used to upload a "foray distance distribution" formatted as specified in Appendix B. Alternatively, to use the default foray distance distributions, which were derived from 12 years of Hells Canyon area telemetry data, click on the checkboxes located to the left of the numbers 3 and 4 in FIGURE 4.47.

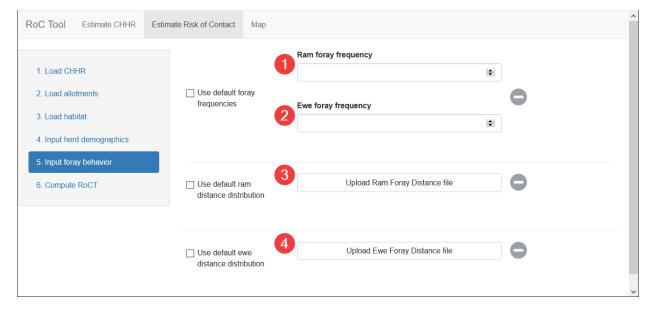
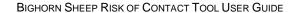


FIGURE 4.47. "INPUT FORAY BEHAVIOR" TAB

Once all four required fields are completed, as indicated by the conversion of all three grey dashes to green checkmarks (FIGURE 4.48), the final sidebar tab, which launches a Risk of Contact analysis, can be selected.





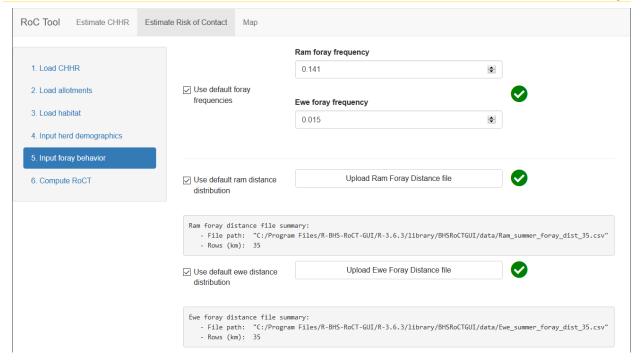


FIGURE 4.48. COMPLETED "INPUT FORAY BEHAVIOR" TAB

## 4.5.6. Tab 6: "Compute RoCT"

Before the Tool runs a Risk of Contact analysis, the user must specify an output directory. Click the **Select output directory** button to launch a directory explorer and navigate to an existing directory into which the Tool should save its output.

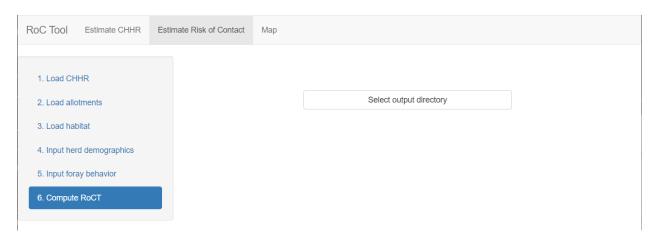


FIGURE 4.49. "COMPUTE ROCT" TAB

Once an output directory has been selected, two additional controls are made visible (FIGURE 4.50). The **Archive inputs** checkbox may be used to indicate whether an "archive" of all inputs used in this Risk of Contact analysis should be saved to the output directory. For a detailed description of the archive's contents and how it may be used to reproduce the Risk of Contact estimate, see Appendix E. Then, to run a Risk of Contact analysis, click the **Compute RoCT** button.



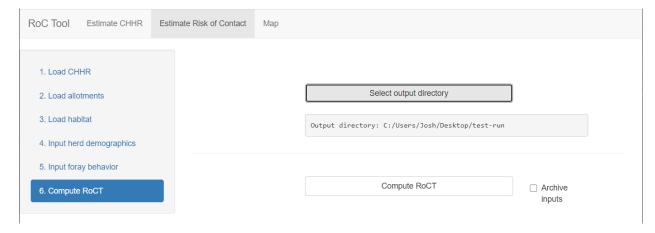


FIGURE 4.50. "COMPUTE ROCT" TAB, WITH ALL CONTROLS VISIBLE

When the **Compute RoCT** button is pressed, before running an analysis, the Tool first checks that the user has supplied all required inputs. If any are missing, it pops up the alert shown in FIGURE 4.51, highlighting the sidebar tab or tabs that are missing required inputs. Click "Dismiss" to close the alert and then visit the indicated tabs to find which elements (marked with grey dashes rather than green checkmarks) are missing their required inputs. After supplying the needed inputs, return to this tab and press **Compute RoCT** again.

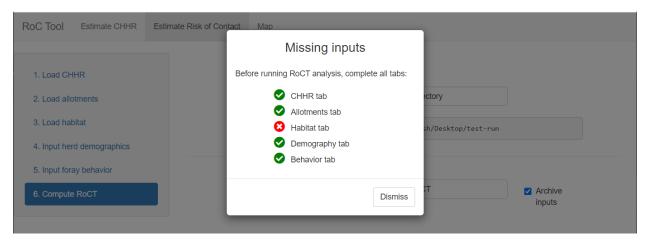


FIGURE 4.51. MISSING INPUTS ALERT

If all required inputs are present, the Tool will pop up a "busy indicator" (FIGURE 4.52) to inform users that RoC estimation is in progress.

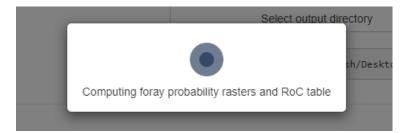


FIGURE 4.52. ROCT COMPUTATION BUSY INDICATOR



When the analysis is complete, the busy indicator will be replaced by the alert in FIGURE 4.53.

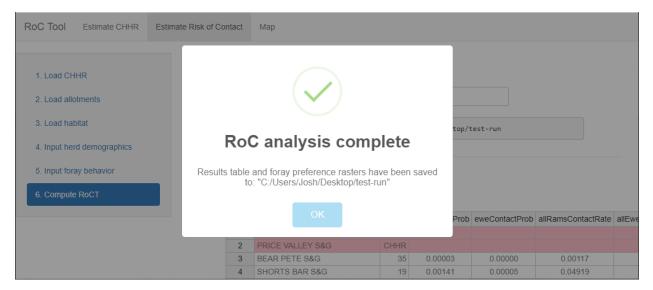


FIGURE 4.53. ROC ANALYSIS COMPLETE

Dismissing the alert, one can view the Risk of Contact Table that summarizes the results of the analysis. The same table is saved to the output directory in a file named RoC-results.csv. Explanations of the meanings of each column can be found in Appendix G.4.





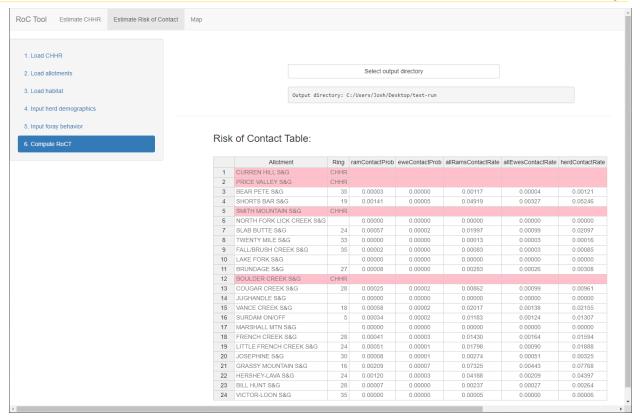


FIGURE 4.54. RISK OF CONTACT TABLE

The Tool also adds the two foray probability raster layers computed during the analysis to the **Map** tab. As shown in FIGURE 4.55, the Ram Foray layer is initially selected. To view the Ewe Foray layer instead, use the checkboxes in the layer control box located in the screen's upper right. In addition to being displayed on the **Map** tab, these layers are also saved to the output directory as rasters named ForayPrefRam.tif and ForayPrefEwe.tif.



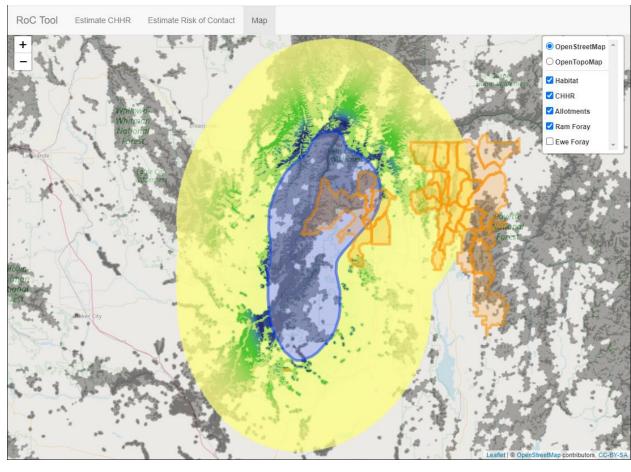


FIGURE 4.55. MAP WITH RAM AND EWE FORAY PROBABILITY SURFACES