

New Approaches to Space Use Workshop

Lab No. 7 ***SYNOPTIC MODEL OF SPACE USE IN R***

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We will use location data from 2 caribou cows from the Ray Mountain herd off the Dawson highway south of Prudhoe Bay on the North Slope Alaska. They were fitted with VHF collars and were located from the air irregularly over a couple years by BLM biologists as part of surveys to count the herd and monitor changes in its abundance in response to development of the transportation corridor bringing oil south from Prudhoe Bay.



We will use an R script to fit a number of synoptic models evaluating their home range size while simultaneously assessing the importance of elevation, roads, slope, deciduous shrubs, non-vegetated areas and wet community types to predicting their space use.

Lab Exercise No. 7

1. Place the R scripts, text files of data, etc. in a directory that will be your working directory.
2. Start R and load MASS by clicking on Packages, select Load and choose MASS from list.
3. Open the R script for the Synoptic Model for Caribou in a text editor.
Look through the script with your instructor focusing on the program flow described in the comments (each begins with #).
4. Change the working directory in the 7th line (following #(1))to insure it matches the location where you placed all the text files etc. for the caribou data.
5. Make sure that the correct file name is included following #(2) for the program to find functions that are called during the analysis.
6. Modify the LocationfileList following #(3) to select caribou number 565 (R151_565_1.txt) for your first analysis. Note that this script allows you to batch file a number of individual animals to run the same analysis on one after another by simply listing each them in double quotes separated by commas.
7. Following #(4) you can specify which variables will be used in each model and choose how many models you want to run by commenting out or uncommenting some of the models listed. Simply place a 1 in the appropriate place for each variable you want to include in a model or a 0 for any variable to be excluded.
8. For this lab exercise divide the models up amongst yourselves so that each person runs 2 different models in addition to the null model (ModelsList[1]) which is the bivariate normal modeling describing random movement from a single home range center.
9. After you've laid out your file of R commands paste it into your R gui and R will begin processing the statements and running the analyses. You should get all red statements indicating statements were processed. If you see any blue, statements read them to see what is wrong and correct the errors to continue the processing. It only takes a minute or less to estimate Model 1 parameters and output results to your working directory. Processing other Models to obtain maximum likelihood parameters can take 20 minutes or more depending on number of parameters in the model, etc. While they are processing open the files containing animal locations (R151_565_1.txt) and the grid of points containing habitat covariates (Avail_Ray.txt) to see the proper format and layout to estimate a synoptic model with data of your own.
10. Write the results of your analysis for caribou 565 into the table on the blackboard for comparison to other student's results. As time allows, go on to caribou705 and/or modify

the scripts for caribou 565 to run more models of interest, remembering to always start a series of analyses with the null model of a bivariate normal pattern of random movement for a single center of the home range.

Question 1: Compare the results of the 8 synoptic models to identify the best model and explain why it is best.

Question 2: What do your analyses imply about the importance and pattern of selection of this caribou with respect to the predictive variables analyzed here?

Question 3: How did the results for caribou 705 differ, if you had time to run some of them, and how would you combine analyses across multiple animals?