Comparison of Programs for Fixed Kernel Home Range Analysis

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Introduction

There is a bewildering array of methods for estimating animal home ranges, including minimum convex polygons, bivariate ellipses, adaptive and fixed kernels, and even a Brownian bridge technique (Bullard 1991; Kernohan et al. 2001).
Many people believe that the fixed kernel method using least-squares cross validation (LSCV) is the best approach currently available (Seaman and Powell 1996; Powell 2000; Kernohan et al. 2001).

Kernel estimators are based on probability "kernels", which are regions around each point location containing some likelihood of animal presence.
The width of the kernel is based on the smoothing parameter (h), which can be determined in a number of different ways.
The main automated methods for smoothing parameter selection are reference (which is based on assumptions of bivariate normality) and least-squares cross validation (which is based on properties of the data).
Kernel methods are either adaptive (where the kernel width increases as the distance between kernels increases) or fixed (always the same kernel width). Adaptive kernels tend to perform poorly, often over-estimating home range areas (Powell 2000; Kernohan et al. 2001).

Kernel estimators have a number of features that make them useful for home ranges: they work well with small amounts of data (approximately 50 locations), they are robust to autocorrelation, they are nonparametric, they allow multiple centers of activity, and they result in a utilization distribution (UD) rather than a simple home range outline (Kernohan et al. 2001). A UD is a grid where the value for each cell represents the probability of the animal occurring in that cell. Among other uses, a UD allows for a more precise estimate of home range overlap than a simple outline.

Although there have been occasional articles comparing home range programs (e.g., Lawson and Rodgers [1997]), I am not aware of any articles that address whether common packages produce equivalent fixed kernel with LSCV home ranges.
I used telemetry locations of a territorial male coyote to examine how closely home ranges correspond between several programs: Animal Movement Extension 2.0 for ArcView 3.x (http://www.absc.usgs.gov/glba/gistools/), Biotas 1.02.1 (http://www.ecostats.com/software/biotas/biotas.htm), Home Range Extension for ArcView 3.x (http://blue.lakeheadu.ca/hre/), Home Ranger 1.5 (http://nhsbig.inhs.uiuc.edu/wes/home_range.html), and KernelHR 4.27 (http://nhsbig.inhs.uiuc.edu/wes/home_range.html). I am aware of three other packages that I was unable to test: adehabitat for R (http://cran.r-project.org/src/contrib/Descriptions/adehabitat.html), Home Range Tools for ArcGIS 9.x (http://blue.lakeheadu.ca/hre/), and Ranges 6 (http://www.anatrack.com/).
Home Range Tools is the ArcGIS version of the Home Range Extension and the two programs should produce similar results.
In addition, Hawth's Tools (http://www.spatialecology.com/htools/tooldesc.php) includes a module for kernel analysis, but it does not use LSCV so it was not included in this comparison.

Given that all of the programs purport to use the same algorithm for calculating h, and that the kernel calculations are fairly straightforward, my hope was that the programs would produce equivalent home ranges.

However, I suspected that differences in programming and implementation of the cross-validation and kernel calculations could easily result in non-trivial differences between software packages.

Methods

I used 115 locations of a territorial male coyote tracked in Tehama County, California, between 27 February 2001 and 15 April 2002.

I followed software instructions to import the locations into the various home range packages. I attempted to standardize input parameters as much as possible, and specific settings are described below. Table 1 lists some of the basic features of the programs I reviewed.

Table 1: Programs for generating fixed kernel home ranges

Program	Probability Contours	Utilization Distribution	LSCV Option	Platform
Animal Movement Extension	Yes	No	Yes	ArcView 3.x
Biotas	Yes	No	Yes	Windows
Hawth's Tools	Yes	Yes	No	ArcGIS
Home Range Extension	Yes	No	Yes	ArcView 3.x
Home Ranger	Processing Needed	Yes	Yes	DOS
KernelHR	Processing Needed	Yes	Yes	DOS

When running the Animal Movement Extension, I used the option to auto-calculate the extent, with a 10 meter cell size.

For most of the programs I evaluated, I used a 50 meter cell size, but in the Animal Movement Extension this cell size produced rough contours.

In Biotas, I used the default settings, except that I changed the grid cell size to 50 meters (Format Grid… Size… Center Distance parameter).

In the Home Range Extension, I selected unit variance standardization, fixed smoothing, volume contours, and a raster resolution of 200 (which corresponded to a cell size of approximately 50 meters). When I ran Home Ranger, I selected standardized data and a grid resolution of 200. Finally, for KernelHR I used a grid spacing of 50 meters.

Results

Each of the programs reported different statistics to a different level of detail, so directly comparing summary statistics was not possible.

Also, since some of the programs did not produce a UD, I resorted to comparing the 50% and 95% probability contours (i.e., the smallest area that encloses 50% or 95% of the probability distribution). I compared the overall area of each contour across the programs, and I produced maps in ArcGIS 8.2 to examine how well the contours overlaid each other.

For Animal Movement Extension, Biotas, and Home Range Extension, areas were calculated using XTools

3.1 for ArcGIS 8.x.

For Home Ranger and Kernel HR, areas were calculated based on the number of cells with an adjusted cumulative probability below the target contour area (Table 2). The adjusted cumulative probability is calculated from a utilization distribution that is sorted from highest to lowest probability (see Appendix). Home Range Extension and KernelHR had nearly identical areas, while Home Ranger was slightly larger. The 50% contours for Biotas and Animal Movement Extension covered approximately half the area of the 50% contours from the other programs, and the 95% contours were somewhat smaller.

Table 2: Contour areas from several home range programs.

Program	50% Contour Area (ha)	95% Contour Area (ha)
Animal Movement Extension	115.60	840.23
Biotas	95.81	876.09
Home Range Extension	199.52	946.95
Home Ranger	209.26	1013.52
KernelHR	199.00	954.50

When I compared actual contours in ArcGIS 8.2, I found that KernelHR and Home Range Extension were very similar (Figure 1).

The differences included a very small 3rd 50% core polygon and a slight extension to the main 50% contour in the Home Range Extension output.

The output from Home Ranger was also very similar to KernelHR (Figure 2) and Home Range Extension, with Home Ranger contours typically slightly larger than KernelHR contours. Animal Movement Extension and Biotas did not include the second core area that was seen in home ranges from the other programs, and when compared to KernelHR (Figures 3 and 4), both had contours that fell inside the KernelHR contours. Animal Movement Extension and Biotas generally agreed with each other, although Biotas had a smaller core area than Animal Movement Extension and more area around outlying points (Table 2 and Figure 5).

Figure 1. KernelHR output (red) compared to Home Range Extension (black). Background points are animal locations.
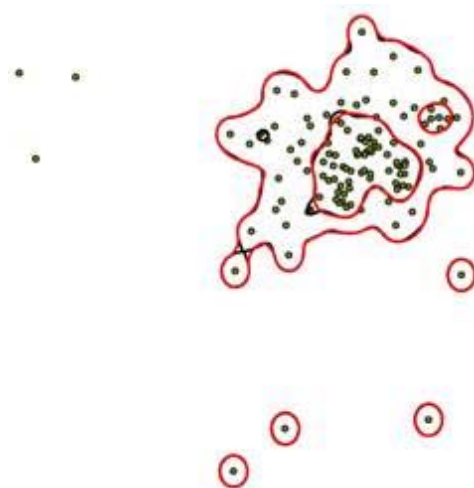

Figure 2. KernelHR output (red) compared to Home Ranger (blue).
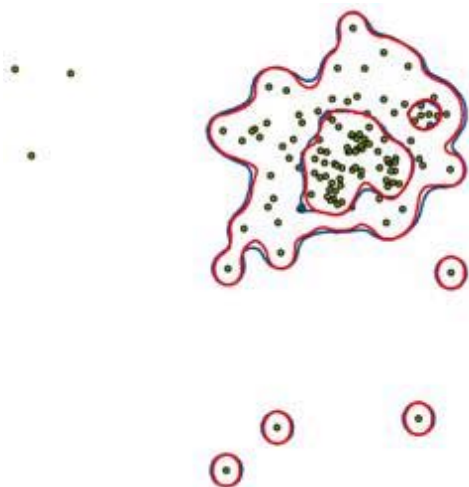
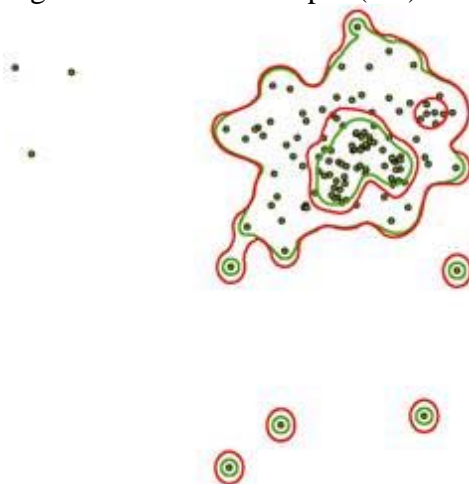Figure 3. KernelHR output (red) compared to Animal Movement extension (green).

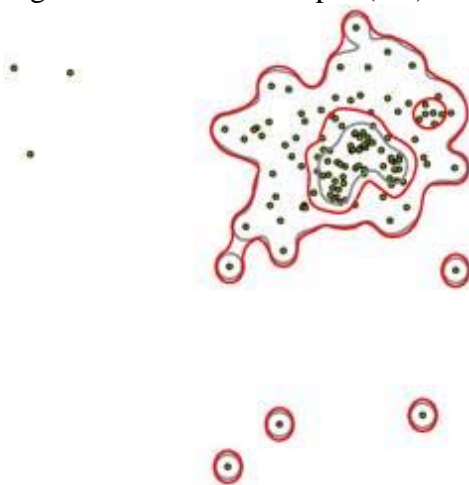Figure 4. Kernel HR output (red) compared to Biotas (gray).

Figure 5. Animal Movement Extension output (green) compared to Biotas (gray).

Discussion

My findings supported my suspicion that different home range programs would produce different results. Most strikingly, the Animal Movement Extension and Biotas produced 50% core areas that were about half the size of cores produced by the other programs, and that lacked a second area of interest. If these differences are consistent across different data sets, significant biases could be introduced by attempts to compare results obtained from different programs. Given the inconsistencies I detected, I do not recommend use of Animal Movement Extension or Biotas at this time. These programs produced results that differed from each other and from the other three programs, and they also lack options for outputting utilization distributions.

Home Range Extension, Home Ranger, and KernelHR all produced similar home ranges with the data set I used.
Comparison with additional data sets would be useful, but for now I would recommend any of these programs.
If the goal is to produce home range probability contours, then the Home Range Extension is easy to use and fully integrated into ArcView 3.x. If the analysis involves comparing different utilization distributions (e.g., calculating a grid-based volume of intersection between home ranges [Kernohan 2001]), then I recommend KernelHR over Home Ranger.
KernelHR allows the user to set the grid cell size, while Home Ranger specifies overall grid dimensions. In addition, Home Ranger only outputs values to 2 significant digits. If the analysis requires overlaying grids, it will help to have KernelHR's higher number of significant digits and the assurance that all grids have the same cell size.
Unfortunately, KernelHR and Home Ranger are not particularly user friendly, since both are DOS-based and processing is required to import the program output into ArcGIS. Instructions for using KernelHR and importing the results into ArcGIS are provided in the Appendix to this article.

Home range programs are continually evolving, and hopefully a package will be available soon that integrates into ArcGIS, outputs utilization distributions as well as probability contours, produces results that agree with other programs, and allows a variety of methods for choosing the smoothing parameter. Until then, wildlife biologists should be aware of the pros and cons of different programs, and they should remember that different software packages will produce different home ranges with the same data.

Literature Cited
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Appendix: Using KernelHR and importing the results into ArcGIS
RUNNING KERNELHR:

1) Download and unzip the KernelHR program files into c:/kernelhr. I find it easiest to run KernelHR from the DOS command line (Start… Programs… Accessories… Command Prompt in Windows 2000 or XP).
   I prepare a command line in a text editor, and then copy and paste it into the command prompt as follows.

2) Here is a sample DOS command line:
   > *kernelhr temp.txt temparea.txt 1 M 50 LSCV 1 tempgrid.txt UD*

   Kernelhr runs the program executable file

   Temp.txt is the name of the input file (must be a space delimited text file with animal ID, east coordinate, and north coordinate only).

   Temparea.txt is the name of the summary results file

   1 is the number of meters per unit of the data (keep this the same for UTM or StatePlane data

   M is for the output units (for home range area estimation). You may want KM for animals that cover a lot of ground

   50 is the number of meters per grid line (in other words, the grid coarseness or cell size). You'll likely use a value between 10 and 100 for real data; plot your biggest HR first, and decide if you have a fine enough grid.

   LSCV is for smoothing with Least Squares Cross Validation

   1 is a placeholder (no meaning for LSCV)

   tempgrid.txt is the name of your output grid

   UD specifies utilization distribution rather than density

3) Start the command prompt, and navigate to the directory where KernelHR is installed:
   > *cd c:\kernelhr*

4)
   Copy the command line from your text editor, then right-click in the command prompt to paste the command. Press Enter to run KernelHR. NOTE: if LSCV "crashes" in KernelHR (ratio = 0.05, MISE <-4, and/or volume <0.95 or >1.05, OR if LSCV fails (many disjunct 95% contours that also contain 50% contours), review the information in the KernelHR documentation for dealing with "pathological LSCV". This is most common when many locations are very close together.

FORMATTING YOUR GRID:

1) Open the output grid text file in Excel.
   Delete column "E"; this is the adaptive kernel probability and is not needed. Sort the data on column D (the fixed kernel probability) in descending order. Reformat the cells in Column D to Number, 10 decimal places. NOTE:
   if your grid is too large to open in Excel (> 65,536 rows), display in ArcGIS, decide on sections to cut, cut them in a word processor, export to a new text file, and then continue.

2) In cell E1, use the formula: = D1.
   In cell E2, use the formula: =E1+D2, then copy this formula down the column. In cell F1, use the formula = E1/E#### where #### is the last row with data. Insert a new first row, and use the following labels: ID, X_Coord, Y_Coord, FK_Prob, Cum_Prob, Adj_CP. NOTE: This can be sped

up with a macro in Excel! FK_Prob is the probability of the animal being in a given cell. Cum_Prob is the cumulative probability.

Cells with a cumulative probability below a certain value N define the smallest region of the grid where there is an N probability of the animal occurring. Adj_CP is the adjusted cumulative probability; this corrects the cumulative probability so that it sums to one.

3)   Highlight columns A-F, and Save As… Text.

IMPORTING INTO ARCGIS

1)   Open ArcGIS and click "Add Data"
2)   Navigate to the appropriate directory, find your file, and double-click on it.
3)   Right-click on the table in ArcGIS, and select "Display XY Data". The X and Y field names should fill in automatically. Hit OK.
4)   In Spatial Analyst, select Convert… Features to Raster. Select FK_Prob from the Field drop-down to make a grid of probabilities, and Adj_CP for a grid of cumulative probabilities (for making contours). The adjusted probability assures that the probabilities sum to 1.000. Select an output cell size equal to the cell size used in KernelHR. Then name it and click "OK".
5)

If you want to produce contours, use the grid based on the Adj_CP, and select Spatial Analyst… Surface Analysis… Contour.

Use a 0.05 contour interval and name the resulting shapefile before hitting OK.