

# Using GIS to Analyze Animal Movements in the Marine Environment

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\*Abstract

Advanced methods for analyzing animal movements have made few inroads in the aquatic research environment compared to the terrestrial. In addition, despite obvious advantages of integrating Geographic Information Systems (GIS) with spatial studies of movement behavior, movement analysis tools have not been integrated into GIS. In response, we developed software that integrates one of the most commonly used GIS programs (ArcView®) with a large collection of animal movement analysis tools. This application, Animal Movement, can be loaded as an extension under multiple operating system platforms (PC, Unix, and Mac OS). The extension contains more than 50 functions, including parametric and nonparametric home range analyses, random walk models, habitat analyses, point and circular statistics, tests of complete spatial randomness, tests for autocorrelation and sample size, point and line manipulation tools, and animation tools. This paper will demonstrate the use of these functions in analyzing locational data; some examples will be drawn from a sonic-tracking study of Pacific halibut (*Hippoglossus stenolepis*) in Glacier Bay, Alaska. The extension is available on the Internet at <http://www.absc.usgs.gov/glba/gistools/index.htm>.

\*Introduction

Studies investigating patterns of movement in aquatic species can be very informative regarding many issues of concern in fisheries, including population regulation, local depletion, migration, marine reserve design, and habitat selection (Freire and Gonzalez-Gurriaran 1998, Hooge and Taggart 1998, Kramer and Chapman 1999). However, little of the rich analytic field of analyzing movement patterns that has been developed and utilized in the terrestrial environment (see White and Garrott 1990) has been applied to aquatic species. A literature

review of scientific papers about fish and crabs referenced in the BIOSIS Previews® bibliographic database since 1994 indicates that of 374 articles investigating movement, only 48 examined home range patterns, no study calculated probabilistic home ranges, and none rigorously examined patterns of site fidelity, serial autocorrelation, or sample size effects. This record is in sharp contrast to studies of terrestrial species, and can partly be attributed to the difficulty of obtaining large sample sizes in the aquatic environment. However, these analysis methods have not been applied even in many movement studies of aquatic species that did have adequate sample size.

Despite the extensive development and use of analytical methods in studies of movement in terrestrial species, employing these techniques with Geographic Information Systems (GIS) has been hampered by a lack of tools. GIS provides a rich environment within which to analyze movement patterns; it allows the integration of multiple layers of habitat data into a framework capable of complex two- and three-dimensional analysis. In response to this lack of tools, we wrote a program that implements a suite of movement analysis functions within a GIS. In this paper we will discuss the program and examine methods to prepare data, conduct exploratory data analysis, perform home range and habitat selection analyses, and test other hypotheses. Discussion about much of the methodology is brief, as many of the details are beyond the scope of this paper. We have, however, referenced a wide variety of literature, which workers should peruse before utilizing the program. Data used in examples have been taken from a sonic-tracking study of Pacific halibut (*Hippoglossus stenolepis*) in Glacier Bay, Alaska between 1991 and 1996 (Hooge and Taggart 1998).

\*The Animal Movement Analyst Extension (AMAE) to ArcView® GIS

Multiple criteria need to be met by software synthesizing movement analysis with GIS. The program must be able to be integrated completely with a widely used GIS available on multiple operating systems. It should be able to work with any point data that are otherwise usable by the GIS and to create both raster (grid) and vector (polygon) results in the output data structures of the chosen GIS. It should have a full suite of analysis routines, including data exploration and animation, home range analysis, spatial statistics, habitat selection, modeling, and hypothesis testing. Ideally this program would be written in an object-oriented programming language capable of easily being extended with additional code; it should also make each of its routines available to be called by other parts of the GIS so they can be used in new and unforeseen ways.

The Animal Movement Analyst was written as an ArcView® extension. ArcInfo/ArcView® (Environmental Systems Research Institute, Inc., Redlands, California) is the most widely used GIS throughout the world at this time. The extension capability of ArcView® allows code written in the object-oriented programming language Avenue (and Visual Basic in the near future) to be loaded and unloaded at will from the GIS. While AMAE would be much faster if written in a language capable of producing compiled dynamic link libraries, doing so would make the program processor-specific. Keeping the code in the scripting language Avenue allows the code to work on multiple operating systems and processors as well as to be modified easily for other uses. By employing as many compiled routines built into ArcView® as possible, the speed of the program on newer computers is quite reasonable. AMAE is capable of utilizing any point data usable by ArcView® and produces completely compatible raster and vector outputs. It can work on any selected subset of data resulting from queries in ArcView® or other ArcView® Extensions. More than 50 functions are implemented in AMAE (Table 1). All the

major functions are written as call-able routines that can be integrated into other Avenue programs. AMAE is in the public domain and is available from the principle author or on the Internet at: <http://www.absc.usgs.gov/glba/gistools/index.htm>.

### **\*\*Preparation of the Data**

Preparing data for Animal Movement is relatively easy. The program directly utilizes Point Shape files, which can import point data from delimited text, dBase files, SQL databases, and many CAD and GIS file structures. Data can also be directly digitized onto the screen or through a digitizer tablet. Utilizing the Tracking Analyst Extension® (ESRI) with AMAE allows the real-time collection of data from GPS units or other data sources. We are working on additional modules that will allow integration with three-dimensional tracking systems from Desert Star Systems (Marina, California) and Lotek Marine Technologies, Inc. (Newfoundland, Canada). The only fields required for data analysis are X and Y coordinates. AMAE will work in any projection, but the theoretical underpinnings of some routines require coordinate systems with equal X and Y units (geographic units can be handled by re-projecting them in the View Window). AMAE's time-based functions require date in the dBase standard of ddMMyy and time of day in the 24-hour clock format of hours:minutes:seconds. Attribute tables for points and those functions of AMAE that utilize attribute data can handle any data that can be brought into ArcView®.

### **\*\*Exploratory Data Analysis**

One of the first exercises after entering or importing data into the GIS is to explore some of the general movement patterns. The Point to Polyline creation tool produces travel paths (see

Fig. 1B), which can then be used in AMAE's display and animation tools. The movement path can be displayed either one point at a time via mouse clicks or as an automated animation. The user can choose to display the attribute fields associated with each point at the bottom of the screen or in a window next to each point. If there is a date field, distance traveled as well as speed and average speed are also displayed. Animation can be set to run either forwards or backwards and at various speeds with different types of lines and point symbols. Simple or complex attribute queries can be conducted so that travel paths are restricted to certain types of events, such as daylight movements or positions within a particular depth range. Attribute sorting or summarizing routines in AMAE can also be used to restructure these travel paths. This type of exploratory analysis is helpful for generating hypotheses to be tested and for observing patterns in the data not evident from the point distributions.

#### **\*\*Home Range**

Home range calculation is often performed next. However, a home range is an analytical construct that has biological meaning only when the assumptions of the individual home range model are met and the limitations of the model understood (White and Garrott 1990). First, for a home range to exist at all the animal must exhibit site fidelity (Spencer et al. 1990, Hooge 1995). We have implemented a robust and powerful test for site fidelity in AMAE (Fig. 1A). This test is an extension of the Monte Carlo random walk test developed by Spencer et al. (1990). The test has been modified to use the actual sequence of distances traveled by the animal during each interval and has also been extended to work within a more realistic world of constrained movements (Hooge 1995). A polygon representing the space within which the random walk test is to occur can be created from any type of spatial data that can be brought into ArcView® (e.g.

bathymetry, oceanographic constraints, or substrate; see Fig. 1A). After generating the user-specified number of random walks, AMAE calculates for each walk both the mean squared distance from the center of activity and the linearity of the path; these two values are measures, respectively, of the data dispersion and of directed movement. The actual movement path's values are then compared to the ranked values of the random walks to determine significance. To be site-faithful the animal's real locations should exhibit neither significant dispersion nor significant linearity. This test can be used to discern changes in behavior between site fidelity and random or directed explorations by choosing a "time window" and then iterating the test along the entire set of points.

One other assumption common to all home range models is adequate sample size, a parameter that nonetheless varies considerably with different home range methods (Worton 1987, Boulanger and White 1990, White and Garrott 1990). Minimum convex polygons (MCP's) are the most sensitive to the sample size effect. AMAE implements a bootstrap test to examine the mean and variance of MCP home range size with varying sample size. Some other assumptions do exist for certain home range models and are discussed later.

If the preliminary data analysis indicates that site fidelity exists, the next step is to analyze the animal's home range. A full discussion of the home range concept and of the advantages and disadvantages of each home range analysis method is beyond the scope of this paper (see Burt 1943, Worton 1987, Boulanger and White 1990, White and Garrott 1990). We have chosen to implement several models based on their robustness and common usage and will discuss these only briefly. The most basic of these is the MCP (Fig. 1B), which can be considered as the space that the animal both uses and traverses. We include it primarily to allow comparisons with the many previous studies using the MCP, since it is the oldest and most

simple method. However, the MCP suffers from sample size effects, is greatly affected by outliers, and contains much area never used by an animal. Removing a certain percentage of points, such as 5%, can mitigate the outlier effect. AMAE implements a harmonic mean outlier removal method (White and Garrott 1990). Also, with knowledge of habitat relationships, areas can be clipped out of the MCP by ArcView® functions to more accurately represent the areas actually used. However, in order to avoid circular reasoning, habitat analyses should not be conducted on the resulting home range.

Probabilistic home range techniques are better than MCP's for describing how animals actually use the area within their home ranges (Jennrich and Turner 1969, Ford and Krumme 1979, Anderson 1982, Worton 1989). These are often also called utilization distributions; each cell within a probabilistic home range has an associated probability that the animal is at that location. Probabilistic models can be sensitive to serial autocorrelation, and the point statistics function in AMAE will generate a serial autocorrelation value (the  $t^2/r^2$  ratio, Swihart and Slade 1985). However, the corrections for autocorrelation may lead to more bias than the autocorrelation itself (see \*\*Future Additions). All the home range functions described here allow the user to select the desired probability contours; all produce vector output and either directly produce raster output or produce output that is easily changed into raster files with ESRI's Spatial Analyst®. When choosing output contours, it is useful to consider the 95% contour as that area the animal actually uses and the 50% contour as the core area of activity. Statistical comparisons between individuals are best done with the 50% contour, as it is less affected by deviations from the assumptions of the home range models. All of the home range methods can be batch-processed in AMAE using multiple attribute fields to separate different home ranges.



One of the most robust of the probabilistic techniques is the kernel home range (Fig 1D; Worton 1989). Animal Movement implements a fixed kernel with the smoothing factor calculated via least-squares cross-validation (LSCV), which is widely considered the most robust technique (Seaman and Powell 1996). However, the ad hoc value is often quite close to the LSCV, especially with large sample sizes, despite its dependence on a normal distribution of the kernels created around each point; the ad hoc value may offer a smoothing factor that is more comparable between studies.

Animal Movement also implements the Jennrich-Turner home range (Fig. 1C; Jennrich and Turner 1969). While having the advantages of speed and simplicity, this algorithm assumes the data follow a bivariate normal distribution, a requirement that is often not met by animals in the wild. The random normal point generation tool in AMAE does allow the user to test the actual point pattern against a random normal distribution with the same axis and variance. The Jennrich-Turner method, like the MCP, is principally useful for comparison with older studies as well as for generating the principle axis of the data.

The harmonic mean home range method is also included (Dixon and Chapman 1980). This technique is especially useful in determining animal activity centers. AMAE does not calculate area values for the harmonic mean home range, though, as this method is considered less robust than the kernel (Worton 1987).

When sample sizes are very large (thousands of points per individual) and serial autocorrelation is a significant issue, AMAE provides triangulation and tessellation as two alternative home range models (Silverman 1986). Both techniques essentially calculate the density of location points without any assumptions about the underlying distribution of the data. The Delaunay triangulation builds a triangulated irregular network (TIN) from each point to all

other points possible without intersecting such lines from other points. The Dirichlet tessellation creates a polygon around each location such that all parts of the polygon are closer to the enclosed point than to any other point. To determine density, the output from these routines can be run through AMAE's area calculation tool and then contoured based on inverse area of the triangles or polygons. The triangulation routine is also useful for looking at slope relationships, and the tessellation routine for examining spatial relationships between points and nearest features.

### **\*\*Hypothesis Testing**

The ultimate goal of most movement studies is to compare the patterns of observed movement against a null hypothesis to elucidate such processes as habitat selection, relationships between individuals, population dispersion patterns, or marine reserve efficacy. There are multiple tools within AMAE to accomplish such hypothesis testing. Currently, there are only limited statistical capabilities in AMAE, with some additional functions available through Spatial Analyst®. However, attribute data created in AMAE can easily be exported to stand-alone statistical applications, particularly those that readily accept delimited data or dBase files such as SPSS® (SPSS Inc., Chicago, Illinois), SAS®, and StatView® (SAS Institute Inc., Cary, North Carolina). Also, many of the functions in AMAE can easily be called from Avenue, allowing the creation of hypothesis-specific bootstrapping or Monte Carlo tests.

One of the primary advantages of integrating GIS with the study of animal movements is the powerful environment available for examining species-habitat relationships. Several functions have been programmed into AMAE to aid in examining habitat selection. The first of these is the classification tool, which allows animal locations to be classified by the polygon,

line, or grid cell on which the points lie. These classified attribute tables can then be exported to a statistical package to conduct the appropriate test (Allredge and Ratti 1992). Not all the habitat that exists in the study area or home range is available to an organism at any particular time. To address this issue we have implemented an extension to the habitat selection algorithm used by Arthur et al (1996). This availability function uses the movement patterns of the animal to determine the area that could be utilized at each location and then compares that to the choice made at the next movement. This method is especially relevant when the home range is much larger than the animal's daily movements.

The two methods described above are prone to the loss of both power and robustness when there are significant errors in either the animal locations or habitat polygon mapping (Nams 1989), and such errors are common. For these situations, habitat analysis techniques that utilize either probabilistic home ranges or univariate distance measures are appropriate. AMAE implements a version of compositional analysis (Aebischer et al. 1993) that uses the utilization distribution of the animal rather than its point locations to determine habitat selection.

Alternatively, converting the spatial relationship between the location points and habitat into a univariate distance measure decreases the effect of small errors in location by converting categorical data into a continuous variable. This distance analysis, named "spider" because of the graphics that it produces, calculates the distance between points and the nearest habitat (to either the edge or center of a polygon or line) or between the points and all habitats (Fig. 2). These distance tables can then be exported to a statistical package for parametric or nonparametric analyses of variance.

There are two functions in AMAE to examine hypotheses about directed movement. For movements that are directed but occur both to and from locations, the site fidelity function can

be used to examine either attachment to that location or directed movement towards it. For movement that occurs in only one direction, circular statistics can be employed. AMAE implements a test for significant circular angle (Batschelet 1981) and produces a graphical circular histogram with mean vector.

Movements of one individual may affect the movements of others through such processes as territoriality, competition, or reproduction. The relationship between the movements of two individuals can be examined for both dynamic and static interaction (Doncaster 1990). Dynamic interaction is the spatial relationship between the simultaneous movements of two individuals. AMAE implements a moving time-window bootstrap test (Hooge 1995) to determine whether two movement paths exhibit either positive or negative dependence or are random with respect to each other. Static interaction is the comparison of the movements of two individuals without regard to time. This test is implemented by calculating the correlation between two individuals' probabilistic home ranges (Hooge 1995). For the null hypothesis, random points are generated within the area of MCP home range overlap and are then compared with the actual correlation.

Many spatial hypotheses that users may wish to investigate do not have specific tests available in the literature. AMAE has multiple tools to create Monte Carlo or bootstrap tests; these can either be used manually at the graphical user interface or can be strung together by calls in Avenue scripts to build complex analyses. These tools include random point generation functions (utilizing several different distributions; see Fig. 2), random walk functions, and random selection functions, in addition to aggregation and summarizing functions. There are also two tests for complete spatial randomness (CSR) in AMAE, nearest neighbor analysis (Clark and Evans 1954) and a Cramer-Von Mises test of CSR (Zimmerman 1993). The point statistics

function also produces nearly 40 different statistical values for point patterns, including graphical output of many values (e.g. principle axis, harmonic mean, and geometric mean).

#### \*\*Future Additions

In future versions we hope to provide several commonly requested functions that are not yet available in AMAE. These include triangulation capability to build point location files from multiple bearings, additional habitat selection routines, Fourier home range analysis, more modeling tools, more flexible time formats, tests for serial autocorrelation, and three-dimensional home range methods. Currently we have a population viability analysis module that we hope to expand with spatially specific individual-based modeling tools and incorporate into Animal Movement, in order to integrate individual movement analysis with population-level modeling. We have purposefully omitted a test for serial autocorrelation from AMAE other than calculating the overall  $t^2/r^2$  ratio. We have done so because we feel that such tests, as currently constructed, are flawed and produce a greater bias by excluding points from analysis than that caused by autocorrelation (for example see Andersen and Rongstad 1989, Reynolds and Laundré 1990, Otis and White 1999). We are currently working on more robust methods to determine when serial autocorrelation is a serious problem and what to do about it. We are also working on extending the home range methods implemented in AMAE into three dimensions; however, this effort is hampered by the limitations of present three-dimensional GIS systems such as ArcView's® 3D Analyst® (ESRI), which lack the true volumetric capabilities of programs such as PV-Wave® (Visual Numerics, Inc., Houston, Texas).

#### \*Conclusion

Animal Movement significantly extends the capabilities of ArcView® GIS into the study of movement patterns and habitat selection. It permits the user to conduct a wide range of spatial analyses and hypothesis testing on movement data taken from observation and from radio-, sonic-, and satellite-tracking data. AMAE is completely integrated within the GIS environment, allowing complex animal-habitat relationships or movement hypotheses to be examined. The use of a non-compiled language can result in significant processing times for large data sets or for the more numerically intensive routines that cannot take advantage of built-in compiled code. However, the Avenue language permits the program to run on multiple platforms and operating systems and to be extended easily by the user. In addition, the use of batch routines allows processing of large data sets to occur without user input. We hope that Animal Movement will help encourage other workers also to produce GIS extensions rather than stand-alone code.

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Figure 1. A test for site fidelity and the existence of a home range (A), with land as a constraining polygon for ten random walks; and three different home range models: a minimum convex polygon (B), here shown enclosing the actual movement path of the animal tested in (A); a Jennrich-Turner 95% ellipse home range (C) with the major and minor axes of the data shown; and a fixed kernel home range (D) with least-squares cross-validation of the smoothing factor, showing the 50%, 75%, and 95% utilization distribution contours. Data are from sonic-tracking locations of Pacific halibut in Glacier Bay, Alaska.

Figure 2. Distance analysis between Pacific halibut locations and rocky habitat found on reef tops in Glacier Bay, Alaska. The distance to edge (spider) function was first run on 96 randomly-selected actual halibut locations; an equal number of random points was then generated uniformly-randomly within the study area (in water only), and the spider distance function was run between the random points and the rocky-reef habitat. There was a significant association of halibut positions with these reefs compared to the random locations (Mann-Whitney  $U$ ,  $Z = 6.23$ ,  $P < 0.001$ ).

Table 1. Tools implemented in the Animal Movement Analyst Extension. Column 1 refers to whether the function is found within the View document (V) or the Table document (T).

Column 2 is whether the function is presented as a Menu (M), Tool (T) or Button (B). An asterisk indicates routines with functions that can easily be called by other Avenue programs.

1	2	Name of Function	Description
V	M	Create Polyline from Point File	Creates a Polyline Theme connecting points in the order of the records
V	M	Animate Movement Path	Animates the movement path with the user-selected values
V	T	Display Movement Path	Moves through the movement path one position at a time via mouse clicks
V	M	Set Movement Path Variables	Allows user to set the graphics and field display for the two path functions
V	M	Static Interaction*	Analyzes spatial correlation between two individuals without regard to time
V	M	Dynamic Interaction*	Analyzes the simultaneous spatial correlation between two individuals
V	M	Location Statistics*	Generates 38 location statistics and graphical output from Point Themes
V	M	Nearest Neighbor Analysis*	Conducts a Nearest Neighbor Analysis for CSR in the specified Polygon
V	M	Cramer-Von Mises CSR*	Conducts a C-VM test for CSR within the specified Polygon
V	M	Circular Point Statistics*	Determines the mean angle, significance, and creates a graphic histogram
V	M	Harmonic Mean Point Theme*	Conducts a harmonic mean home range analysis, producing a Point Theme
V	M	Spider Distance Analysis*	Conducts multiple types of distance analysis for habitat selection
V	M	Compositional Analysis*	Conducts a compositional analysis of habitat selection
V	M	Availability Analysis*	Conducts an availability analysis of habitat selection
V	M	Classify Points by Polygons	Classifies each Point by the Polygon or Line on or within which it lies
V	M	Random Selection*	Randomly selects a user-specified number of points
V	M	Outlier Removal*	Removes the user-specified % of points via the harmonic mean method
V	M	Generate Random Points*	Generates several types of random distributions within a Polygon
V	M	Add XY Coordinates to Table	Adds X and Y coordinate Fields to the Attribute Table
V	M	Calculate Successive Distances	Calculates the distance between sequential Points
V	M	Calculate Distance	Calculates the distance between a Point and all objects in another Theme
V	M	Summarize Attributes	Aggregates the Attribute Table based on the user-specified requests
V	M	Sort Shape File	Permanently sorts the Point File
V	M	Histogram	Creates a histogram based on a Theme's Legend Classification
V	M	Batch Home Range Processing	Performs the selected home range analysis on multiple Point Themes
V	M	Minimum Convex Polygon*	Calculates the minimum convex polygon home range
V	M	Kernel*	Calculates a fixed kernel home range with multiple options
V	M	Jennrich-Turner*	Calculates a Jennrich-Turner bivariate normal home range
V	M	Harmonic Mean*	Calculates a harmonic mean home range, but no area
V	M	Delaunay Triangulation*	Generates a TIN between points for a distribution-free home range
V	M	Dirichlet Tessellation*	Generates polygons around points for a distribution-free home range
V	M	MCP Sample Size Bootstrap	Bootstrap test examining the effect of sample size on MCP home range area
V	M	Site Fidelity Test*	Performs a site fidelity test with or without a constraining Graphic
V	B	Recalculate area, length...	Updates area, length, and circumference in the units of the View projection
V	B	Point Buffer	Creates a Buffer Shape File of the specified distance around each Point
V	B	Delete Graphics	Deletes all Graphics in the View
V	T	Display Coordinates	Displays the geographic and UTM coordinates at the specified location
V	T	Nearest Neighbor*	Allows the user to draw a rectangular extent and conduct an NN test
V	T	Random Normal Points	Allows the user to draw a circle and generate a random normal distribution
T	M	Field Properties	Displays the Field properties of the selected Field in the active Table
T	M	Add Record Numbers	Adds the record numbers in either the Table or Vtab order
T	M	Selection to DBF	Exports the selected records to a new .dbf-formatted Table
T	M	Create Cumulative Field	Creates a new Field with the cumulative total from the selected Field
T	M	Histogram	Creates a histogram based on a selected Table Field



