

# Genetic Landscapes GIS Toolbox

*Tools to create genetic divergence  
and diversity landscapes in ArcGIS.*

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## Website

[http://www.werc.usgs.gov/products/MGL\\_toolbox](http://www.werc.usgs.gov/products/MGL_toolbox)

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## Overview

The Genetic Landscapes GIS Toolbox contains tools created to map the patterns of genetic divergence and diversity for multiple species within the Geographic Information System software package ArcGIS® (ESRI, Redlands, CA). There are four tools in the package. The **“Single Species Genetic Divergence”** tool creates a genetic divergence raster surface from pairwise population genetic distances for a single species or marker/locus. The **“Single Species Genetic Diversity”** tool creates a raster surface based on intra-population genetic diversity for a single species. The **“Multiple Species Genetic Landscape”** tool creates three raster surfaces; an average, variance and a count of input surfaces per cell, from multiple divergence or diversity surfaces that have geographic overlap (as created with the first two tools). The **“Create Feature Class from Table”** tool is a utility that creates a feature class from a table. The Multiple Species Genetic Landscape tool was scripted in the Python computing language. The remaining three tools were created in ModelBuilder® (ESRI).

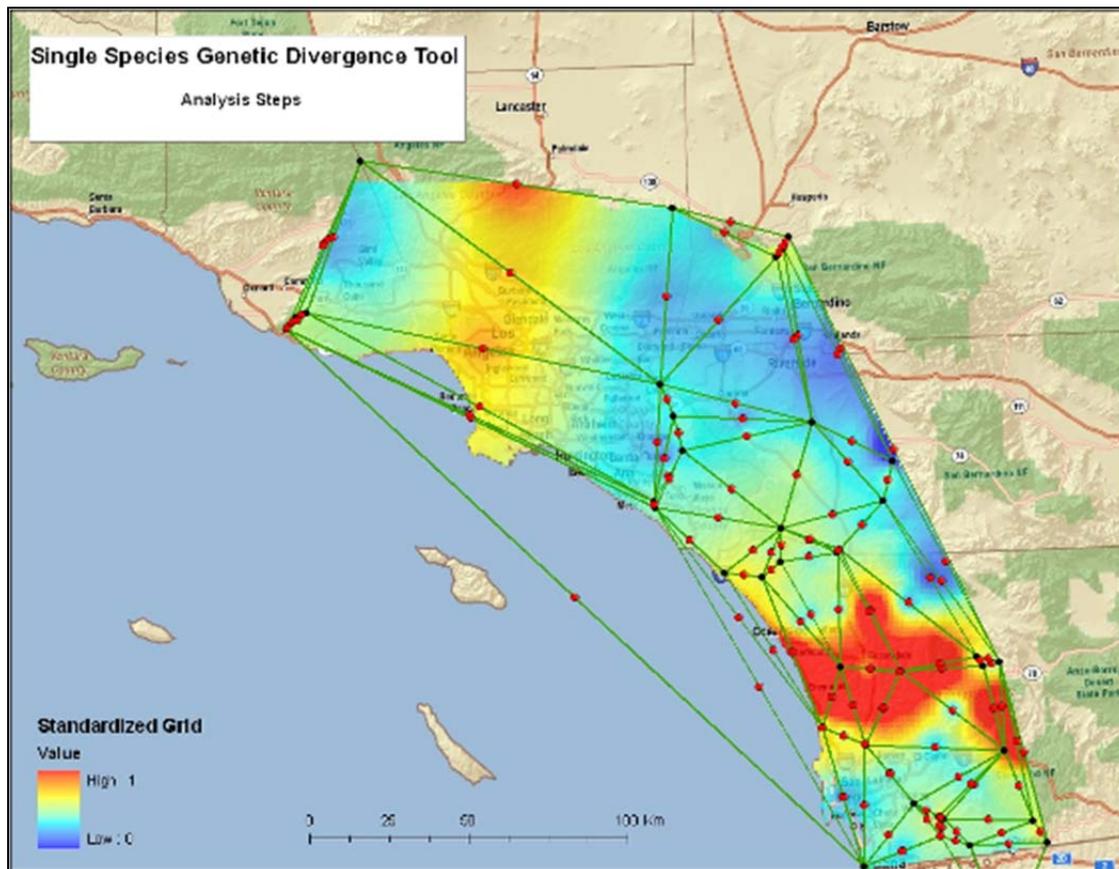
## Rationale and Methodology

The rapidly growing field of landscape genetics aims to investigate the influences of landscape features on microevolutionary processes, for example gene flow and genetic differentiation (Keller and Largiadere 2003; Manel et al. 2003). A promising new analysis approach is the creation of “genetic landscapes” to visualize the distribution of genetic diversity across geographic space (Miller 2005). A potentially powerful application of this approach is visualization and analysis of genetic landscape surfaces in combination with other georeferenced environmental data layers in a Geographic Information System (GIS). Using this approach, one can evaluate hypothesized geographic barriers to movement and gene flow, and other landscape features associated with patterns of genetic diversity. Additionally, it is possible to overlay genetic landscapes from multiple sources (e.g. different types of genetic data: mtDNA/nuDNA sequences, microsatellites; or multiple species or taxa) to examine patterns of concordance and to locate geographic regions that are important reservoirs of genetic diversity across taxa.

We have developed a series of GIS tools to map genetic landscapes and to summarize multiple genetic landscapes as average and variance surfaces in the ArcGIS software package. Together, the tools contained within this toolbox automate a series of calculations and data manipulations to create genetic landscape surfaces directly from tables containing genetic distance or diversity data and sample location coordinates. This allows users with little GIS experience to create and analyze these complex raster surfaces with efficiency and accuracy. The multiple species genetic landscape approach provides an avenue to incorporate measures of genetic differentiation (and evolutionary history and potential) into GIS-based systematic conservation assessment and land-use planning. A more detailed description and application of these methods can be found in Vandergast et al. (2008). The series of calculations is briefly described below for each tool.

## Single Species Genetic Divergence Tool

The single species divergence tool creates a genetic landscape based on pairwise population genetic divergence as measured among multiple collection locations or populations. The method is similar to those implemented in the program Alleles in Space (<http://www.marksgeneticsoftware.net/AISInfo.htm>; Miller 2005). A network connecting all collection locations to their nearest neighbors with non-overlapping edges is drawn. The midpoints between each connected edge are mapped and genetic divergence values are attached to these points. A spatial interpolation algorithm, inverse distance weighted interpolation, is used to generate a surface from the mapped genetic distance values (Figure 1). To avoid extrapolating beyond the original collection locations, the genetic landscape is clipped to the extent of the original network (sampling extent) and to the boundaries of the region of analysis (as determined by the user). The tool will create a surface with the raw genetic divergence values, and another surface with values scaled between 0 and 1 to allow equal weighting of multiple surfaces for inclusion in the Multiple Species Genetic Landscape Tool.



**Figure 1:** Image displaying the results of the analysis steps of the Single Species Genetic Divergence Tool. Black points represent collection locations. Green lines represent the non-overlapping edges connecting each collection point to its nearest neighbors. Red points represent the midpoints between collection locations where genetic divergence values are mapped. The raster surface is the Inverse Distance Weighted interpolation of these genetic divergence values. The surface edges that fall outside of the green lines are clipped by the tool to avoid extrapolation. This image has also been clipped to the coastline of southern California.

*Calculating genetic divergence values:* The tools provided in this package are designed to map and visualize patterns of genetic divergence, but do not calculate these values directly from raw genetic data. We leave it to the discretion of the user to determine the most appropriate measure of genetic divergence for their data. Pairwise genetic divergence values (e.g.  $F_{ST}$ ,  $\Phi_{ST}$ ) can be calculated following several different methods (Hartl and Clark 1989) as implemented in Arlequin (Excoffier et al. 2005) and other population genetic analysis software packages. It is commonly found that genetic differences accumulate as a function of increasing geographic distance (Slatkin 1993). Utilizing residual values from a regression of geographic distance on genetic divergence allows one to remove the effects of simple distance on genetic divergence to reveal regions of unusually high or low divergence (Manni et al. 2004). We recommend using reduced major axis regression for this, which can be implemented in the software Isolation by Distance Web Service (IBDWS) (Jensen et al. 2005). Therefore, for visualizing genetic surfaces on a landscape, we recommend first regressing geographic distance against genetic divergence, and utilizing the residuals from this analysis as the input genetic distance values.

### ***Single Species Genetic Diversity Tool***

The single species diversity tool creates a genetic landscape similar to the genetic divergence tool, but it is based on within-site population genetic diversity for multiple populations or collection locations within a species. From a starting file containing latitude, longitude and a genetic diversity measure for each population, inverse distance weighted interpolation is used to generate a surface from the mapped genetic distance values. To avoid extrapolating beyond the original collection locations, the genetic landscape is clipped to the extent of the input collection points (sampling extent) and to the boundaries of the region of analysis (as determined by the user). As with the single species divergence tool, two output surfaces will be created, one with the raw values and another with the values scaled between 0 and 1.

There are multiple estimators of genetic diversity that can be calculated, and we leave it to the user to determine the metric best suited to their data. Genetic analysis software packages such as PAUP (Swofford 2002), Arlequin (Excoffier et al. 2005), FSTAT (Goudet 1995) and GENEPOP (Rousset 2008) can be used to calculate these values from raw genetic data.

### ***Multiple Species Genetic Landscape Tool***

This tool calculates the average and sample variance of multiple single species divergence or diversity surfaces (as calculated with the previous tools) and displays these as a multiple species genetic landscape. From the input genetic surfaces, a raster calculator is employed to calculate a simple arithmetic mean in each grid cell:

$$\bar{X} = \frac{\sum X_i}{n}$$

To better explore data, a second surface, sample variance, which represents the dispersion of the individual species' genetic landscape values from the average multiple species genetic landscape, is calculated using the standard formula:

$$s^2 = \frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n-1}$$

Finally, a third output surface is generated that shows the count of input surfaces that overlap in each cell of the multiple species genetic landscape. This allows the user to visually assess how many individual species are contributing to the multiple species genetic landscape for any given cell, in cases where individual species surfaces do not show complete overlap.

### ***Create Feature Class from Table Tool***

This tool is included to assist in creating the feature class that is necessary for running the Single Species Genetic Divergence Tool. This tool creates a feature class from an input table. The table can be an ASCII file, dbf or a Microsoft Excel<sup>®</sup> worksheet. The input coordinate system is defined and the output feature class coordinate system is specified.

## **Operation**

### ***Hardware***

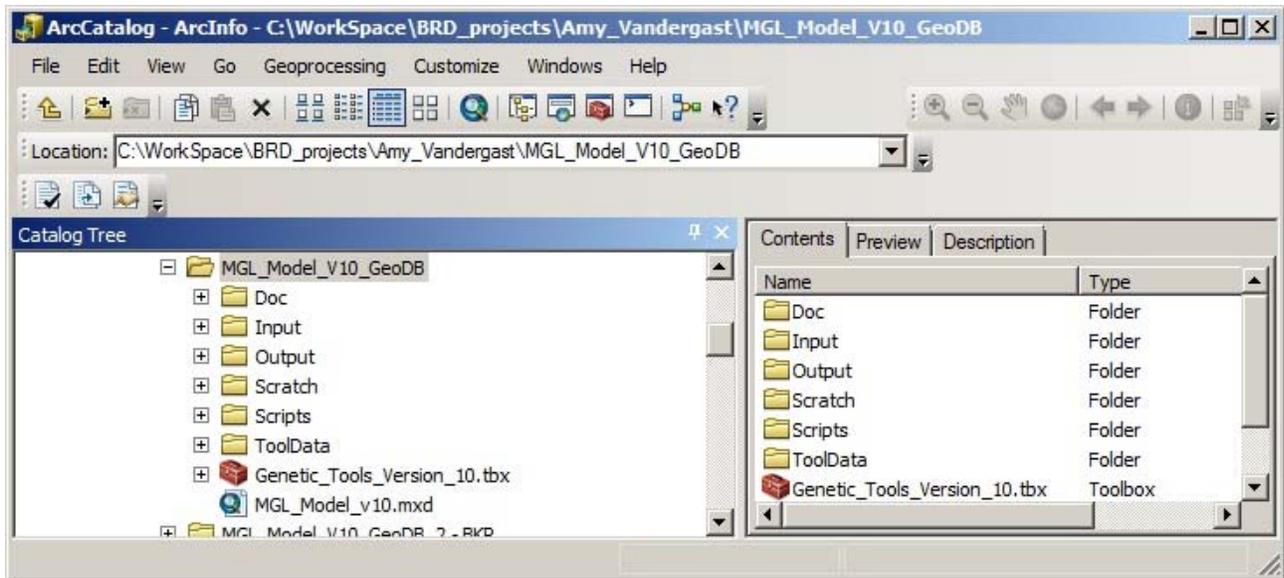
ArcGIS is supported on Windows 2000 or later. A CPU speed of 1.6 GHz with an Intel Core Duo, Pentium 4 or Xeon Processors, a minimum of 1GB RAM and 2.4 GB of hard drive space are required. More information can be found at the ESRI Support Center (<http://wikis.esri.com/wiki/display/ag93bsr/ArcGIS+Desktop>).

### ***Software***

The Genetic Landscapes GIS Toolbox was originally developed using ArcGIS 9.3.1 and requires ArcMap Spatial Analyst and 3D Analyst extensions to run. The tools have been updated to run in ArcGIS version 10.

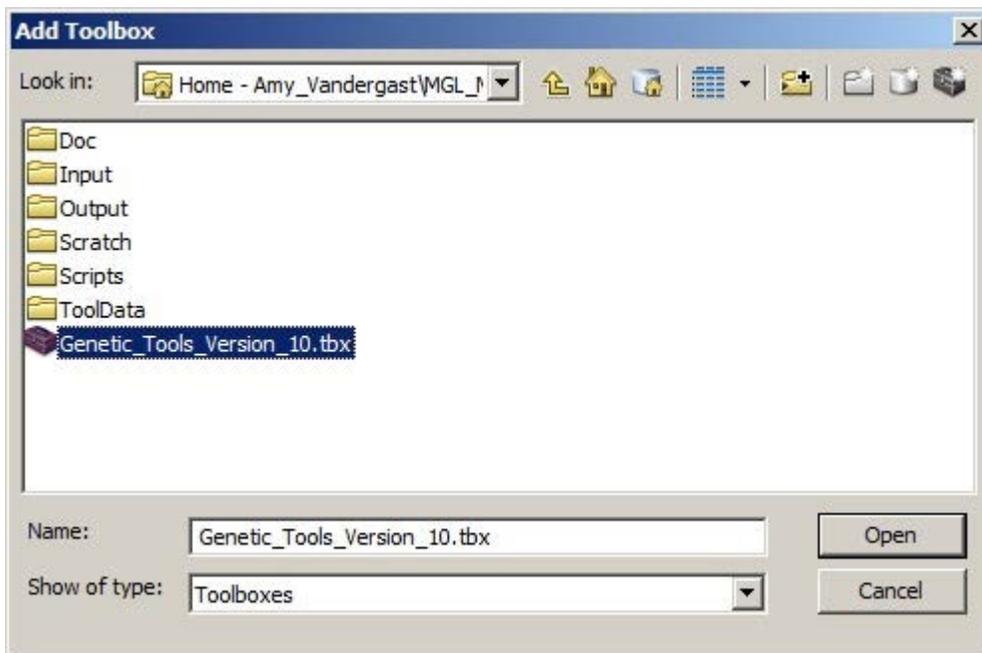
### ***Installation***

The tools and associated files and folders are contained in the zip file, MGLModel.zip. Copy this file to a local or network drive and extract the zip file. You should get a file structure similar to that shown below in ArcCatalog with the model contained in the Genetic\_Tools\_Version\_10.tbx toolbox file.

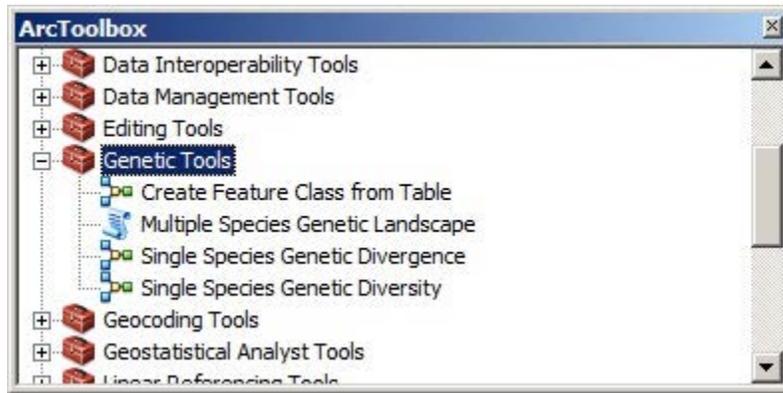


To use the tools, you can either open the provided MGLModel\_v10.mxd map document or open a new or preexisting ArcMap document. The tools will be accessible in the ArcToolbox. Double clicking on the red toolbox icon on the ArcMap toolbar will bring up the ArcToolbox.

To open the Genetic Landscapes GIS Toolbox in a new ArcMap document right click in the white space area of the ArcToolbox window and select Add Toolbox. Navigate to the drive and directory where you copied the toolbox and select it. Then click Open. For more help on adding toolboxes to ArcMap, see ESRI help page at [http://help.arcgis.com/en/arcgisdesktop/10.0/help/Tour\\_of\\_managing\\_tools\\_and\\_toolboxes](http://help.arcgis.com/en/arcgisdesktop/10.0/help/Tour_of_managing_tools_and_toolboxes)



It should add a new toolbox called ‘Genetic Tools’ to your ArcToolbox. The toolbox contains four tools (Single Species Genetic Divergence, Single Species Diversity, Create Feature Class from Table, and Multiple Species Genetic Landscape).



*Note: Make sure to have the Spatial Analyst and 3D Analyst extensions enabled in the ArcMap project. Click the Tools menu in ArcMap. Click Extensions and check the Spatial Analyst and 3D Analyst check boxes. Click Close. If these extensions are not enabled, the tools will not run.*

*Also Note: The Multispecies Genetic Landscape Tool will not run if there are any spaces in the path name of the working directory.*

## Running the Single Species Genetic *Divergence* Tool

### Step 1: Creating Input Files

The single species divergence tool requires three separate files to run, a feature class containing required attributes of collection location points, a table containing pairwise population divergence values in column format, and a grid that defines the spatial boundaries for the analysis. Feature classes can be easily created from spreadsheet format containing an alpha numeric code for each population and coordinates using the "Create Feature Class from Table" tool that is also included in this package.

**Location feature class attributes:** This is an example of an attribute table from a feature class representing the sampling points of the species of interest. The model will look for an attribute labeled popcode that contains alpha numeric population codes, all other fields are optional.

*Note: field names are not case sensitive.*

The attribute table should look like this:

OBJECTID*	Shape*	Popcode	Population	Longitude	Latitude	Datum
1	Point	1	SycamoreCanyon	-118.94862	34.08848	NAD83
2	Point	2	LosAlisosCanyon	-118.89697	34.06314	NAD83
3	Point	3	PointDume	-118.79942	34.05922	NAD83
4	Point	4	SolsticeCanyon	-118.74751	34.03771	NAD83
5	Point	5	OldTopangaCanyon	-118.6163	34.0986	NAD83
6	Point	6	PacificPalisades	-118.5304	34.0622	NAD83
7	Point	7	PalosVerdes	-118.40751	33.77734	NAD83
8	Point	8	GriffithCityPark	-118.30818	34.14543	NAD83
9	Point	9	SunsetCanyon	-118.2898	34.201	NAD83
10	Point	10	MillardCanyon	-118.1624	34.2103	NAD83
11	Point	11	ChantryFlats	-118.023	34.19606	NAD83
12	Point	12	RinconFireStation	-117.86337	34.23798	NAD83

The field definitions for the fields included in this example are:

Name	Data type	Length	Precision	Scale	Definition
Popcode	String	50	-	-	population number
Latitude	Double	16	15	6	decimal degrees
Longitude	Double	16	15	6	decimal degrees

The required field, popcode, must be the first field in the attribute table (after ObjectID and Shape). Additional data fields placed after popcode are optional. The feature class must have a defined coordinate system so that ArcMap can correctly map the data and produce accurate results. It can be in the geographic coordinate system (as shown above in decimal degrees with North American Datum 1983 (NAD 83), or a projected coordinate system such as USA Contiguous Albers Equal Area Conic with NAD 83 (as is used in the included ArcMap document (MGLModel\_v10.mxd), or any other projection appropriate for the user designated study area. We recommend using a projection with a Cartesian coordinate system (eg. NAD 83 Albers), with a map unit such as meters.

*Note: The map projections must be identical for the feature class and study area grid.*

**Table with genetic distance values:** This table can be formatted as a Microsoft Excel spreadsheet, an ASCII or dbf file. The table must contain three specifically labeled data columns that the model will use. (See example below). If they do not exist, the model will fail. The first two columns denote the two populations for which the pairwise genetic distance value is calculated. These must be labeled Pop1 and Pop2 and the **values in these data fields should exactly match the alpha numeric codes in the Popcode attribute of the feature class.** The Pop1 and Pop2 fields are used as a composite key to match up the Gen\_Dist values from the table with the Popcode field in the species feature class. (Each population or location sampled must have a unique Popcode). These values can be alpha numeric. The model looks for a third specific column name Gen\_Dist. This contains the pairwise genetic distance or residual genetic distance values that will be assigned to the geographic midpoints between collection locations.

	A	B	C	D	E	F
1	Pop1	Pop2	Gen_Dist			
2	1	2	0.3827			
3	1	3	-1.3444			
4	1	4	5.1975			
5	1	5	3.7890			
6	1	6	0.5135			
7	1	7	-8.5822			
8	1	8	-7.5842			

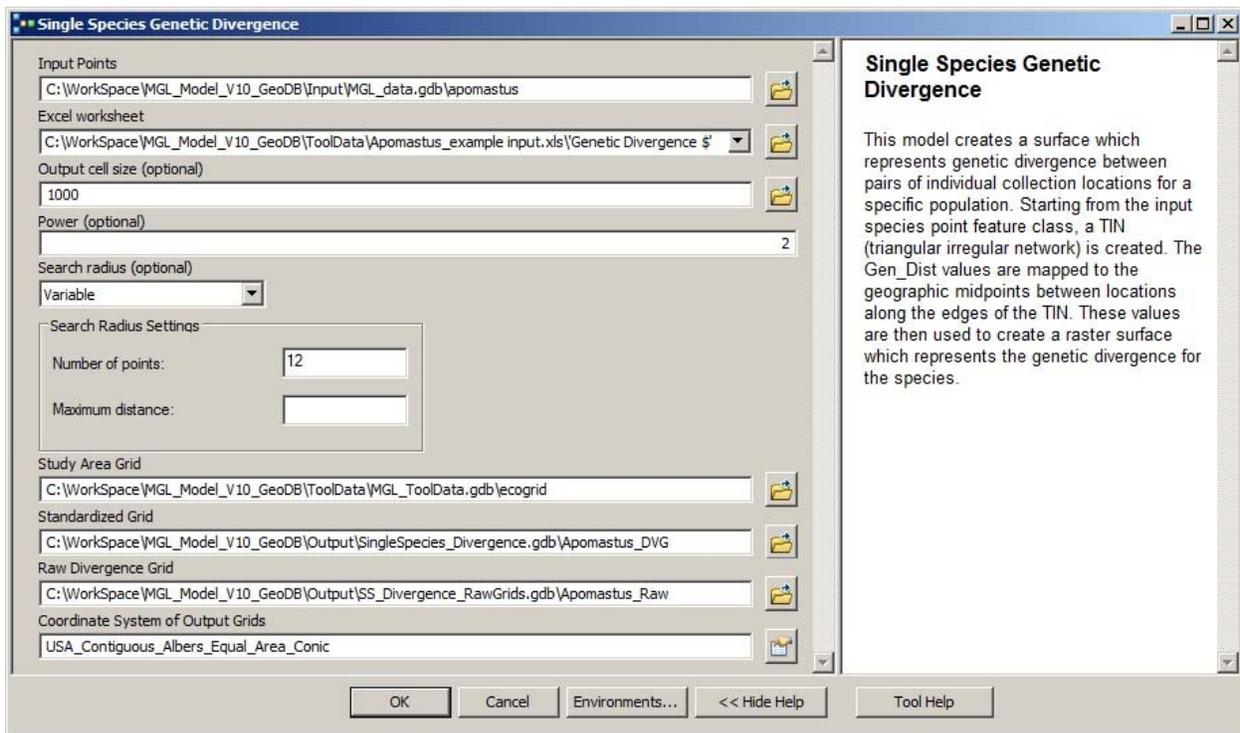
**Creating a Study Area Grid:** The study area grid file is a user defined raster grid that encompasses the study area. To convert a polygon (a feature class or shape file) into raster (grid) format, use the “Polygon to Raster” Tool in the Conversion Tools -> To Raster toolbox with the following steps:

1. Click the Input features drop-down arrow and select the feature layer you want to convert to raster. Alternatively, click the browse button to navigate to the location of a feature dataset.

2. Click the Field drop-down arrow and click the field you want to use in the conversion process. This is the field used to assign values to the output raster. It can be any field in the input feature attribute table. The field you choose will be added to the output raster's attribute table.
3. Type a value for the cell size of the output raster.
4. Type a name for the output raster.
5. If you accept the default path for the output, or you just type a name, the output raster will be written to the location set for your working directory on the General tab of the Options dialog box. You can also type the path to a different location on disk, for example, c:\data\myresult (myresult being the name of an output GRID).

## Step 2: Running the Divergence Tool

Double click the Single Species Genetic Divergence tool. You should see the model dialog box:



## Divergence Tool Parameters

**1. Input points** – Navigate to the drive and directory of the feature class that represents sampling points for the species of interest. If you don't have your data in feature class format you can use the Create Feature Class from Table tool in the Genetic Landscapes GIS Toolbox.

**2. Excel worksheet** - Navigate to the drive and directory of the table containing the population codes (Pop1 and Pop2), and the genetic distances (Gen\_dist) corresponding to the feature class of the species of interest above.

**3. Output cell size** - Enter the cell size for the output genetic surface (default 1000 map units).

**4. Power** - The exponent of distance. Controls the significance of surrounding points on the interpolated value. A higher power results in less influence from distance points. It can be any number greater than zero, but the most reasonable results will be obtained using values from 0.5 to 3. The default is 2.

**5. Search radius** - Defines which surrounding points will be used to control the raster. There are two options; variable and fixed. Variable is the default. It has two search radius settings {Number of points} (with a default of 12) and {Maximum distance}. For more complete help, see <http://help.arcgis.com/en/arcgisdesktop/10.0/help/IDW>

**6. Study area grid** - This is the grid which is used to clip the final single species genetic divergence grid. There is no default set for this parameter. The user should create or select a grid that represents the spatial extent of the area of interest for their specific study, for example, an ecoregion. When you use the GIS genetic tools you will need to navigate to the drive and directory of the ecoregion grid of interest.

**7. Standardized grid** – Create a name for the final output genetic divergence grid. The grid name must be 13 characters or less with no spaces or special characters. The default location to write output to is: \MGLModel\Output\SingleSpecies\_Divergence.gdb file geodatabase. The tool will also generate a second grid, called Rawgrid in the \MGLModel\Scratch\MGL\_Scratch.gdb geodatabase. This one will contain the raw genetic distance values.

*Note: If you use the Landscape Genetics GIS Toolbox in a new project or from a drive and directory other than the one the tool was extracted to from the zipped file, you will need to navigate to the drive and directory you would like the output to be written to. Also, make sure all the datasets (input points, study area grid) and the data frame in ArcMap are set to the same map projection.*

The output grids (Figure 2) can be used as input files for the Multiple Species Genetic Landscape tool.

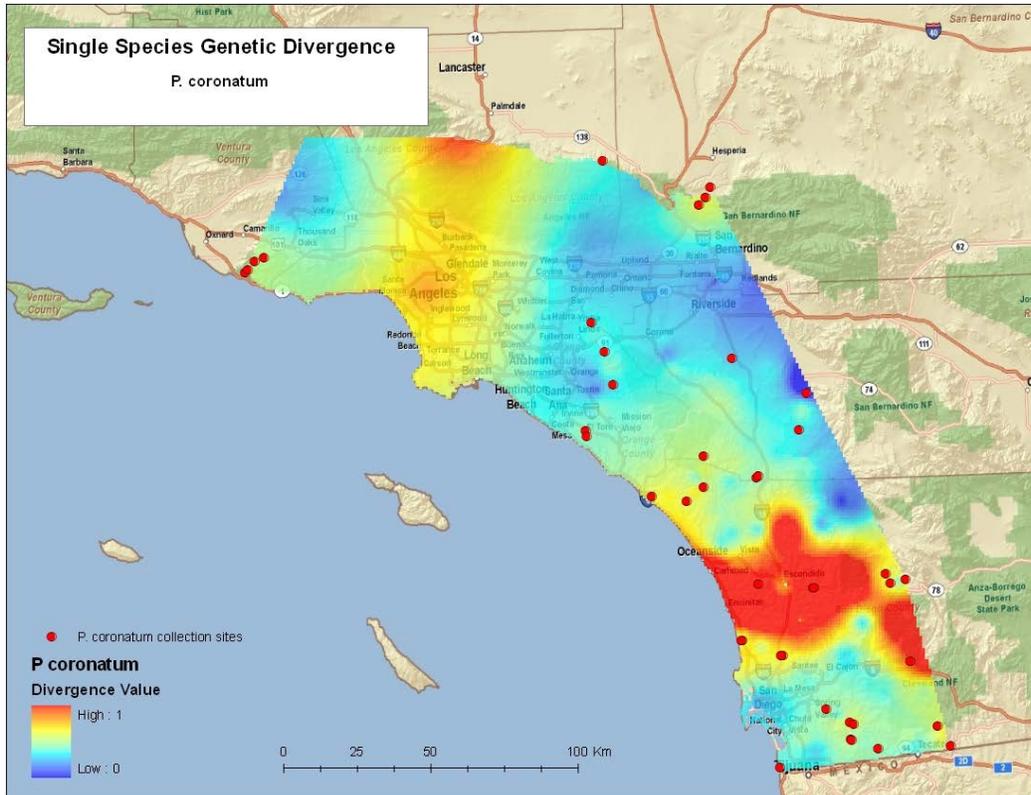


Figure 2. Example output of the Single Species Genetic Divergence Tool.

## Running the Single Species Genetic *Diversity* Tool

### Step 1: Creating Input Files

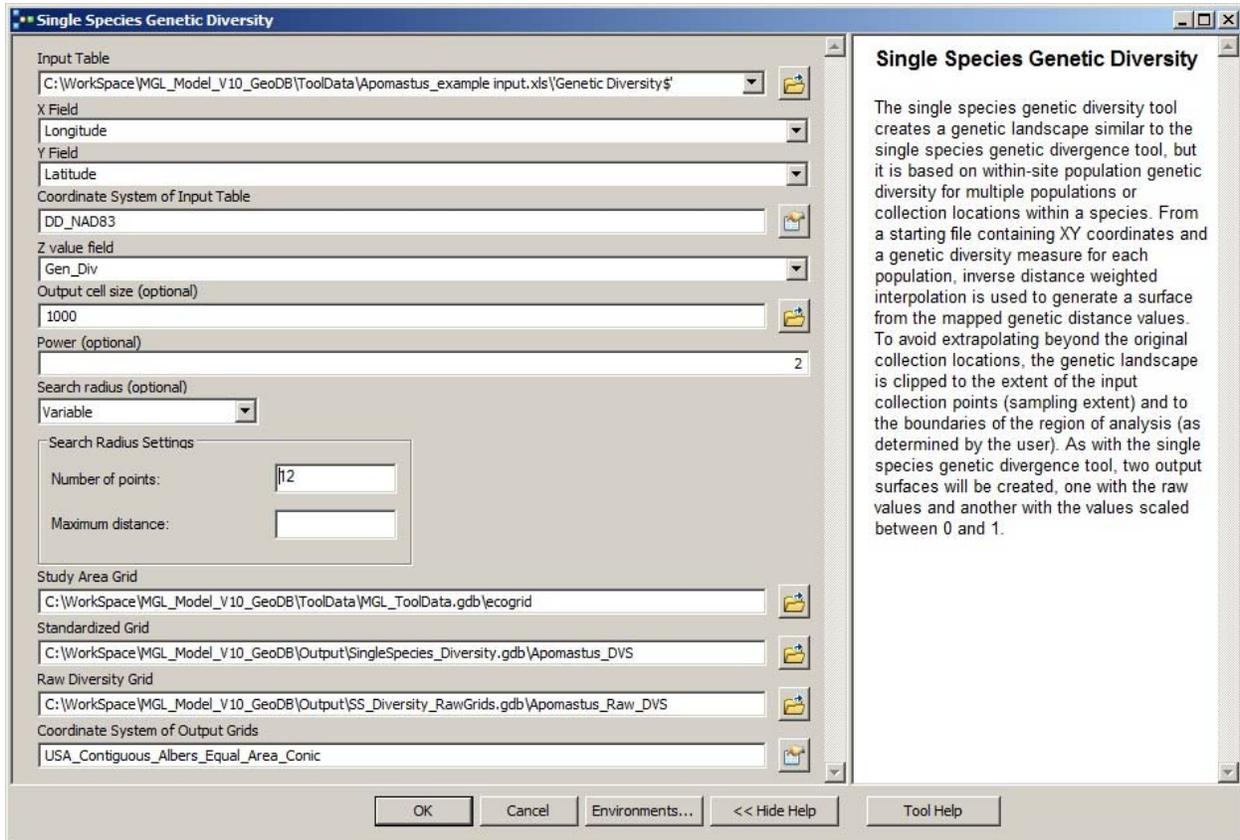
The input file for the single species diversity tool is a table containing two coordinate columns (Latitude: Y field, and Longitude: X field) and a column containing within site genetic diversity estimates. The table can be formatted as an ASCII file, dbf, or Microsoft Excel<sup>®</sup> worksheet.

OID	popcode	Latitude	Longitude	PWITHTH
0	1	32.8663	-117.19603	1.00285
1	2	32.878283	-117.18975	5.37906
2	3	32.94494	-117.16603	4.03368
3	4	32.94563	-117.16328	4.70617
4	5	32.95127	-117.16696	6.05616
5	6	32.95105	-117.1668	4.03744
6	7	32.94549	-117.16374	4.43775
7	8	32.91315	-117.11806	0
8	9	32.92679	-117.15054	0.50077
9	10	32.92664	-117.15162	0
10	11	32.9119	-117.15676	4.86016
11	12	32.91178	-117.15808	7.0766

Record: 0 Show: All Selected Is

## Step 2: Running the Diversity Tool

Double click the Single Species Genetic Diversity tool. You should see the model dialog box:



### Diversity Tool Parameters

1. **Input table** - Navigate to the drive and directory of the table that represents sampling points for the species of interest.
2. **X field** - Select the field that represents the longitude values.
3. **Y field** - Select the field that represents the latitude values
4. **Spatial Reference** - Select the spatial reference for the input sample point locations. The default DD\_NAD83 assumes that the point coordinate data are in decimal degrees North American Datum 1983 and should be changed if necessary to match the Input Table data.
5. **Z value field** - Select the genetic diversity value field to use to create the surface.
6. **Output cell size** - Select the output cell size for the genetic surface (typically 1000m).

7. **Power** - The exponent of distance. Controls the significance of surrounding points on the interpolated value. A higher power results in less influence from distance points. It can be any number greater than zero, but the most reasonable results will be obtained using values from 0.5 to 3. The default is 2.
8. **Search radius** - Defines which surrounding points will be used to control the raster. There are two options; variable and fixed. Variable is the default. It has two search radius settings: {Number of points}(with a default of 12) and {Maximum distance}. For more complete help, see <http://help.arcgis.com/en/arcgisdesktop/10.0/help/IDW>
9. **Study area grid** - Select the study area grid to define the area of interest.
10. **Standardized grid** - Name for the final output genetic diversity grid. The grid name must be 13 characters or less with no spaces or special characters. Default geodatabase to write output to: \MGLModel\Output\SingleSpecies\_Diversity.gdb. If you use the ArcGIS genetic tools in a new project or from a drive and directory other than the one the tool was extracted to from the zipped file, you will need navigate to the drive and directory you would like the output to be written to. These grids (for example see Figure 3) can be used as input files for the Multiple Species Genetic Landscape Tool.

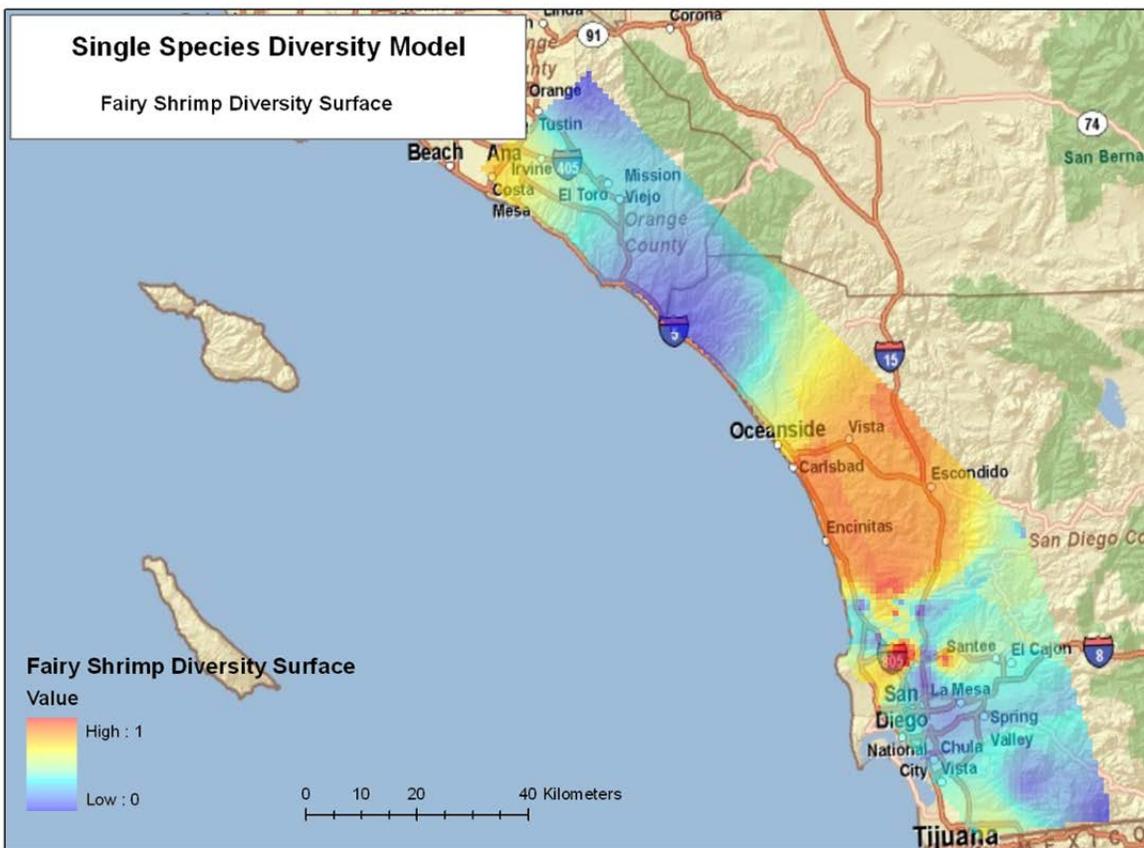


Figure 3. Sample output from the Single Species Genetic Diversity Tool.

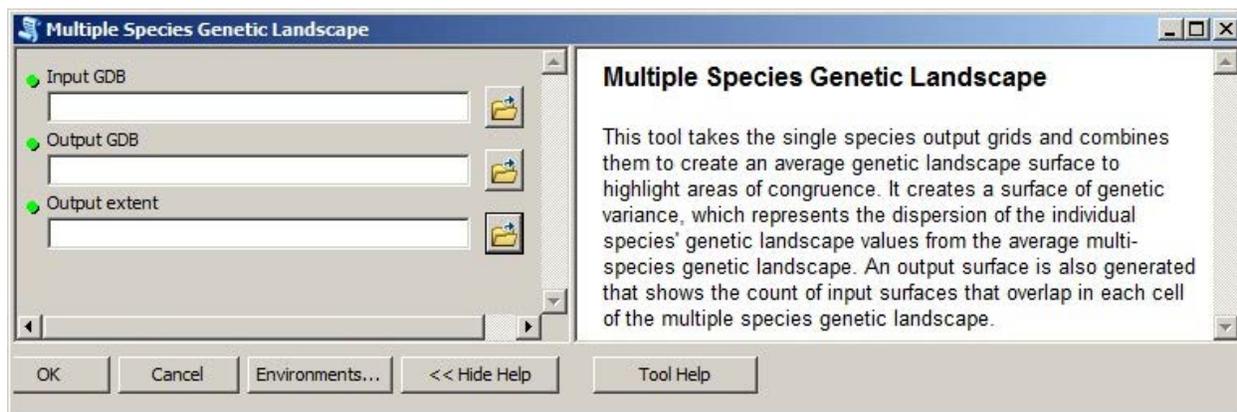
## Running the Multiple Species Genetic Landscape Tool

### Step 1: Creating Input Files

This tool is a Python script which reads in all the single species genetic divergence or diversity grids created with either of the first two tools.

### Step 2: Running the Tool

Double clicking the Multiple Species Genetic Landscape Tool will bring up this dialog;

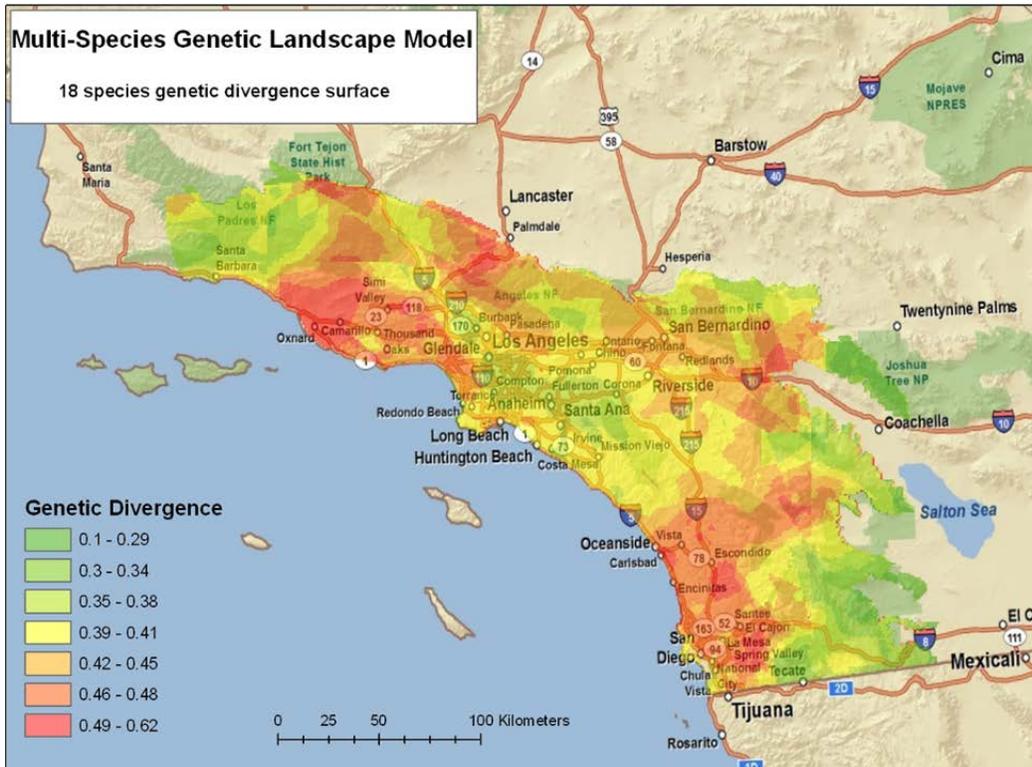


### Tool parameters

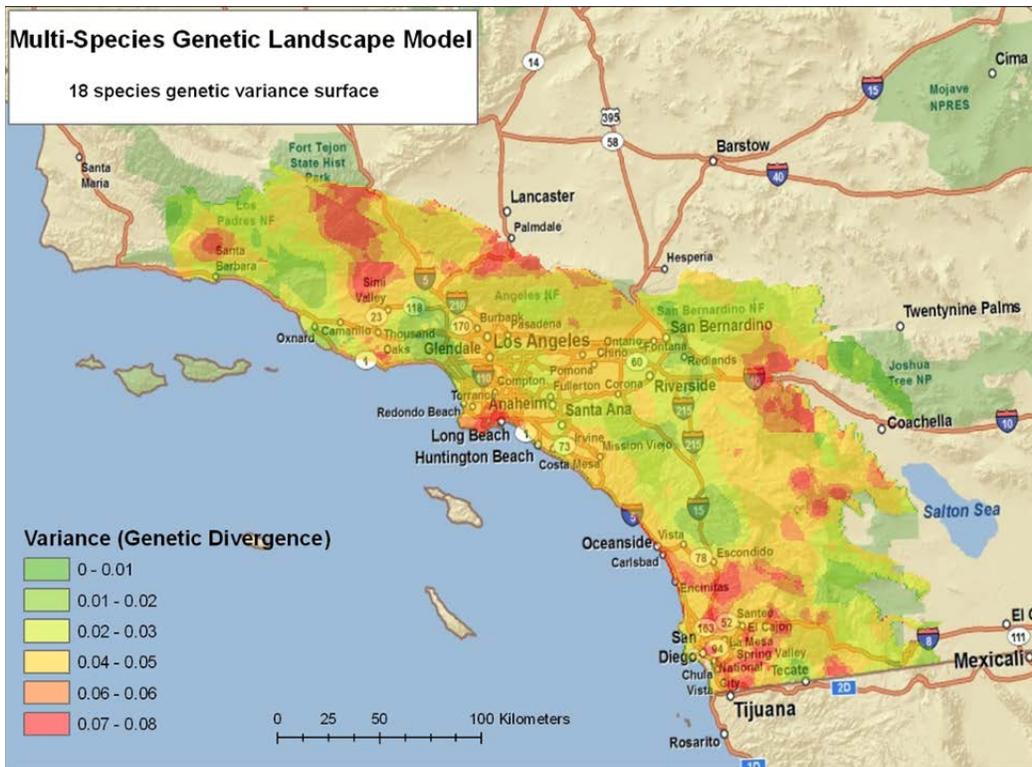
1. **Input GDB** – Navigate to the location of the file geodatabase that contains the single species genetic grids created in the first step. Make sure that only the grid files you wish to analyze are contained in this geodatabase. The script will read in all the ESRI grids located here.
2. **Output GDB** – Navigate to the location of the geodatabase where you want to have the average multiple species genetic landscape, the variance, and species count grids to be written. Default location, \MGLModel\Output\FinalResults\Final\_MGL\_Surface.gdb.
3. **Output extent** – This is the same study area grid used in the single species tools described above. It is used to set the analysis extent when processing the grids.

Examples of an “average genetic landscape” and a “variance genetic landscape” based on 18 individual species genetic divergence grids are shown in Figures 4 and 5.

*Note: The output extent for average and variance multiple species genetic landscapes will be clipped to grid cells where 2 or more input surfaces overlap.*



**Figure 4:** Example output showing an average genetic divergence surface created with the Multiple Species Genetic Landscape Tool using 18 species.

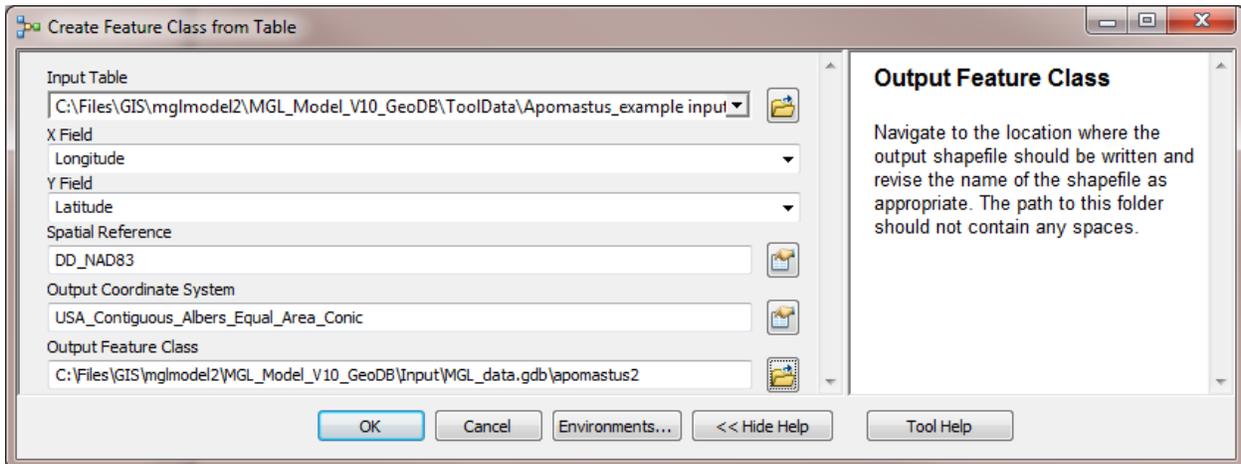


**Figure 5:** Example output showing the variance genetic surface for 18 species.

## ***Running the Create Feature Class from Table Tool (optional)***

This simple tool was created in Model Builder and is here as a utility if needed. It will create a feature class from an input table. The table can be in the form of an ASCII file, dbf, or Microsoft Excel worksheet.

Double clicking the Create Feature class from Table tool will bring up this dialog:



### ***Feature Class Tool parameters***

- 1. Input Table** – Navigate to the drive and directory of the folder that contains the table. The tool will read in an ASCII file, dbf file or Microsoft Excel<sup>®</sup> worksheet.
- 2. X Field** – Select the field which contains the longitude or easting values. *This must be labeled “Longitude” in your input table.*
- 3. Y Field** – Select the field which contains the latitude of northing values. *This must be labeled “Latitude” in your input table.*
- 4. Spatial Reference** – Select the spatial reference of the input sample points.
- 5. Output Coordinate System** - Select the output coordinate system for the feature class.
- 6. Output Feature Class** – Navigate to the location where the output feature class should be written and revise the default name of the feature class as appropriate.

## Version History

Genetic\_Tools\_Version\_1.tbx released June 15, 2010. This version was developed using ArcGIS 9.3.1 and will only run using that version.

Genetic\_Tools\_Version\_10.tbx released June 1, 2011. This version was updated to run using ArcGIS 10 and will not run in ArcGIS 9.3.1 because of its use of version 10 geodatabases.

1. The shapefile format was replaced by feature classes in file geodatabases. All the raster datasets are now stored in geodatabases. We switched to file geodatabases for several reasons; to prevent the schema locking bug (listed below), more efficient file management and to avoid the truncation of field names when using the shapefile format.

## Known Bugs

1. **The single species divergence tool cannot be run multiple times.** There is a schema lock problem that prevents this tool from being used multiple times in a single session. We are working on fixing this problem. As a work around, simply close and reopen the ArcMap project and the tool should run fine. Note: this bug is for the ArcGIS 9.3 version only. The ArcGIS 10 version does not have this problem.

## Trouble Shooting

**If any of the tools fail to run, check the following:**

1. Do the column headings on the input files match exactly as described in the manual?
2. Are the Spatial Analyst and 3D Analyst extension enabled in the ArcMap project?
3. Are the map projections identical for the collection location feature class, the study area grid file and the data frame?
4. If you get an error message stating that you do not have a license to use a tool, check to see what license level of ArcGIS you have. Is it Basic, Standard, or Advanced (formerly ArcView, ArcEditor, or ArcInfo)? The Single Species Divergence Tool requires the highest license level (Advanced or ArcInfo).
5. Are there any spaces or unusual characters in the path name to the working and output directories? These should be removed.

## Contacts

Questions and comments regarding the operation and programming of the Genetic Landscapes GIS Tools can be directed to William Perry ([wmperry@usgs.gov](mailto:wmperry@usgs.gov)) or Roberto Lugo ([rlugo@usgs.gov](mailto:rlugo@usgs.gov)).

Questions and comments regarding the genetic analyses can be directed to Amy Vandergast (avandergast@usgs.gov).

### **Tool Citation**

Perry, W., R. Lugo, S. A. Hathaway and A. G. Vandergast 2010. Genetic Landscapes GIS Toolbox: Tools to create genetic divergence and diversity landscapes in ArcGIS. U.S. Geological Survey.

## References

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