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Project Summary

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 Largiader 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.

For my class project, I used Python to automate a series of calculations and data manipulations to create genetic landscape surfaces directly from input data containing genetic distance values and sample location coordinates. The initial sequence of steps was written out by exporting a model I created in ModelBuilder to python. My goal was to make the python script more efficient, cleaner and faster.

Some of the geoprocessing steps include, Create TIN, spatial joins, delete fields, Add XY coordinates, Add Join, Copy Rows, Make Table View, Add Fields, Calculate fields, Make XY Event Layer, IDW, Extract by Mask, Copy Raster, and Single Output Map Algebra. The final output is a raster dataset. I initially converted the Model to a python script to use as a guide for the steps I needed to take. I quickly learned that the python output from ModelBuilder takes quite a bit of modification in order to get it to run correctly. Another problem I had was the change of tool syntax from different versions of ArcGIS. The Model was originally developed in ArcGIS 9.3.1 and my python script was written using ArcGIS 10.1 SP1. The big change was in how I had to code to use Python Map Algebra. Two examples were using a Con statement and Zonal Statistics. Another problem I ran into was that Excel tables (.xls, .xlsx) are not supported in 64 bit processing. One of my data inputs was from an Excel file, but it kept throwing an error saying ‘data does not exist or is unsupported’. It took a lot of digging on the ESRI help forums to find the answer. My workaround was to convert the input table to dbf format and I was able to read it in fine.

References

- Keller, I. and C. R. Largiader. 2003. Recent habitat fragmentation caused by major roads leads to reduction of gene flow and loss of genetic variability in ground beetles. *Proceedings of the Royal Society of London Series B-Biological Sciences* 270:417-423.
- Manel, S., M. K. Schwartz, G. Luikart, and P. Taberlet. 2003. Landscape genetics: combining landscape ecology and population genetics. *Trends in Ecology and Evolution* 18:189-197.

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