Vertex Sequence

- The purpose of the vertex sequence is to produce data structures that are useful for variography and mapping of vertex data.
- Scripts make use of patch vertex data, which is normally included in patches, but can be from other sources. As patches or vertex tables change (e.g. variable names), these scripts may need to be updated.
- All paths are relative to the directory containing the spatial_toolbox folder. Adjust as needed before running scripts. Directory organization and file naming conventions should be maintained.
- Scripts should be run in terminals (see ***Usage*** sections).

Required Packages

- compiler
- concaveman
- data.table
- dismo
- dplyr
- raster
- rgdal
- rgeos
- sf
- sp
- spdep

Vertex_1_Save.R – read patch vertex data tables from patches and save them as .csv. If already starting with .csv vertex tables or obtaining them by some other means, proceed to step 2 of this process provided that vertex data is the same as patch vertex tables (objective d).

Arguments

1. **PATCHES** – path to folder containing input patch .rds files
2. **ORIGINALS** – path to folder to export output .csv files
3. **REGIONS** – which regions of the patch to include based on “labels” column in vertex data table; corresponds to key in **Vertex_Definitions_Regions.R** (see script to define region)
4. **HEMISPHERES** – list of hemispheres (as any number of additional arguments) to export

Objectives

a. Read in patch files
b. Export vertex tables with all variables in table for the given region

Notes

- Although the option exists to select which hemisphere to use, both hemispheres are expected in later scripts and sequences
- Vertex table will have the following columns – *ipvx, ivx, ibnd, xp, yp, zp, x, y, z, avH.mean, wH.mean, H.mean, Th.mean, Sc.mean, labels*

- Only a unique identifier, *x*, *y*, and *z* coordinates for three-space, *x*, *y* for flattened patch, and *labels* column denoting regions are required for most subsequent scripts

Usage

```
Rscript Vertex_1_Save.R vertex_directory/patches vertex_directory/originals
temporal lh rh
```

Vertex_2_Aggregate_Midpoint.R – aggregate vertices to change resolution of the data. The aggregation function takes a set of points, on each iteration aggregates *pairs* of points to a single point. The location of the aggregated point is the midpoint between the two original points. The pairs that are nearest in distance are aggregated first. This process continues until the distance between any two points is greater than **RESOLUTION**.

Arguments

1. **ORIGINALS** – path to folder containing the original vertex tables
2. **AGGREGATES** – path to folder to output the aggregated vertex tables
3. **RESOLUTION** – distance beyond which points are no longer aggregated. A resolution of 3 (mm), for example will produce points that are separated by no less than 3 (mm).
4. **STANDARD** – 0 (false) or 1 (true) to specify whether using standard space data structures

Objectives

a. Read in original vertex tables
b. Aggregate vertex structure
c. Output aggregated vertex tables

Notes

- The values of the vertices produced by this script are not their final values. See **Vertex_3_Remap.R**
- To reduce computation time, each sub-region (ROI) is aggregated individually.
- Can run multiple instances simultaneously by running the same Rscript command in multiple terminals

Usage

```
Rscript Vertex_2_Aggregate_Midpoint.R vertex_directory/originals
vertex_directory/aggregates 3 0
```

Vertex_3_Remap.R – aggregation performed in the previous script produces the structure alone without values. This script assigns values to aggregated vertices as the mean of the values of the original vertices that comprise each aggregated vertex. Any other function can be used here (min, max, etc.). The second function performed is to remap the aggregated vertices to their closest original vertex location. While this may compromise some of the aggregation (by bringing some vertices closer together), it is done to preserve the integrity of the original structure.

Arguments

1. **AGGREGATES** – path to folder containing the *aggregated* vertex tables
2. **ORIGINALS** – path to folder containing the *original* (un-aggregated) vertex tables

3. **FINALS** – path to folder to output the *remapped* aggregated vertex tables
4. **STANDARD** – 0 (false) or 1 (true) to specify whether using standard space data structures

Objectives

a. Read in aggregated vertex tables
b. Read in original vertex tables
c. Assign values to aggregated vertices from original vertices
d. Assign location of aggregated vertices to their closest location from the original set of vertices

Notes

- Can run multiple instances simultaneously by running the same Rscript command in multiple terminals

Usage

```
Rscript Vertex_3_Remap.R vertex_directory/aggregates vertex_directory/originals
vertex_directory/final_tables 0
```

Vertex_4_Polygon.R – produces polygon objects from vertex data. Polygons are useful for visualizing choropleth and other maps for various data that may be associated with vertices. Some errors such as stray polygons—those which are not contiguous with the main set of polygons—are handled. Vertices which produce these strays will also be removed from the final aggregated data tables.

Arguments

1. **FINALS** – path to folder containing the remapped, final aggregated vertex tables
2. **POLYGONS** – path to folder to output the polygons
3. **REGIONS** – which regions of the patch to use based on “labels” column in vertex data table; corresponds to key as defined in **Vertex_1_Save.R**
4. **STANDARD** – 0 (false) or 1 (true) to specify whether using standard space data structures

Objectives

a. Read in final vertex tables
b. Produce polygon data structure from vertex tables
c. Export polygon data structure

Notes

- Can run multiple instances simultaneously by running the same Rscript command in multiple terminals

Usage

```
Rscript Vertex_4_Polygon.R vertex_directory/final_tables vertex_directory/polygons
temporal 0 lh rh
```

Vertex_5_Distance_List.R – produces a list containing two lists of key-value pairs. The keys in each list are the identities (row numbers) corresponding to each polygon in the set of polygons for a patch.

In the first list, the values for each key are the identities (row numbers) for all of the other polygons in the dataset sorted by their distance (nearest to furthest) from the given polygon. In the second list are the actual distances to those polygons.

Arguments

1. **FINALS** – path to folder containing the remapped, final aggregated vertex tables
2. **POLYGONS** – path to folder containing polygon .rds files
3. **DISTANCES** – path to folder to output the distance list .rds files
4. **STANDARD** – 0 (false) or 1 (true) to specify whether using standard space data structures

Objectives

a. Read in aggregated vertex tables
b. Read in polygon files
c. Output distance list and neighbors data structures

Notes

- Distance as defined in all parts of these scripts refers to three-space distance. With modifications, flattened patch distance may be used.
- This is a time-consuming process. Percent complete is printed to screen.
- Can run multiple instances simultaneously by running the same Rscript command in multiple terminals

Usage

```
Rscript Vertex_5_Distance_List.R vertex_directory/final_tables
vertex_directory/polygons vertex_directory/distance_lists 0
```

Vertex_6_Distance_Matrix.R – this script converts the distance list produced by the previous script to a distance matrix. The distance matrix contains the distance from each feature (vertices, polygons, etc.) to every other feature—n features produces an n by n matrix. The distance matrix is more useful for some spatial analysis applications than the outputs of the previous script.

Arguments

1. **DISTANCES** – path to folder containing distance lists
2. **MATRICES** – path to folder to output distance matrices
3. **STANDARD** – 0 (false) or 1 (true) to specify whether using standard space data structures

Objectives

a. Read in distance lists
b. Convert lists to distance matrices
c. Output distance matrices

Notes

- Can run multiple instances simultaneously by running the same Rscript command in multiple terminals

Usage

```
Rscript Vertex_6_Distance_Matrix.R vertex_directory/distance_lists vertex_directory/distance_matrices 0
```

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September 2019