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| Executive Summary | How is culture spatially transmitted? | **27-Jul-16** | **VHS model** |

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VHS (vertical, horizontal, or selection) model

Overview:

We are part of a larger working group studying the ecology of human cultural evolution. This group has identified a critical knowledge gap, which is to identify the mechanisms by which ideas are transmitted through the environment. There are four possible modes of transport for ideas, vertical transmission between generations, horizontal transmission between cultures, and selection from the environment or society. These four mechanisms are all playing a role in the transmission of language and we would like to disentangle their relative contributions to the process. These questions are currently beyond the scope of field experimentation, so we will use a modeling approach to establish the boundaries of our current understanding and inform future experimental designs. A key function of this model must be that it outputs phylogenetic trees that can be compared against the most trustworthy data on the spread of cultural ideas, language phylogenies. This contribution should provide valuable contributions to both ongoing studies (e.g. the spread of agriculture) and future questions that generically involve the spatial spread of cultural ideas. We must maintain independence between the modes in the model so that we can isolate the roll of each in a nested experimental design.

Scientific question

* What relative contributions do the four modes of cultural transmission make to the spatial spread of cultural ideas? Can changes in these mechanisms be detected in the phylogenies of cultures that have undergone spatial change?

Hypotheses:

1. When provided a phylogenetic tree, it is possible to reconstruct the spatial process that created that tree from the information in the tree.
2. Each of the four spatial mechanisms alone will produce a different phylogenetic outcome.
3. Each combination of spatial mechanisms will produce a different phylogenetic outcome.

Explicit assumptions:

1. Vertical transmission is described by two different processes, speciation (where a society splits into un-colonized space by creating a new branch on the tree) or neighbor takeover (where a society drives a neighbor extinct so the invader speciates into the neighbors spot and the extinct society is removed from the tree).
2. Horizontal transmission is described by a simple diffusion process where one culture gives their neighbor a trait, but the neighbor maintains their own tip on the tree.
3. Selection is cause by the underlying habitat. Currently this habitat, and therefore the fitness surface, is defined as a binary choice between matching or mismatching habits for each transmission mode.

Discussion points:

1. A priori, what shape do we expect each transmission mode to produce?

Vertical Horizontal Env Selection Social selection

1. Do we have any way of identifying the geographic location of different nodes in the tree?
2. How good are our time estimates for the time between nodes?
3. Agriculture: will societies that are successful with ag be more likely to take over another ag society because they have

Design:

The model for this project is a sequence of three separate modules. The first module produces simulated data by running the simulation. These data are written to the hard drive at the end of the simulation. The second module loads those files and analyzes the data they produced. The third module plots the analysis outputs from the second module.

We are designing the model using the R(CRAN) programming language. This is a graphical schematic of our algorithm design.

%20Spread%20phylogeny%20algorythm%20diagram.pdf

Methods:

Simulation module –

1. myWorld: The simulation module begins by defining the world within which the simulation will perform.
2. Define probabilities: This is a phenomenological model where the probabilities of different events are defined by the user.
3. Randomize the order that processes (speciation, extinction, arisal, takeover, diffusion) will happen. Different models use different combinations or numbers of these processes to test different hypotheses, but the order they are applied each time step is always randomized.
4. Run the modules, which operate according to the following rule sets:
   1. Speciation –
   2. Extinction –
   3. Arisal –
   4. Takeover –
   5. Diffusion –
5. Track the development of both spatial pattern and phylogenetic pattern through time.
6. Write a file with the spatial and phylogenetic data that the simulation produced. The file name for each file embeds the parameters used for that simulation including, the probabilities used for each module, the replicate number of each simulation, and the number of time steps each simulation ran for.

Data analysis module –

1. Load files from simulation output and extract data
2. Subset data from files to analyze each model results separately.
3. There are 5 subcategories of analysis.
   1. Spatial analyses
   2. Richness tree metrics (sum of tree units)
   3. Divergence tree metrics (mean of tree units)
   4. Regularity tree metrics (variance of tree units)
   5. Macro evolutionary tree metrics (rate and rate change in tree units)
4. Write a file with all of the output values.

Data plotting module –

1. Load analysis files
2. Subset analysis files for plotting
3. Use layout() function to make a display dashboard

Dates: