**Summary of the project**

Historians, arqueologists and geneticits have been trying for a long time to answer how the spread of farming has occurred. Currently, there are two main competing hypothesis that can potentially explain it: (1) farming was transmitted by the diffusion of ideas and technology between societies (hereafter cultural diffusion); or, alternatively, (2) by population expansion of the first farmers that subsequent displaced foraging societies (hereafter demic diffusion). So far, the scarcity of data and the limited application of quantitative analysis have restricted the conclusions to local and regional scales. Here, we propose that the two process (cultural and demic diffusion) would lead to different patterns of language evolution and that this could help us understand the spread of farming at global level. We expect that the spread of farming through demic diffusion would lead to more speciation (new societies driven by expansion and conquering), more societies extinctions (caused by conflicts) and an aggregation of farming technology among societies that descend from the first farmers. By the other side, the cultural diffusion of farming would represent an adaptation of already established societies, only decreasing extinction rates. We propose that such different processes could be identified using modern methods of macroevolution applied to phylogenies generated from comparative linguistics. Assuming that the selection of farming should be at the society level, we used a society based modelling approach to investigate if our expectations hold and if other effects should be also expected. After, we plan to compare the modelling results with the real world linguistic phylogeny to indicate what process was more likely to have happen in human history.

**The model**

* In our model, a society can only occupy one location. The locations are determined by the occurrence points in the real dataset (n = 1253). So, the maximum number of societies is determined by the number of locations.
* The locations are connected by the 7 closest neighbors that keep all the connections symmetric.
* All the societies have one trait associated, either foraging or farming. Each location has a value indicating whether a society could farm or not, determined by previous studies using real data.
* The model starts with one foraging society.
* Every society has a chance to expand into un-colonized locations at each time step. Because societies can only occupy one location, a speciation occurs, and a new society is created (hereafter speciation module). The decedent society will keep the same trait of the parent society.
* Every society has a chance to go extinct at each time step (hereafter extinction module). For now, farming societies in locations that are not suitable for farming have higher extinction probability.
* Every society has a chance to change their trait from foraging to farming at every time step (hereafter arisal module). For now, in locations that are not suitable for farming it is impossible to change from foraging to farmer.
* Every society has a chance to diffuse their trait to other society at every time step (hereafter diffusion module). For now, in locations that are not suitable for farming it is X times harder to diffuse farming and it is X times harder to diffuse foraging to farming societies that are in suitable locations for farming.
* Every society has a chance to takeover other society (with speciation of the source society and extinction of the target society) at every time step (hereafter takeover module). Takeover only happens when all neighbor cells are occupied. For now, farming societies have X times higher probability of takeover and resistance from takeover when in suitable locations for farming. Farming societies will always prefer to invade locations suitable for farming if they are available.