Using phylogenetic methods to explore culinary innovations in culture

# Introduction

Cultural innovations are passed down through generations within a populace. Cultures have been able to maintain relative development in isolation bar their near neighbors until the invention of modern modes of travel. Horizontal transmission of cultural elements have been relatively slow even during the age of ship travel. As the world becomes more connected through air travel by the use of airplane, and we continue to move towards a global economy, cultures are beginning to merge into a continuum. It can be expected that in the near future, cultural elements may become merged to the point where no distinct signal of cultural origin can be distinguished with it extensive look to the past, highlighting the importance of this work.

Because of the linear direction of culture, phylogenetic methods can be used.

## Caveats of cultural

# Methods

## Assembling the dataset

The top 20 recipes from a set of countries/regions were scrapped from AllRecipes.com using a public script that had been repurposed by Dr. Jennifer Chang. The data scraped from the page included recipe country/region, recipe id, recipe title, and recipe ingredients. The ingredients were used as the characters for phylogenetic reconstruction. This data was further processed to be in a format where the characters were presented in a binary manner. This file was reprocessed into tnt, phylip, and nexus format for us with different tools.

## Assessing Treeness

## Inferring relatedness by parsimony methods

TNT was used to infer a tree using parsimony methods

The characters of each recipe were defined as discrete and binary. TNT was used to to analyze the characters (see recipes.tnt in the data folder), using the following two string of commands;

tnt p renamedfood.txt, log newfound.out, rep+1, hold 1000, mult=replic 10, le, majority, taxname=,export - newtree.tre, quit

tnt p renamedfood.txt, log newfound.out, rep+1, hold 1000, mult=replic 10, le, resample, taxname=,majority,export - newtree2.tre, quit

## Distance methods

Pairwise distances between recipes were calculated by summing the results of an exclusive or (XOR) between binary characters. If one recipe had an ingredient that was not present in the compared recipe, the distance between recipes was incremented by one. Trees were built using neighbor-joining methods, made available through the APE package in R. Code is available in the repository.

## Maximum likelihood methods

Maximum likelihood trees were built using RAxML.

raxmlHPC-PTHREADS-SSE3 -p 777 -m MULTIGAMMA -s test.phy -n maxlikefood

## Bayesian methods

Bayesian analysis were run using mrbayes. After 10,000,000 runs on two chains, the analyses failed to converge.

# Results

# Discussion

With modern modes of transportation and the innovation of the internet, cultures are able to horizontally integrate at a much faster rate than ever before. It is increasing becoming difficult to find cultures in isolation with unique hallmarks. Despite globalization, many countries still maintain culinary traditions which were developed based on regional availability as well as locally defined palettes. Globalization is spreading ‘invasive species’ of food around the world, some which sustain very well. An example of this would be how curry was introduced to Britain during colonization, or the rise of the hamburger in Japan.

The source of the data, AllRecipes.com, would not be the best

Distance methods were able to separate between Asiatic and African/European dishes. This supports the idea that there are distinct ingredients used specifically in these two hemispheres of the world. The implementation of neighborjoining was not able to distinguish well between the different countries, expectedly because distance methods only relied on distances without taking into account the characters.

Maximum likelyihood methods were able to begin to cluster individual countries together.

## Caveats of using allrecipes