Mantel test for 238 samples

1. Covert VCF file to Fasta using Spider
2. Pairwise FST was generated from fasta file using POPGENOME

get.F\_ST(GENOME\_class, pairwise=TRUE)

GENOME\_class@Nei.G\_ST.pairwise # Based on Nei's Fixation Index

1. Get pairwise distance between province

* Prepare you input file (text file contains name, lat, and log )

https://biodiversityinformatics.amnh.org/open\_source/gdmg/

1. Calculate average province data and prepare mantel input file