

1. INPUT DATA

Input Data Filename: 

Browse...

OR: 

File Data Here

2. BASIC SETTINGS

(Raw data format only): If $F \leq 0$, what value should be assigned to Slatkin's M for RMA regression (Should be a large number)?

For IBD plots, would you like a background grid? ☒

Number of randomizations (1-30,000):

Also perform analysis on Logarithmic (Genetic Distance)? ☒

Also perform analysis on Logarithmic (Geographic Distance)? ☒

(Raw data format only): Calculate Rousset's distance? ☐

Calculate RMA regression residuals? ☐

3. DETAILED SETTINGS

(Raw data format only): Calculate summary stats for each locus? ☐

For first set of analyses, use negative genetic distances? (Otherwise, they will be set to zero.) ☒

When log-transforming (genetic distance), set genetic distances less than zero to:

When log-transforming (genetic distance), negative genetic distances will be:

☒ Set to value above

☐ Thrown out

If calculating Rousset's distance, set genetic distances of 1.00 to:

4. SUBMIT

Submit