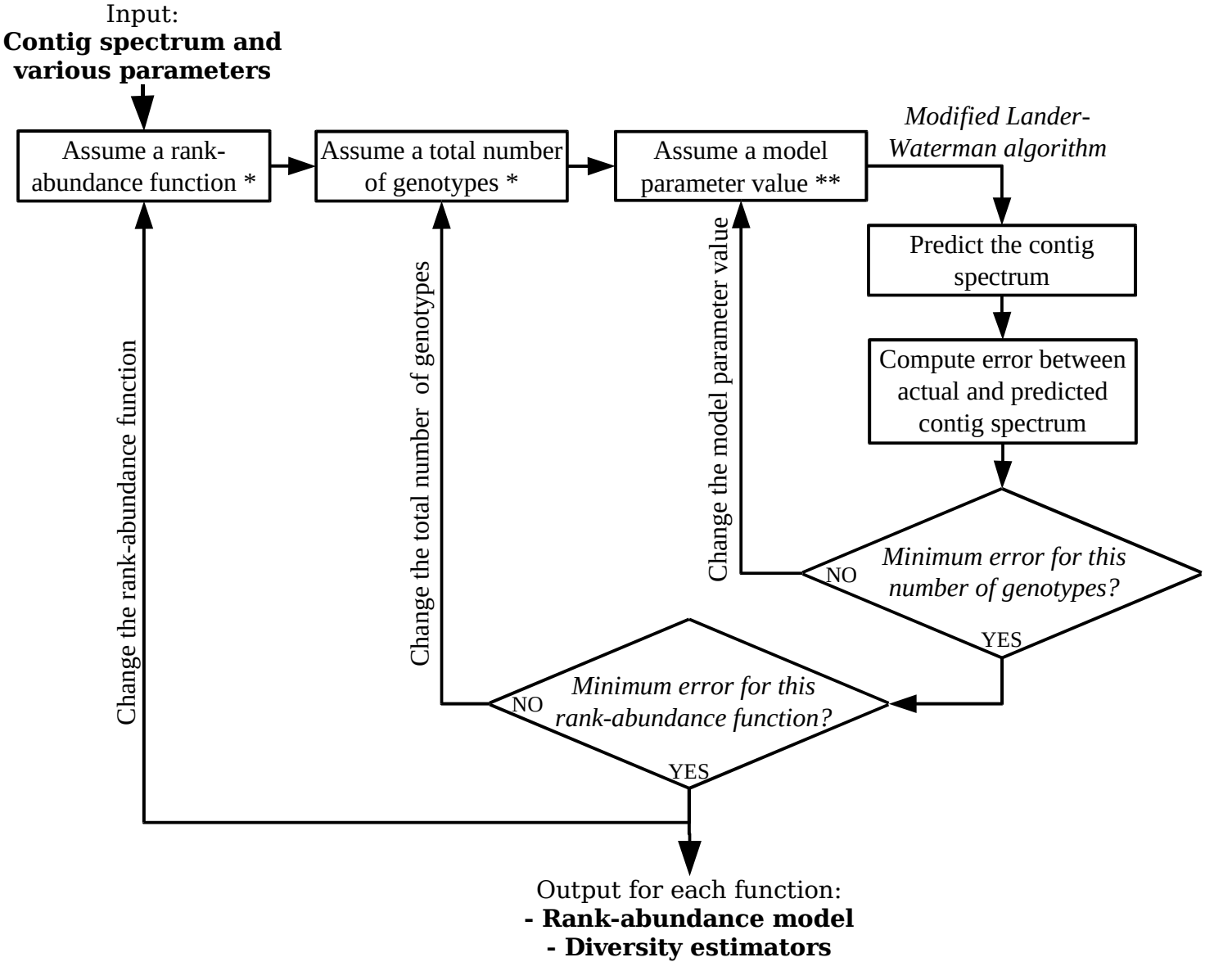
Input:
Contig spectrum and various parameters
Assume a rank-abundance function *
Assume a total number of genotypes *
Assume a model parameter value **
Modified Lander-Waterman algorithm
Predict the contig spectrum
Compute error between actual and predicted contig spectrum
Minimum error for this number of genotypes?
NO
YES
Minimum error for this rank-abundance function?
NO
YES
Change the model parameter value
Change the total number of genotypes
Change the rank-abundance function
Output for each function:
- Rank-abundance model
- Diversity estimators