

MATH 660
INFORMATION ON THE MIDTERM

The midterm in MATH 660 is Friday, March 9. You should bring a (dumb) calculator so that you can do some elementary arithmetic quickly. The exam will have two sorts of questions:

1) those that test that you can apply the algorithms and methods we have learned effectively. These include: unweighted parsimony, parsimony, tree-popping, tree consensus methods, UPGMA, using the 3-point formula, and one iteration of NJ (see below); and counting the number of rooted and unrooted leaf-labeled n -taxon trees or checking that a collection of splits is compatible.

2) those that ask you to qualitatively discuss the pros and cons of the various methods we have learned.

For NJ, I do not expect you to memorize the formulas used to compute the M_{ij} , but you should know how to pick a pair of taxa to join, and how to fit this pair onto a tree. A sample problem might be that you see a table of M_{ij} and pairwise dissimilarity values and ask you to perform one step of the NJ algorithm.

The other information you need to know are definitions and statements of important theorems. This includes the *Splits Equivalence Theorem* and an informal understanding of Theorem 16 (NJ is consistent on dissimilarity maps from tree metrics for trees with positive edge lengths.) You also will need to know definitions for terms like cherry, sister taxa, vertex, rooted, metric, unrooted, binary, quartet tree, etc. You should be able to use the terms ‘dissimilarity map’ and ‘tree metric’ correctly and precisely, and be fluent with all terminology we have used in the course (purine, pyrimidine, nucleotide, aligned sequences, leaf-labelled tree, additive dissimilarity, etc.)

There will be a review session on W March 7 at 7 pm in a location TBA. For our Anchorage student, we can set up a skype link for him to join in if he is interested. Please bring questions and suggestions for problems to go over, etc.