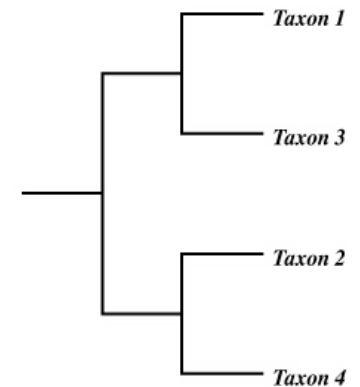
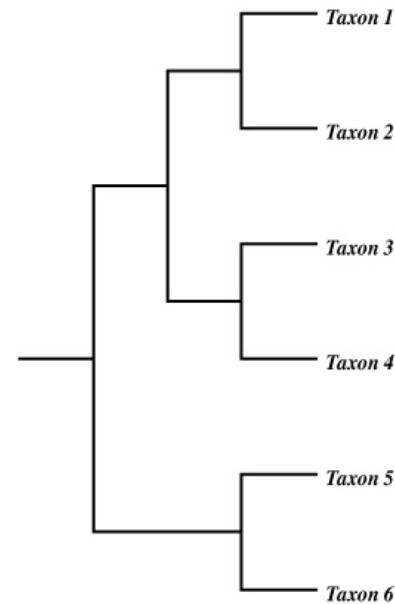


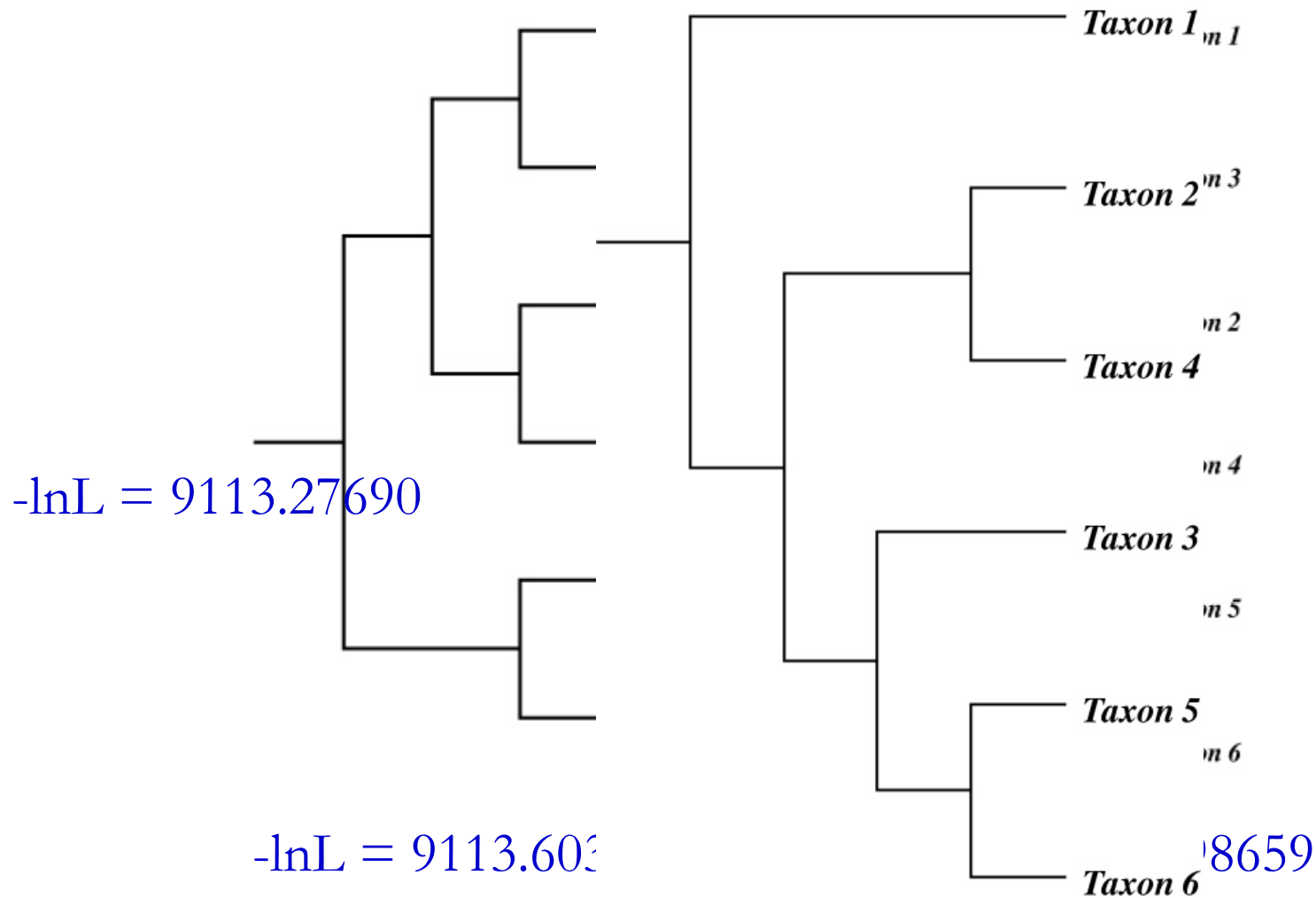
Simulation

- One dataset of six sequences.
- Second dataset pruned with recombination
 - Taxa 5 and 6 removed
 - Taxa 2 and 3 exchange sequences
- Simulates LGT
- Any results not due to sequence variation -sequences are the same in both datasets.



$$-\ln L = 5113.27 \quad -\ln L = 3585.33$$

Likelihoods of concatenated data using the Optimal tree for concatenated data intuitive trees



- 4 genomes
 - *Neisseria meningitidis* serogroup A
 - *N. meningitidis* serogroup B
 - *N. meningitidis* serogroup C
 - *N. gonorrhoea*
- 390 alignments (single gene families)
- ntax=4 nchar=390,085;

Topology	100%	70%	SHtest
A+B	51 (31.5%)	116 (30%)	106 (30.5%)
B+C	58 (35.8%)	127 (33%)	114 (32.7%)
A+C	53 (32.7%)	143 (37%)	128 (36.8%)
Number of trees	162	386	348

Total number of families used = 390

Total number of families that have more than 70% support for a particular topology=386

Total number of families that have 100% support for a particular topology=162

Total number of families that have a significantly better topology as per SH test 348

Results - best trees

Method	Topology I	Topology II	Topology III
Maximum Likelihood (GTR+I)			75%
Distance NJ (GTR+I)	98%		
Maximum Parsimony		100%	