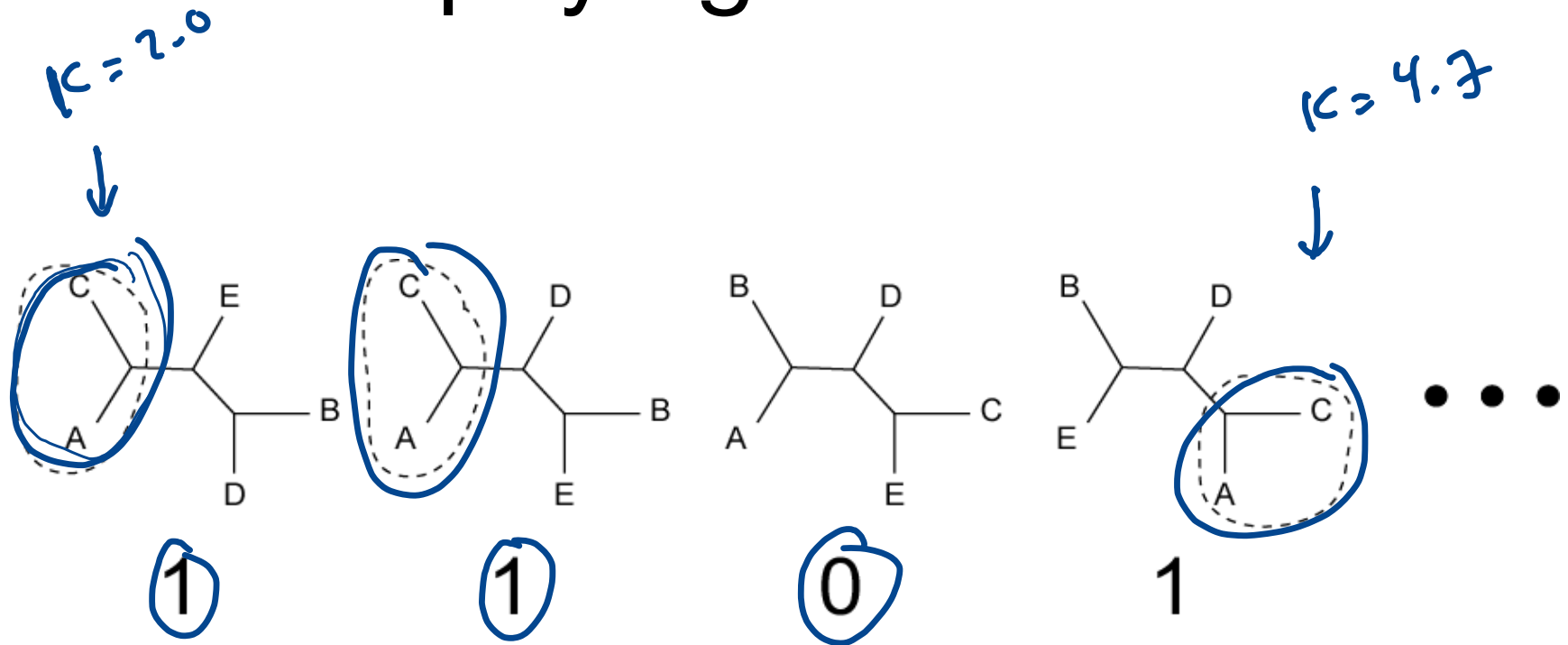
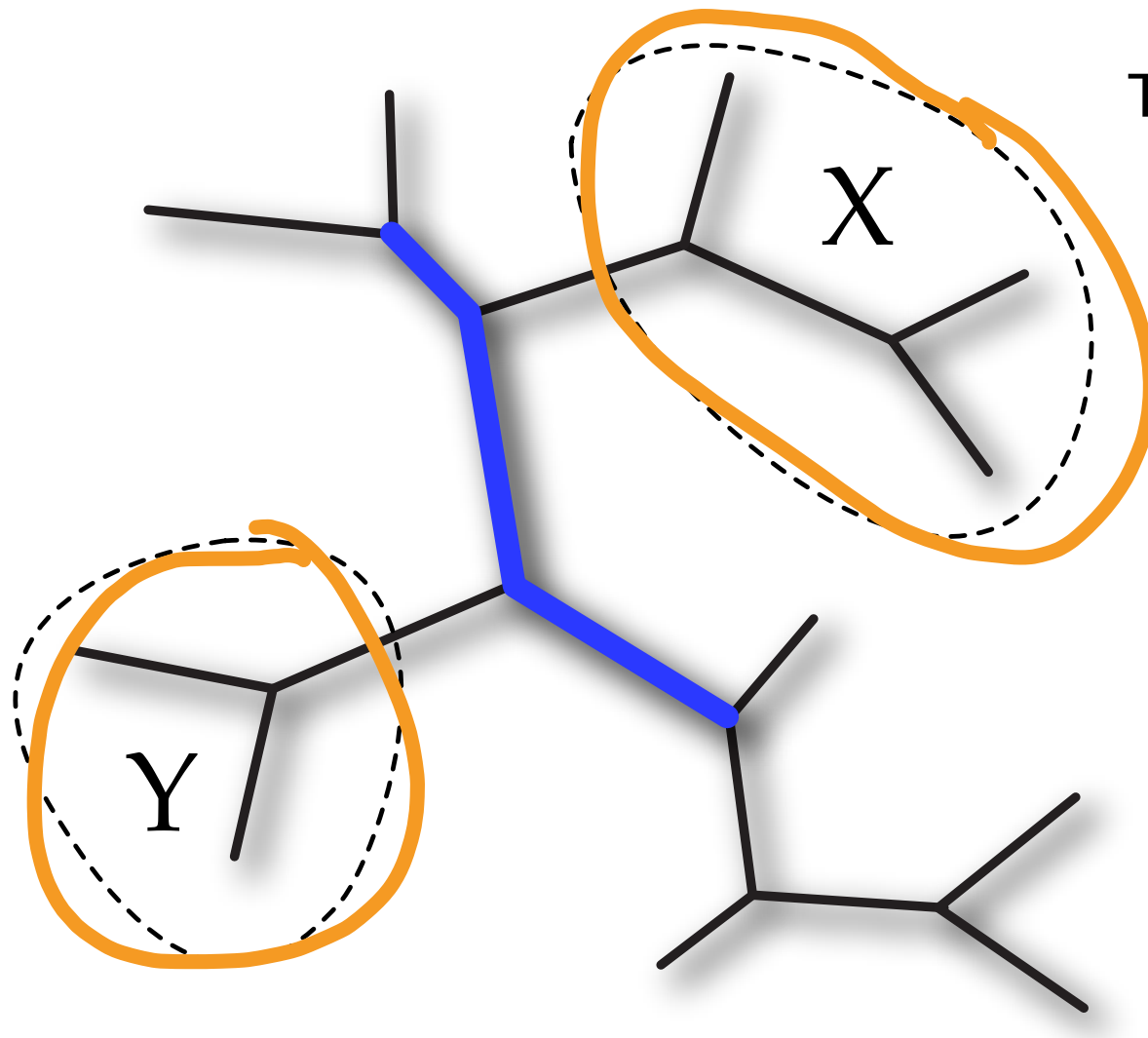


So, what's all this got to do with phylogenetics?



80% → 0.80 ← marginal
posterior
probability
that clade
A,C exists

Moving through treespace

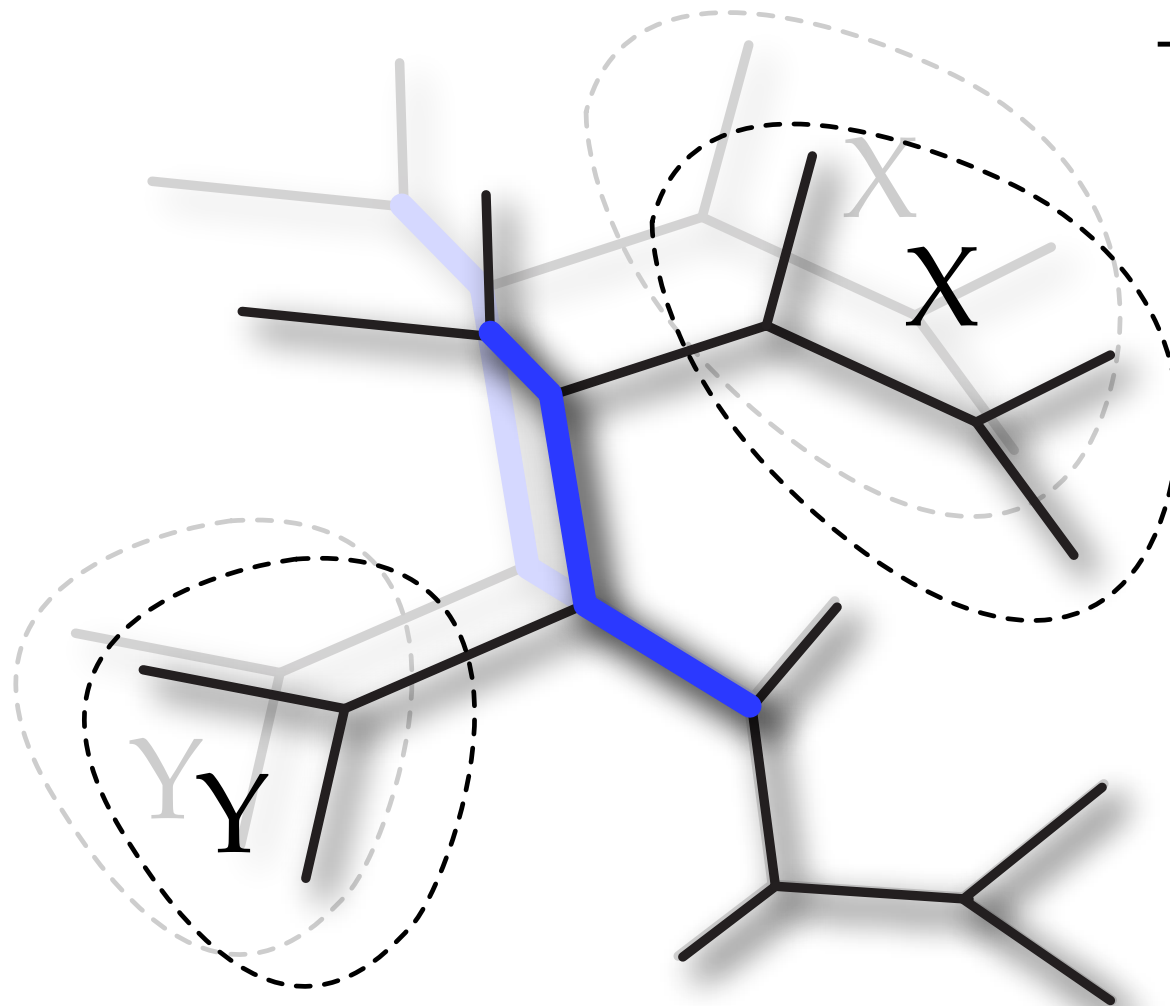


The Target-Simon move

Step 1:

Pick 3 contiguous edges randomly, defining two subtrees, X and Y

Moving through treespace



The Target-Simon move

Step 1:

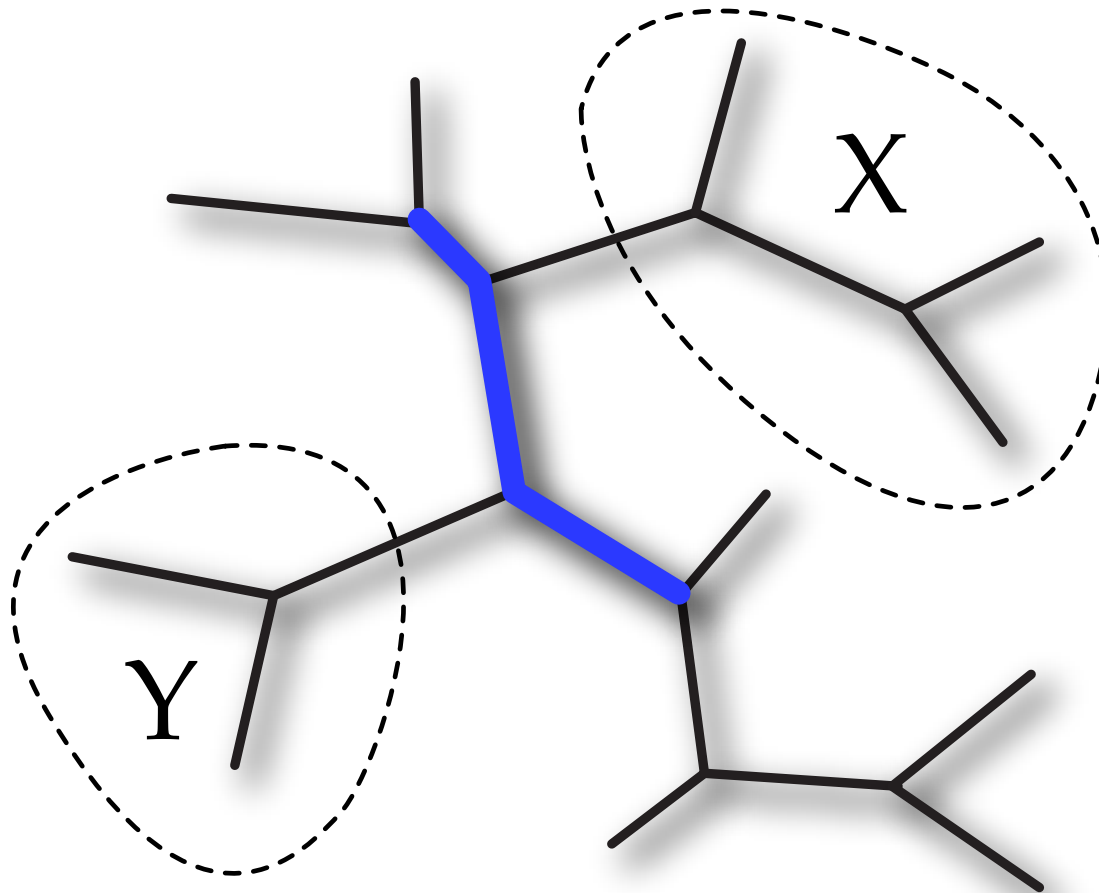
Pick 3 contiguous edges randomly, defining two subtrees, X and Y

Step 2:

Shrink or grow selected 3-edge segment by a random amount

Moving through treespace

Thearget-Simon move



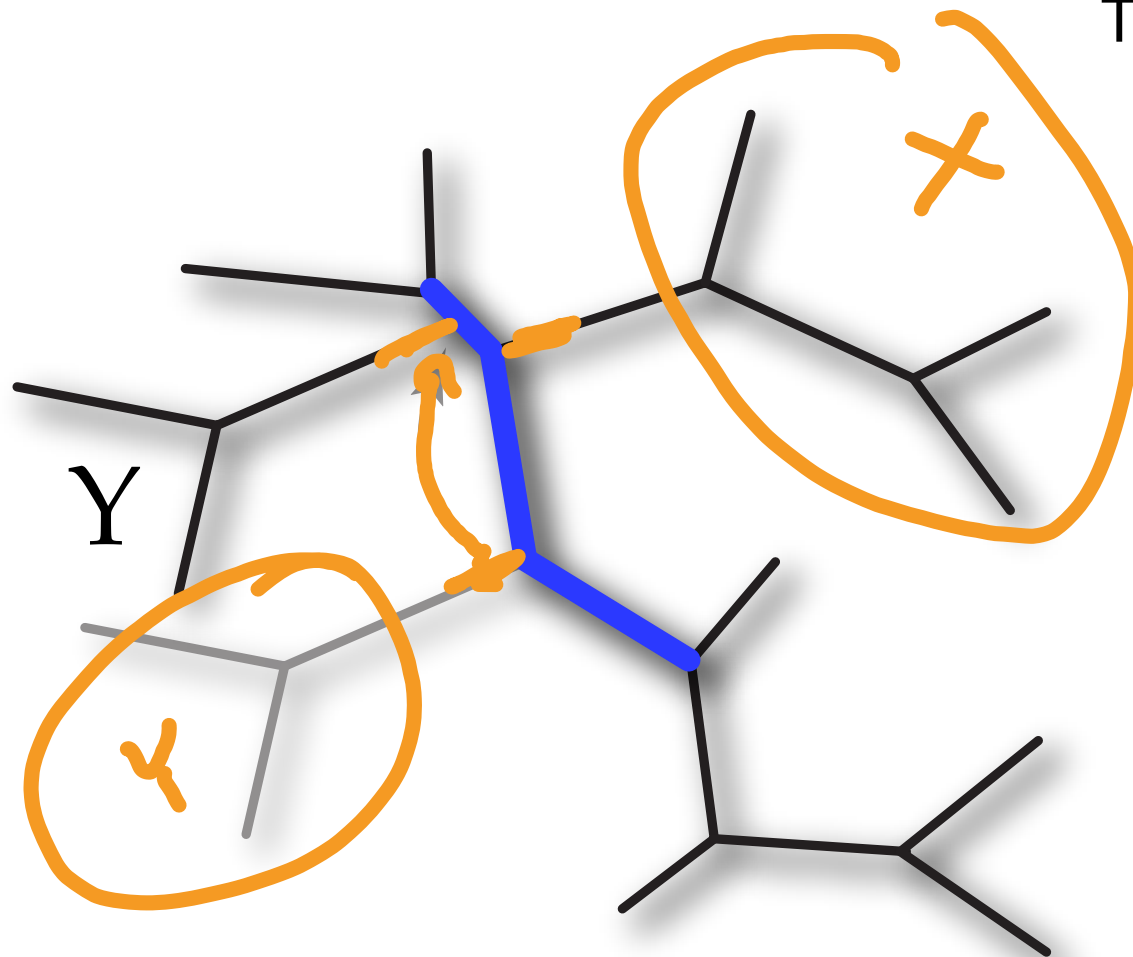
Step 1:

Pick 3 contiguous edges randomly, defining two subtrees, X and Y

Step 2:

Shrink or grow selected 3-edge segment by a random amount

Moving through treespace



The Target-Simon move

Step 1:

Pick 3 contiguous edges randomly, defining two subtrees, X and Y

Step 2:

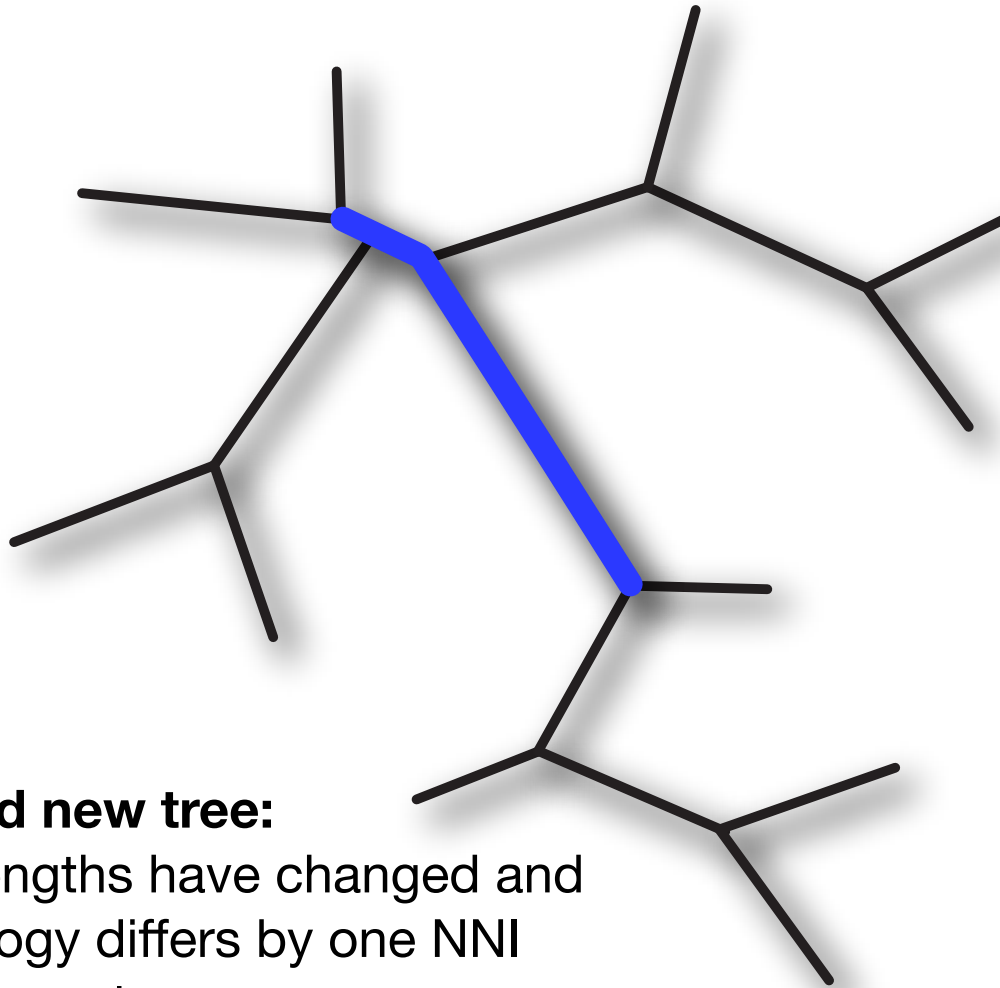
Shrink or grow selected 3-edge segment by a random amount

Step 3:

Choose X or Y randomly, then reposition randomly

Moving through treespace

The Target-Simon move



Proposed new tree:

3 edge lengths have changed and the topology differs by one NNI rearrangement

Step 1:

Pick 3 contiguous edges randomly, defining two subtrees, X and Y

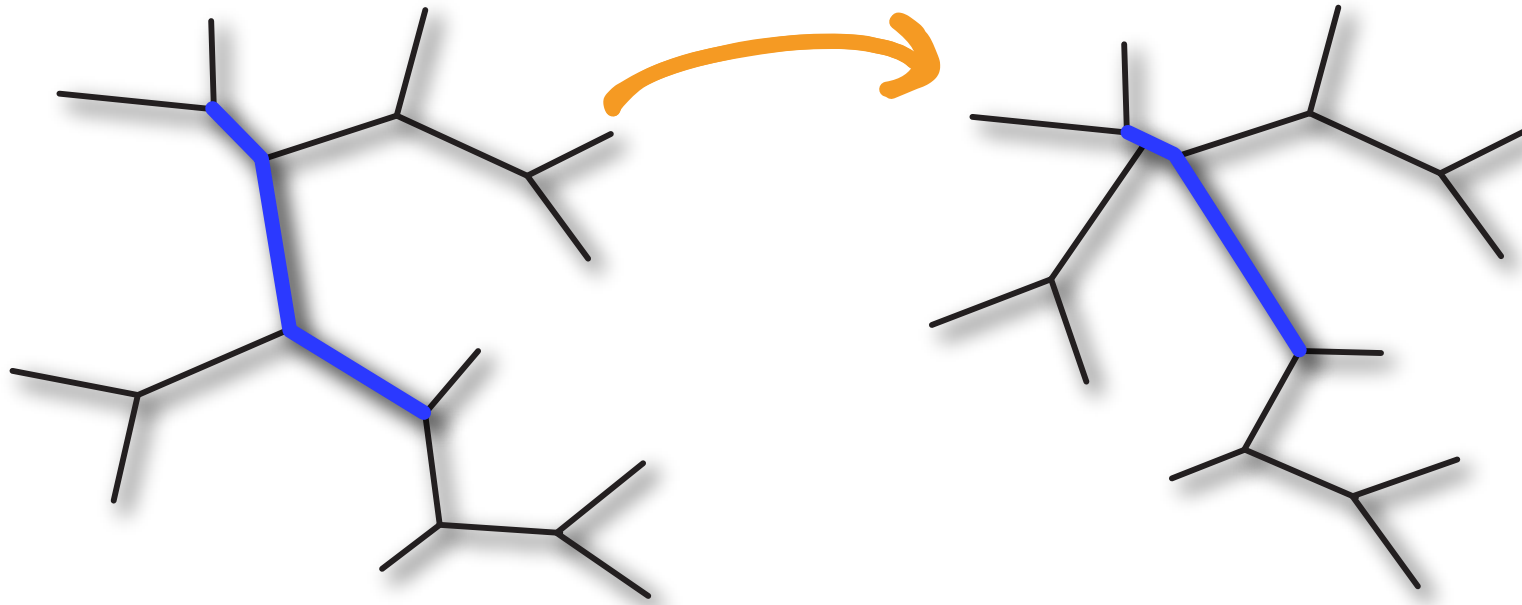
Step 2:

Shrink or grow selected 3-edge segment by a random amount

Step 3:

Choose X or Y randomly, then reposition randomly

Moving through treespace



Current tree

log-posterior = -34256

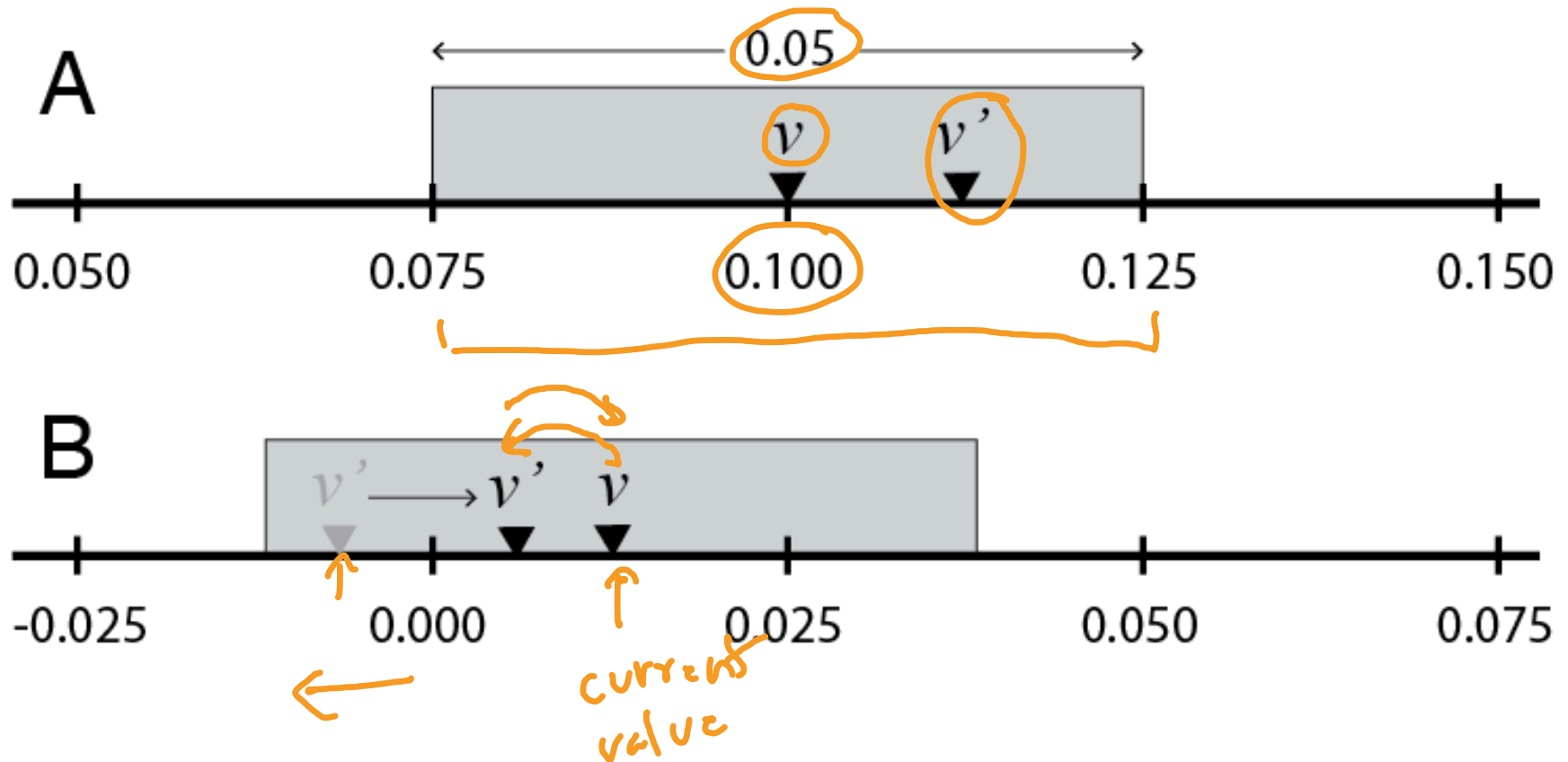
Proposed tree

log-posterior = -32519

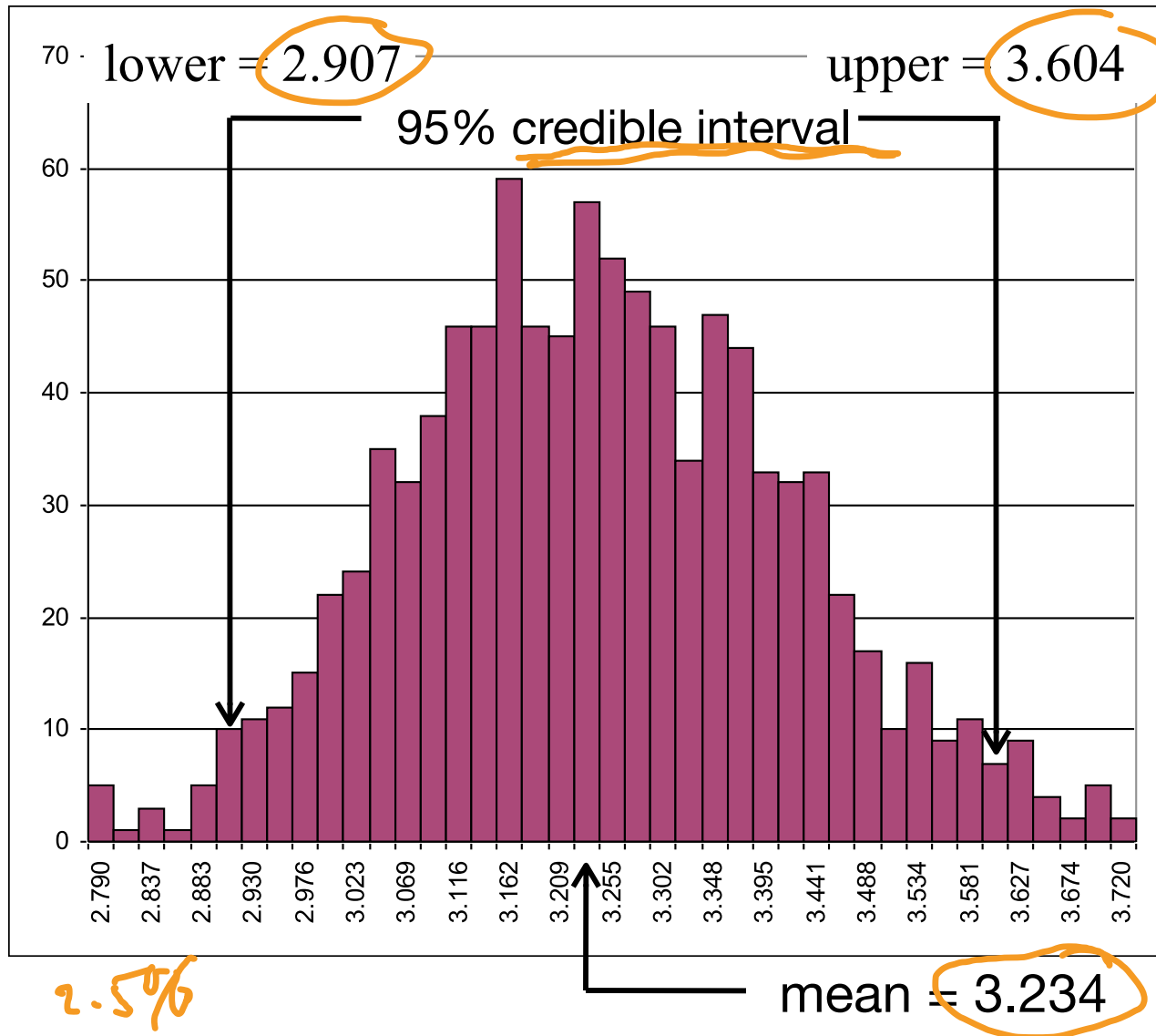
(better, so accept)

log likelihood + log prior

Proposing a new value of a model parameter



Marginal Posterior Distribution of κ



HPD interval
(Highest Probability
Density)

Histogram
created
from a
sample of
1000 kappa
values.

Kernel Density Estimation (KDE)

Estimate density function using sampled points

