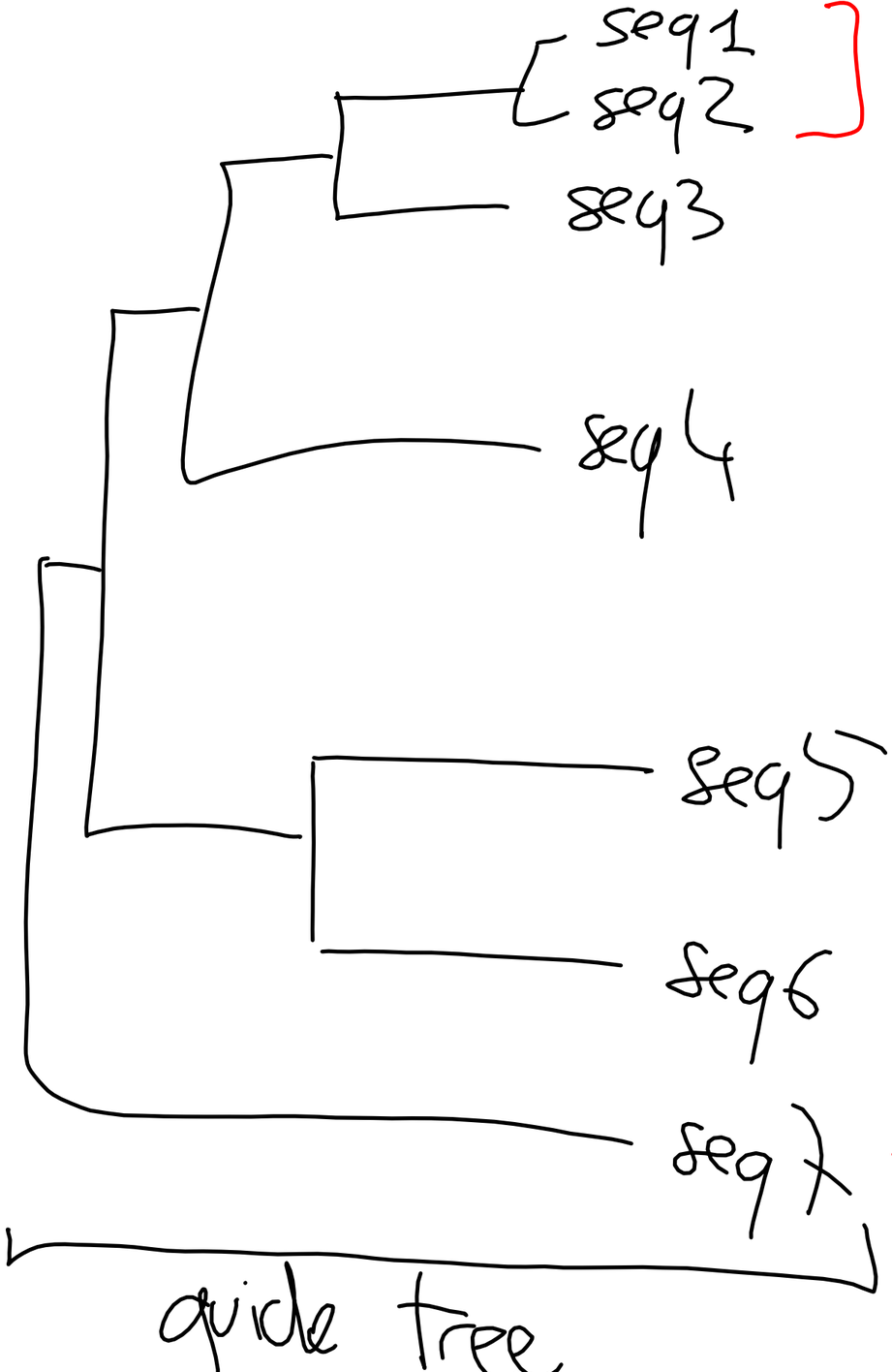
ALIGNMENTS (PAIRWISE)



order: 1 2 3 6

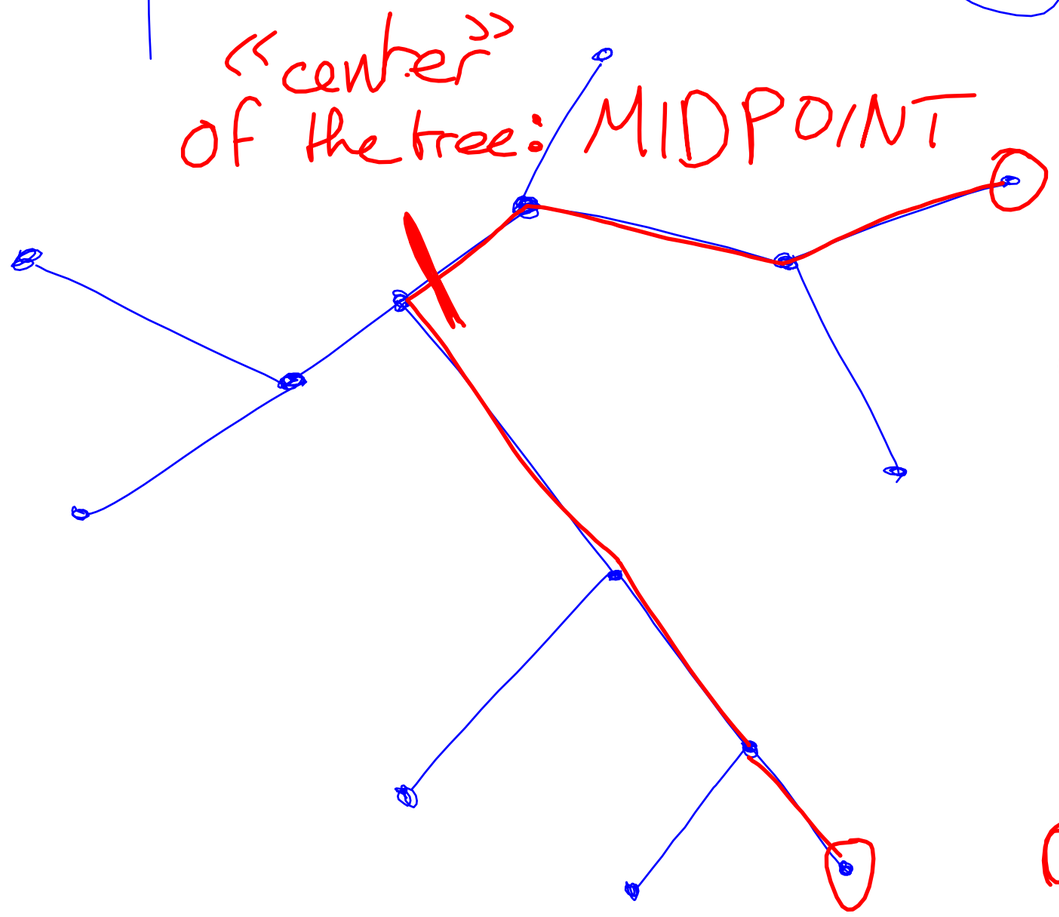
AATA
AAGA

? ?

AATA
AAGA

AAT-A
AA-GA

Midpoint rooting



diameter of a tree

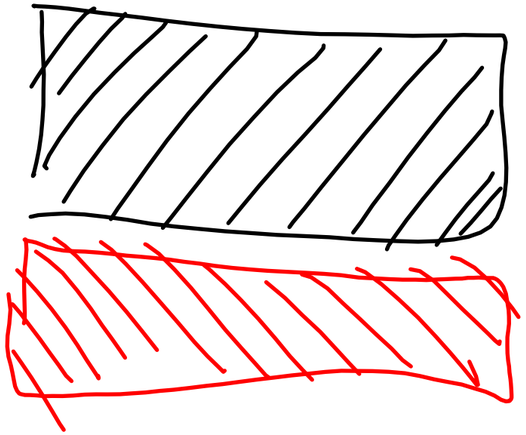
= =

distance between the two most distant leaves

align:

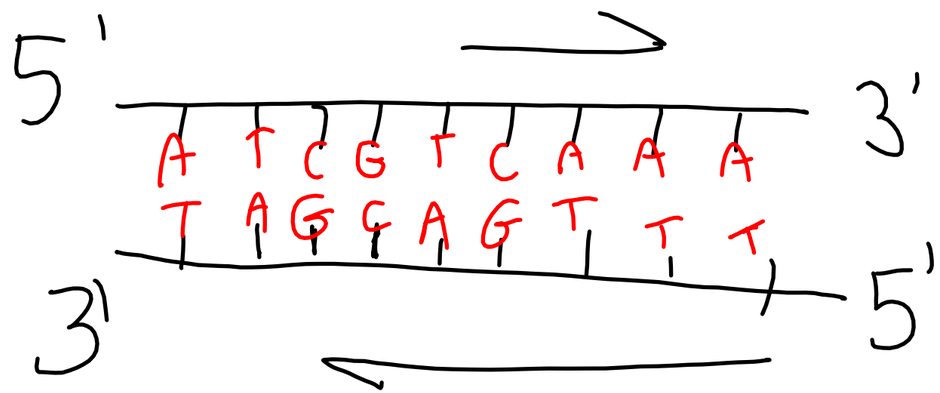
ATCGTCAAATGC

GCATTTTGACGAT

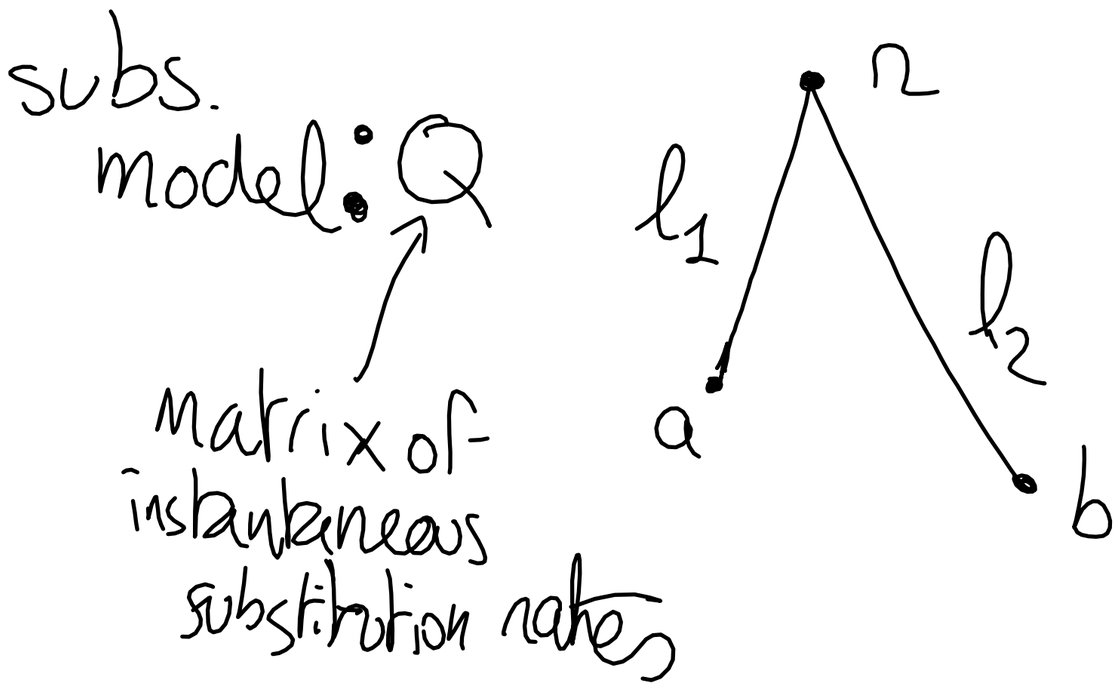


well aligned block

completely ≠ block



phylogenetic models from a generative viewpoint



I can calculate the a priori distribution on the root (π) as well as probability distrib.

$Pr(a \mid r, l_1)$ and

$Pr(b \mid r, l_2)$

I can generate sites according to these.