1. Combinations didn't work.

These dist and tree combinations didnt work

sequences are very different, most evolutionary distances are undefined and a non-finite value (Inf or NaN) is returned.

JC69 nj

K80 nj

F81 nj

K81 nj

F84 nj

BH87 nj

T92 nj

TN93 nj

GG95 nj

logdet nj

paralin nj

paralin NJ

raw bionj

JC69 bionj

K80 bionj

F81 bionj

K81 bionj

F84 bionj

BH87 bionj

T92 bionj

TN93 bionj

GG95 bionj

logdet bionj

paralin bionj

ml fastme.ols

F81 fastme.ols

F84 fastme.ols

T92 fastme.ols

TN93 fastme.ols

raw fastme.bal

2. Ml and dist method with same aligned seq

dist.ml

dist.hamming

nj

3. Change parameters for the alignment