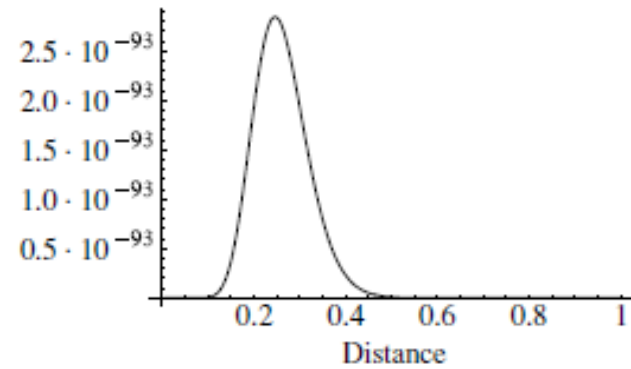
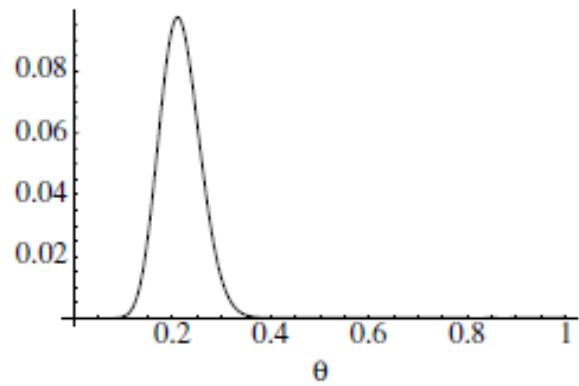


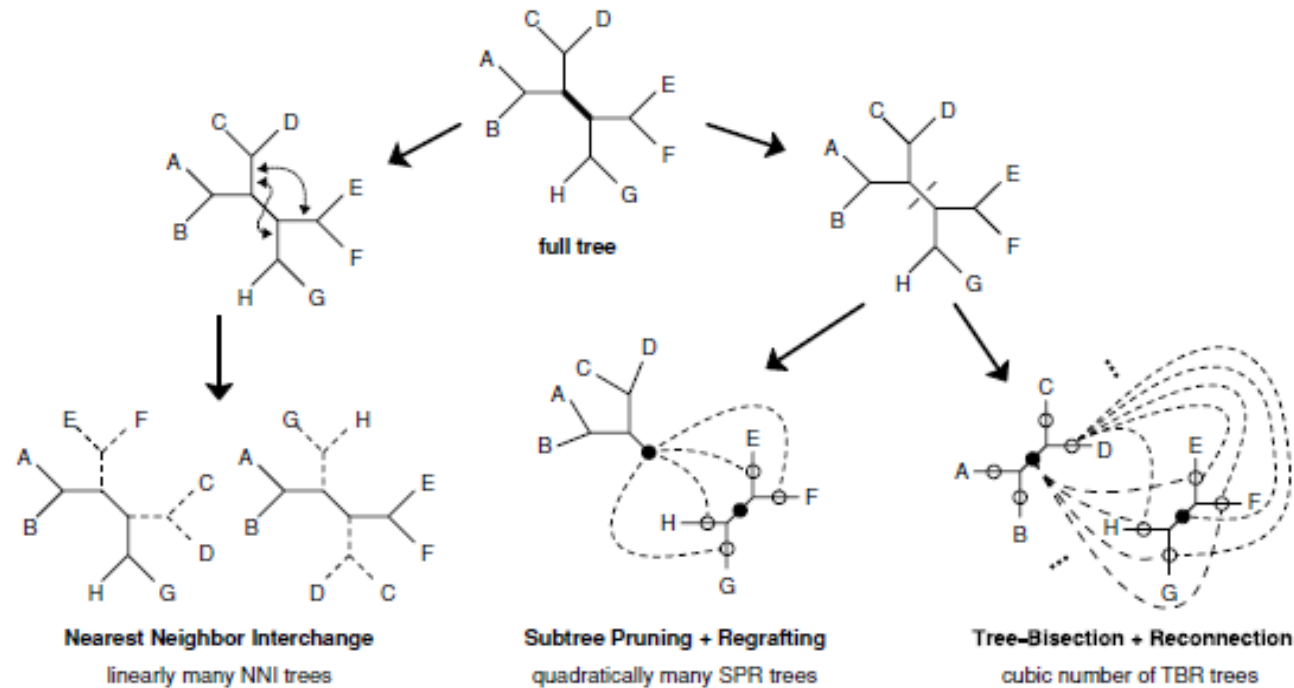
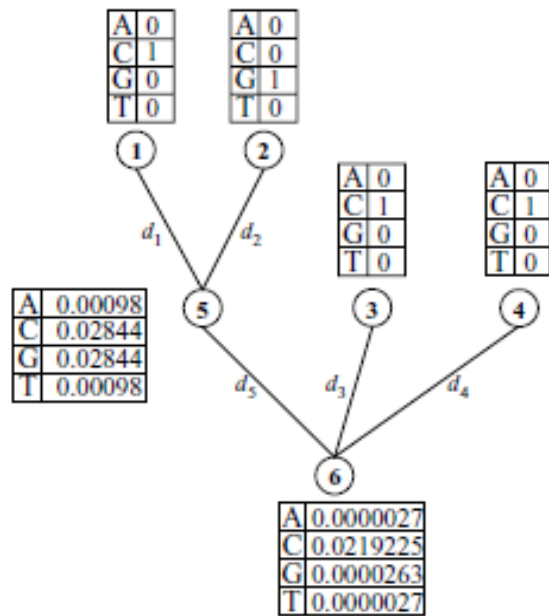
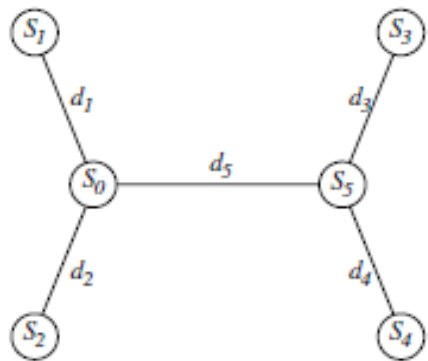
6. Maksimum benzerlik yöntemleri

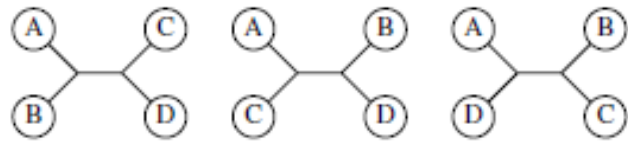


```

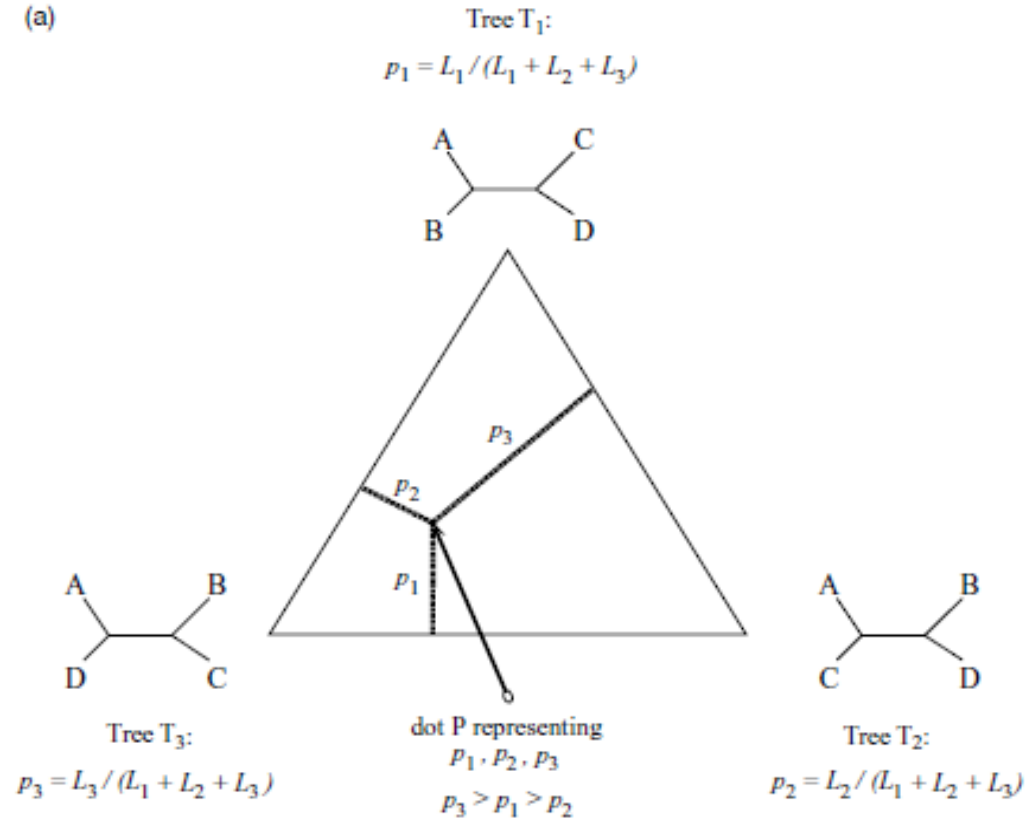
L20571   . . . AAAGTAATGAAGAAGAACAACAGGAAGTCATGGAGCTTATACATA . . .
AF10138  . . . ATGGAGAAGAAGAAG-----AGACTCTGGCTAAGTTATTGT . . .
X52154   . . . ATGGAGAAGAAGAAG-----AGAGACTGGAACAGCTTATCC . . .
U09127   . . . ATGGGGATAGAGAGGAATTATCCTTGCTGGTGGACATGGGGGATT . . .
U27426   . . . AGGGGGATACAGATGAATTTGGCAACACTTGTGGAAATGGGGA . . .
U27445   . . . AAGGGGATACGGACGAATTTGGCAACACTTCTGGAGATGGGGA . . .
U067158  . . . AGGGGGACACTGAGGAATTTATCAACAATGGTGGATATGGGGCGTC . . .
U09126   . . . GAGGGGATACAGAGGAATTTGAAAACAATGGTGGATATGGGGCATC . . .
U27399   . . . AGGGAGATGAGGAGGAATTTGTCAGCATTTGTGGGGATGGGGCACC . . .
U43386   . . . AGGGAGATGCAGAGGAATTTATCAGCATTTATGGAAATGGGGCATC . . .
L02317   . . . AAGGAGATCAGGAAGAATTTATCAGCACTTGTGGAGATGGGGCACC . . .
AF025763 . . . AAGGGGATCAGGAAGAATTTGTCAGCACTTGTGGAGATGGGGCATG . . .
U08443   . . . AAGGAGATGAGGAAGCATTTGTCAGCACTTATGGAGAGGGGGCACC . . .
AF042106 . . . AAGGGGATCAGGAAGAATTTATCGGCACCTTGTGGACATGGGGCACC . . .

```

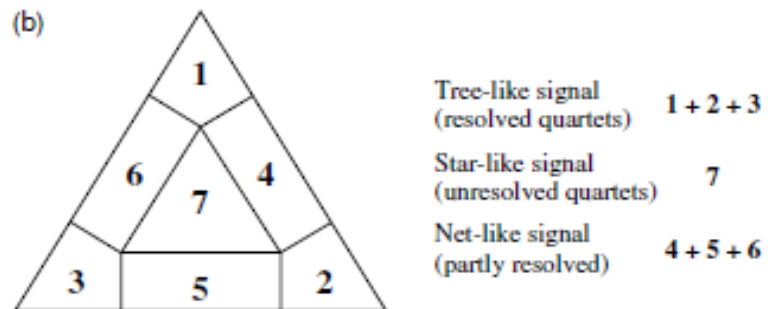




(a)



(b)



RATE HETEROGENEITY

r Model of rate heterogeneity? Uniform rate

quit [q], confirm [y], or change [menu] settings:

GENERAL OPTIONS

o Display as outgroup? L20571
n Number of iterations? 200
s Stopping rule? No, stop after 200 iterations

IQP OPTIONS

p Probability of deleting a sequence? 0.3
k Number representatives? 4

SUBSTITUTION PROCESS

d Type of sequence input data? Nucleotides
m Model of substitution? HKY85 (Hasegawa et al. 1985)
t Ts/Tv ratio (0.5 for JC69)? Estimate from data
f Base frequencies? Estimate from data

GENERAL OPTIONS

o Display as outgroup? L20571
n Number of iterations? 200
s Stopping rule? No, stop after 200 iterations

IQP OPTIONS

p Probability of deleting a sequence? 0.3
k Number representatives? 4

SUBSTITUTION PROCESS

d Type of sequence input data? Nucleotides
m Model of substitution? HKY85 (Hasegawa et al. 1985)
t Ts/Tv ratio (0.5 for JC69)? Estimate from data
f Base frequencies? Estimate from data

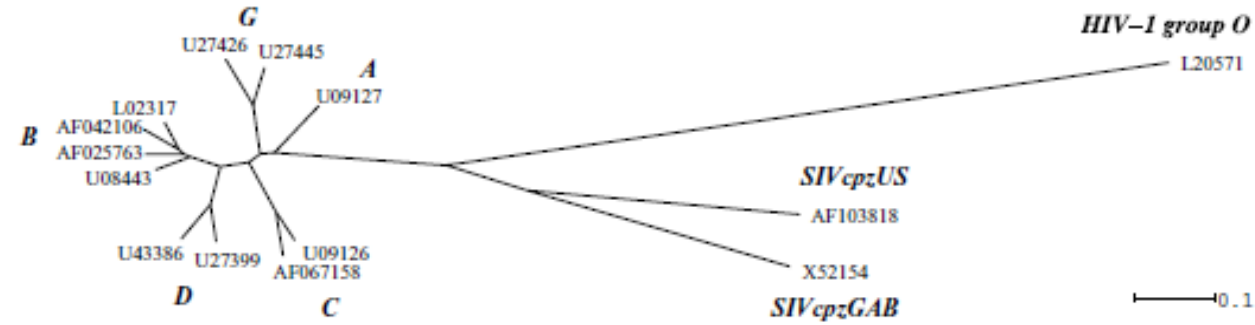
RATE HETEROGENEITY

r Model of rate heterogeneity? Gamma distributed rates
i Proportion of invariable sites? No
a Gamma distribution parameter alpha? Estimate from data
c Number of Gamma rate categories? 4

quit [q], confirm [y], or change [menu] settings:

(a)

HIV-1 group M



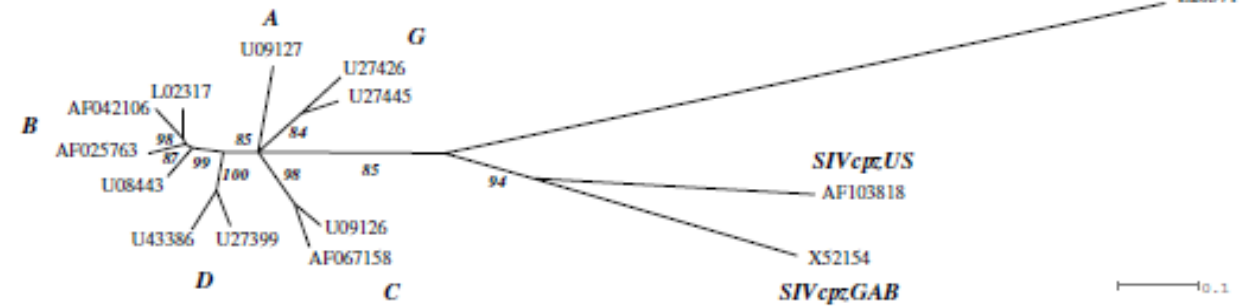
Input data set (hivALN.phy) contains 14 sequences of length 2352

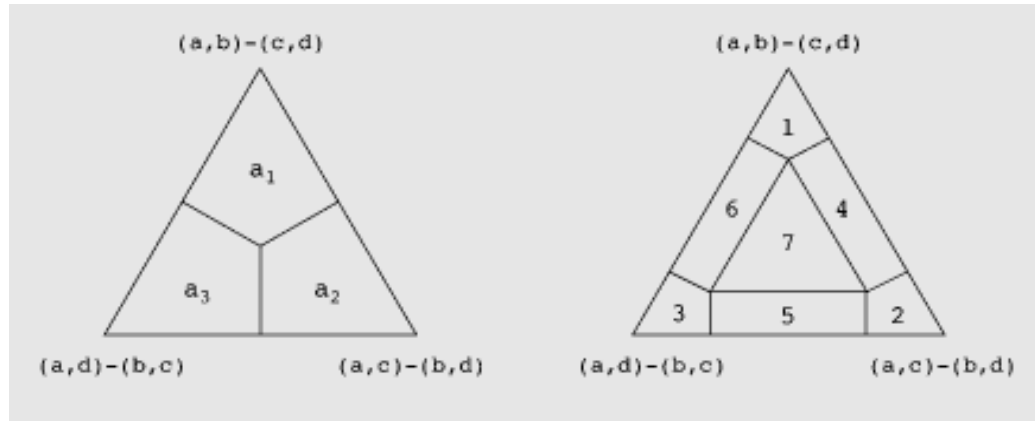
1. L20571
2. AF103818
3. X52154
4. U09127
5. U27426
6. U27445
7. AF067158
8. U09126
9. U27399
10. U43386
11. L02317
12. AF025763
13. U08443
14. AF042106

(consists very likely of nucleotides)

(b)

HIV-1 group M





	name	#quartets	resolved	partly	unresolved
1	L20571	286	261 (91.26)	12 (4.20)	13 (4.55)
2	AF103818	286	271 (94.76)	14 (4.90)	1 (0.35)
3	X52154	286	260 (90.91)	13 (4.55)	13 (4.55)
4	U09127	286	255 (89.16)	17 (5.94)	14 (4.90)
5	U27426	286	260 (90.91)	15 (5.24)	11 (3.85)
6	U27445	286	273 (95.45)	11 (3.85)	2 (0.70)
7	AF067158	286	261 (91.26)	18 (6.29)	7 (2.45)
8	U09126	286	263 (91.96)	13 (4.55)	10 (3.50)
9	U27399	286	270 (94.41)	9 (3.15)	7 (2.45)
10	U43386	286	264 (92.31)	8 (2.80)	14 (4.90)
11	L02317	286	268 (93.71)	12 (4.20)	6 (2.10)
12	AF025763	286	268 (93.71)	13 (4.55)	5 (1.75)
13	U08443	286	267 (93.36)	12 (4.20)	7 (2.45)
14	AF042106	286	271 (94.76)	9 (3.15)	6 (2.10)
		1001	928 (92.71)	44 (4.40)	29 (2.90)

Input data set (hivALN.phy) contains 14 sequences of length 2352

1. L20571
2. AF103818
3. X52154
4. U09127
5. U27426
6. U27445
7. AF067158
8. U09126
9. U27399
10. U43386
11. L02317
12. AF025763
13. U08443
14. AF042106

GENERAL OPTIONS

b Type of analysis? Tree reconstruction
k Tree search procedure? Quartet puzzling
v Quartet evaluation criterion? Approximate maximum likeli-
hood (ML)
u List unresolved quartets? No
n Number of puzzling steps? 1000
j List puzzling step trees? No
9 List puzzling trees/splits (NEXUS)? No
o Display as outgroup? L20571 (1)
z Compute clocklike branch lengths? No
e Parameter estimates? Approximate (faster)
x Parameter estimation uses? Neighbor-joining tree

SUBSTITUTION PROCESS

d Type of sequence input data? Auto: Nucleotides
h Codon positions selected? Use all positions
m Model of substitution? HKY (Hasegawa et al. 1985)
t Transition/transversion parameter? Estimate from data set
f Nucleotide frequencies? Estimate from data set

RATE HETEROGENEITY

w Model of rate heterogeneity? Uniform rate

Quit [q], confirm [y], or change [menu] settings:

GENERAL OPTIONS

b Type of analysis? Tree reconstruction
k Tree search procedure? Quartet puzzling
v Quartet evaluation criterion? Approximate maximum likelihood (ML)
u List unresolved quartets? No
n Number of puzzling steps? 10000
j List puzzling step trees? No
9 List puzzling trees/splits (NEXUS)? No
o Display as outgroup? L20571 (1)
z Compute clocklike branch lengths? No
e Parameter estimates? Approximate (faster)
x Parameter estimation uses? Neighbor-joining tree

SUBSTITUTION PROCESS

d Type of sequence input data? Auto: Nucleotides
h Codon positions selected? Use all positions
m Model of substitution? HKY (Hasegawa et al. 1985)
t Transition/transversion parameter? Estimate from data set
f Nucleotide frequencies? Estimate from data set

RATE HETEROGENEITY

w Model of rate heterogeneity? Gamma distributed rates
a Gamma distribution parameter alpha? Estimate from data set
c Number of Gamma rate categories? 8

Quit [q], confirm [y], or change [menu] settings:

Optimizing missing substitution process parameters
Optimizing missing rate heterogeneity parameters
Optimizing missing substitution process parameters
Optimizing missing rate heterogeneity parameters
Optimizing missing substitution process parameters
Optimizing missing rate heterogeneity parameters
Writing parameters to file hivALN.phy.puzzle
Writing pairwise distances to file hivALN.phy.dist
Computing quartet maximum likelihood trees
Computing quartet puzzling trees
Computing maximum likelihood branch lengths (without clock)

All results written to disk:

Puzzle report file: hivALN.phy.puzzle
Likelihood distances: hivALN.phy.dist
Phylip tree file: hivALN.phy.tree

The parameter estimation took 11.00 seconds (= 0.18 minutes = 0.00 hours)

The ML step took 8.00 seconds (= 0.13 minutes = 0.00 hours)

The puzzling step took 2.00 seconds (= 0.03 minutes = 0.00 hours)

The computation took 23.00 seconds (= 0.38 minutes = 0.01 hours)

including input 272.00 seconds (= 4.53 minutes = 0.08 hours)

```
[1. 657 6.57 14 68510000](L20571,((AF10138,X52154),
(U09127,(((U27426,U27445), (U067158,U09126)),
((U27399,U43386),(((L02317,AF042106),AF025763),
U08443))))));
```

GENERAL OPTIONS

```
b          Type of analysis? Tree reconstruction
k          Tree search procedure? Evaluate user defined trees
z          Compute clocklike branch lengths? No
e          Parameter estimates? Approximate (faster)
x          Parameter estimation uses? Neighbor-joining tree
```

SUBSTITUTION PROCESS

```
d          Type of sequence input data? Auto: Nucleotides
h          Codon positions selected? Use all positions
m          Model of substitution? HKY (Hasegawa et al., 1985)
t          Transition/transversion parameter? Estimate from data set
f          Nucleotide frequencies? Estimate from data set
```

RATE HETEROGENEITY

```
w          Model of rate heterogeneity? Gamma distributed rates
a          Gamma distribution parameter alpha? Estimate from data set
c          Number of Gamma rate categories? 8
```

Quit [q], confirm [y], or change [menu] settings: y