Tracing phylogenetic signal in datasets

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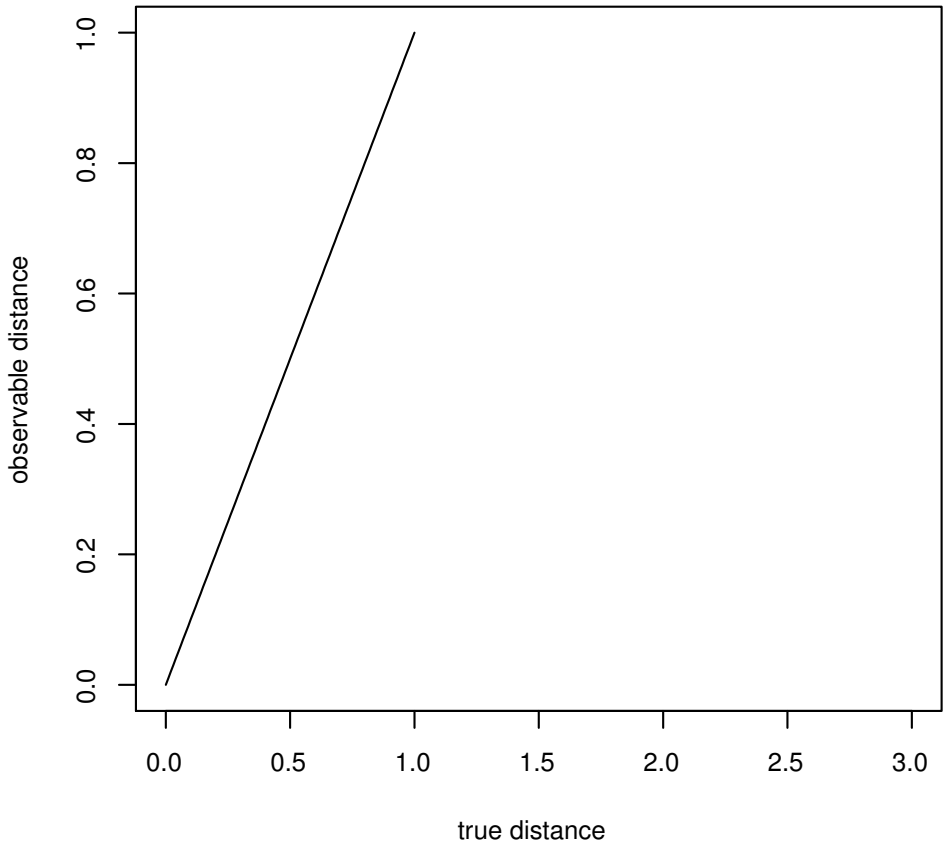
Are there ways to check for this?

Reminder: Jukes-Canter Correction for Multiple Hits



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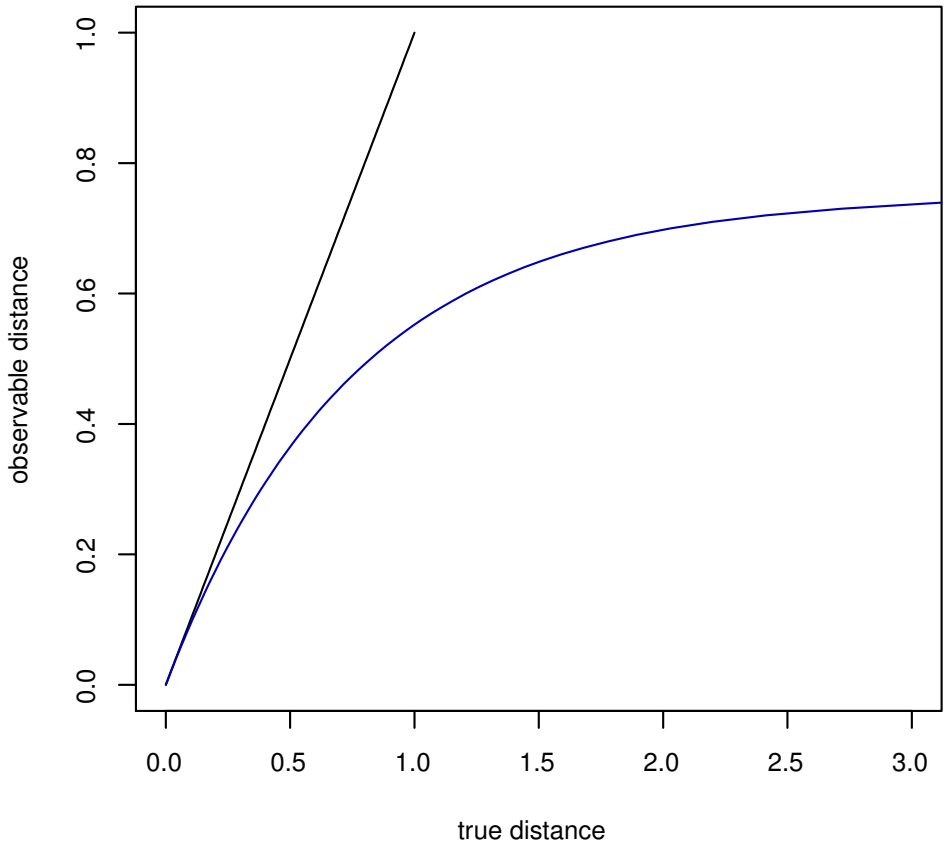
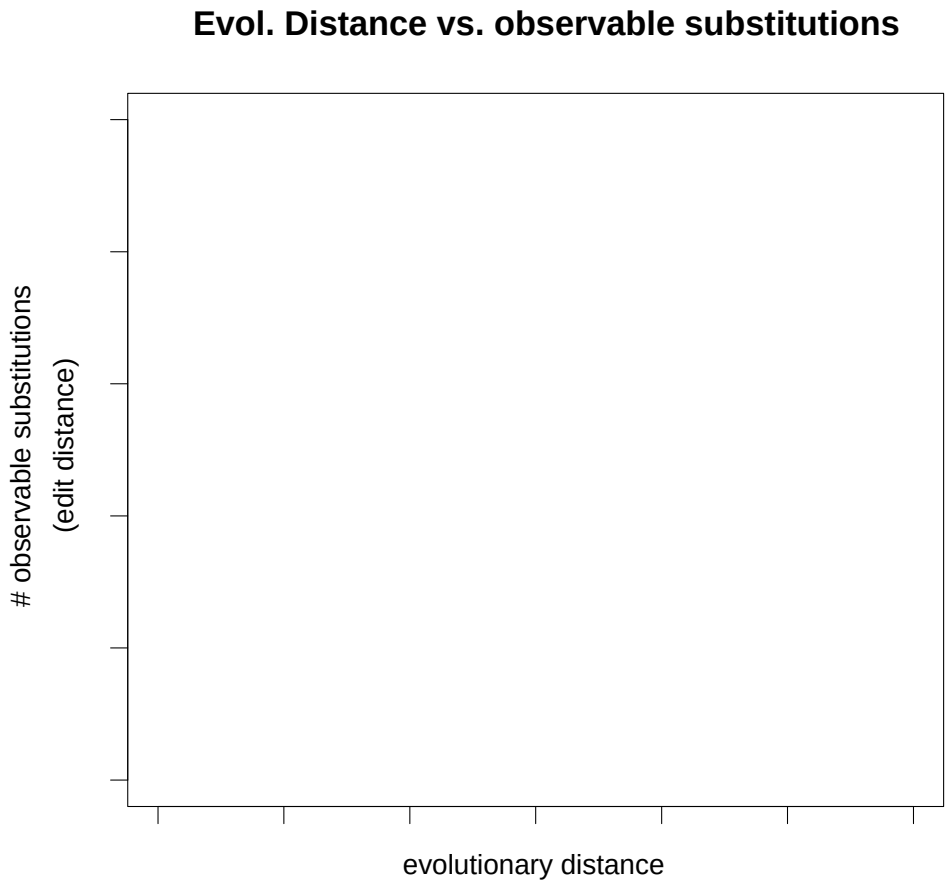


Plotting Substitutions vs. Distance for DNA



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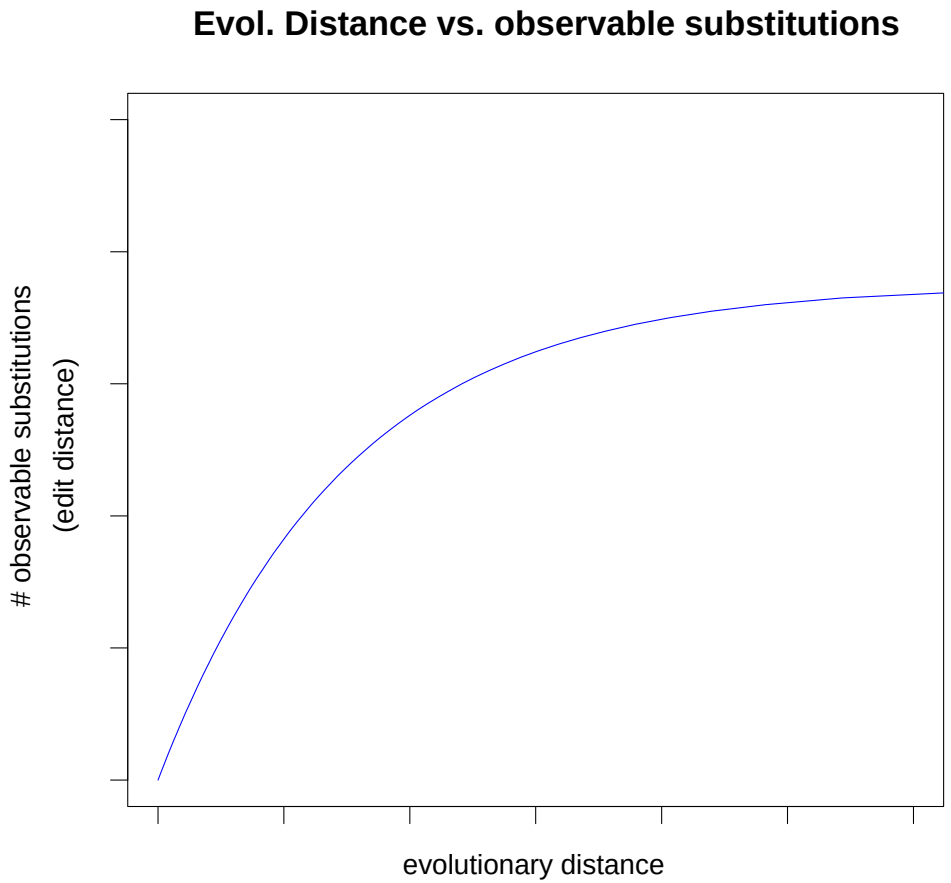

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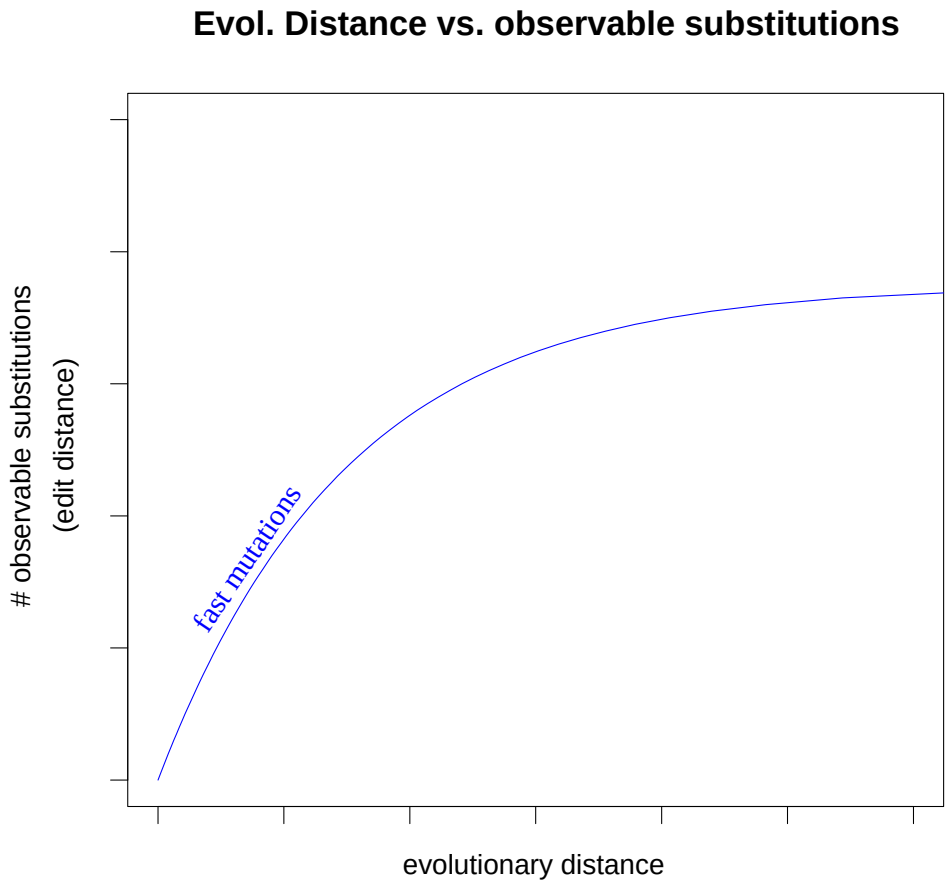

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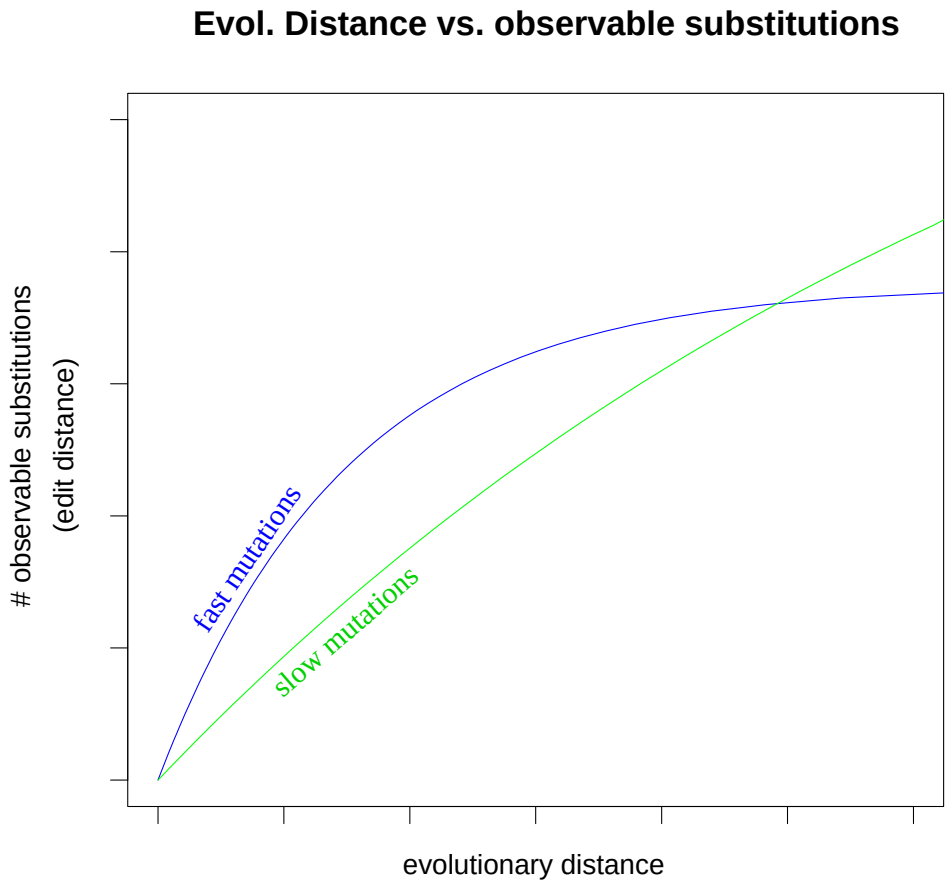

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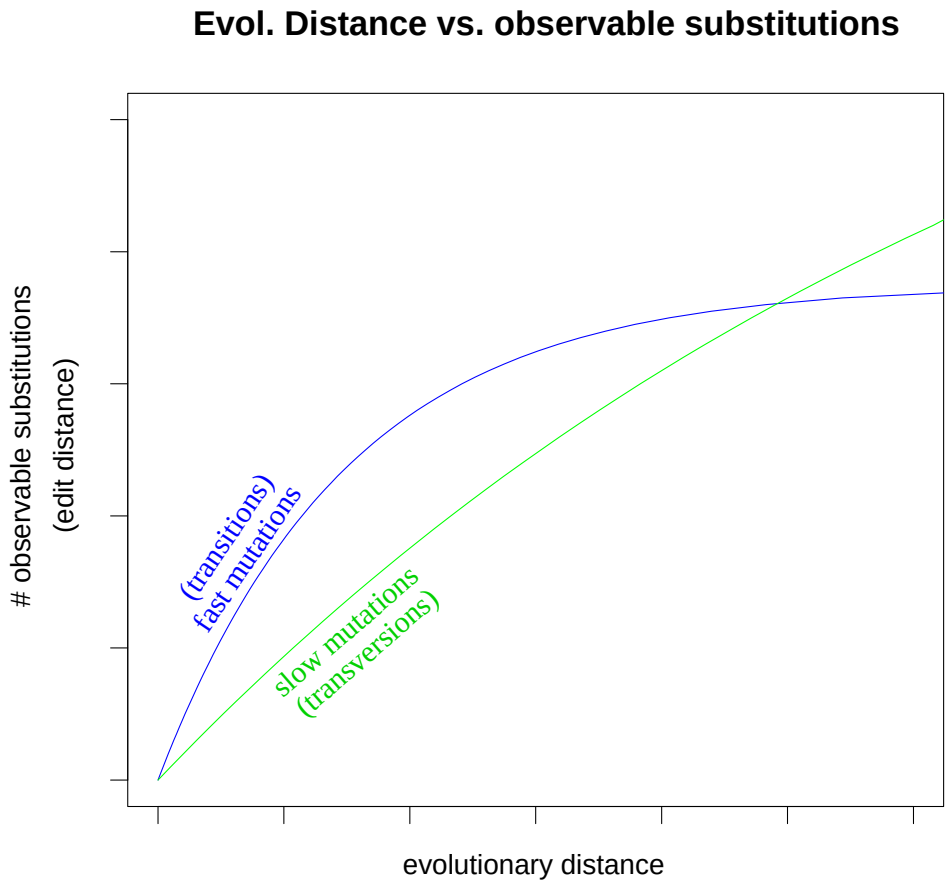

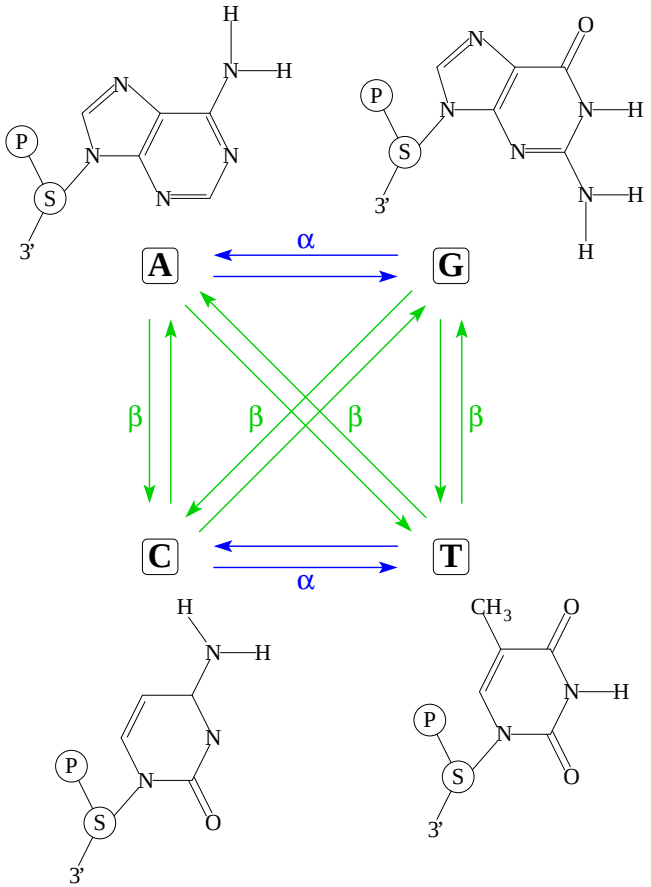

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Thus, the ts-curve rises faster but reaches the plateau earlier.

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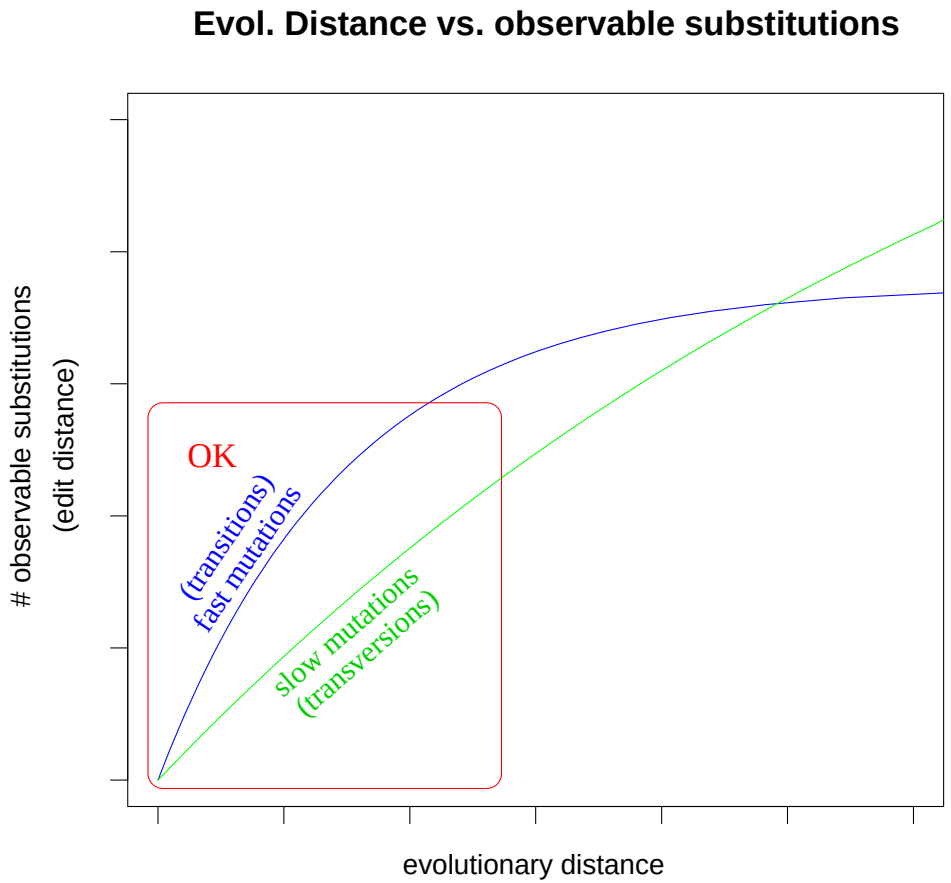

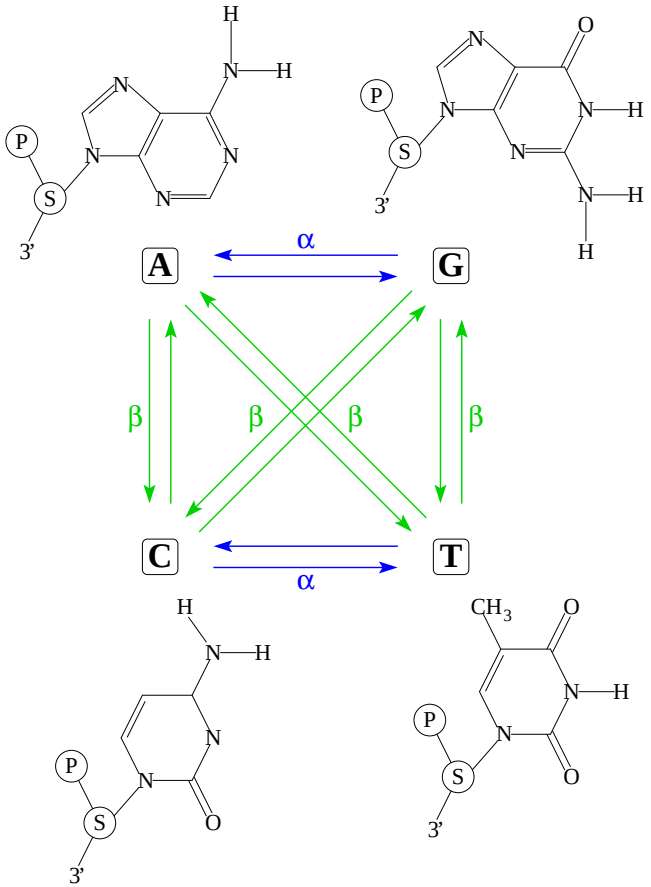

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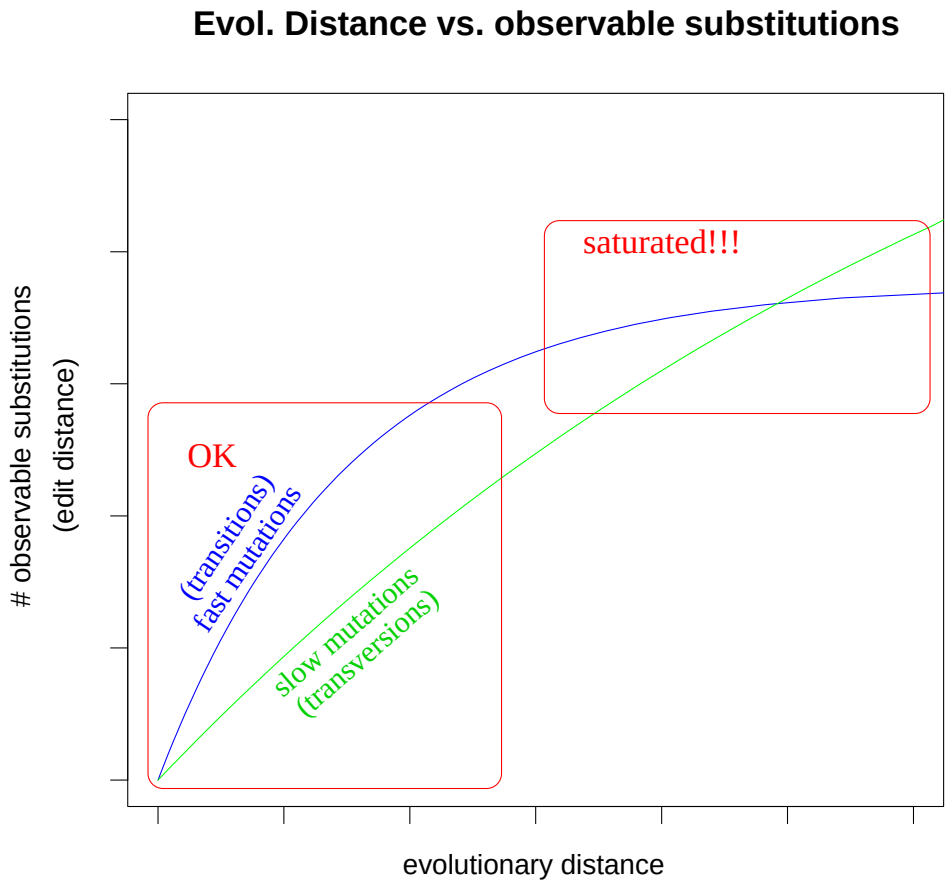

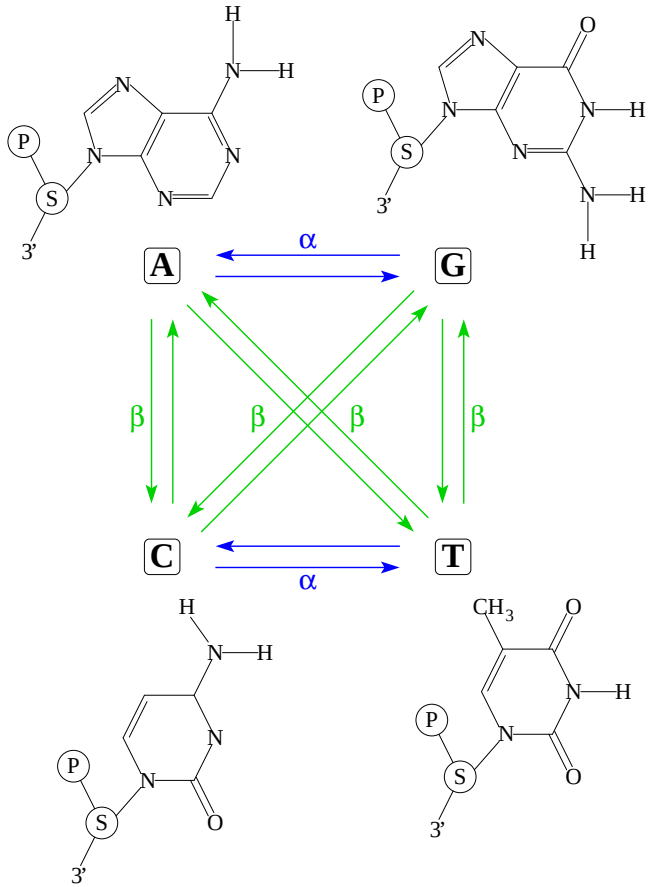

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The tv-curve can only 'overtake' the ts-curve if the latter is quite saturated!

Saturation Plots for DNA

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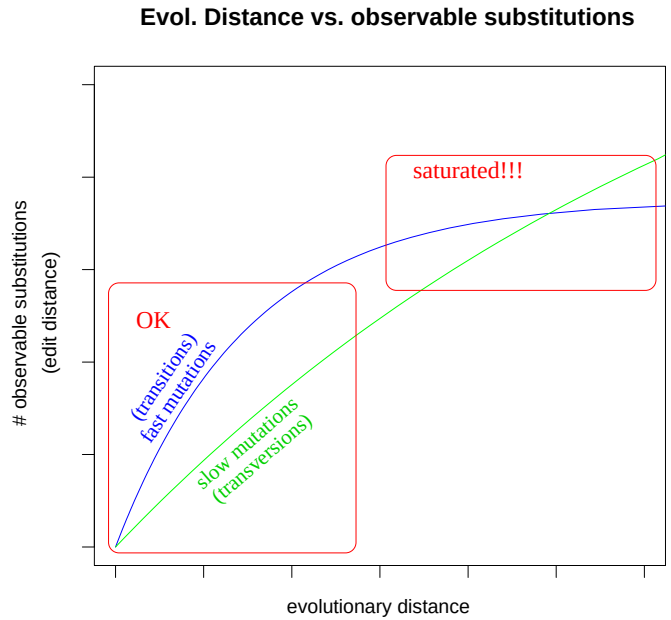
- . . . and plot the evolutionary distance (x-axis) against the observed substitutions (y-axis) for each class of mutations.



Software for DNA Saturation Plots

Saturation Plots can be created using

- **Windows:** DAMBE (Xia and Xie, 2001)

```
→ Graphics menu
→ Transition and transversion vs. divergence
```

- **All OS:** TREE-PUZZLE (Schmidt *et al.*, 2001), plotting the data in `*.tstv` with a few lines in the `R` program (`www.r-project.org`):

```
tstvtab = read.table("ali.phy.tstv", header=T)  # read data
attach(tstv)                                    # use headers as names
pdf(file="tstv.pdf")                            # open PDF file
maxsubst=max(ts,tv)                             # find maximum
plot(distance,ts,col=2,ylab="observed substitutions",ylim=c(0,maxsubst))
points(distance,tv,col=3)                       # plot
dev.off()                                       # close PDF file
detach(tstvtab)                                 # release names
q()                                             # quit R program
```

Saturation Plots for AA (AsaturA, van de Peer et al. 2002)

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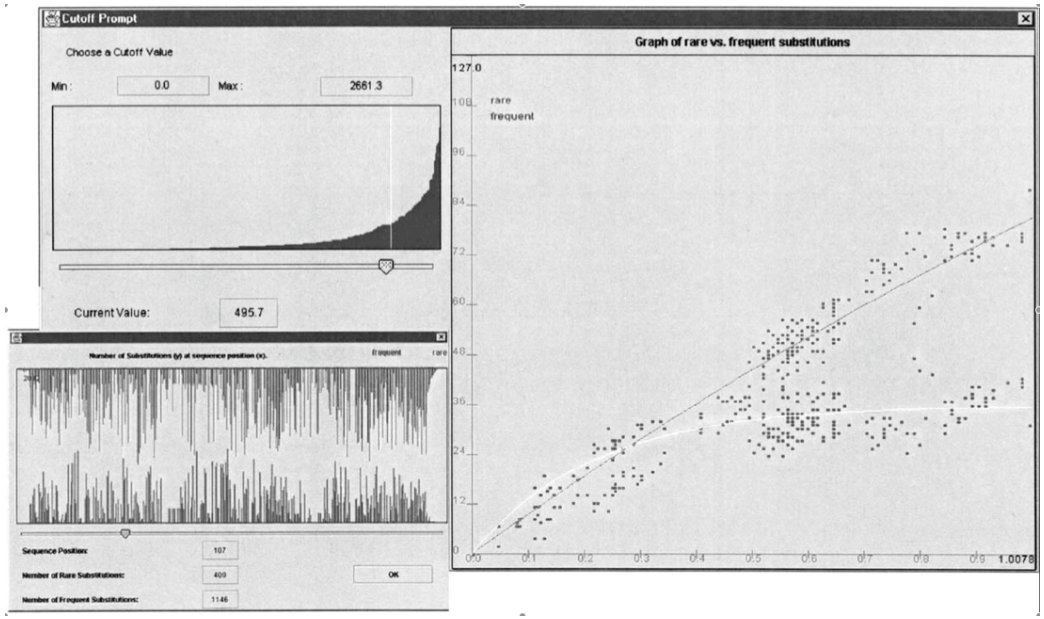
The same can be done for amino acids, but

- There is not intuitive division into fast and slow substitutions,
- AsaturaA orders the the substitution types according to the probabilities in a substitution probability matrix (e.g., PAM, WAG).
- Then, the user has to set a cutoff between *fast* and *slow*. (But there are no guidelines for that choice.)
- Then the numbers of fast and slow substitutions are plotted against the distance accordingly.



Likelihood Weights, Posterior Prob., and Empirical Bayes

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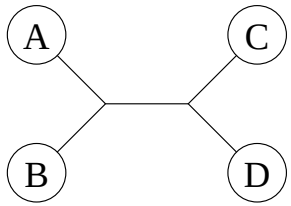
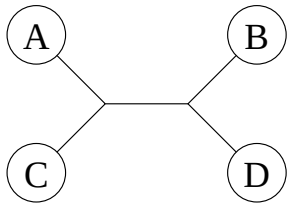
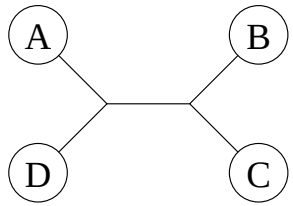
- Problem: How different are the likelihoods?
  Just from the value of likelihoods one often cannot tell whether they are significantly different.
- Normalization: Posterior probabilities are computed:

$$p_i = \frac{L_i}{\sum_n L_n}$$

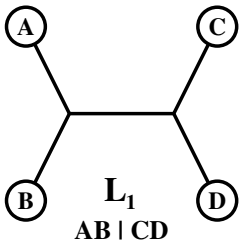
- We can use that on the three different quartet topologies to assess phylogenetic information in our data.

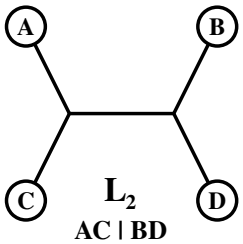


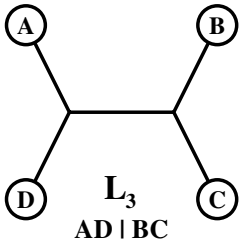




Plotting Posteriors: Likelihood Mapping







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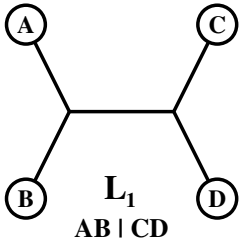
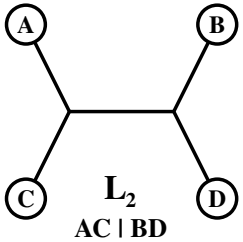
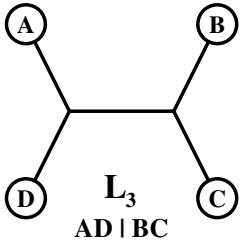


$$p_1 = \frac{L_1}{L_1 + L_2 + L_3}$$



$$p_2 = \frac{L_2}{L_1 + L_2 + L_3}$$



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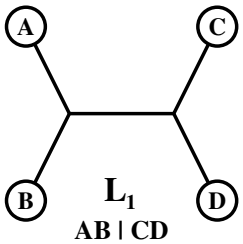

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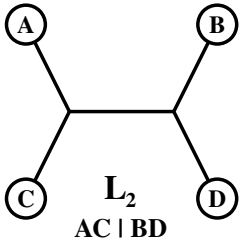

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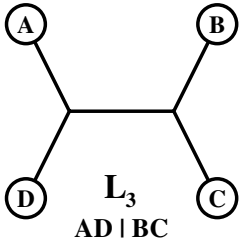

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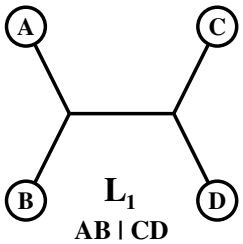

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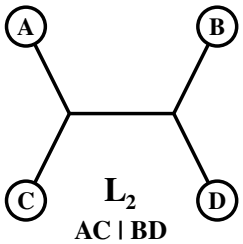

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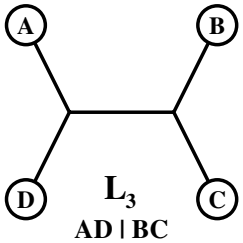

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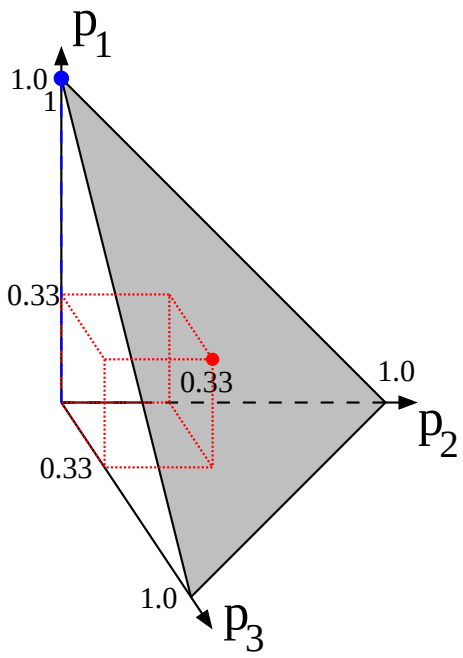

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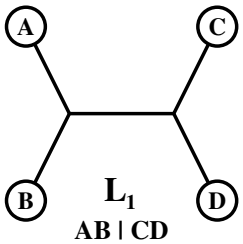

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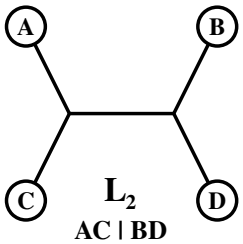

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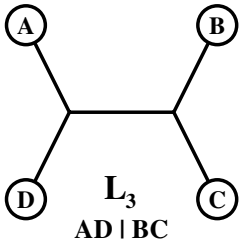

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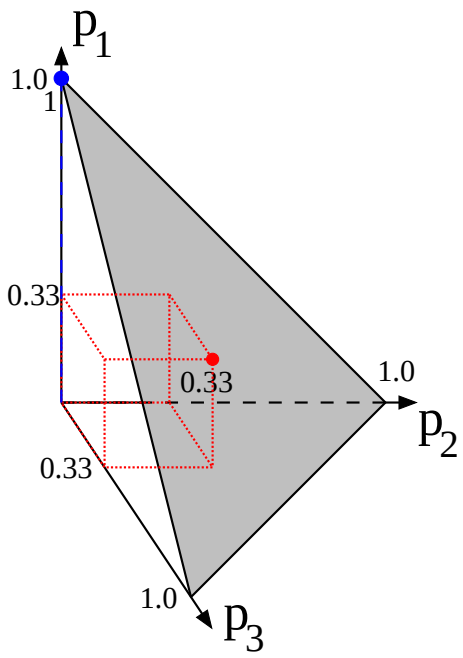

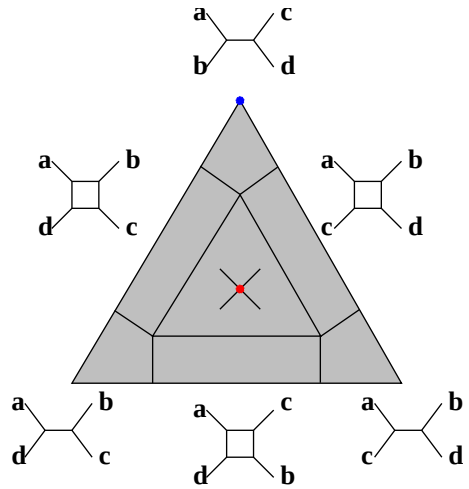

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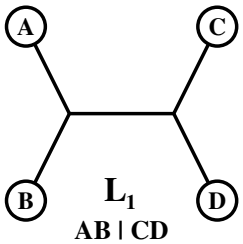

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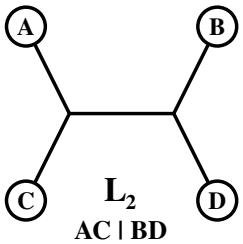

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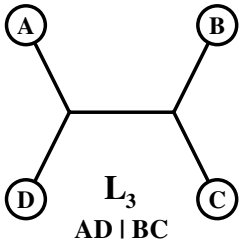

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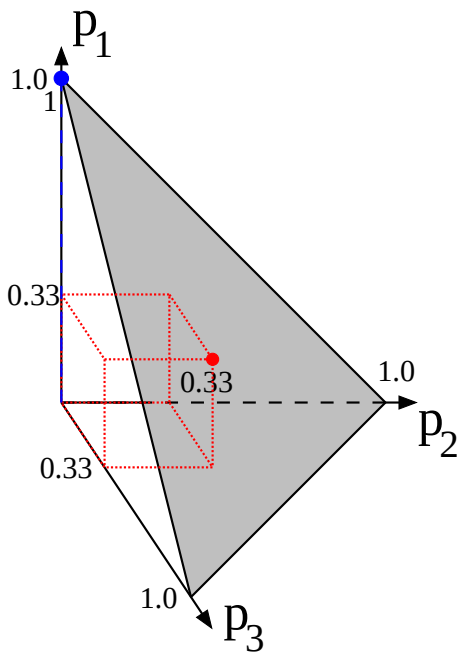
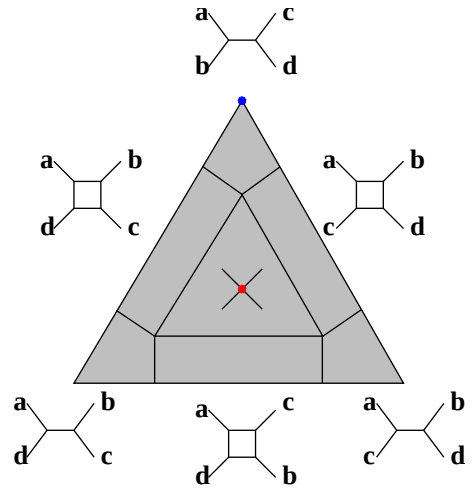
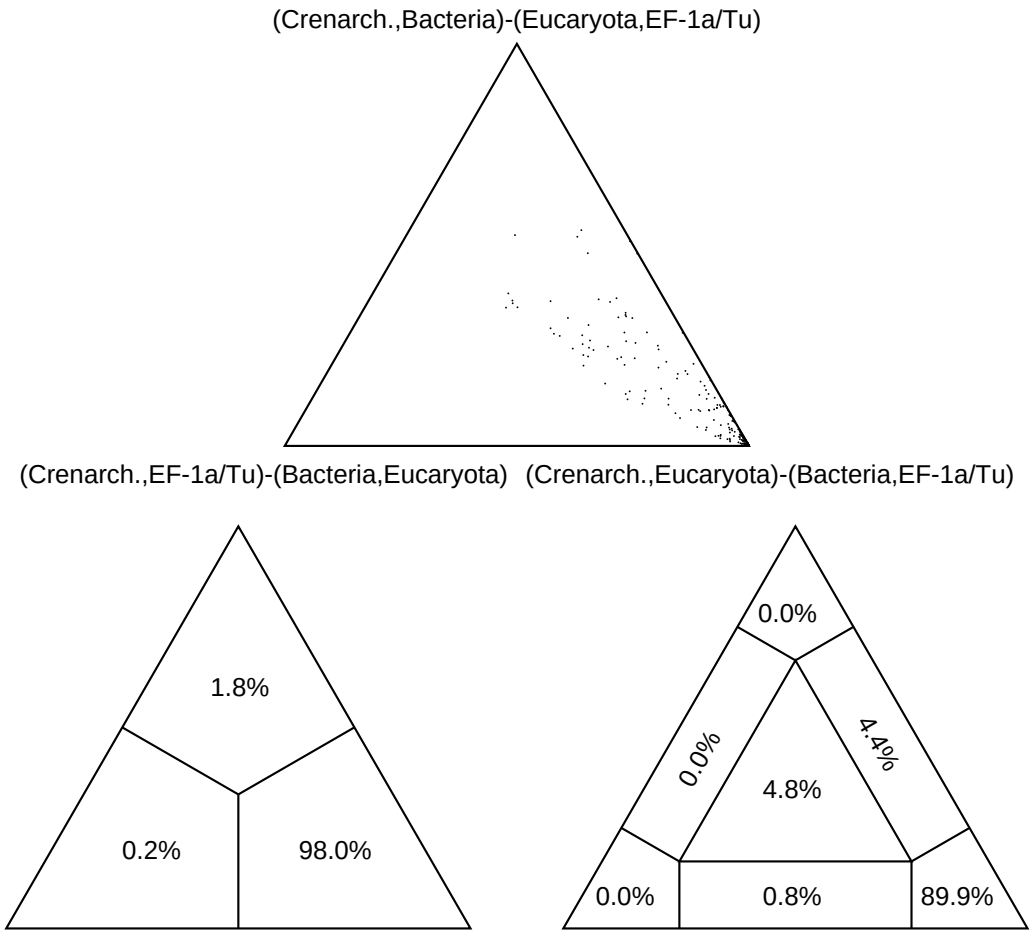




Since $p_1 + p_2 + p_3 = 1$, 3D points (p_1, p_2, p_3) fall into a triangular (simplex).

If we repeat this for all quartets (or a large random subset) in a dataset we can assess the amount of phylogenetic signal in the dataset.

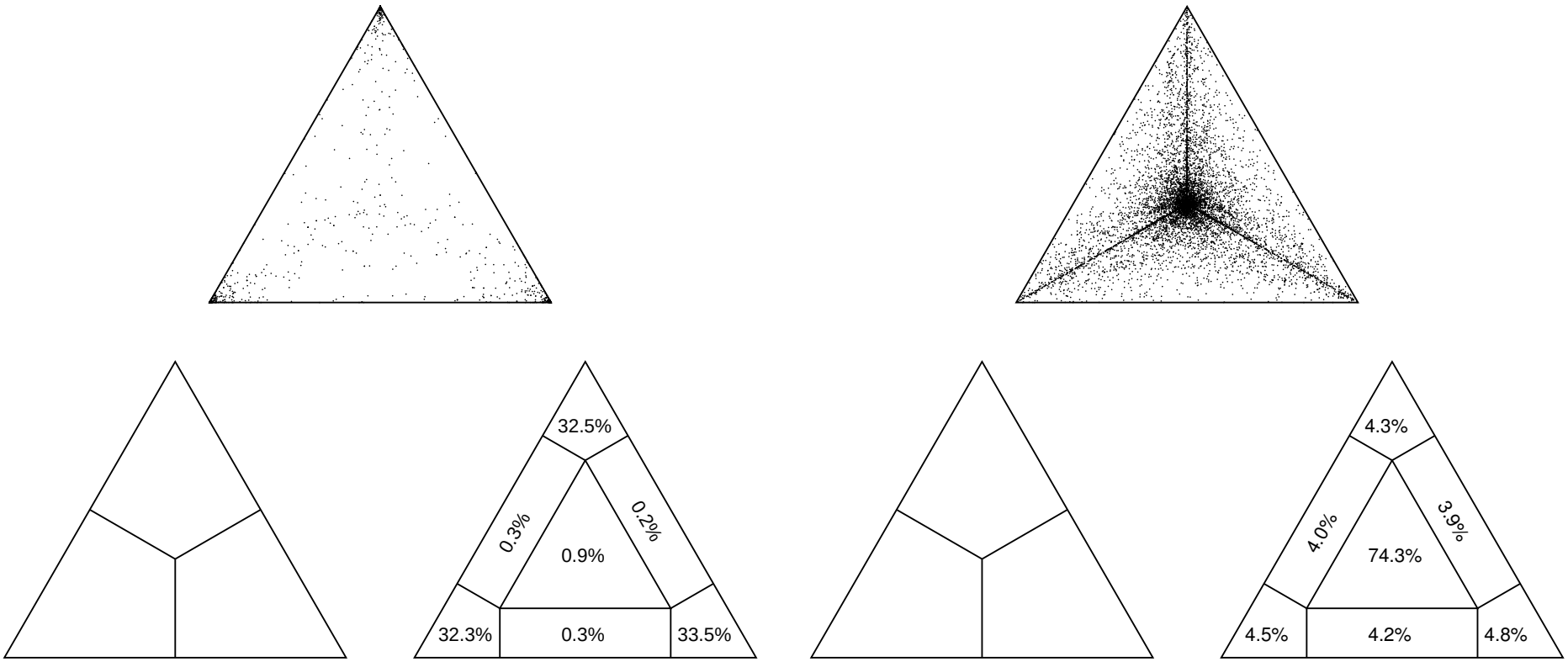
Likelihood Mapping (Cluster Analysis)



The Simplex Plot can visualize the relationship among (4) sets of taxa.

The taxa/sequences are assigned to four sets (A,B,C,D) one for each leaf of a quartet tree.

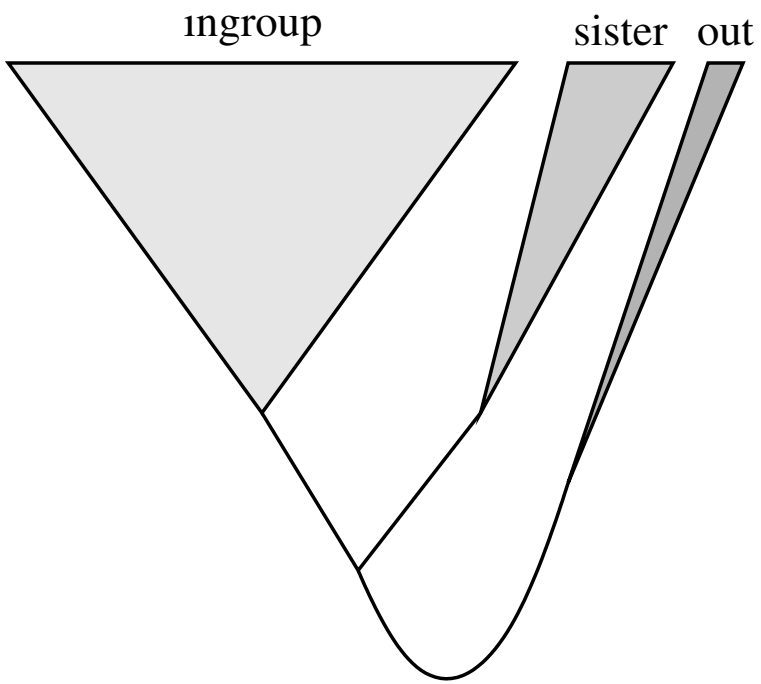
Likelihood Mapping (Information Content)



The Simplex Plot can also visualize the information content in an alignment.

By not assigning taxa to clusters, four are chosen randomly for each leaf. We have to add the percentages in the corners (resolved) or rectangles (partly resolved), respectively. Center means unresolved.

Likelihood Mapping to Validate Outgroups



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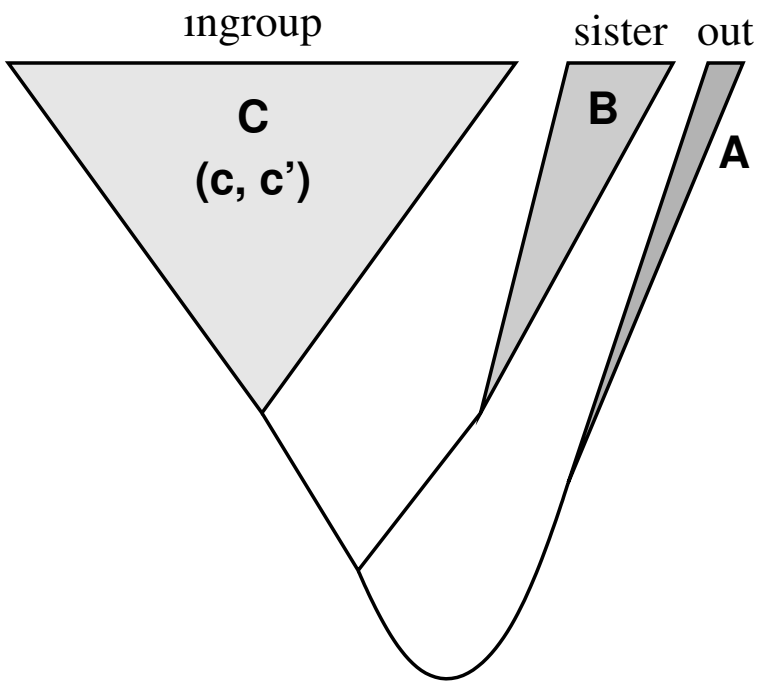
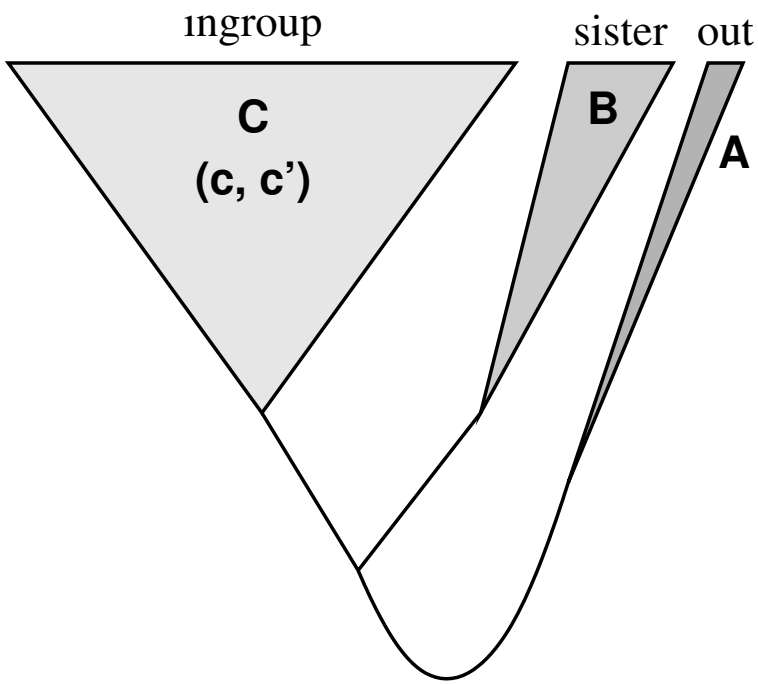


Likelihood Mapping to Validate Outgroups



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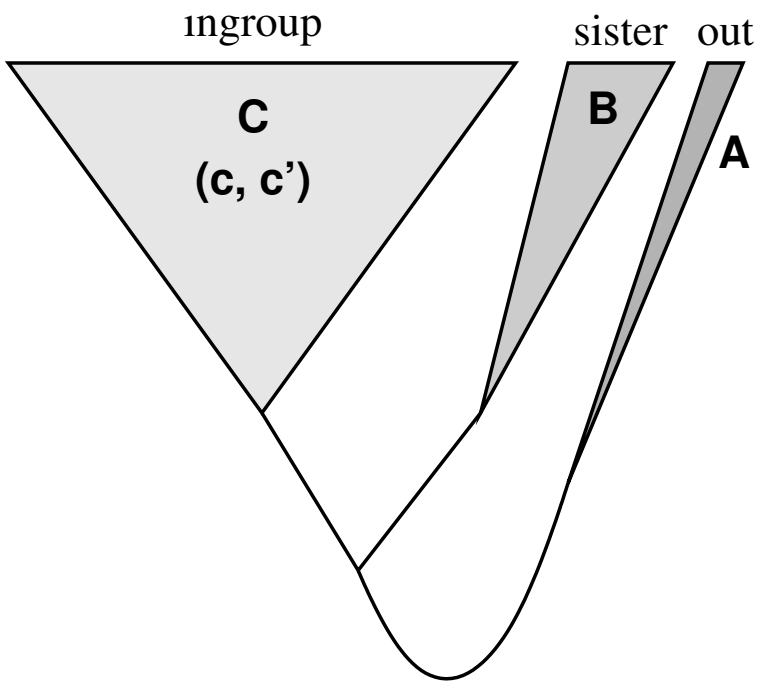

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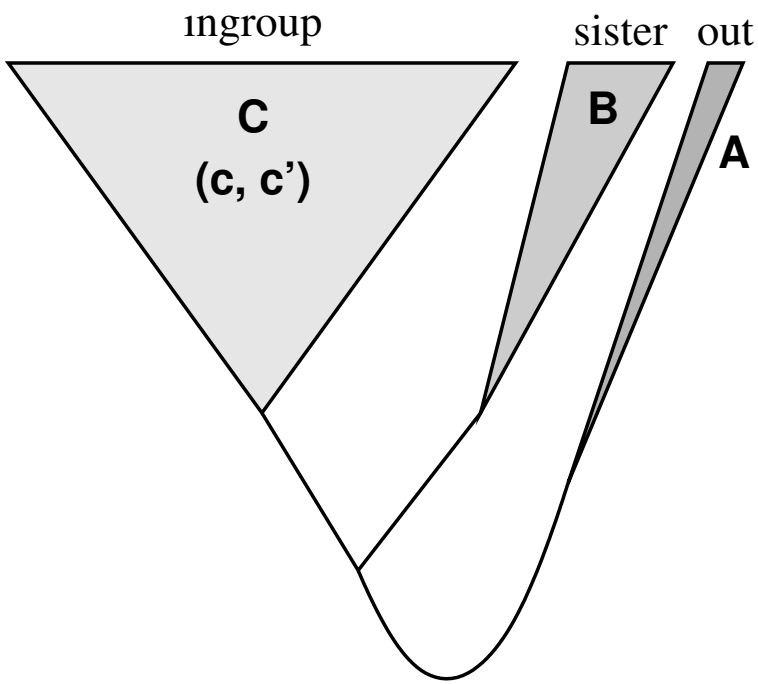

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- random quartets are drawn from the sets: two from C and one each from B and A.
- if not $a, b|c, c'$ (upper corner) is the support topology, A is not a good outgroup (or B is not a proper sister group).

Exercises:

the exercises can be found at

`http://www.cibiv.at/~hschmidt/VEME`