See also 18-Apr-2018 and 16-May-2018 at http://phyloseminar.org/recorded.html

Likelihood in Phylogenetics

Workshop on Molecular Evolution Woods Hole, Massachusetts 28 May 2023

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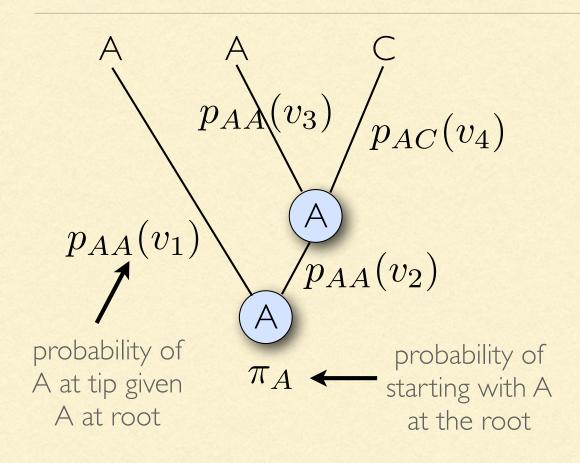
Probability

Probabilities: the AND rule

Rolling 2 dice, what is the probability of seeing (simultaneously) a I on the first die and a 6 on the second die?



AND rule in phylogenetics

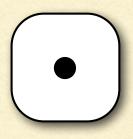


One use of the AND rule in phylogenetics is to combine probabilities associated with individual branches to produce the overall probability of the data for one site.

$$Pr(A, A, C, A, A) = \pi_A \ p_{AA}(v_1) \ p_{AA}(v_2) \ p_{AA}(v_3) \ p_{AC}(v_4)$$

Probabilities: the OR rule

Rolling I die, what is the probability of seeing either a I or a 6?

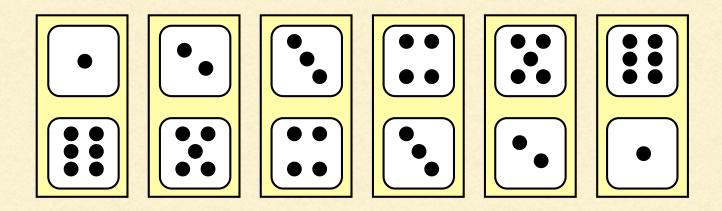




$$+ \qquad (1/6) =$$

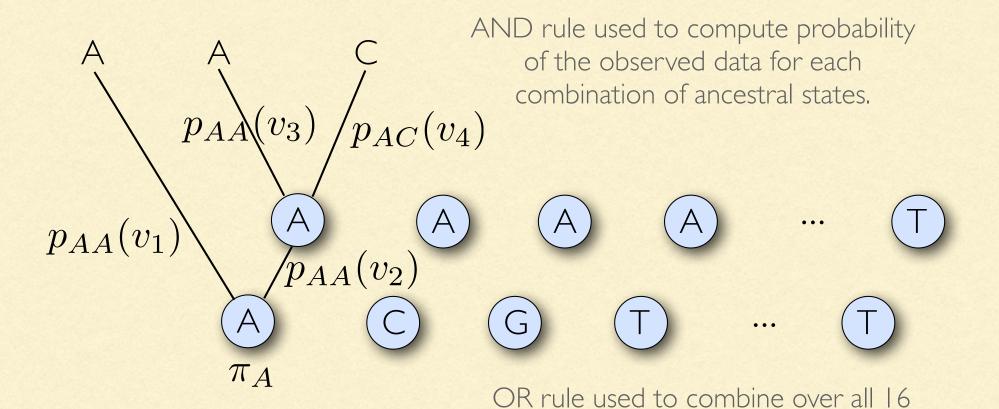
Combining AND and OR

What is the probability that the sum of two dice is 7?



$$(1/36) + (1/36) + (1/36) + (1/36) + (1/36) + (1/36) + (1/36) = 1/6$$

Using both AND and OR in phylogenetics



Pr(A,A,C) = Pr(A,A,C,A,A) + Pr(A,A,C,A,C) + ... + Pr(A,A,C,T,T)

combinations of ancestral states.

Independence

$$Pr(A, B) = Pr(A) Pr(B)$$

Probability of flipping a coin twice and getting heads both times:

$$Pr(H,H) = Pr(H) Pr(H)$$

Non-independence

$$\Pr(A,B) = \Pr(A)\Pr(B|A)$$

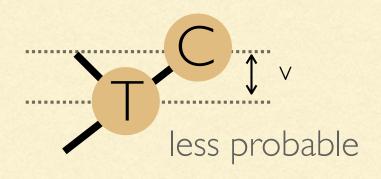
† conditional probability of A and B of B given A

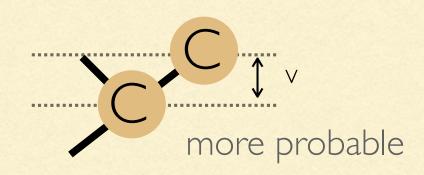
Pr(walk to work|sunny) = 0.99 Pr(walk to work|raining) = 0.50

Non-independence in phylogenies

Normally, for a given rate of substitution and time, the probability of the end state is dependent on the starting state

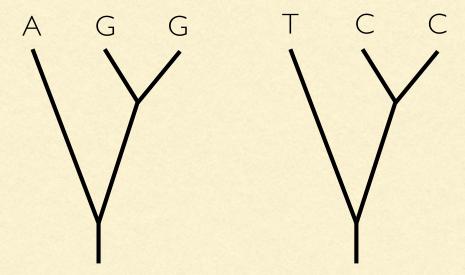
$$p_{CC}(v) > p_{TC}(v)$$
common notation for transition probabilities





Conditional Independence

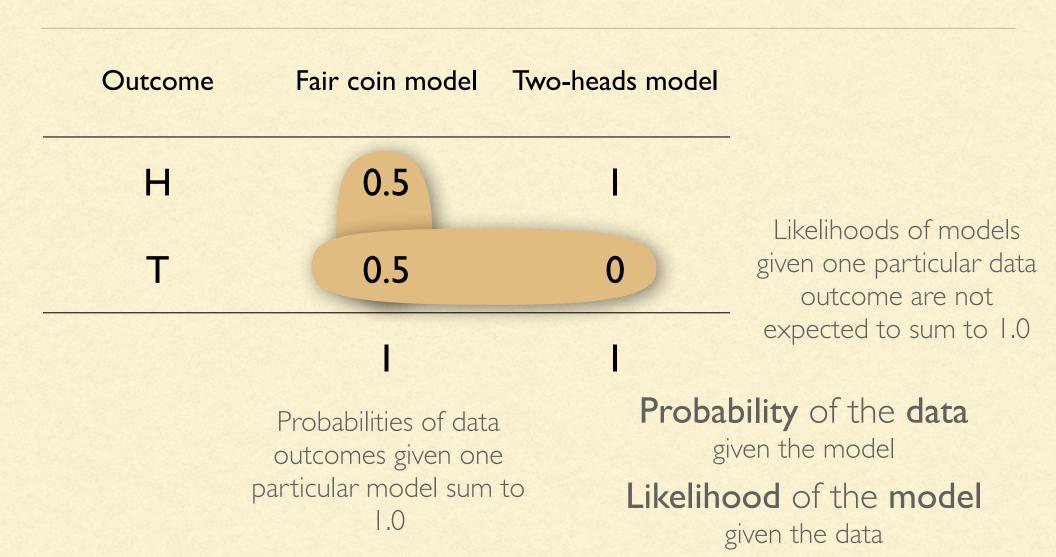
$$Pr(A,B|C) = Pr(A|C) Pr(B|C)$$



Pr(AGG,TCC|tree) = Pr(AGG|tree) Pr(TCC|tree)



Why do we need the term likelihood?



Likelihood of a single vertex

First 32 nucleotides of the $\psi\eta$ -globin gene of gorilla:

GAAGTCCTTGAGAAATAAACTGCACACACTGG

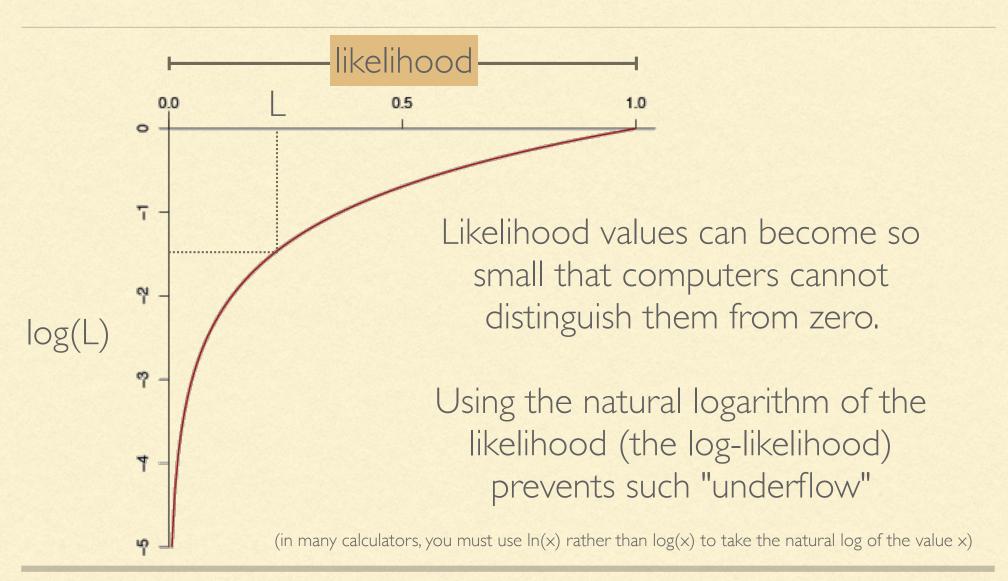
$$L = \Pr(G) \Pr(A) \Pr(A) \Pr(G) \Pr(T) \cdots \Pr(G)$$

$$L = \pi_G \; \pi_A \; \pi_A \; \pi_G \; \pi_T \; \cdots \; \pi_G$$

$$L = \pi_A^{12} \ \pi_C^7 \ \pi_G^7 \ \pi_T^6$$

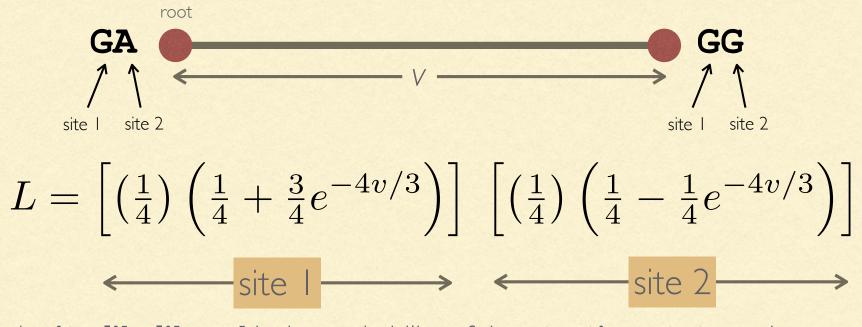
$$\log L = 12\log(\pi_A) + 7\log(\pi_C) + 7\log(\pi_G) + 6\log(\pi_T)$$

Natural logarithm



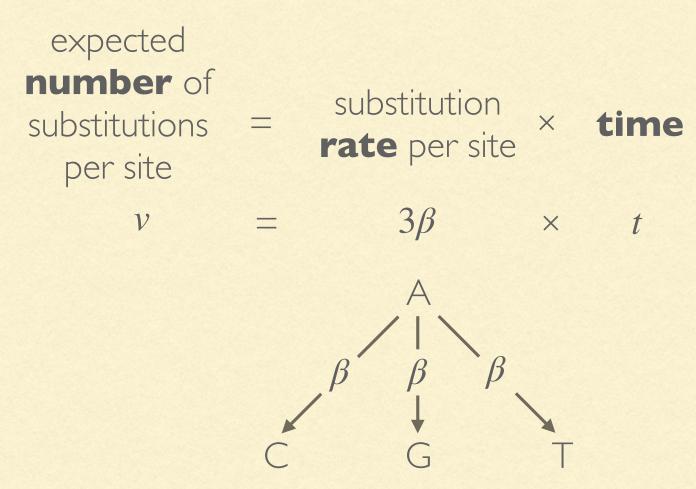
Likelihood of a single-edge tree

Two nodes have sequence data (but only for two sites)



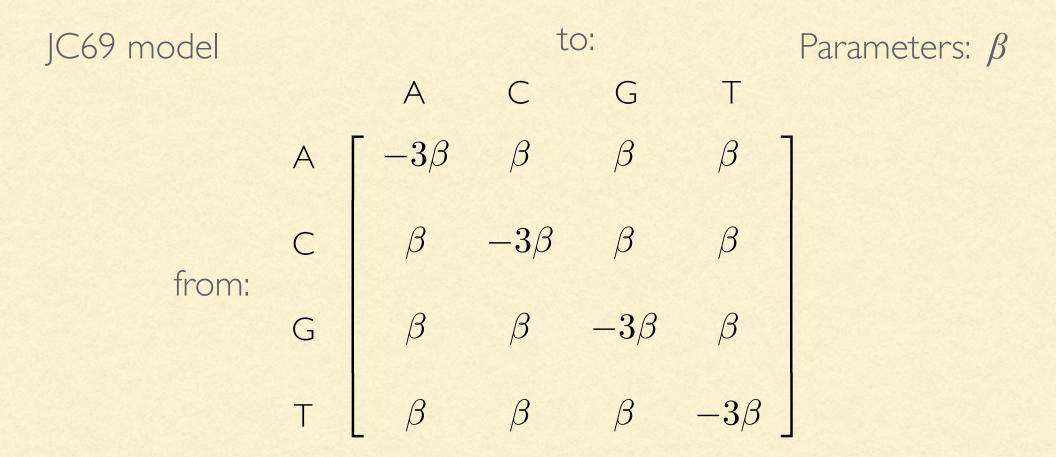
Each **site likelihood** is the probability of the **starting state** at the root (1/4) times the **transition probability** (probability of the end state given the starting state)

What is the edge length v?



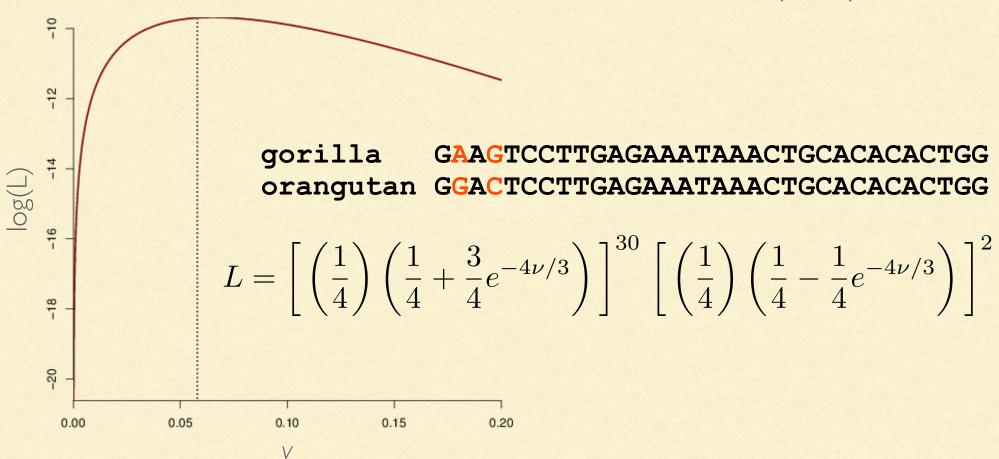
3 possible substitutions, each of which happens with rate β

Jukes and Cantor (1969)



Maximum likelihood estimation

0.065 is the maximum likelihood estimate (MLE) of v

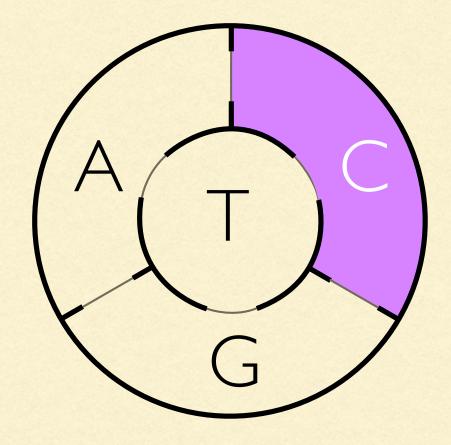


Equilibrium Frequencies

Imagine a bottle of perfume has been spilled in room C.

The doors to the other rooms are closed, so the perfume has, thus far, not been able to spread.

What would happen if we opened all the doors?



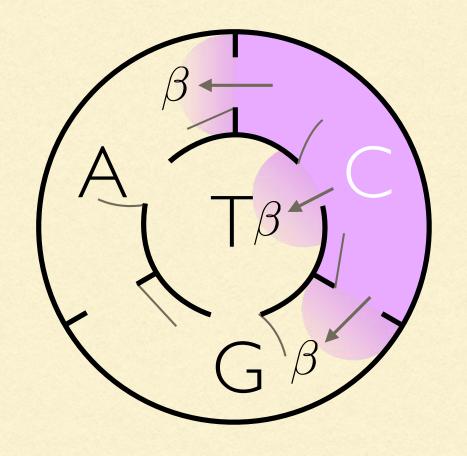
Architect: Joe Bielawski

Equilibrium Frequencies

At the instant the doors open, perfume molecules...

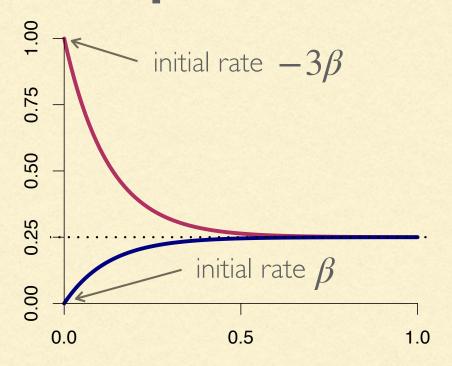
enter room A at rate β enter room T at rate β enter room G at rate β enter room C at rate -3β

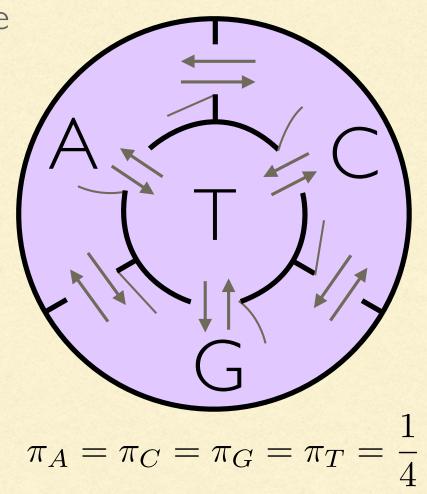
(you could also say they leave C at rate 3β)



Equilibrium Frequencies

At **equilibrium**, the relative concentration of perfume is **equal** in all rooms





Transition probability demo

https://plewis.github.io/applets/jc-transition-probabilities/

Sequence data for four taxa

one site

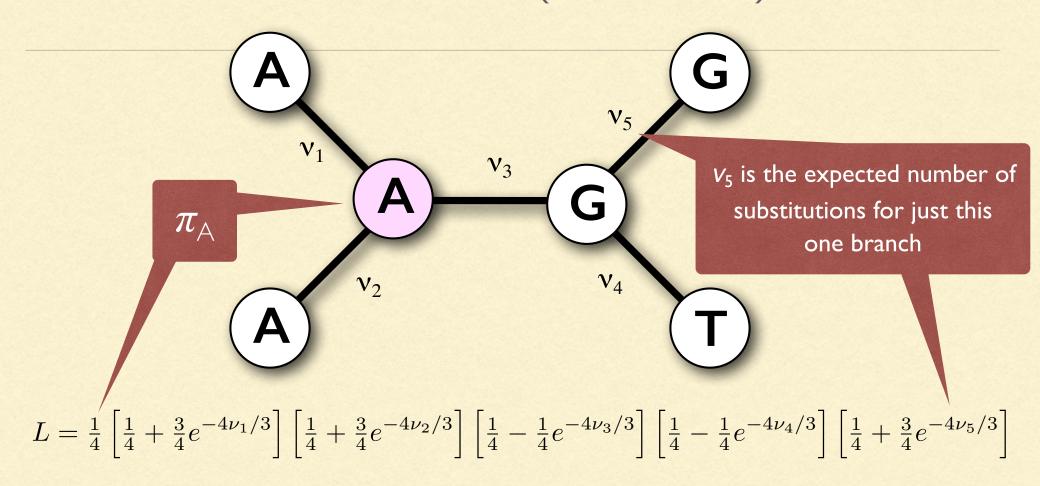
Sphagnum GGCAGCATTTCGAATGACTCCTCAACCTGGAG! A CCACCCG...

Asplenium GGCAGCTTTCCGGATGACCCCACAACCCGGAG! A CCAGCTG...

Picea GGCAGCATTCCGAGTAACTCCTCAACCAGGGG! G CCGCCCG...

Avena GGCAGCATTCCGAGTAACTCCTCAACCTGGGG! T CCGCCGG...

Likelihood for tree (one site)



Total likelihood

Jukes and Cantor (1969)

JC69 model Parameters: β to: from:

Kimura (1980)

K80 (or K2P) model

Parameters: α , β

	Α	С	G	Т
Α	$-\alpha - 2\beta$	eta	α	β
С	β	$-\alpha - 2\beta$	β	α
G	α	β	$-\alpha - 2\beta$	β
Т	lacksquare	α	β	$-\alpha - 2\beta$

Kimura (1980)

K80 (or K2P) model

$$\kappa = \alpha/\beta$$

Parameters: κ , β

A

C

G

A
$$\lceil -\beta(\kappa+2) \rceil$$

 β

 $\kappa\beta$

 β

C

 β

 $-\beta(\kappa+2)$

B

 $\kappa \beta$

G

 $\kappa \beta$

 β

 $-\beta(\kappa+2)$

B

T

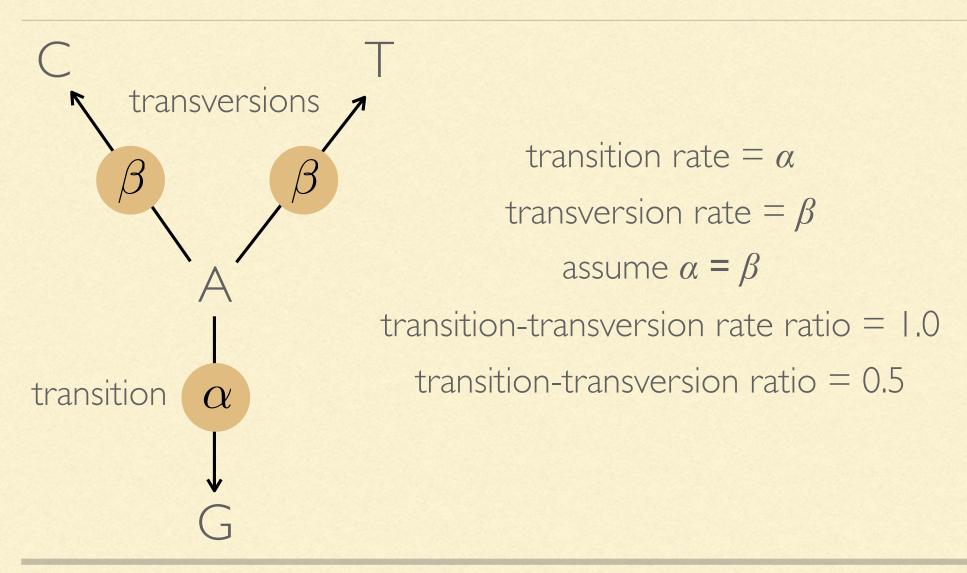
B

 $\kappa\beta$

B

 $-\beta(\kappa+2)$

Transition-transversion (rate) ratio



Felsenstein (1981)

F81 model Parameters: μ , π_A , π_C , π_G $\pi_C \mu$ $\pi_G \mu$ $\pi_T \mu$ $-\mu(1-\pi_C)$ $\pi_A \mu$ $\pi_G \mu$ $\pi_T \mu$ $-\mu(1-\pi_G)$ $\pi_C \mu$ $\pi_A \mu$ $\pi_T \mu$ $-\mu(1-\pi_T)$ $\pi_A \mu$ $\pi_G \mu$ $\pi_C \mu$

JC69 is a special case of F81

Hasegawa, Kishino, and Yano (1985)

HKY85 model

Parameters: μ , κ , π_A , π_C , π_G these are global

one parameter in each model is associated with the length of an edge

hese are globa parameters (apply to all edge lengths)

	A	C	G	Т
Α	$-\mu \left(\pi_C + \pi_G \kappa + \pi_T\right)$	$\pi_C \mu$	$\pi_G \mu \kappa$	$\pi_T \mu$
C	$\pi_A \mu$	$-\mu \left(\pi_A + \pi_G + \pi_T \kappa\right)$	$\pi_G \mu$	$\pi_T \mu \kappa$
G	$\pi_A \mu \kappa$	$\pi_C \mu$	$-\mu \left(\pi_A \kappa + \pi_C + \pi_T\right)$	$\pi_T \mu$
Τ	$\pi_A \mu$	$\pi_C \mu \kappa$	$\pi_G \mu$	$-\mu \left(\pi_A + \pi_C \kappa + \pi_G\right)$

Tavaré (1986)

GTR model

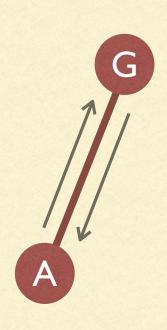
A C G T

A $\begin{bmatrix} - & \pi_C\mu(a) & \pi_G\mu(b) & \pi_T\mu(c) \end{bmatrix}$ C $\begin{bmatrix} \pi_A\mu a & - & \pi_G\mu(d) & \pi_T\mu(e) \end{bmatrix}$ G $\begin{bmatrix} \pi_A\mu b & \pi_C\mu d & - & \pi_T\mu(f) \end{bmatrix}$ T $\begin{bmatrix} \pi_A\mu c & \pi_C\mu e & \pi_G\mu f & - & - & - \end{bmatrix}$

Parameters: ?

exchangeability parameters are circled

Time reversibility



Time reversibility means...

$$Pr(A) Pr(G|A, v) = Pr(G) Pr(A|G, v)$$

Time reversibility allows any point on the tree to serve as the root, and thus has some practical advantages, but time reversibility is not a requirement for substitution models used in phylogenetics

Rate heterogeneity

Green plant rbcL gene

First 88 amino acids (translation is for Zea mays)

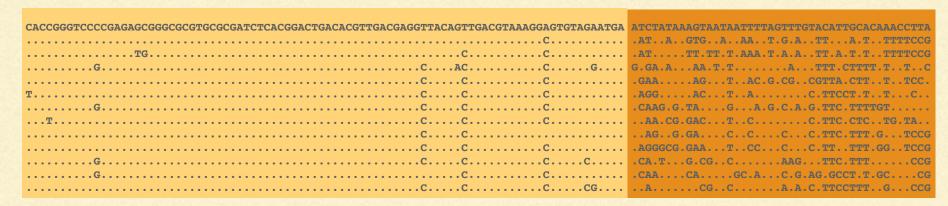
```
{\tt M--S-P-Q-T-E-T-K-A-S-V-G-F-K-A-G-V-K-D-Y-K-L-T-Y-Y-T-P-E-Y-E-T-K-D-T-D-I-L-A-A-F-R-V-T-P-E-Y-E-T-K-D-T-D-I-L-A-A-R-F-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-P-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-V-T-R-
Chara
               (green alga; land plant lineage)
                                              AAAGATTACAGATTAACTTACTATACTCCTGAGTATAAAACTAAAGATACTGACATTTTAGCTGCATTTCGTGTAACTCCA
                                              .....C....C.T...A...G...C.....T...CC...C.A......C....T...C.T...A...G...C...A.G.....T
Chlorella
              (green alga)
                                              ......TC.T....A....C..A.....C..GT.GTA.....C......C...A.....A.G.....
Volvox
               (green alga)
                                              Conocephalum
              (liverwort)
Bazzania
               (moss)
                                              Anthoceros
              (hornwort)
Osmunda
              (fern)
                                              Lycopodium
              (club "moss")
                                              .\mathsf{GG}.\dots\dots\dots.\mathsf{C.T..C.}\dots.\mathsf{T.\dots.G..C.}\dots\mathsf{A..C..T.\dots.C.G..A}\dots.\mathsf{AA.G.\dots.T}
Ginkgo
              (gymnosperm; Ginkgo biloba)
                                              Picea
               (gymnosperm; spruce)
                                              Iris
              (flowering plant)
                                              (fern; spleenwort)
                                              .....TC..C.G....T..C..C..C..A..C..G..C.........C..T..C..G..A..T..C..GA.G..C...
Asplenium
                                              Nicotiana
              (flowering plant; tobacco)
O-L-G-V-P-P-E-E-A-G-A-A-V-A-A-E-S-S-T-G-T-W-T-T-T-V-W-T-D-G-L-T-S-L-D-R-Y-K-G-R-C-Y-H-I-E-
    \dots \text{A..G.} \dots \text{C.T.C.T.C.T.C.T.T.T.T.} \dots \text{G.} \dots \text{T.C.C.C.G}
```

All 4 bases are observed at some sites...

...while at other sites, only I base is observed

Site-specific rates

Each defined subset (e.g. 1st+2nd pos. versus 3rd pos.) has its own relative rate



 r_1 applies to subset I Ist+2nd codon positions (sites I - 88) r₂ applies to subset 2 3rd codon positions (sites 89-132)

Relative rates have mean I.0:
$$r_1 \ p(r_1) + r_2 \ p(r_2) = 1$$

Site-specific rates

$$L = p(\mathbf{y}_1|r_1)\cdots p(\mathbf{y}_{88}|r_1) \ p(\mathbf{y}_{89}|r_2)\cdots p(\mathbf{y}_{132}|r_2)$$

1st+2nd codon positions

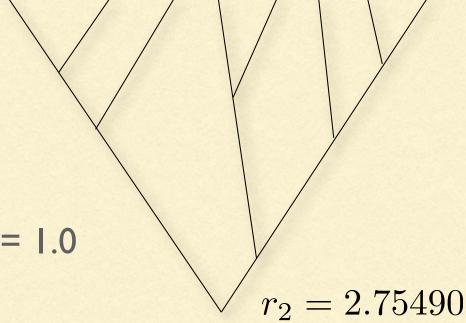
3rd codon positions



$$r_1 = 0.12255$$

mean relative rate:

$$(0.12255)(2/3) + (2.75490)(1/3) = 1.0$$



Site-specific rates

JC69 transition probabilities that would be used for every site if rate *homo*geneity were assumed:

$$P_{ii}(t) = \frac{1}{4} + \frac{3}{4}e^{-4\beta t} \quad \text{C} \quad \text{identity} \quad \text{C}$$

$$P_{ij}(t) = \frac{1}{4} - \frac{1}{4}e^{-4\beta t} \quad \text{C} \quad \text{difference} \quad \text{T}$$

Site specific rates

JC69 transition probabilities that would be used for sites in subset 1:

$$P_{ii}(t) = \frac{1}{4} + \frac{3}{4}e^{-4r_1\beta t}$$

$$P_{ij}(t) = \frac{1}{4} - \frac{1}{4}e^{-4r_1\beta t}$$

JC69 transition probabilities that would be used for sites in subset 2:

$$P_{ii}(t) = \frac{1}{4} + \frac{3}{4}e^{-4r_2\beta t}$$

$$P_{ij}(t) = \frac{1}{4} - \frac{1}{4}e^{-4r_2\beta t}$$

Mixture models

All k relative rates applied to every site

OLGVPPEE	-AGAAVA	AESS-	TCTW'	r	ТWТ	DGTT-	STD	RYK	GRCY	HTE
CAACCTGGCGTTCCACCTGAAGAA										
ATA	GTG	.A	A	. G	A	T T	A	T	TC.TT.	.TCCG
AT	TGTTTT.	TA	AAT	. <mark>. A</mark>	A	TT	.AC.T	T	TC.TT.	.TCCG
GGAG.A	AAT.	T		A		TTC.T.	ACC.TT	TT	TC	.T.GC
GAA								–		
TAGG										
CAAGGG								– – –		
TAACG										
AGGGCG								–		
CATG										
AAG								–		
				А	A	.стс.т.	.ссс.тт			

site i

$$L_i = p(\mathbf{y}_i|r_1)p(r_1) + p(\mathbf{y}_i|r_2)p(r_2) + \dots + p(\mathbf{y}_i|r_k)p(r_k)$$

Common examples

Invariable sites (I) model

Discrete Gamma (G) model

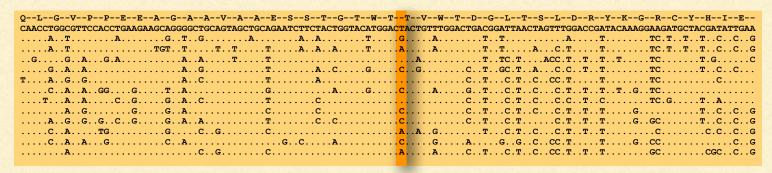
Invariable sites model (Reeves 1992)

$$L_i = p(\mathbf{y}_i|r_1)p(r_1) + p(\mathbf{y}_i|r_2)p(r_2)$$

$$L_i = p(\boldsymbol{y}_i|0.0)p_{\text{invar}} + p(\boldsymbol{y}_i|r_2)(1 - p_{\text{invar}})$$

Discrete Gamma model (Yang 1994)

No relative rate is exactly 0.0, and all are equally probable

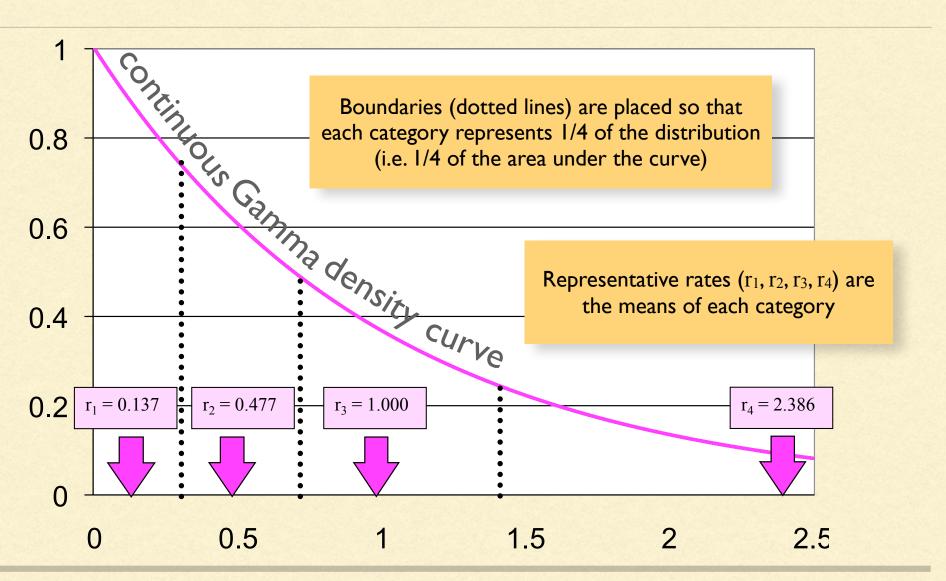


site i

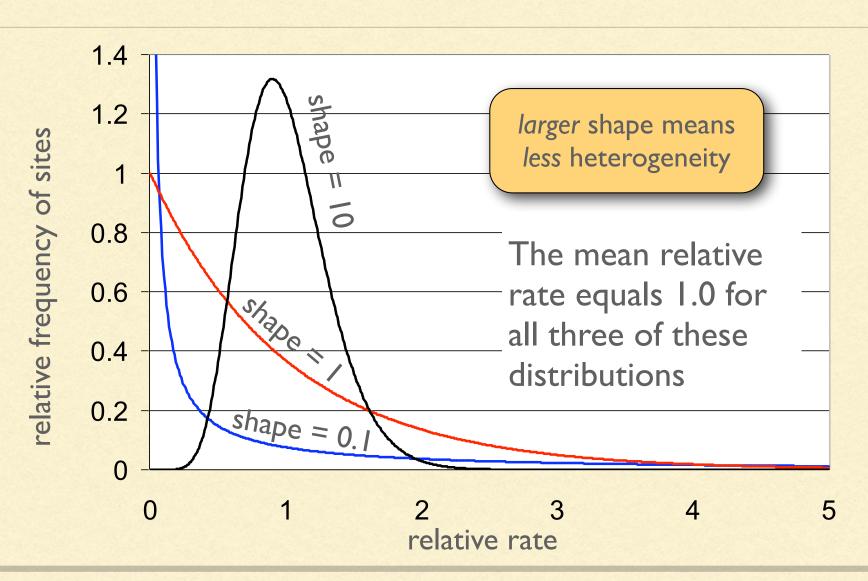
$$L_i = p(\mathbf{y}_i|r_1) \left(\frac{1}{4}\right) + p(\mathbf{y}_i|r_2) \left(\frac{1}{4}\right) + p(\mathbf{y}_i|r_3) \left(\frac{1}{4}\right) + p(\mathbf{y}_i|r_4) \left(\frac{1}{4}\right)$$

Relative rates are determined by a discrete gamma distribution Number of rate categories can vary (4 used here)

Relative rates in 4-category case



Gamma distributions



~ Coffee Break ~