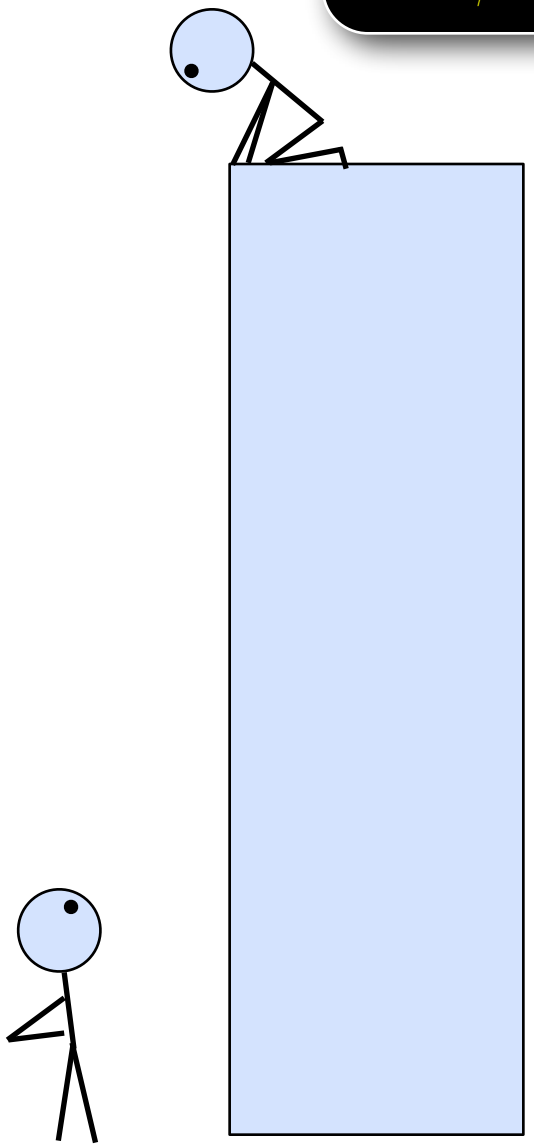
Maximum Likelihood in Phylogenetics

28 January 2015

Paul O. Lewis
Department of Ecology & Evolutionary Biology
UCONN
UNIVERSITY OF CONNECTICUT

Goals

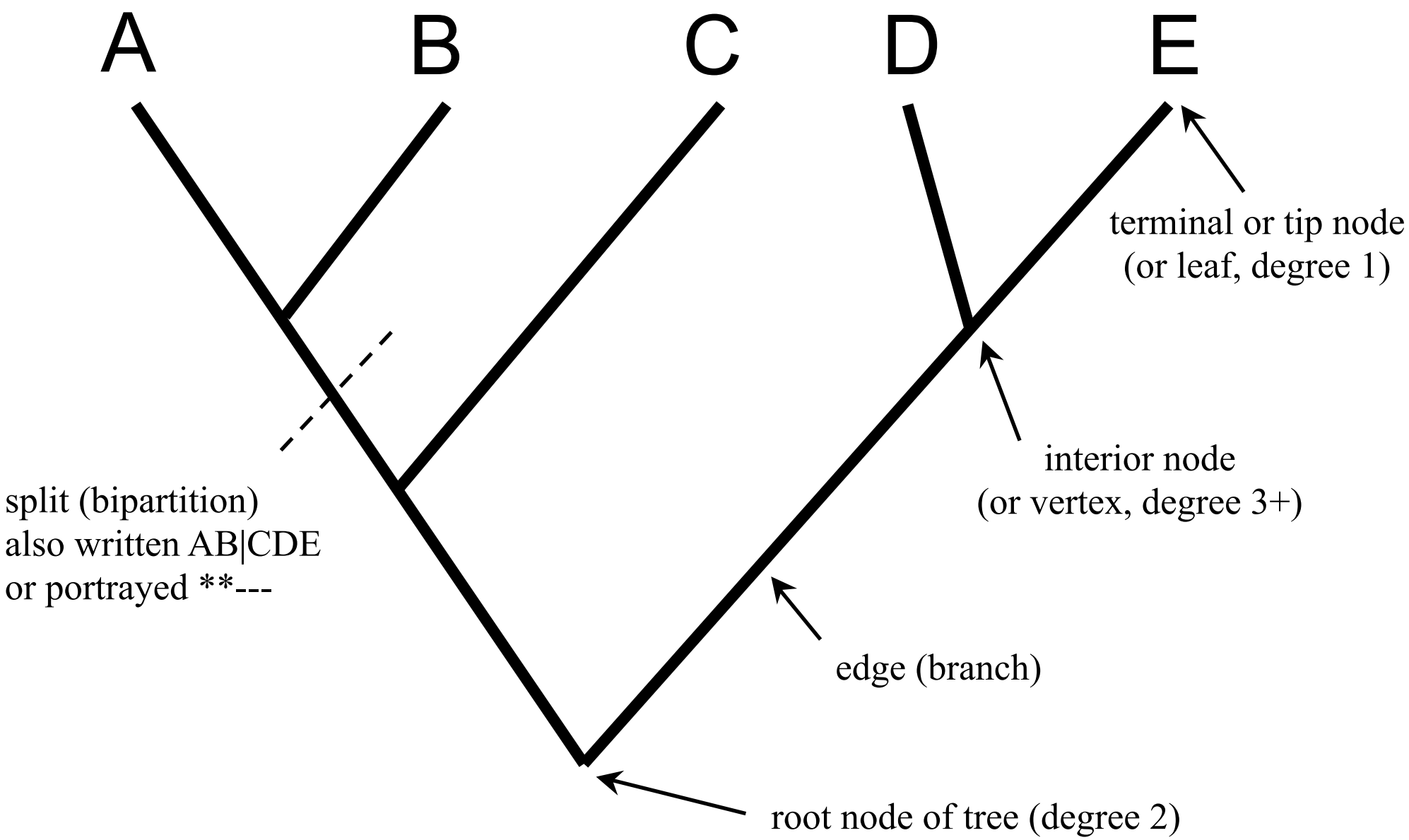
$$f(r) = \frac{r^{\alpha-1}e^{-r/\beta}}{\beta^{\alpha}\Gamma(\alpha)}$$



- Explain jargon
- Increase comfort level
- Provide background

In other words...give a hand up

Tree jargon


A
B
C
D
E
terminal or tip node
(or leaf, degree 1)
interior node
(or vertex, degree 3+)
split (bipartition)
also written AB|CDE
or portrayed **---
edge (branch)
root node of tree (degree 2)

The Plan

- Probability review
- Likelihood
- Substitution models

- The AND and OR rules
- Independence of events

- What does it mean?
- Likelihood of a single sequence
- Maximum likelihood distances
- Likelihoods of trees

- Markov model basics
- Transition probabilities
- Survey of models
- Rate heterogeneity
- Codon models
- Amino acid models

Combining probabilities

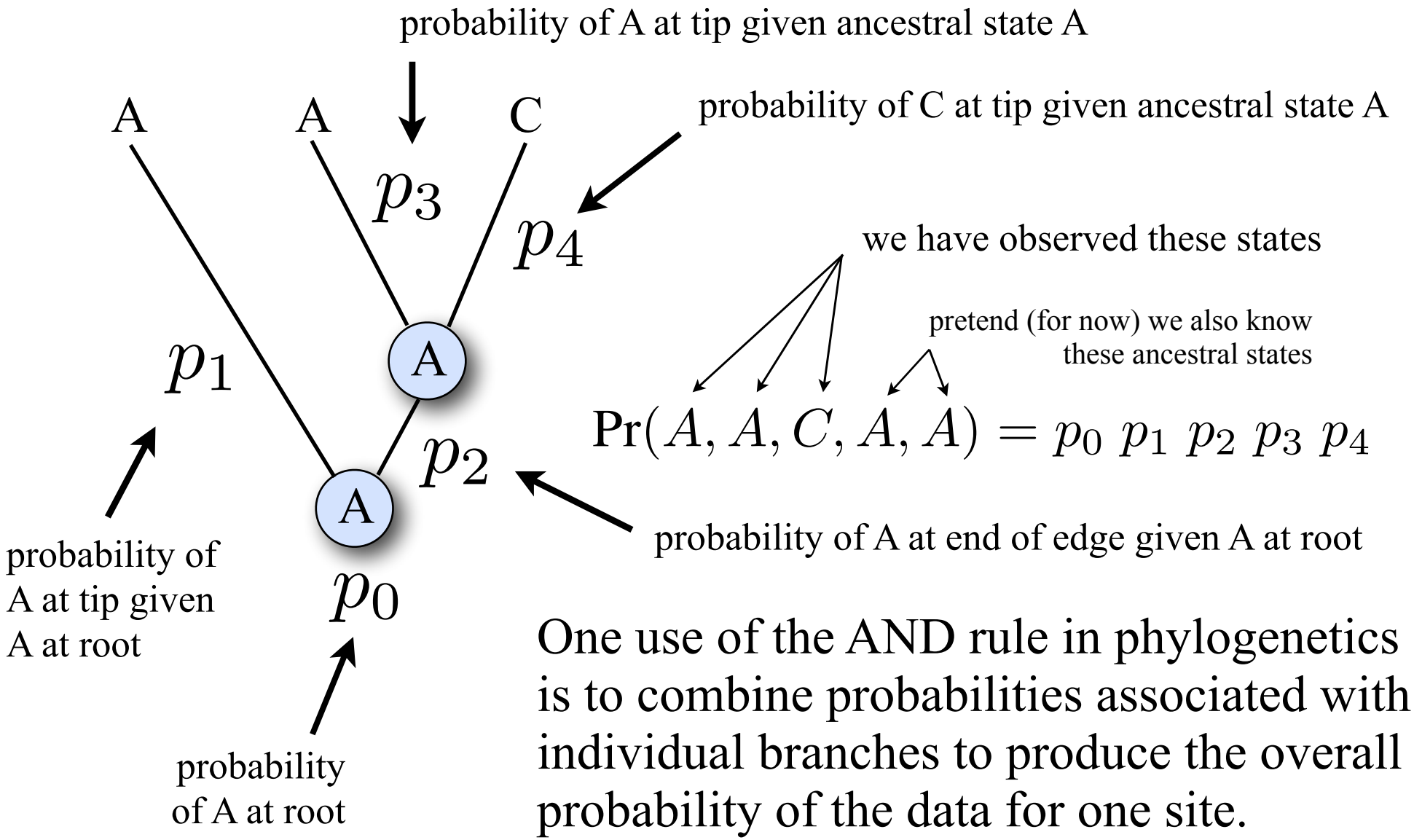
- *Multiply* probabilities if the component events must happen **simultaneously** (i.e. where you would naturally use the word AND when describing the problem)

Using 2 dice, what is the probability of

 AND ?

$$(1/6) \times (1/6) = 1/36$$

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.

Combining probabilities

- *Add* probabilities if the component events are **mutually exclusive** (i.e. where you would naturally use the word OR in describing the problem)

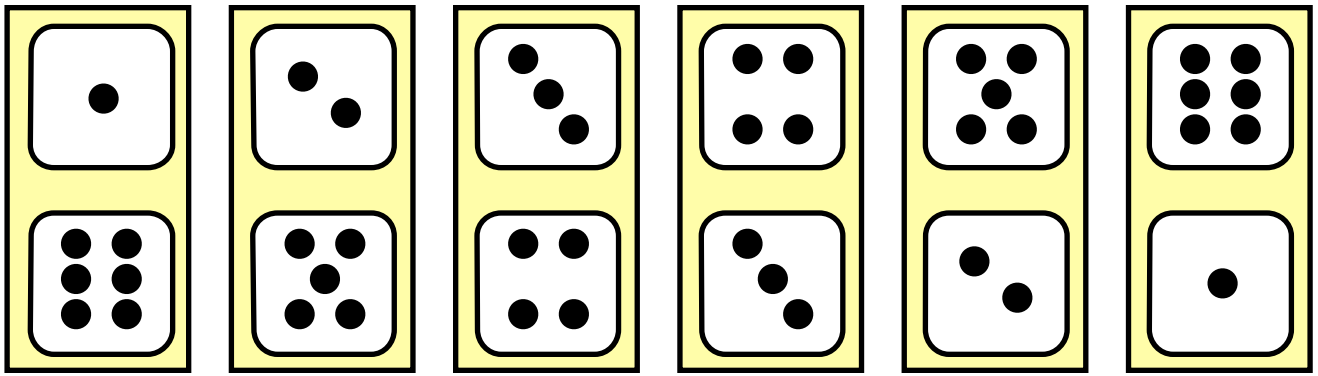
Using one die, what is the probability of

 OR ?

$(1/6) + (1/6) = 1/3$

Combining AND and OR

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



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

1 and 6

2 and 5

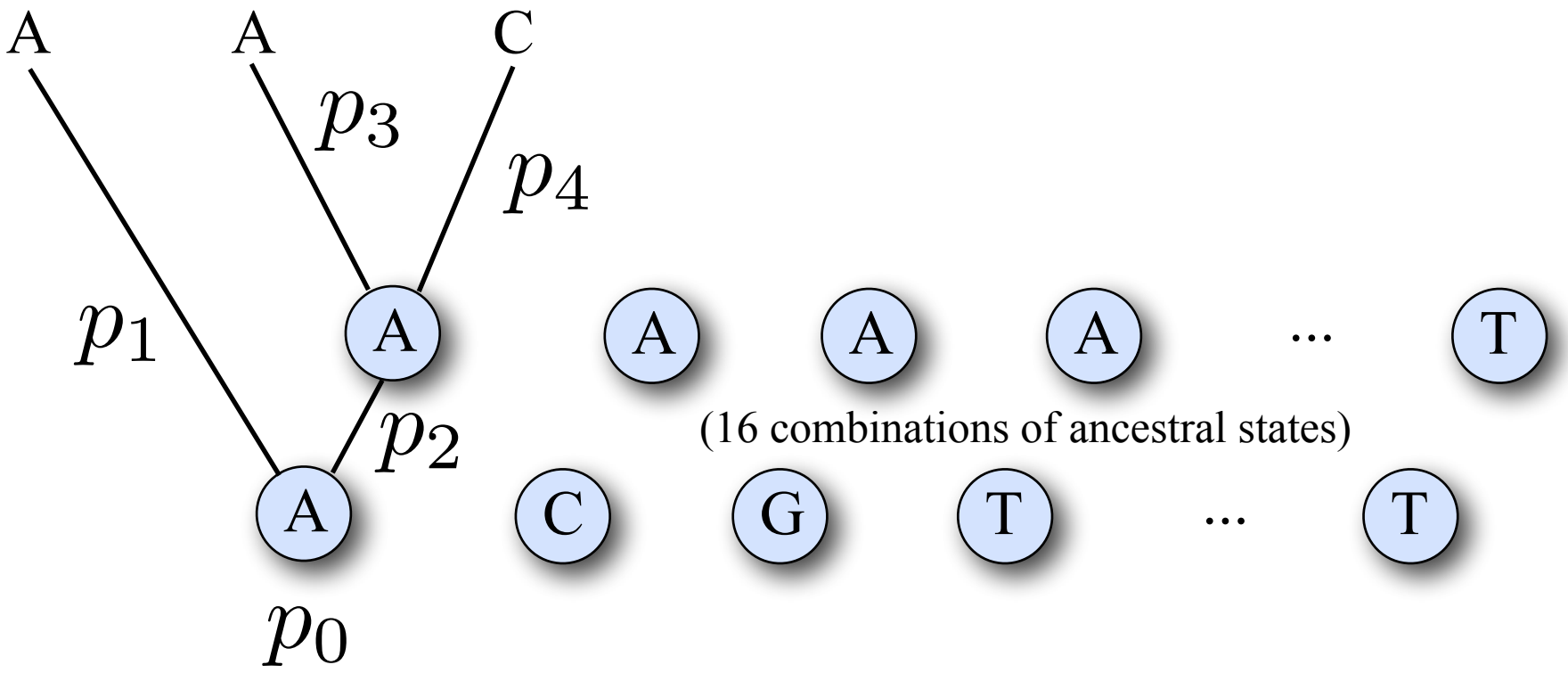
3 and 4

4 and 3

5 and 2

6 and 1

Using both AND and OR in phylogenetics



AND rule used to compute probability of the observed data for *each combination* of ancestral states.

OR rule used to combine different combinations of ancestral states.

Independence

This is always true...

$$\Pr(A \text{ and } B) = \Pr(A)\Pr(B|A)$$

joint probability

conditional probability

If we can say this...

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

...then events A and B are **independent** and we can express the joint probability as the product of Pr(A) and Pr(B)

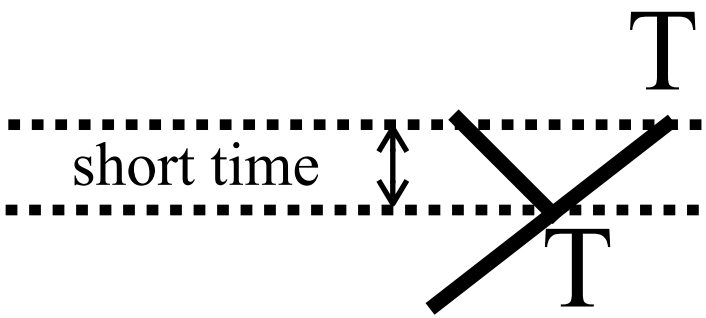
$$\Pr(A \text{ and } B) = \Pr(A)\Pr(B)$$

Non-independence in molecular evolution

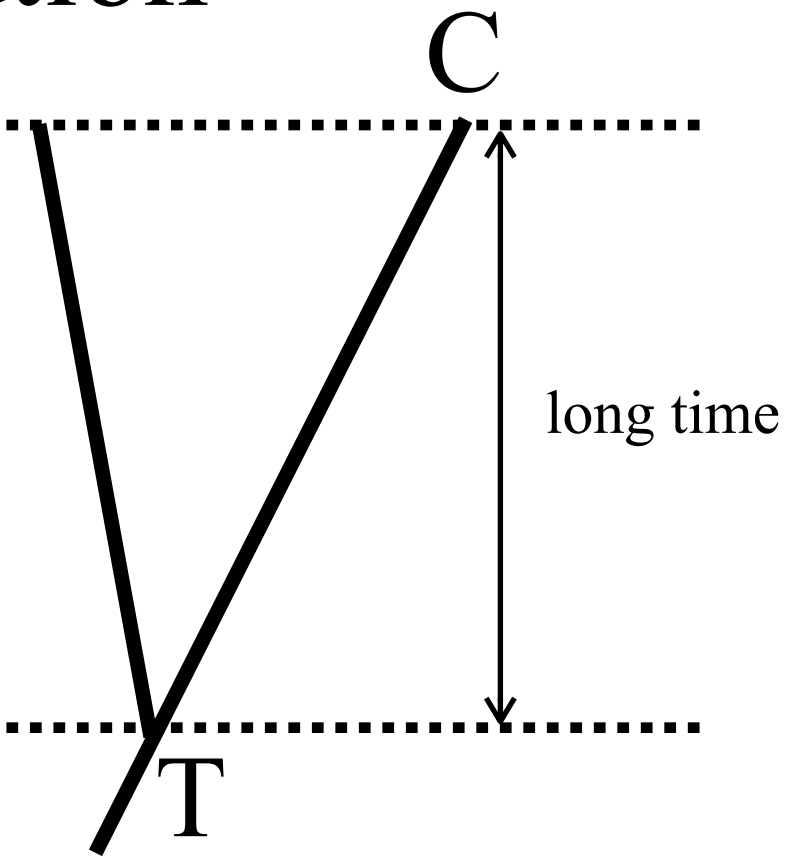
A = state in descendant
B = state in ancestor

$$\Pr(A|B) \neq \Pr(A)$$

That is, the state in the descendant depends on the state in the ancestor



$$\Pr(A|B,t,r)$$



The state in the descendant also depends on the amount time *t* separating ancestor and descendant and the rate of substitution *r*

Conditional Independence

Assume both A and B depend on C:

$$\Pr(A|C) \neq \Pr(A) \quad \Pr(B|C) \neq \Pr(B)$$

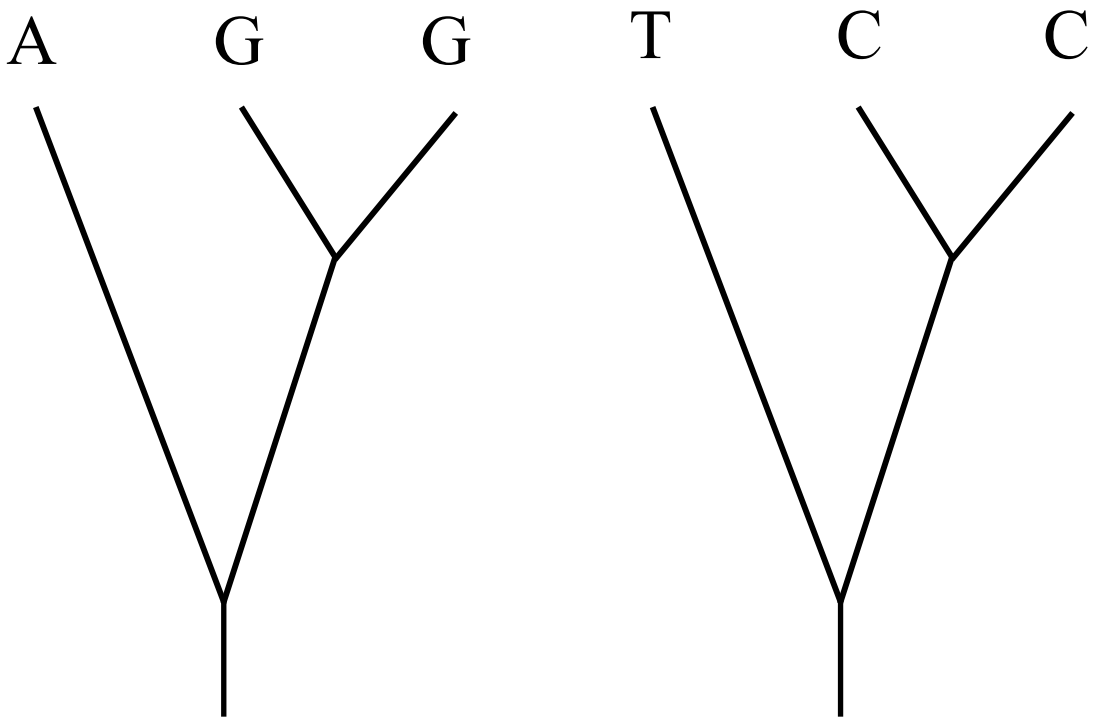
If we can say this...

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

...then events A and B are **conditionally independent** and we can express the joint (conditional) probability as the product of Pr(A|C) and Pr(B|C)

$$\Pr(A \text{ and } B|C) = \Pr(A|C)\Pr(B|C)$$

Conditional independence in molecular evolution



The site data patterns AGG and TCC are conditionally independent.

The patterns all depend on the underlying tree (including edge lengths) and the substitution model.

$$\Pr(\text{AGG and TCC}|\text{tree}, \text{model}) = \Pr(\text{AGG}|\text{tree}, \text{model})\ \Pr(\text{TCC}|\text{tree}, \text{model})$$

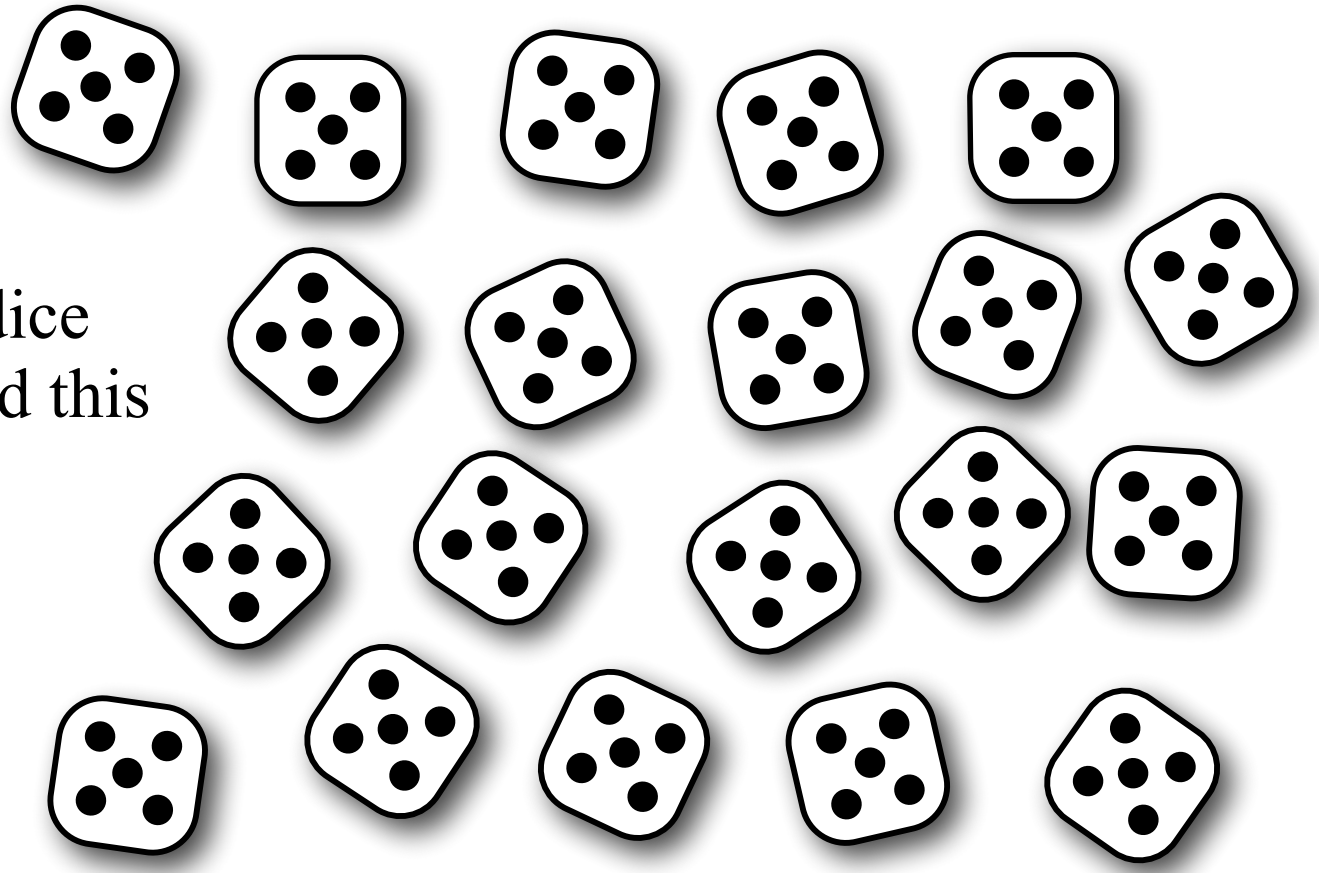
Likelihood

The Likelihood Criterion

The probability of the observations computed using a model tells us how surprised we should be.

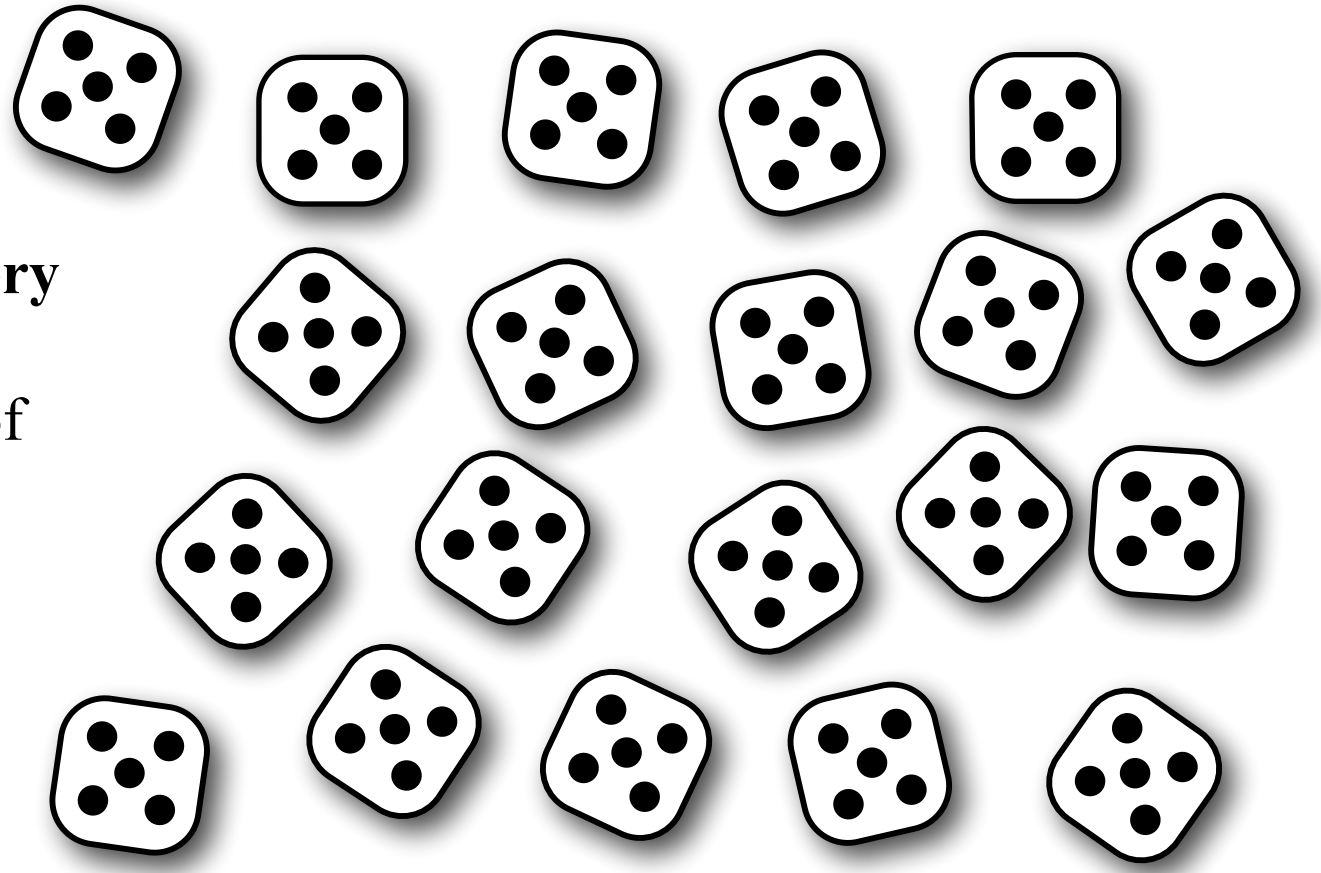
The preferred model is the one that surprises us least.

Suppose I threw 20 dice down on the table and this was the result...



The Fair Dice model

$$\Pr(\text{obs.}|\text{fair dice model}) = \left(\frac{1}{6}\right)^{20} = \frac{1}{3,656,158,440,062,976}$$

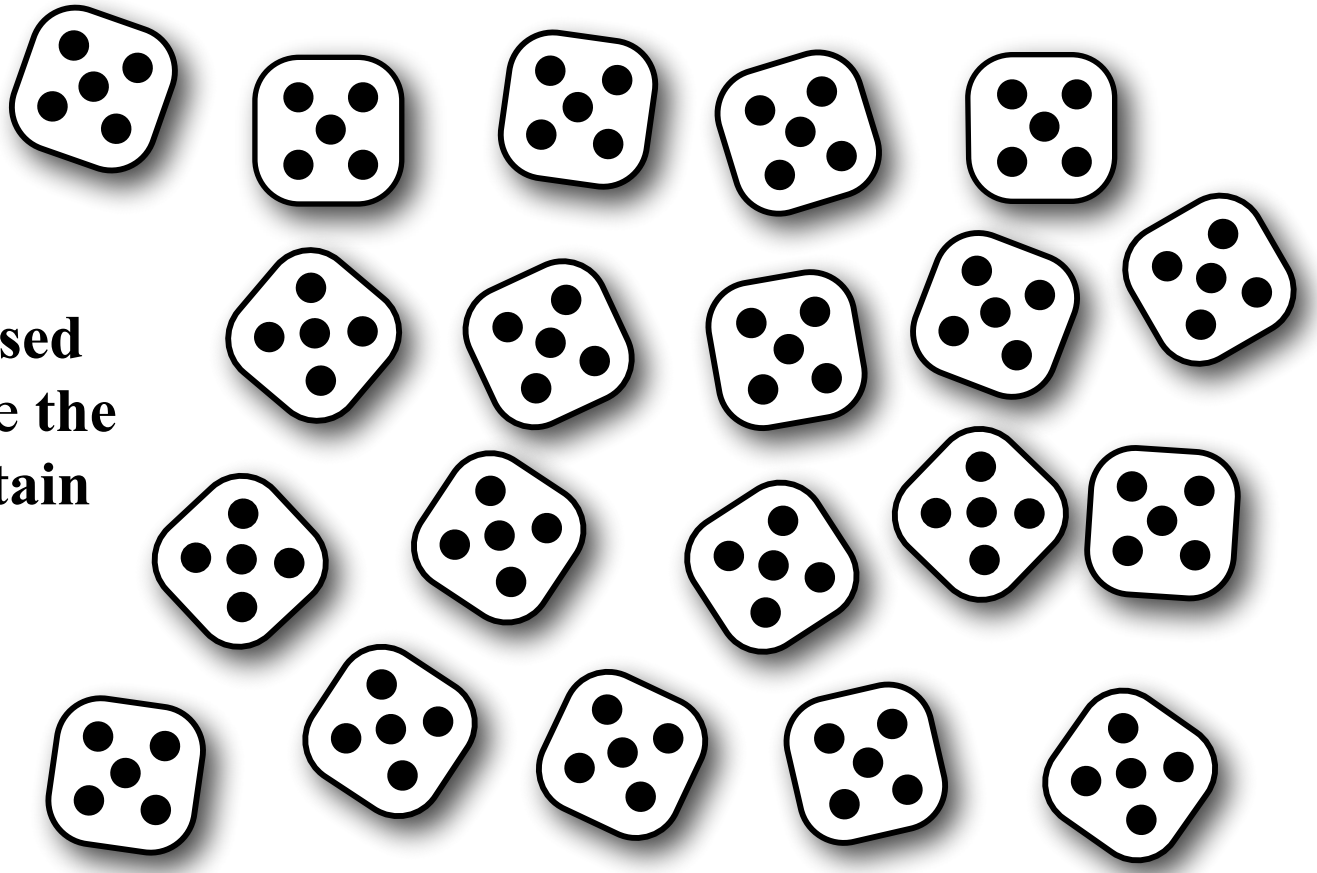


You should have been **very surprised** at this result because the probability of this event is **very small**: only 1 in 3.6 quadrillion!

The Trick Dice model

(assumes dice each have 5 on every side)

$$\Pr(\text{obs.}|\text{trick dice model}) = 1^{20} = 1$$



You should **not be surprised at all** at this result because **the observed outcome is certain** under this model

Results

Model	Likelihood	Surprise level
Fair Dice	$\frac{1}{3{,}656{,}158{,}440{,}062{,}976}$	Very, *very*, ***very*** surprised
Trick Dice	1	Not surprised at all

winning model maximizes likelihood
(and thus minimizes surprise)

Likelihood: why a new term?

Outcome	Fair coin model	Two-heads model
H	0.5	1
T	0.5	0
	1	1

Likelihoods of models given one particular data outcome are *not* expected to sum to 1.0

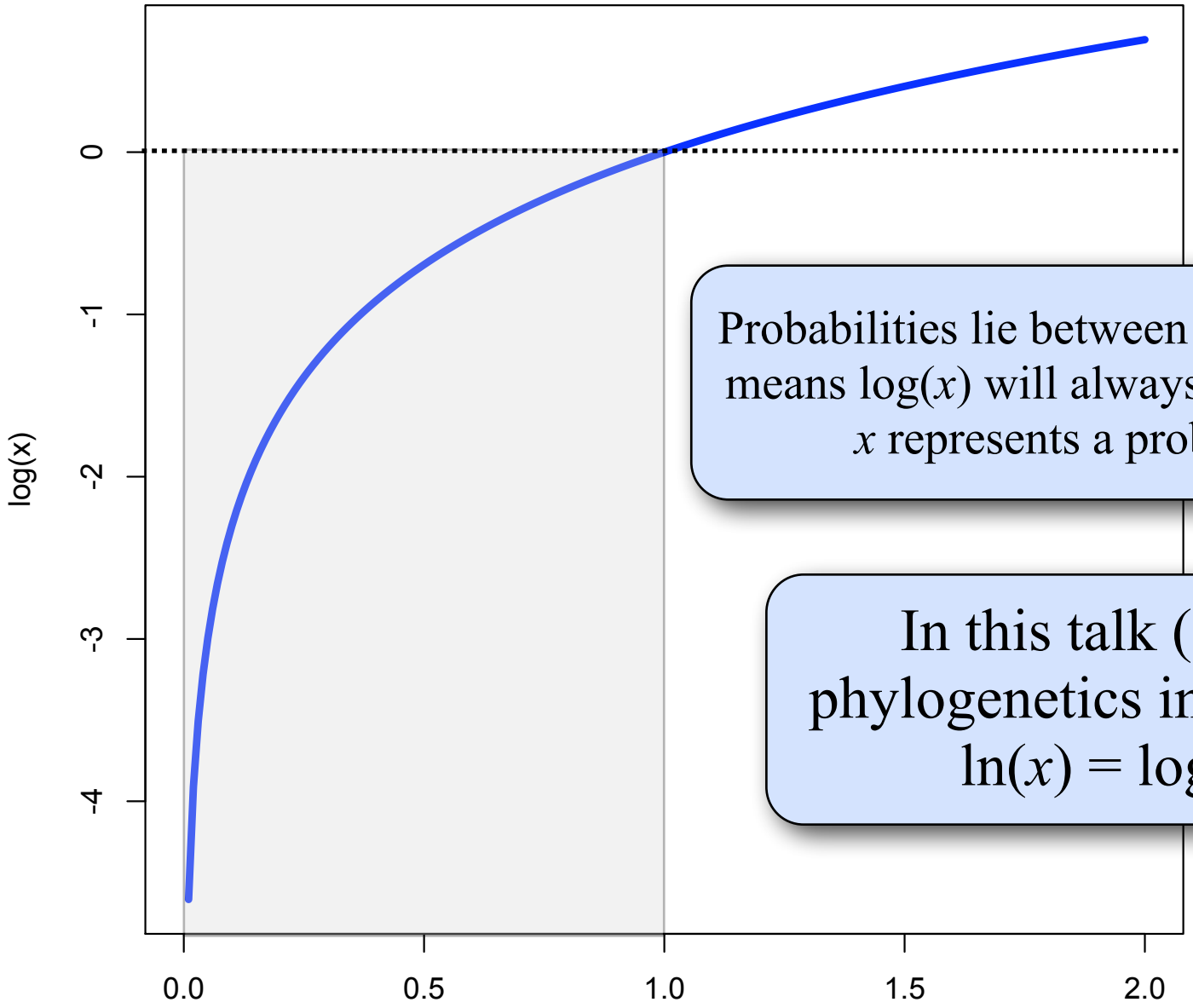
Probabilities of data outcomes given one particular model sum to 1.0

Likelihood and model comparison

- Analyses using likelihoods ultimately involve **model comparison**
- The models compared can be **discrete** (as in the fair vs. trick dice example)
- More often the models compared differ **continuously**:
  - Model 1: branch length is 0.05
  - Model 2: branch length is 0.06

Rather than having an infinity of models, we instead think of the branch length as a **parameter** within one model

Likelihoods vs. log-likelihoods



Probabilities lie between 0 and 1, which means log(x) will always be negative if x represents a probability.

In this talk (and in phylogenetics in general), ln(x) = log(x)

Likelihood of a single sequence

First 32 nucleotides of the ψη-globin gene of gorilla:

GAAGTCCTTGAGAAATAAACTGCACACACTGG

$$L = \pi_G \pi_A \pi_A \pi_G \pi_T \pi_C \pi_C \pi_T \pi_T \pi_G \pi_A \pi_G \pi_A \pi_A \pi_A \pi_T \pi_A \pi_A \pi_A \pi_C \pi_T \pi_G \pi_C \pi_A \pi_C \pi_A \pi_C \pi_A \pi_C \pi_T \pi_G \pi_G$$

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

Note that we are assuming independence among sites here

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

We can already see by eye-balling this that a model allowing **unequal** base frequencies will **fit better** than a model that assumes **equal** base frequencies because there are about twice as many As as there are Cs, Gs and Ts.

Model ranking using LRT or AIC

Likelihood Ratio Tests (LRT) and the Akaike Information Criterion (AIC) provide two ways to evaluate whether an **unconstrained** model fits the data significantly better than a **constrained** version of the same model.

Find *maximum* logL under the *unconstrained* model:

$$\begin{aligned}\log L_{\text{unconstrained}} &= 12\log(\pi_A) + 7\log(\pi_C) + 7\log(\pi_G) + 6\log(\pi_T) \\ &= 12\log(0.375) + 7\log(0.219) + 7\log(0.219) + 6\log(0.187) \\ &= -43.1\end{aligned}$$

This model has 3 estimated parameters

Find *maximum* logL under the *constrained* model:

$$\begin{aligned}\log L_{\text{constrained}} &= 12\log(\pi_A) + 7\log(\pi_C) + 7\log(\pi_G) + 6\log(\pi_T) \\ &= 12\log(0.25) + 7\log(0.25) + 7\log(0.25) + 6\log(0.25) \\ &= -44.4\end{aligned}$$

This model has 0 estimated parameters

Likelihood Ratio Test (LRT)

Calculate the likelihood ratio test statistic:

$$
\begin{aligned}
R &= -2\left[\log(L_{\text{constrained}}) - \log(L_{\text{unconstrained}})\right] \\
&= -2\left[-44.4 - (-43.1)\right] \\
&= 2.6
\end{aligned}
$$

(Note that the log-likelihoods used in the test statistic have been *maximized* under each model separately)

"unconstrained" does fit better than "constrained" (-43.1 > -44.4), but not significantly better (P = 0.457, chi-squared with 3 d.f.*)

*The number of degrees of freedom equals the difference between the two models in the number of estimated parameters. In this case, unconstrained has 3 parameters and constrained has 0, so d.f. = 3 – 0 = 3

Akaike Information Criterion (AIC)

Calculate AIC for each model:

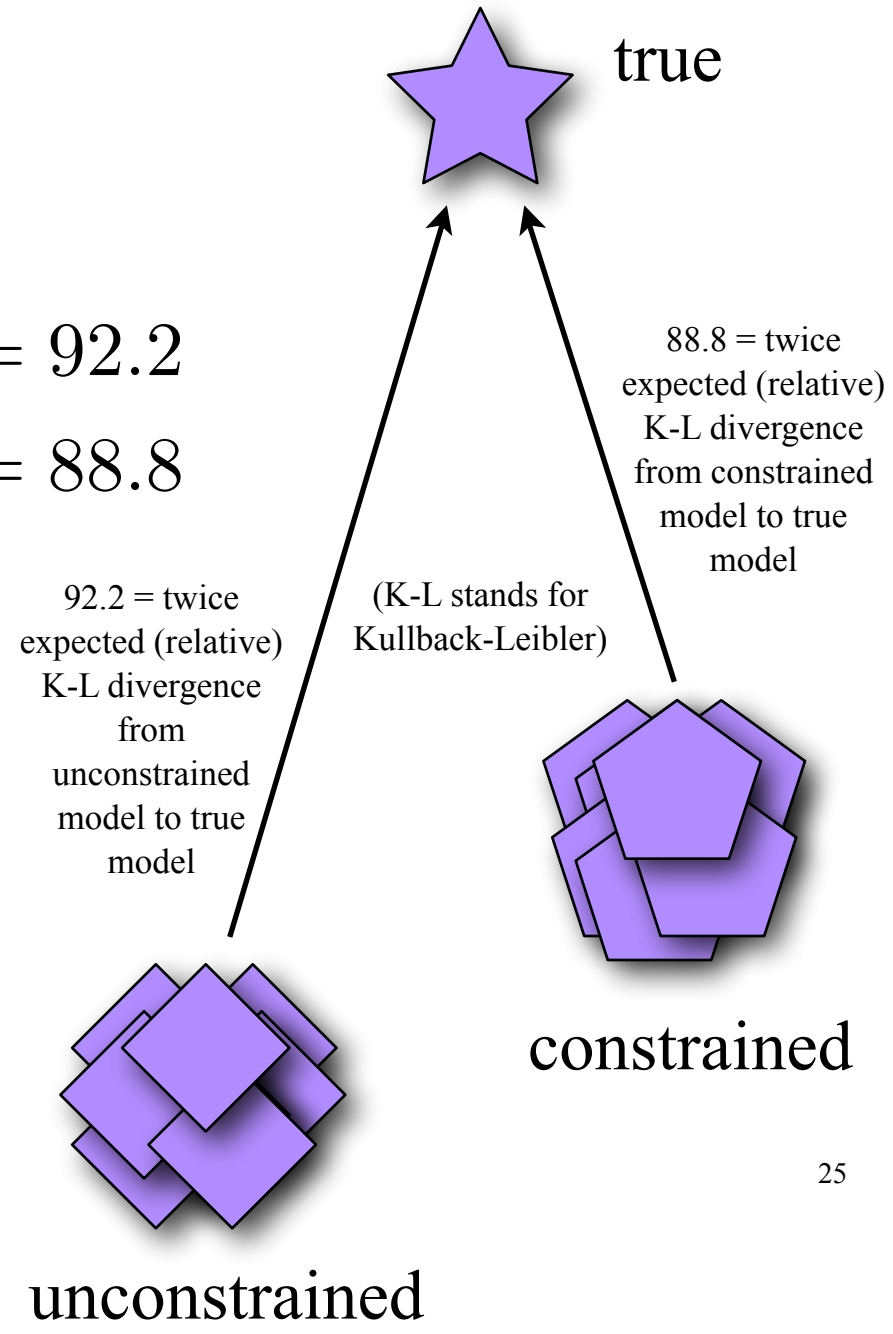
$$AIC = 2k - 2\log(\max(L))$$

$$AIC_{\text{unconstrained}} = 2(3) - 2(-43.1) = 92.2$$

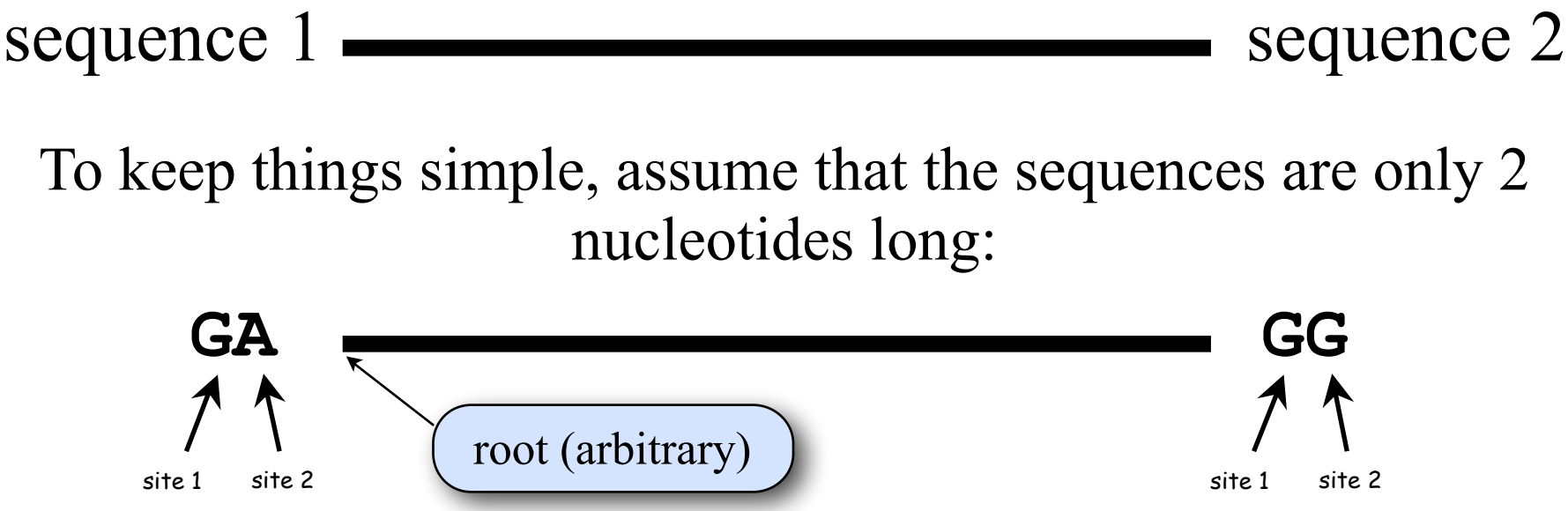
$$AIC_{\text{constrained}} = 2(0) - 2(-44.4) = 88.8$$

The constrained model is a better choice than the unconstrained model according to AIC

Dave Swofford will give you a much more complete explanation of LRT and AIC this afternoon



Likelihood of the simplest tree



$$
\begin{aligned}
L &= L_1 \, L_2 \\
&= \left[\left(\frac{1}{4}\right) \left(\frac{1}{4} + \frac{3}{4}e^{-4\alpha t}\right)\right] \left[\left(\frac{1}{4}\right) \left(\frac{1}{4} - \frac{1}{4}e^{-4\alpha t}\right)\right]
\end{aligned}
$$

Pr(G) Pr(G|G, αt) Pr(A) Pr(G|A, αt)

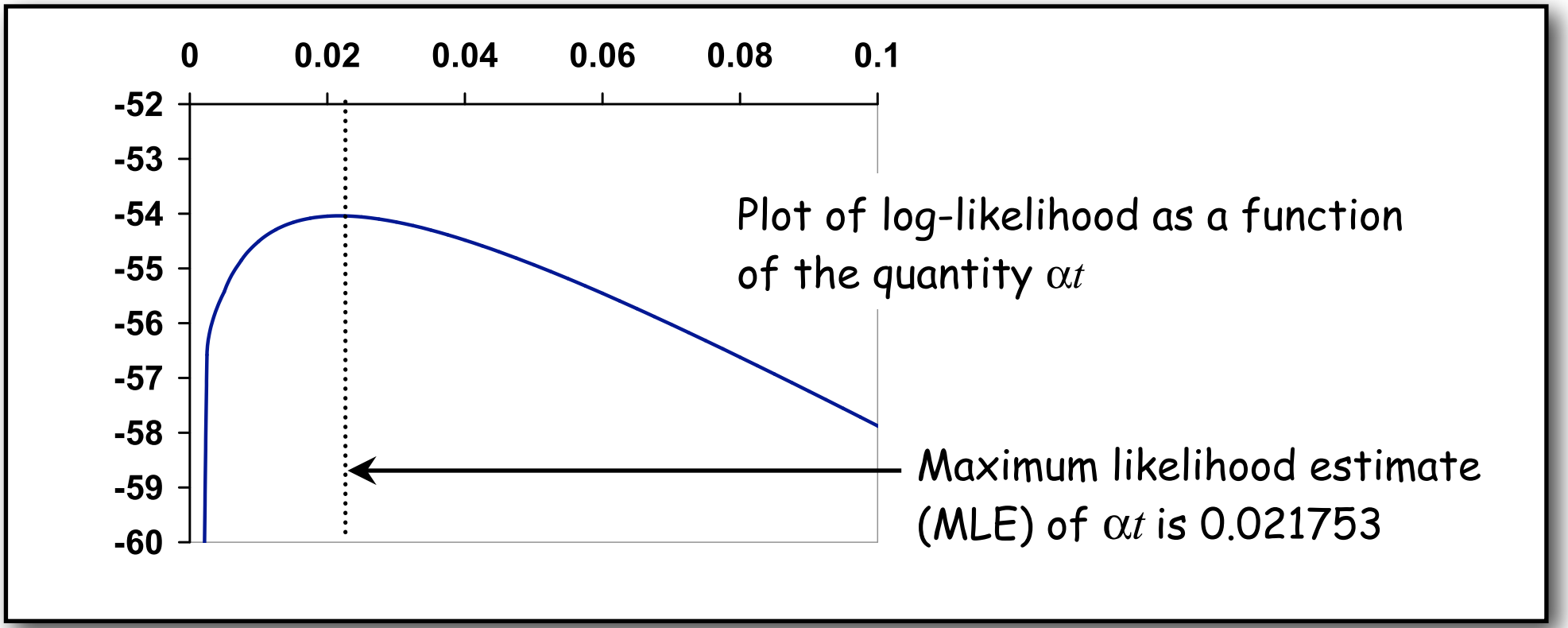
Note that we are NOT assuming independence here

Maximum likelihood estimation

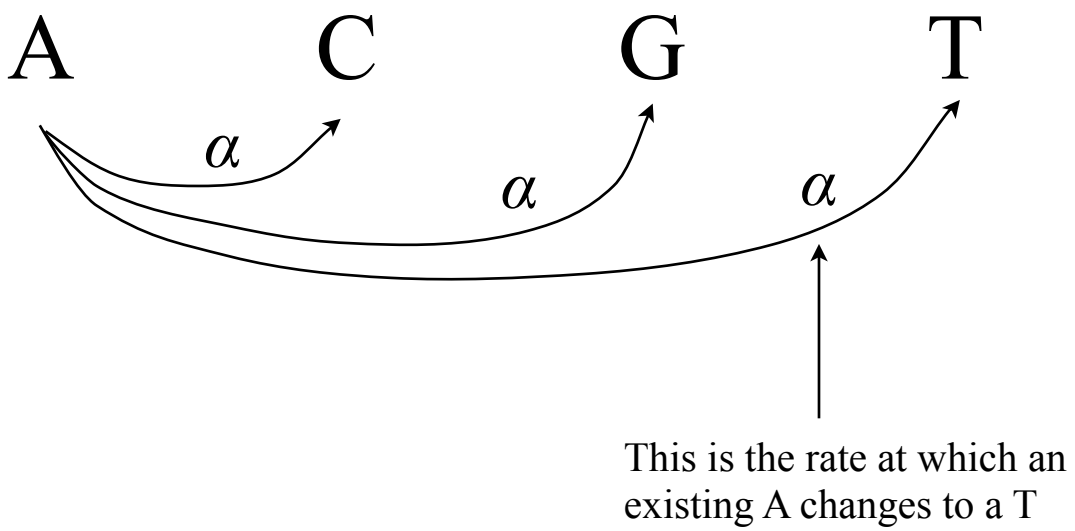
First 32 nucleotides of the ψη-globin gene of gorilla and orangutan:

```
gorilla   GAAGTCCTTGAGAAATAAACTGCACACACTGG
orangutan GGACTCCTTGAGAAATAAACTGCACACACTGG
```

$$L = \left[\left(\tfrac{1}{4}\right)\ \left(\tfrac{1}{4}+\tfrac{3}{4}e^{-4\alpha t}\right)\right]^{30}\left[\left(\tfrac{1}{4}\right)\ \left(\tfrac{1}{4}-\tfrac{1}{4}e^{-4\alpha t}\right)\right]^{2}$$



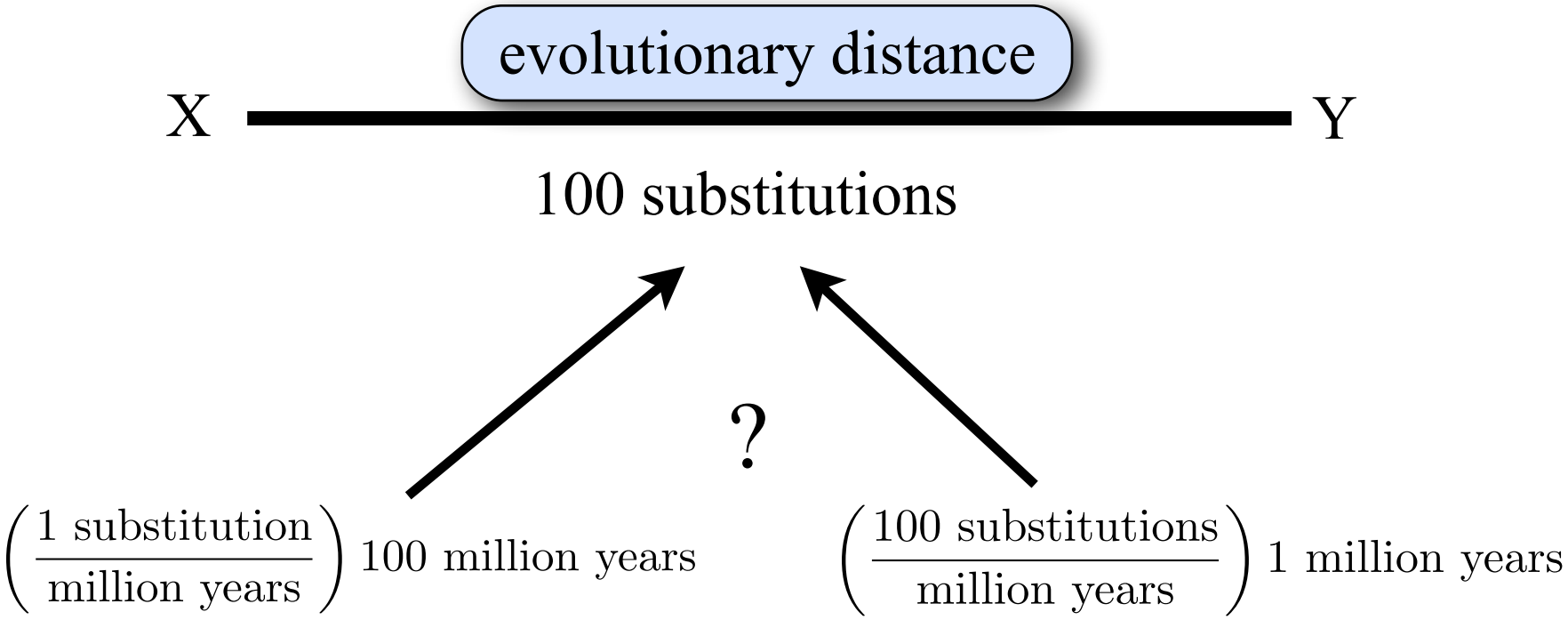
number of substitutions = rate × time



Overall substitution rate is 3α, so the expected number of substitutions (v) is

$$v = 3\alpha t$$

Rate and time are confounded



On Friday, Alexei Drummond will introduce models that allow separate estimation of rates and times, but without extra information/constraints, sequence data allow only estimation of the **number** of substitutions.

A convenient convention

Because rate and time are confounded, it is convenient to arbitrarily standardize things by setting the rate to a value such that **one substitution** is expected to occur in **one unit of time** for each site.

This results in "time" (the length of a branch) being measured in units of **evolutionary distance (expected number of substitutions per site)** rather than years (or some other calendar unit).

evolutionary distance $v = 3\alpha t$

$$v = 3\left(\frac{1}{3}\right)t$$

Setting α=1/3 results in v equalling t

Evolutionary distances for several common models

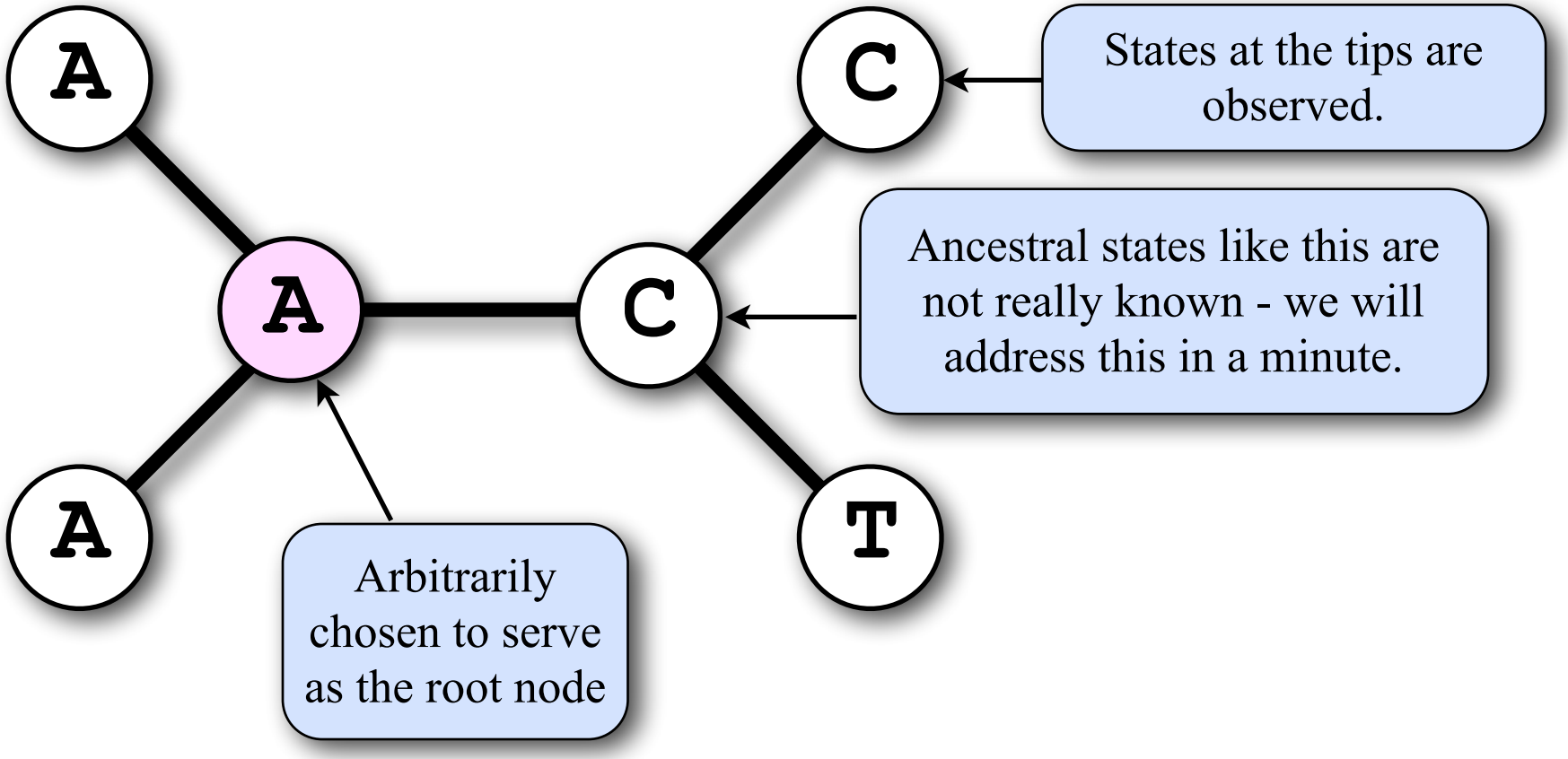
Model	Expected no. substitutions: $v = \{r\}t$
JC69	$v = \{3\alpha\}\, t$
F81	$v = \{2\mu(\pi_R\pi_Y + \pi_A\pi_G + \pi_C\pi_T)\}\, t$
K80	$v = \{\beta(\kappa + 2)\}\, t$
HKY85	$v = \{2\mu\,[\pi_R\pi_Y + \kappa(\pi_A\pi_G + \pi_C\pi_T)]\}\, t$

In the formulas above, the overall rate *r* (in curly brackets) is a function of all parameters in the substitution model.

One substitution model parameter is always determined from the edge length (using our convention that $v = t$); the others are usually global (i.e. same value applies to all edges).

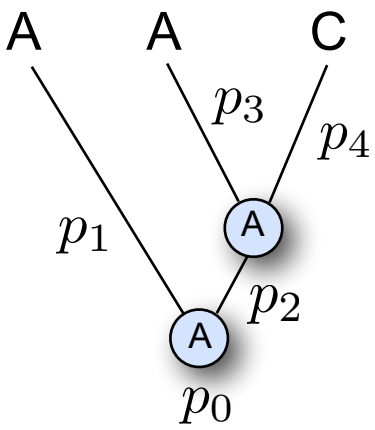
Likelihood of an unrooted tree

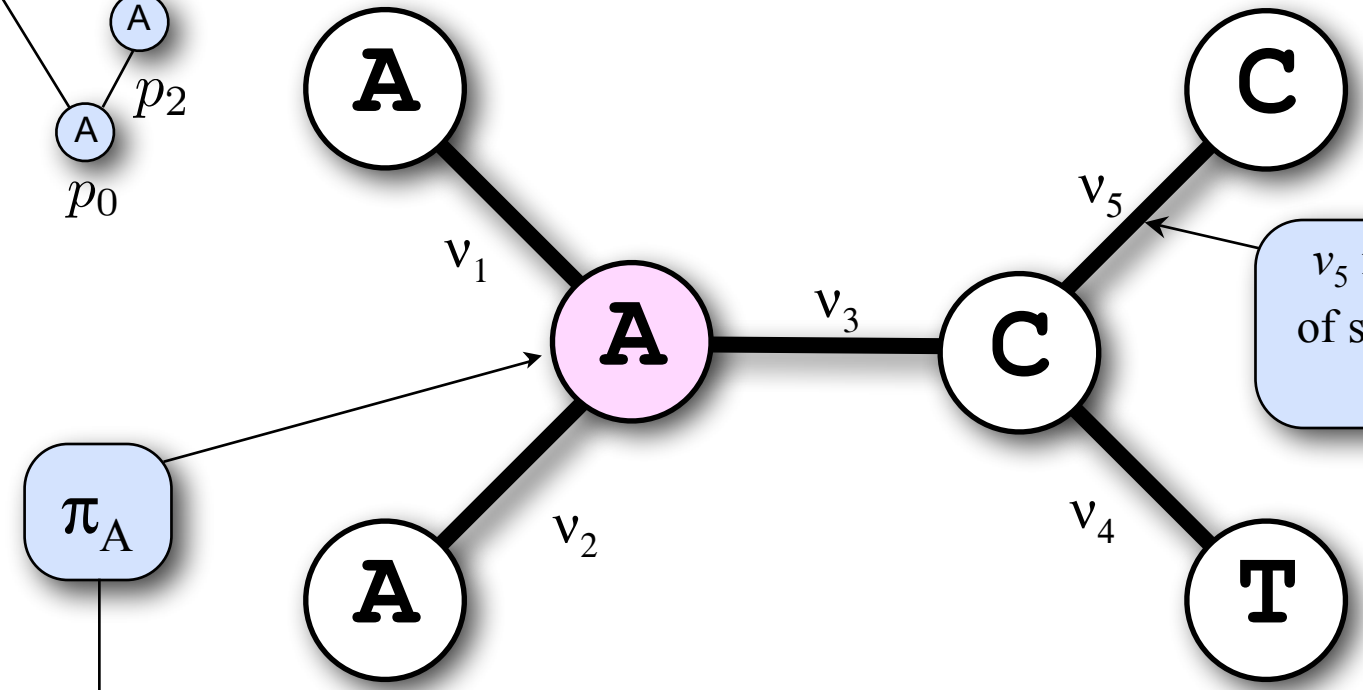
(data shown for only one site)



From slide 6

Likelihood for site k





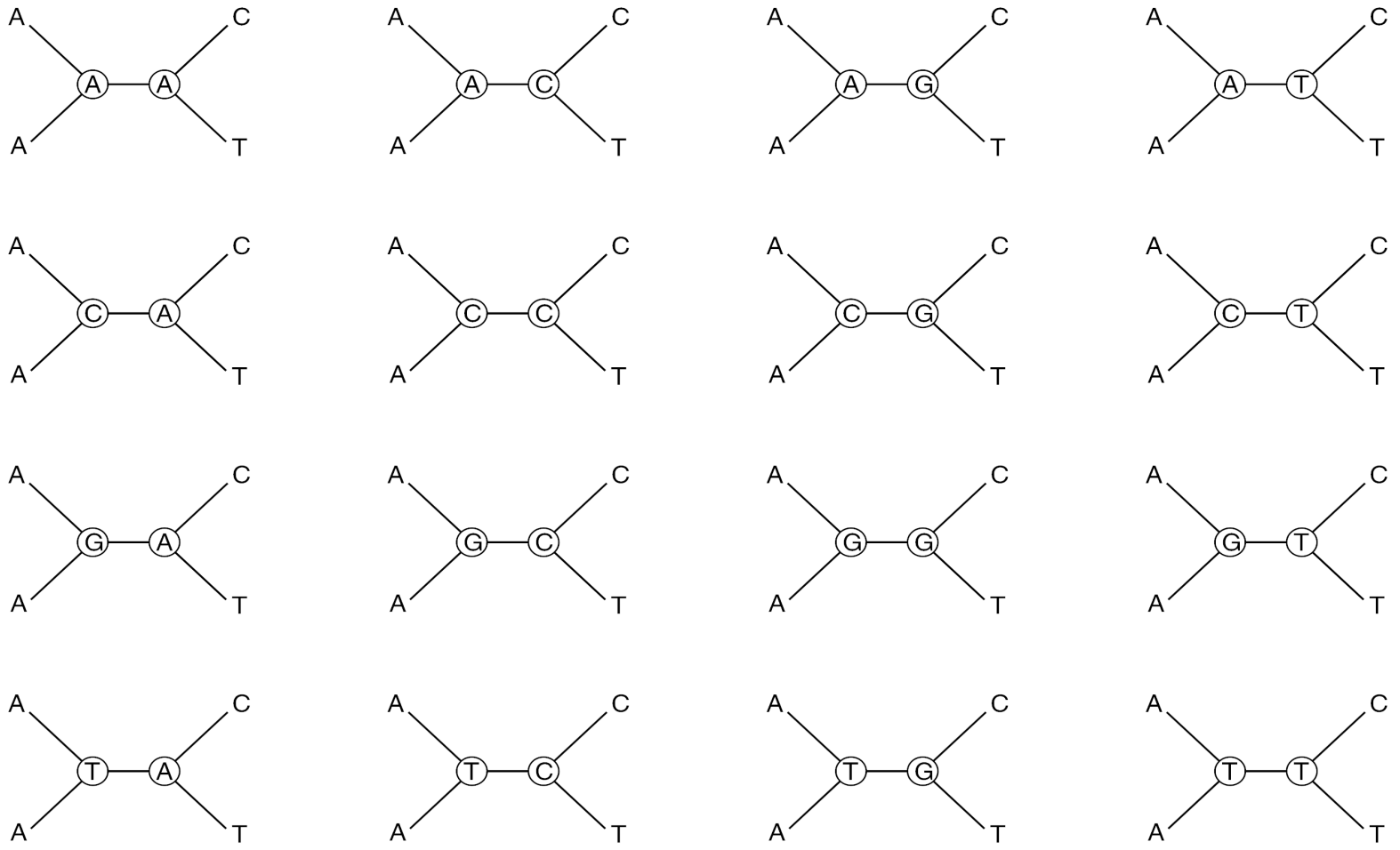
v_5 is the expected number of substitutions for just this one branch

$$L_k = \frac{1}{4}\left[\frac{1}{4}+\frac{3}{4}e^{-4\nu_1/3}\right]\left[\frac{1}{4}+\frac{3}{4}e^{-4\nu_2/3}\right]\left[\frac{1}{4}-\frac{1}{4}e^{-4\nu_3/3}\right]\left[\frac{1}{4}-\frac{1}{4}e^{-4\nu_4/3}\right]\left[\frac{1}{4}+\frac{3}{4}e^{-4\nu_5/3}\right]$$

$P_{AA}(v_1)$ $P_{AA}(v_2)$ $P_{AC}(v_3)$ $P_{CT}(v_4)$ $P_{CC}(v_5)$

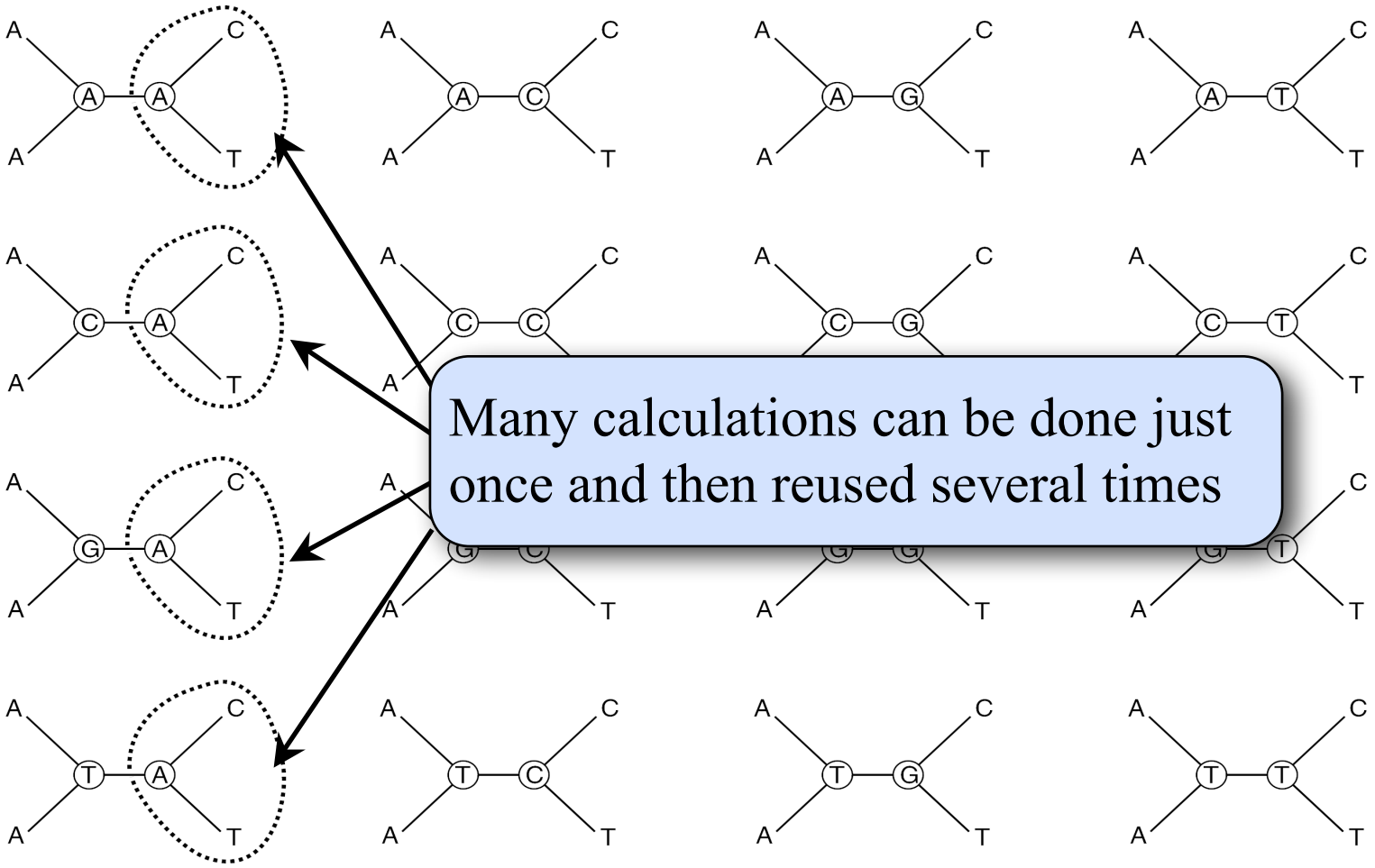
Note use of the AND probability rule

Brute force approach would be to calculate L_k for all 16 combinations of ancestral states and sum them



Note use of the OR probability rule

Pruning algorithm
(same result, less time)



Felsenstein, J. 1981. Evolutionary trees from DNA sequences:
a maximum likelihood approach. *Journal of Molecular Evolution* **17**:368-376

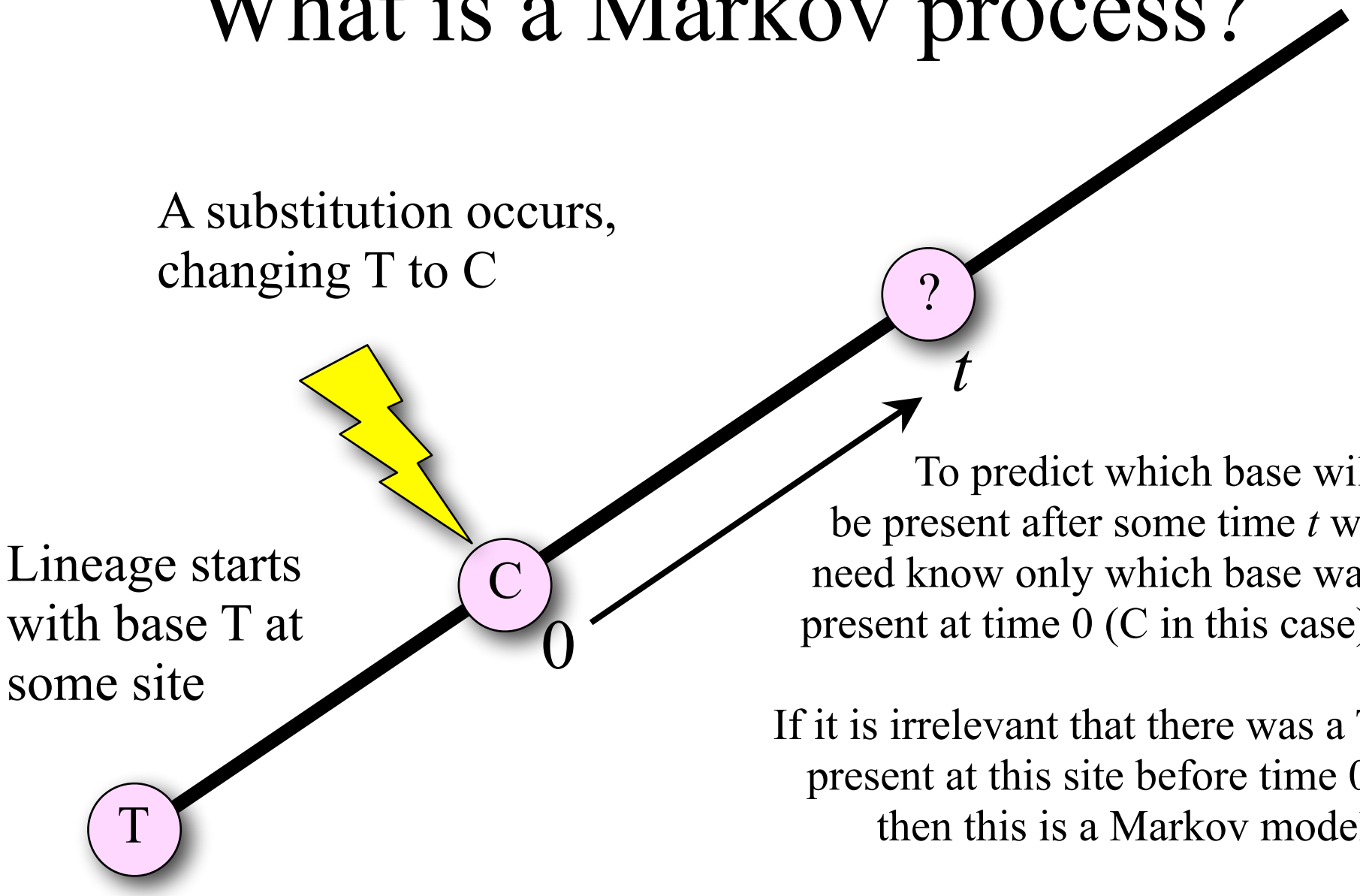
Substitution Models

Jukes-Cantor (JC69) model

- The four bases (A, C, G, T) are expected to be **equally frequent** in sequences ($\pi_A = \pi_C = \pi_G = \pi_T = 0.25$)
- Assumes **same rate** for all types of substitution ($r_{A\rightarrow C} = r_{A\rightarrow G} = r_{A\rightarrow T} = r_{C\rightarrow G} = r_{C\rightarrow T} = r_{G\rightarrow T} = \alpha$)
- Usually described as a **1-parameter** model (the parameter being the edge length)
  - Remember, however, that each edge in a tree can have its own length, so there are really as many parameters in the model as there are edges in the tree!
- Assumes substitution is a **Markov** process...

Jukes, T. H., and C. R. Cantor. 1969. Evolution of protein molecules. Pages 21-132 *in* H. N. Munro (ed.), *Mammalian Protein Metabolism*. Academic Press, New York.

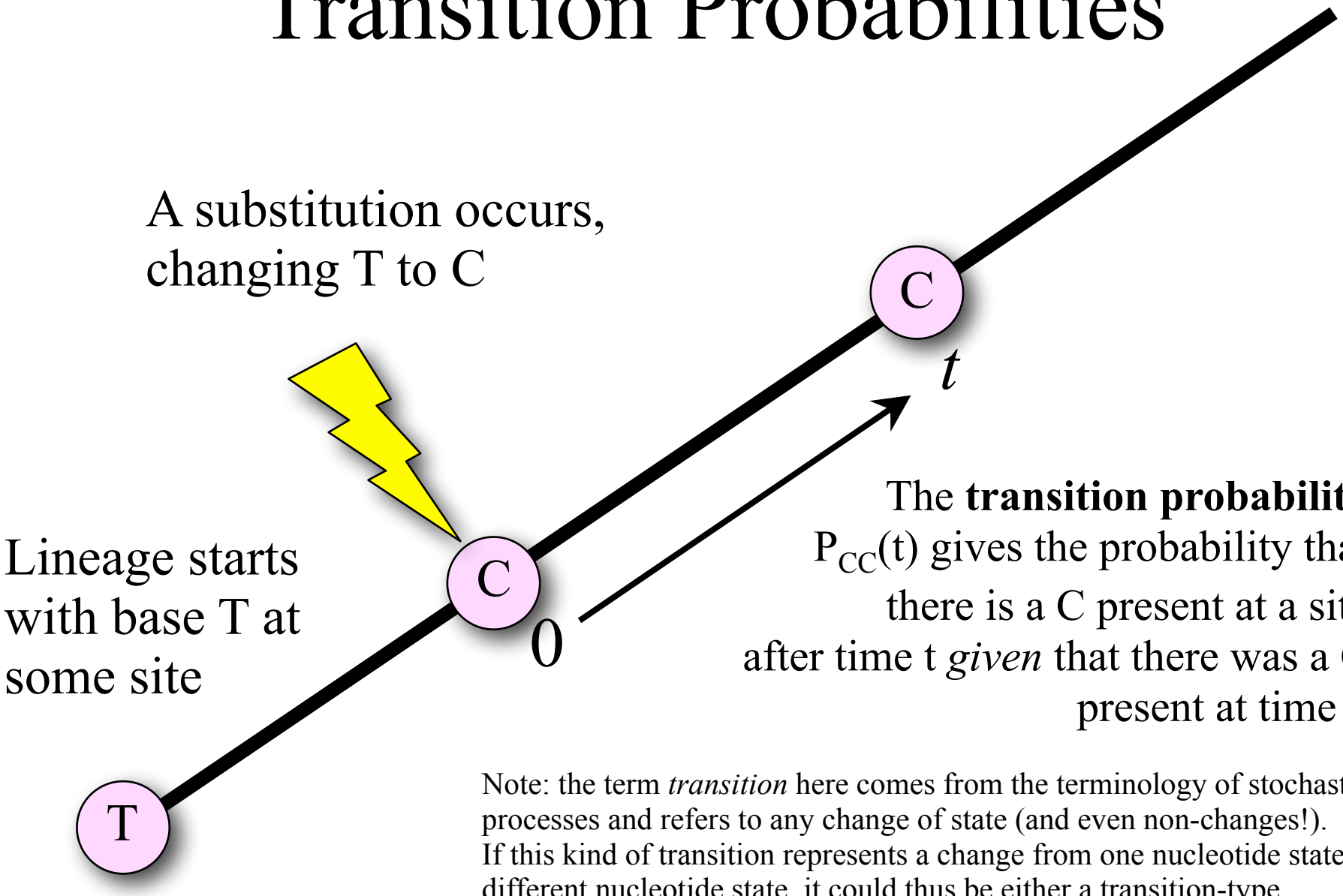
What is a Markov process?



To predict which base will be present after some time *t* we need know only which base was present at time 0 (C in this case).

If it is irrelevant that there was a T present at this site before time 0, then this is a Markov model.

Transition Probabilities



The **transition probability**
$P_{CC}(t)$ gives the probability that
there is a C present at a site
after time t *given* that there was a C
present at time 0

Note: the term *transition* here comes from the terminology of stochastic processes and refers to any change of state (and even non-changes!).
If this kind of transition represents a change from one nucleotide state to a different nucleotide state, it could thus be either a transition-type or a transversion-type substitution.

Jukes-Cantor transition probabilities

Here is the probability that a site starting in state T will end up in state G after time *t* when the individual substitution rates are all α:

$$P_{TG}(t) = \frac{1}{4}\left(1 - e^{-4\alpha t}\right)$$

The JC69 model has only one unknown quantity: αt

(The symbol *e* represents the base of the natural logarithms: its value is 2.718281828459045...)

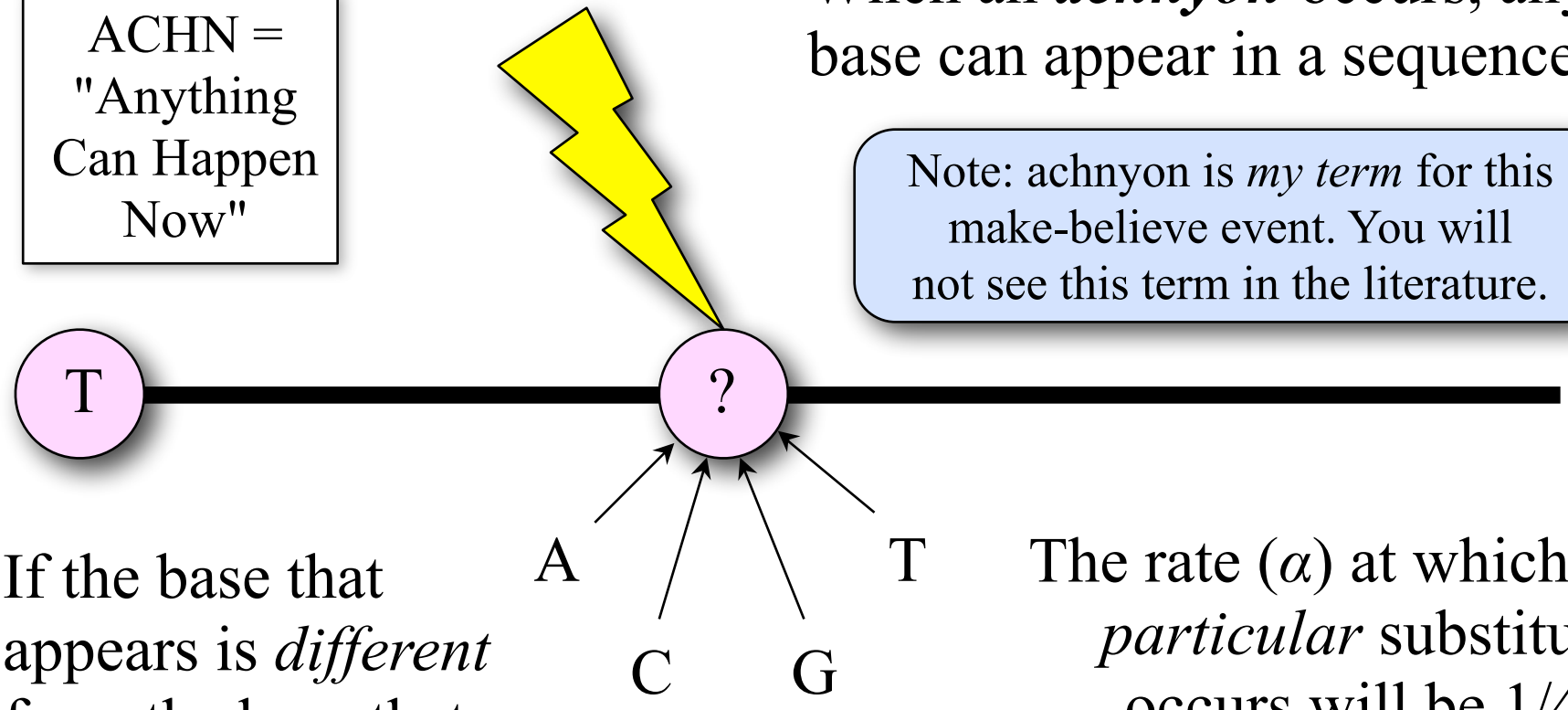
Where does a transition probability formula such as this come from?

"ACHNyons" vs. substitutions

ACHN = "Anything Can Happen Now"

When an ***achnyon*** occurs, any base can appear in a sequence.

Note: achnyon is *my term* for this make-believe event. You will not see this term in the literature.



If the base that appears is *different* from the base that was already there, then a **substitution** event has occurred.

The rate (α) at which any *particular* substitution occurs will be 1/4 the achnyon rate (μ). That is, $\alpha = \mu/4$ (or $\mu = 4\alpha$)

Deriving a transition probability

Calculate the probability that a site currently T will change to G over time *t* when the rate of this particular substitution is α:

Pr(zero achnyons) = $e^{-\mu t}$ (Poisson probability of zero events)

Pr(at least 1 achnyon) = $1 - e^{-\mu t}$

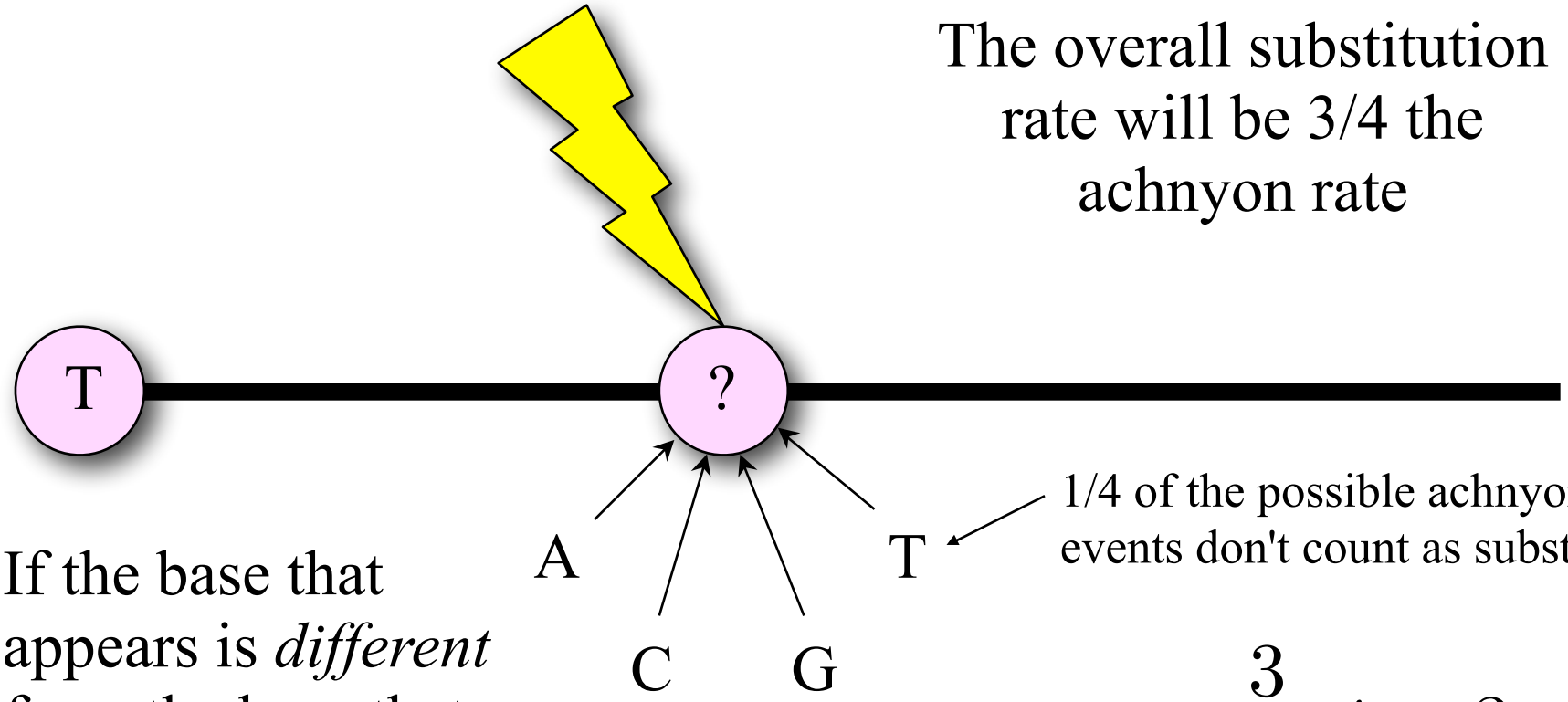
Pr(last achnyon results in base G) = $\frac{1}{4}$

Pr(end in G | start in T) = $\frac{1}{4}\left(1 - e^{-\mu t}\right)$

Remember that the rate (α) of any particular substitution is one fourth the achnyon rate (μ):

$$P_{GT}(t) = \frac{1}{4}\left(1 - e^{-4\alpha t}\right)$$

Expected number of substitutions



The overall substitution rate will be 3/4 the achnyon rate

1/4 of the possible achnyon events don't count as substitutions

If the base that appears is *different* from the base that was already there, then a **substitution** event has occurred.

$$\nu = \frac{3}{4}\mu t = 3\alpha t$$

Transition Probabilities: Remarks

$$
\begin{aligned}
P_{TA}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TC}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TG}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TT}(t) &= \frac{1}{4}(1 - e^{-4\alpha t})
\end{aligned}
$$

$$
\frac{}{1 - e^{-4\alpha t}}
$$

These should add to 1.0 because T *must* change to something!

Doh! Something must be wrong here...

Transition Probabilities: Remarks

$$
\begin{aligned}
P_{TA}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TC}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TG}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) \\
P_{TT}(t) &= \frac{1}{4}(1 - e^{-4\alpha t}) + e^{-4\alpha t}
\end{aligned}
$$

Forgot to account for the possibility of *no* acnyons over time *t*

Equilibrium frequencies

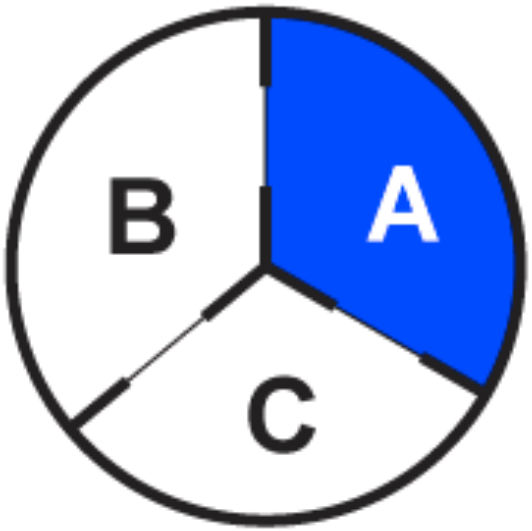
- The JC69 model assumes that the frequencies of the four bases (A, C, G, T) are equal
- The equilibrium relative frequency of each base is thus 0.25
- Why are they called *equilibrium* frequencies?

Equilibrium Frequencies

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

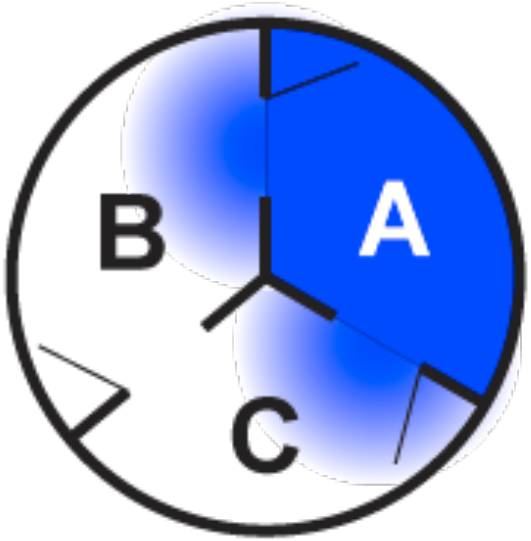
The doors to the other rooms are closed, so the perfume has, thus far, not been able to spread.

What would happen if we opened all the doors?



Equilibrium Frequencies

If the doors are suddenly opened, the perfume would begin diffusing from the area of highest concentration to lowest.

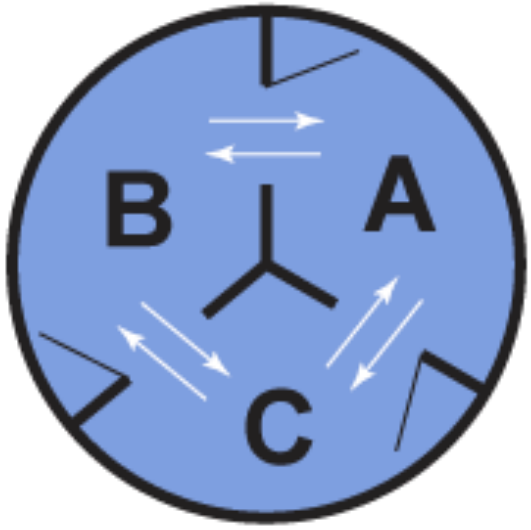


Molecules of perfume go both ways through open doors, but more pass one way than another, leading to a net flow from room A to rooms B and C.

In the instant that the doors are opened, A is losing perfume molecules at *twice the rate* each of the other rooms is gaining molecules. As diffusion progresses, however, the rate of loss from A drops, approaching an equilibrium.

Equilibrium Frequencies

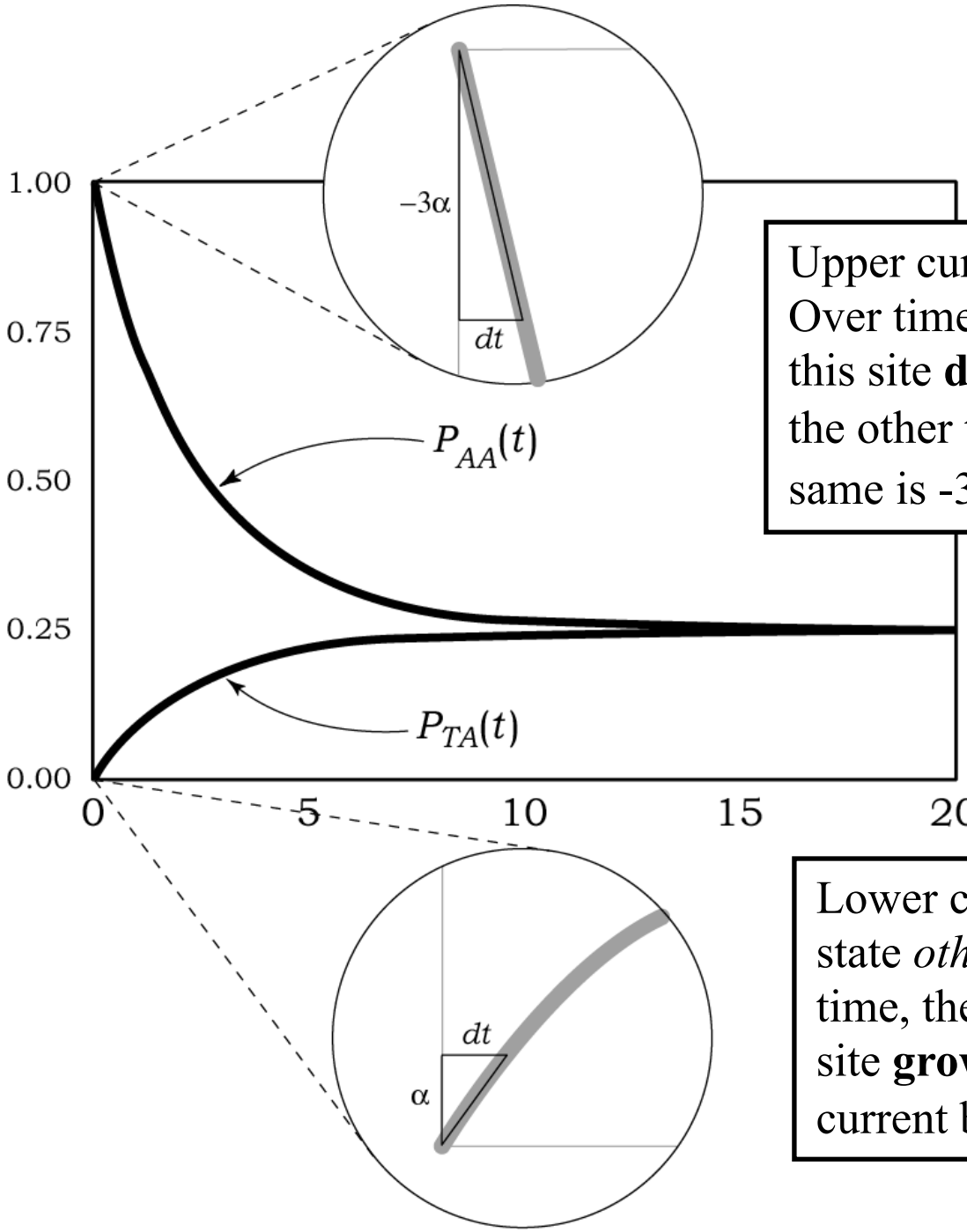
Eventually, all 3 rooms have essentially the same concentration of perfume.



Molecules still move through doors, but now the rates are the same in all directions.

Back to sequence evolution: assume a sequence began with only A nucleotides (a poly-A sequence). Over time, substitution would begin converting some of these As to Cs, Gs, and Ts, just as the perfume diffused into adjacent rooms.

Pr(A|A) and Pr(A|T) as a function of time



Upper curve assumes we started with A at time 0. Over time, the probability of still seeing an A at this site **drops** because rate of changing to one of the other three bases is 3α (so rate of staying the same is -3α).

The equilibrium relative frequency of A is 0.25

Lower curve assumes we started with some state *other* than A (T is used here). Over time, the probability of seeing an A at this site **grows** because the rate at which the current base will change into an A is α.

JC69 rate matrix

1 parameter:
α

From \ To	A	C	G	T
A	-3α	α	α	α
C	α	-3α	α	α
G	α	α	-3α	α
T	α	α	α	-3α

Jukes, T. H., and C. R. Cantor. 1969. Evolution of protein molecules. Pages 21-132 *in* H. N. Munro (ed.), *Mammalian Protein Metabolism*. Academic Press, New York.

K80 (or K2P) rate matrix

2 parameters:
α
β

From \ To	A	C	G	T
A	$-\alpha - 2\beta$	β	α	β
C	β	$-\alpha - 2\beta$	β	α
G	α	β	$-\alpha - 2\beta$	β
T	β	α	β	$-\alpha - 2\beta$

transition rate

transversion rate

Kimura, M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. Journal of Molecular Evolution 16:111-120.

K80 rate matrix
(looks different, but actually the same)

2 parameters:
κ
β

	A	C	G	T
A	$-\beta(\kappa+2)$	β	$\kappa\beta$	β
C	β	$-\beta(\kappa+2)$	β	$\kappa\beta$
G	$\kappa\beta$	β	$-\beta(\kappa+2)$	β
T	β	$\kappa\beta$	β	$-\beta(\kappa+2)$

All I've done is re-parameterize the rate matrix, letting κ equal the *transition/transversion rate ratio*

$$\longrightarrow \quad \kappa = \frac{\alpha}{\beta}$$

Note: the K80 model is identical to the JC69 model if $\kappa = 1$ ($\alpha = \beta$)

Transition/transversion ratio (tratio) versus Transition/transversion *rate* ratio (kappa)

Cobbler analogy:

- 4 cobblers in a factory make loafers
- 8 cobblers in the factory make work boots
- all cobblers produce the same number of shoes per unit time, regardless of shoe type
- what is the loafer/boot *rate ratio* and how does that compare to the loafer/boot *ratio*?

The loafer/boot *rate ratio* is 1.0 because each cobbler cranks out shoes at the same rate.

The loafer/boot *ratio,* however, is 0.5 because there are twice as many cobblers making boots as there are cobblers making loafers.

There are 8 possible transversion-type substitutions and only 4 possible transition-type substitutions: the transition/transversion ratio is thus 0.5 when the transition/transversion rate ratio is 1.

 Image from http://www.gaseenterprise.com/07130%20Shoemaker.jpg

F81 rate matrix

4 parameters:
μ
π_A
π_C
π_G

	A	C	G	T
A	$-\mu(1-\pi_A)$	$\pi_C\mu$	$\pi_G\mu$	$\pi_T\mu$
C	$\pi_A\mu$	$-\mu(1-\pi_C)$	$\pi_G\mu$	$\pi_T\mu$
G	$\pi_A\mu$	$\pi_C\mu$	$-\mu(1-\pi_G)$	$\pi_T\mu$
T	$\pi_A\mu$	$\pi_C\mu$	$\pi_G\mu$	$-\mu(1-\pi_T)$

Note: the F81 model is identical to the JC69 model if all base frequencies are equal

Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal of Molecular Evolution 17:368-376.

HKY85 rate matrix

5 parameters:
κ
β
π_A
π_C
π_G

	A	C	G	T
A	$-$	$\pi_C\beta$	$\pi_G\beta\kappa$	$\pi_T\beta$
C	$\pi_A\beta$	$-$	$\pi_G\beta$	$\pi_T\beta\kappa$
G	$\pi_A\beta\kappa$	$\pi_C\beta$	$-$	$\pi_T\beta$
T	$\pi_A\beta$	$\pi_C\beta\kappa$	$\pi_G\beta$	$-$

A dash means equal to negative sum of other elements on the same row

Note: the HKY85 model is identical to the F81 model if $\kappa = 1$. If, in addition, all base frequencies are equal, it is identical to JC69.

Hasegawa, M., H. Kishino, and T. Yano. 1985. Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. Journal of Molecular Evolution 21:160-174.

F84 vs. HKY85

F84 model:

μ rate of process generating *all types of substitutions*

$k\mu$ rate of process generating *only transitions*

Becomes F81 model if $k = 0$

HKY85 model:

β rate of process generating *only transversions*

$\kappa\beta$ rate of process generating *only transitions*

Becomes F81 model if $\kappa = 1$

F84 first used in Felsenstein's PHYLIP package in 1984, first published by: Kishino, H., and M. Hasegawa. 1989. Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in hominoidea. Journal of Molecular Evolution 29: 170-179.

GTR rate matrix

	A	C	G	T
A	$-$	$\pi_C a\mu$	$\pi_G b\mu$	$\pi_T c\mu$
C	$\pi_A a\mu$	$-$	$\pi_G d\mu$	$\pi_T e\mu$
G	$\pi_A b\mu$	$\pi_C d\mu$	$-$	$\pi_T f\mu$
T	$\pi_A c\mu$	$\pi_C e\mu$	$\pi_G f\mu$	$-$

9 parameters:

π_A
π_C
π_G
a
b
c
d
e
μ

Identical to the F81 model if $a = b = c = d = e = f = 1$. If, in addition, all the base frequencies are equal, GTR is identical to JC69. If $a = c = d = f = \beta$ and $b = e = \kappa\beta$, GTR becomes the HKY85 model.

Lanave, C., G. Preparata, C. Saccone, and G. Serio. 1984. A new method for calculating evolutionary substitution rates. Journal of Molecular Evolution 20:86-93.

Rate Heterogeneity

Green Plant rbc*L*

First 88 amino acids (translation is for *Zea mays*)

```
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--
Chara           (green alga; land plant lineage)   AAAGATTACAGATTAACTTACTATACTCCTGAGTATAAAACTAAAGATACTGACATTTTAGCTGCATTTCGTGTAACTCCA
Chlorella       (green alga)                       .....C...C.T.....................T..CC..C.A.....C.....T...C.T..A..G..C...A.G.....T
Volvox          (green alga)                       ........TC.T.....A.....C..A.....C...GT.GTA.....C........C.....A.........A.G......
Conocephalum    (liverwort)                        ........TC..........T........G..T...G.............G..T........A......A.AA.G.....T
Bazzania        (moss)                             ........T........C..T.....G.....A...G.G..C.....G..A..T.....G..A.........A.G.....C
Anthoceros      (hornwort)                         ........T........CC.T.....C.....T..CG.G..C..G........T.....G..A..G.C.T.AA.G.....T
Osmunda         (fern)                             ........TC....G...C..........C..T...G.G..C..G........T.....G..A.....C..AA.G.....C
Lycopodium      (club "moss")                      .GG..............C.T..C........T.....G..C.....A..C..T...C.G..A........AA.G.....T
Ginkgo          (gymnosperm; Ginkgo biloba)        ..............G.....T...........A...C....C...........T..C..G..A.....C..A........T
Picea           (gymnosperm; spruce)               ...................T...........A...C.G..C........G..T.....G..A.....C..A........T
Iris            (flowering plant)                  ..............G.....T...........T..CG....C...........T..C..G..A.....C..A........T
Asplenium       (fern; spleenwort)                 ........TC..C.G.....T..C..C..C..A..C..G..C........C..T..C..G..A..T..C..GA.G..C...
Nicotiana       (flowering plant; tobacco)         .....G....A...G.....T..............CC....C..G........T..A..G..A.....C..A........T
```

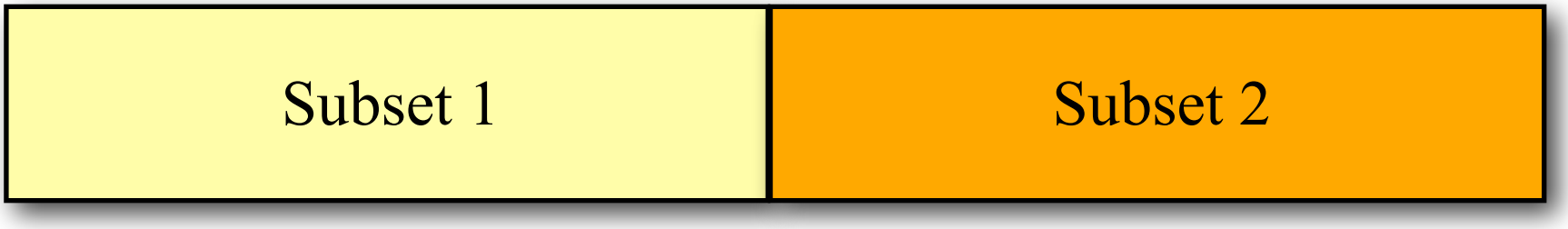
```
Q--L--G--V--P--P--E--E--A--G--A--A--V--A--A--E--S--S--T--G--T--W--T--T--V--W--T--D--G--L--T--S--L--D--R--Y--K--G--R--C--Y--H--I--E--
CAACCTGGCGTTCCACCTGAAGAAGCAGGGGCTGCAGTAGCTGCAGAATCTTCTACTGGTACATGGACTACTGTTTGGACTGACGGATTAACTAGTTTGGACCGATACAAAGGAAGATGCTACGATATTGAA
.....A..T........A........G..T..G........A........A..A........T.....G.....A.........T..T...........A.....T........TC.T..T..T..C..C..G
.....A..T..............TGT..T.....T..T.....T.....A..A..A.....T.....A.....A.........T..T.....A...C.T.....T........TC.T..T..T..C..C..G
..G....G..A...G.A............A..A.....T.....T.............................A...........T..TC.T....ACC.T..T..T..T.....TC.......T.G......C
.....G..A..A..................A..G...........T........A..C.....G.....C..G.........C..T..GC.T..A...C.C..T..T........TC.......T..C..C...
T....A..G..G..................A..C...........T........A.............................C..T...C.T..C..CC.T.....T........TC..........C......
.....C..A..A..GG....G.....T..A..............G...........A.....G.....C.....A.....G..T...C.T..C...C.T..T..T..T..G..TC................
....T...A..A.....C..G.....G..A..C...........T........C.............................C..T...C.T..C...C.C..T..C........TC.G.....T..A......
........A..G........G.....G..A..............C........C..............C...........C..T...C.T..C...C.T..T..T.....G...........T..C..C..G
.....A..G..G..G..C..G.....G..A..A...........T........C..C...........C...........C..T...C.T......C.T..T..T.....G..GC.......T..C..C..G
.....C..A.....TG..........G.....C..G........C.....................A..A..G.........T...C.T..C...C.T..T..T.........C........C.C..C..G
.....C..A..A...G..........C..A.................G..C.....A...........C.....G.....A.....G..G..C..CC.T.....T.....G..CC.............C..G
........A.....................C..G........C.....................A.....A.....C..T...C.T..C..CC.T..T..T........GC........CGC..C..G
```

All four bases are observed at some sites...

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

Site-specific rates

Each defined subset (e.g. gene, codon position) has its own relative rate



r_1 applies to subset 1
(e.g. sites 1 - 1000)

r_2 applies to subset 2
(e.g. sites 1001-2000)

Relative rates have mean 1:

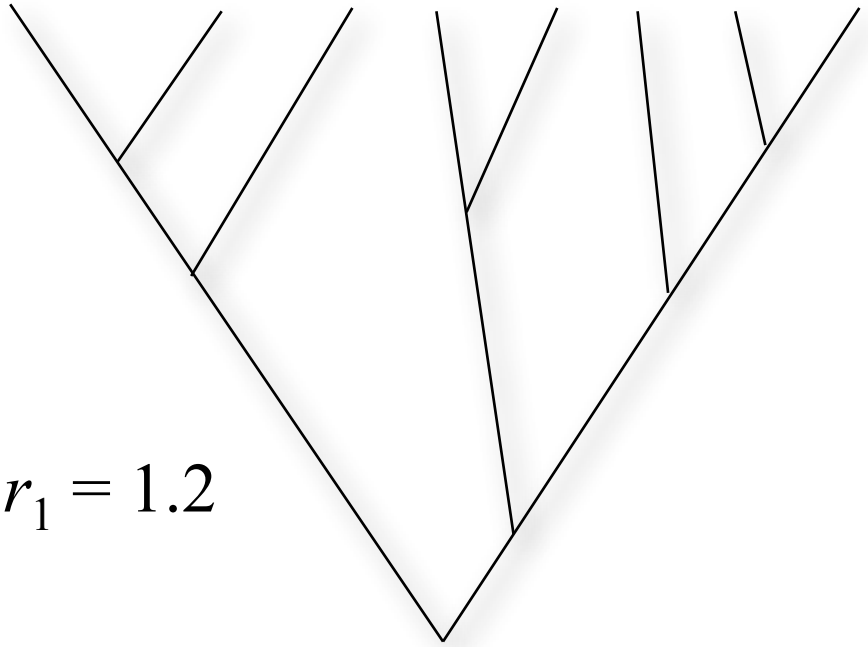
$$\frac{r_1 + r_2}{2} = 1$$

More generally:

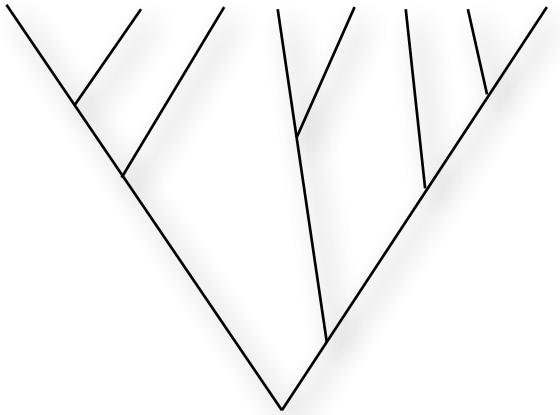
$$r_1\ p(r_1) + r_2\ p(r_2) = 1$$

Site-specific rates

$$L = \underbrace{\Pr(D_1|r_1) \cdots \Pr(D_{1000}|r_1)}_{\text{Gene 1}} \; \underbrace{\Pr(D_{1001}|r_2) \cdots \Pr(D_{2000}|r_2)}_{\text{Gene 2}}$$



$r_1 = 1.2$



$r_2 = 0.8$

Site-specific rates

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

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

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

Site specific rates

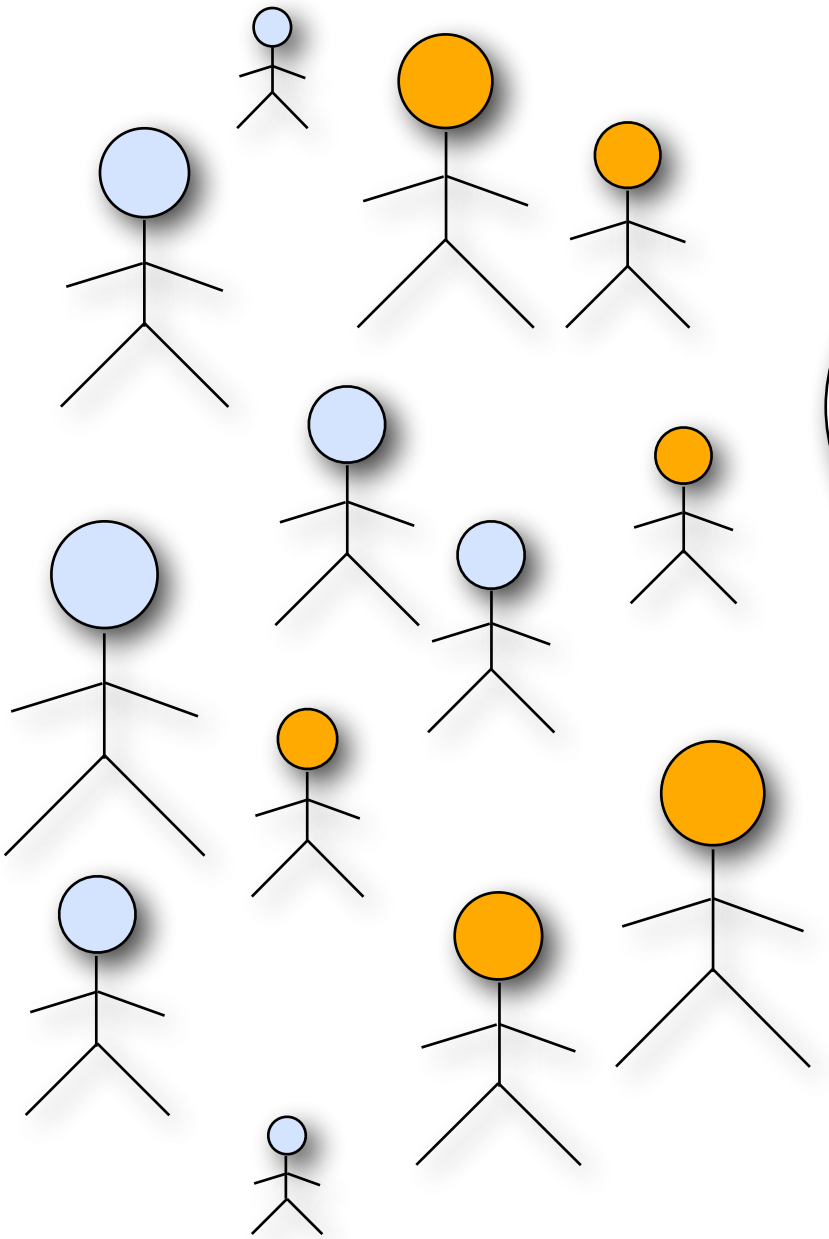
JC69 transition probabilities that would be used for sites in **gene 1**:

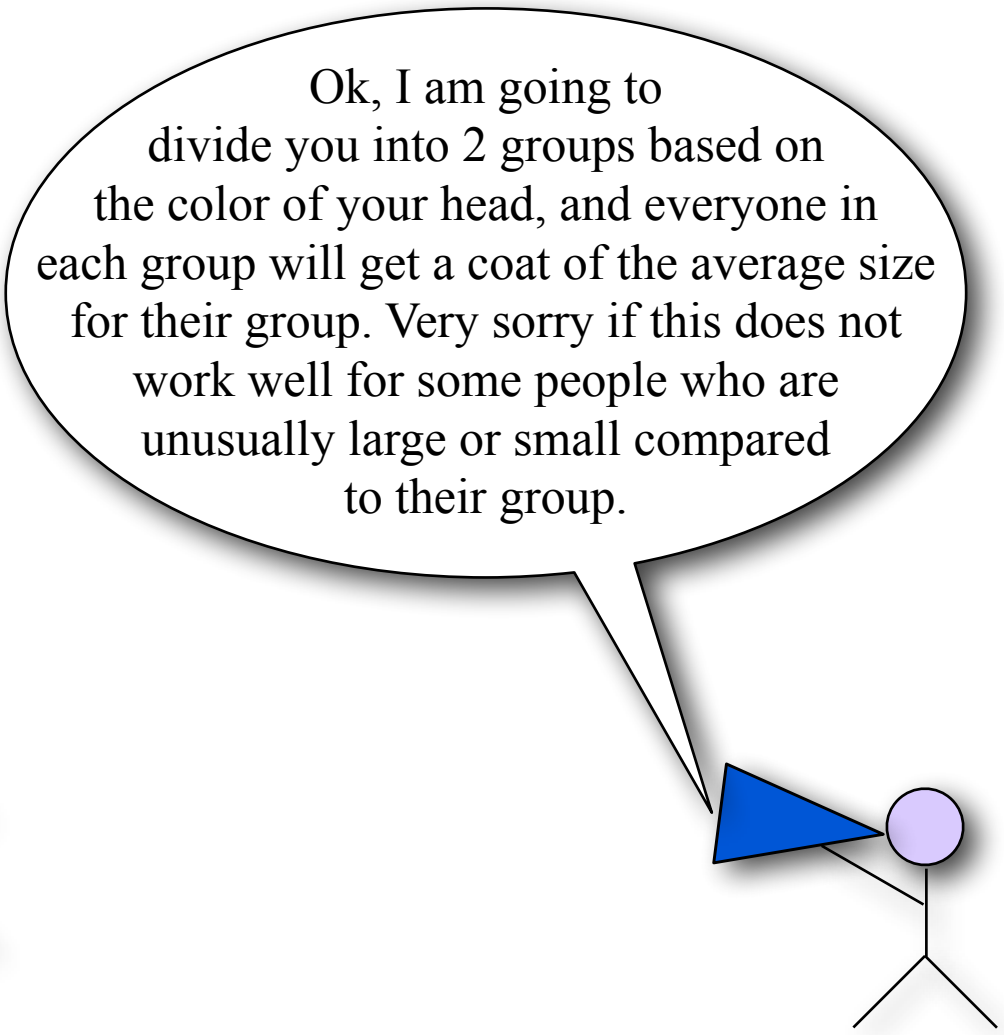
$$
\begin{aligned}
P_{ii}(t) &= \frac{1}{4} + \frac{3}{4}e^{-4r_1\alpha t} \\
P_{ij}(t) &= \frac{1}{4} - \frac{1}{4}e^{-4r_1\alpha t}
\end{aligned}
$$

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

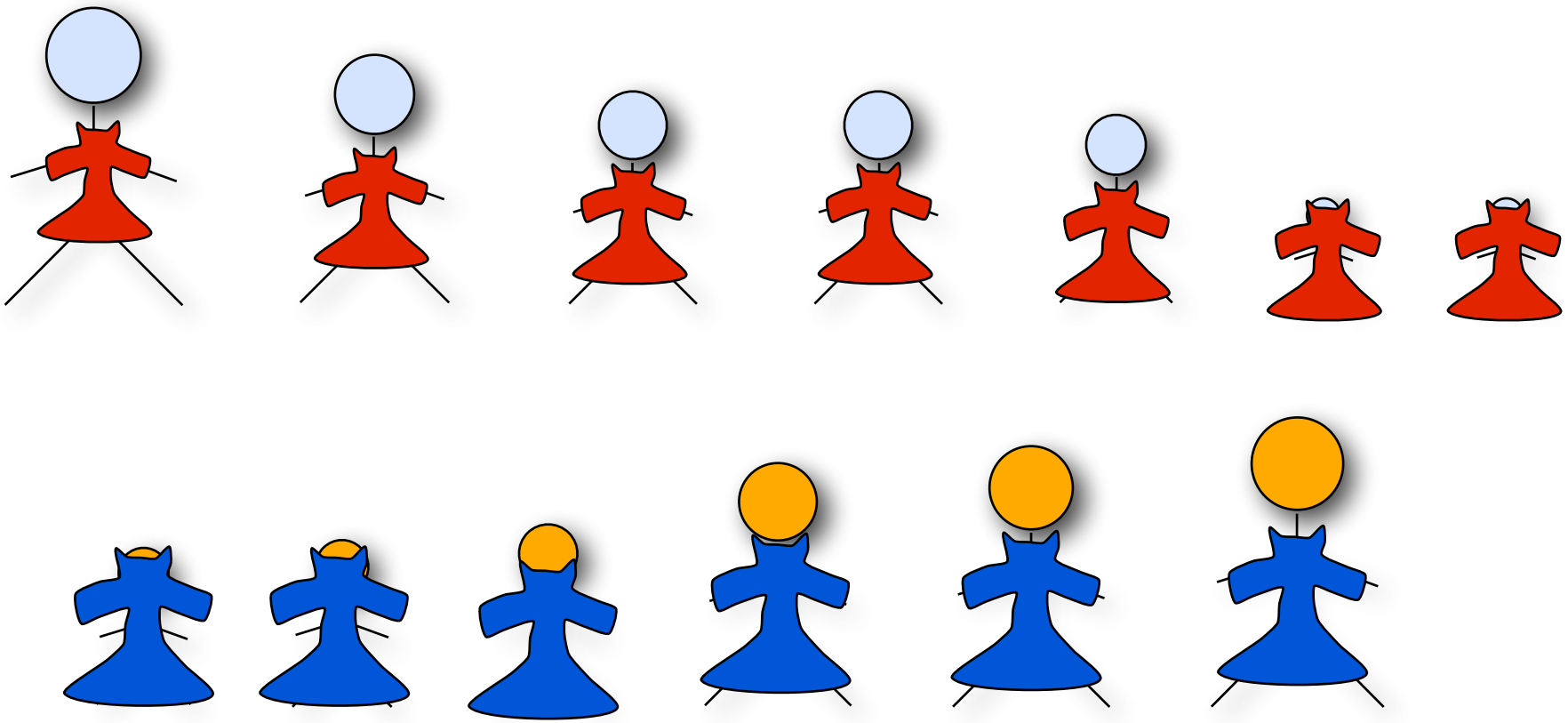
$$
\begin{aligned}
P_{ii}(t) &= \frac{1}{4} + \frac{3}{4}e^{-4r_2\alpha t} \\
P_{ij}(t) &= \frac{1}{4} - \frac{1}{4}e^{-4r_2\alpha t}
\end{aligned}
$$

Site-specific Approach





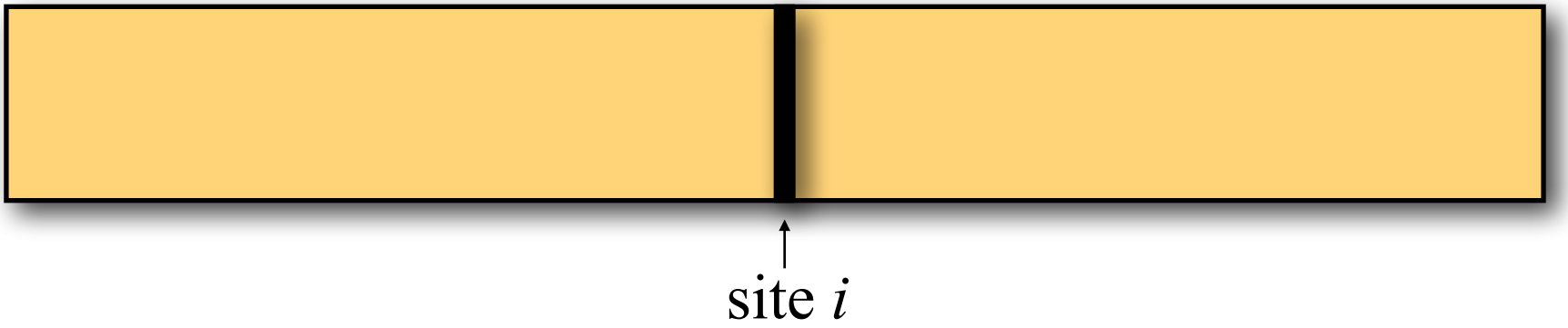
Site-specific Approach



Good: costs less: need to buy just one coat for every person
Bad: every person in a group has to wear the same size coat, so the fit will be poor for some people if they are much bigger or smaller than the average size for the group in which they have been placed

Mixture Models

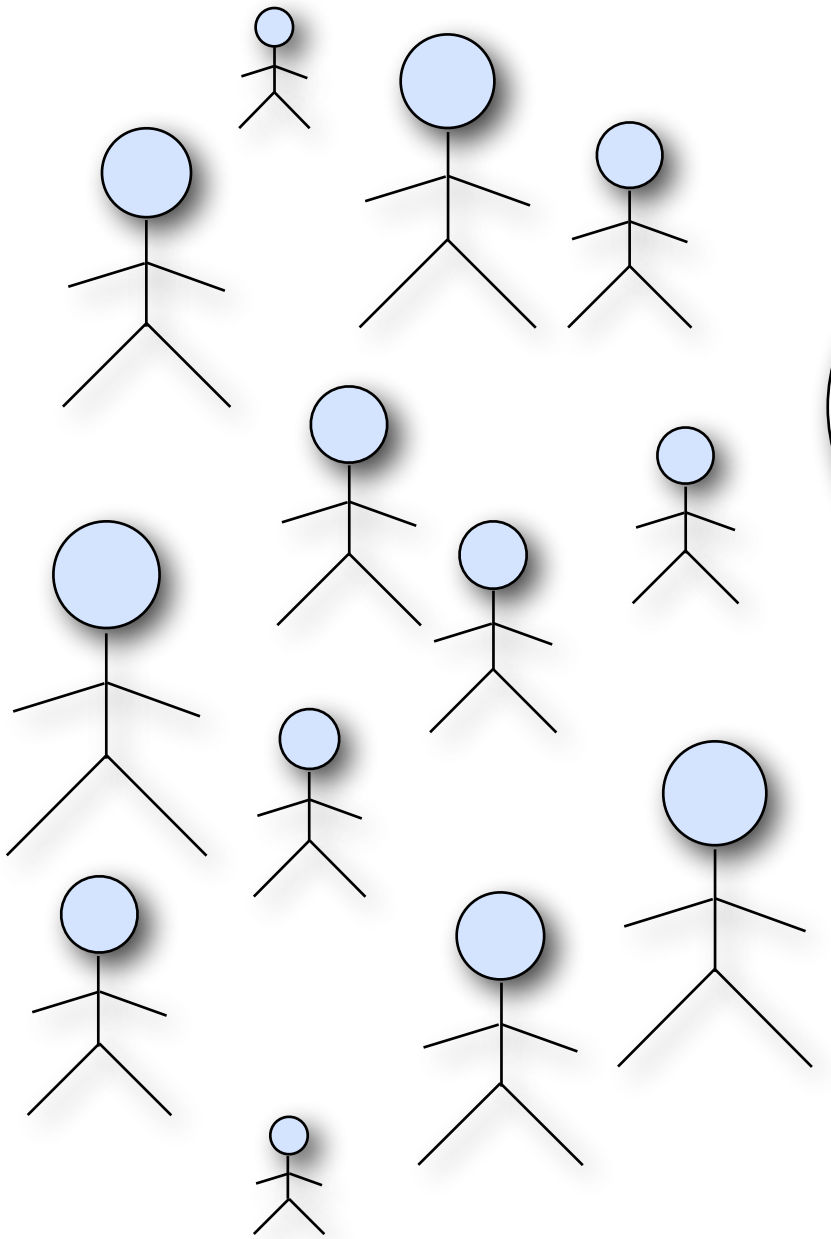
All relative rates applied to every site



$$L_i = \Pr(D_i|r_1)\Pr(r_1) + \Pr(D_i|r_2)\Pr(r_2)$$

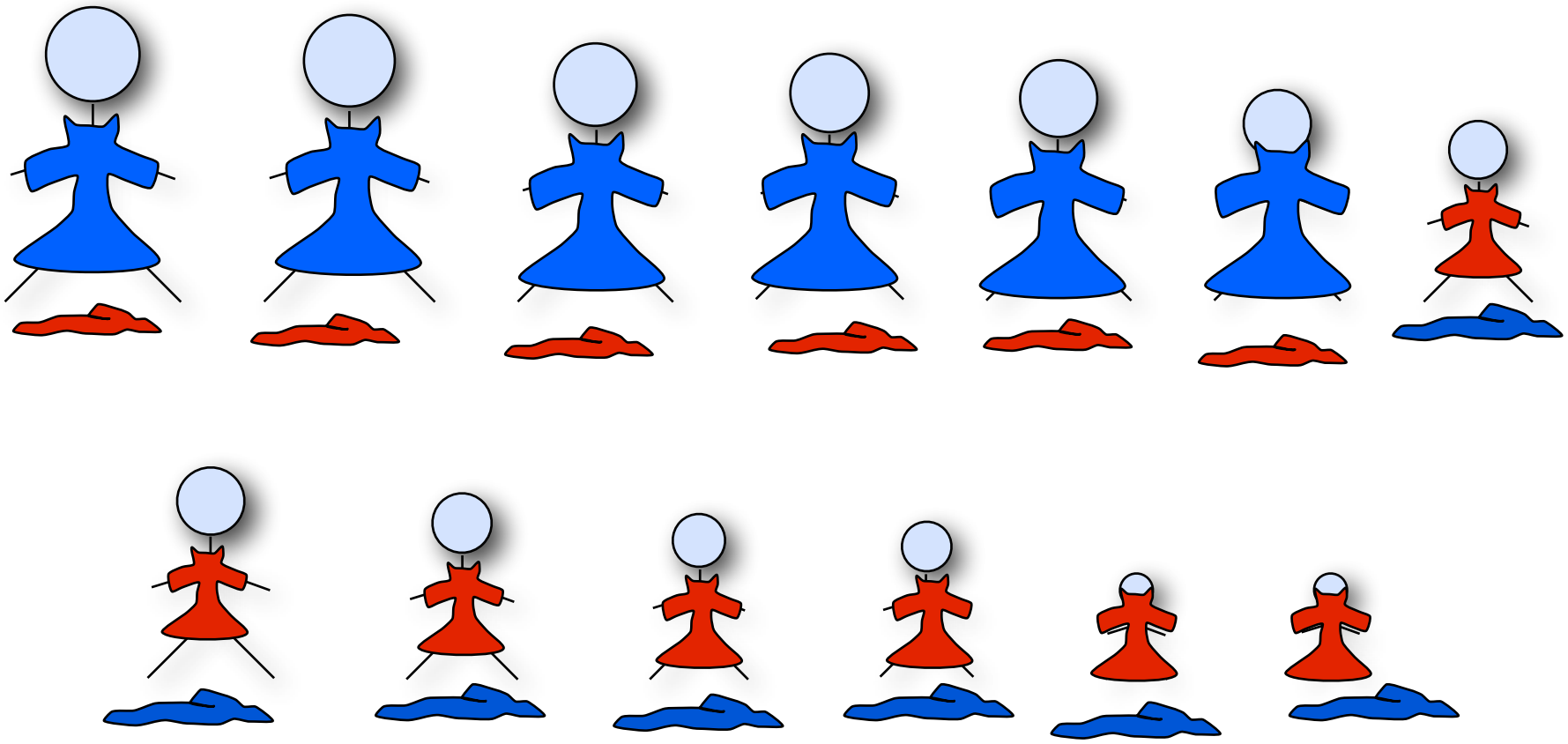
Common examples
- Invariable sites (I) model
- Discrete Gamma (G) model

Mixture Model Approach



Ok, I am going to give each of you 2 coats: use the one that fits you best and throw away the other one. This costs twice as much for me, but on average leads to better fit for you. I have determined the two sizes of coats based on the distribution of your sizes.

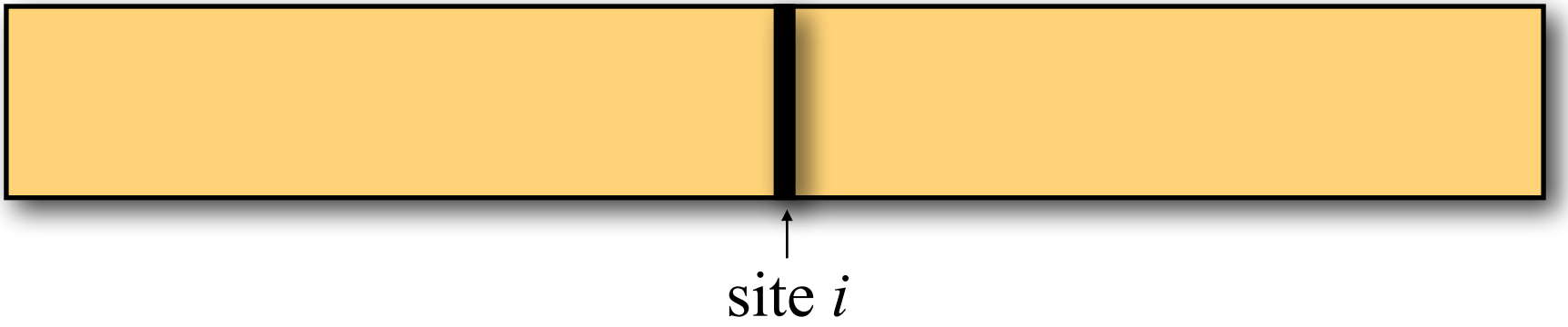
Mixture Model Approach



Good: every person experiences better fit because they can choose the size coat that fits best
Bad: costs more because two coats much be provided for each person

Invariable Sites Model

A fraction p_{invar} of sites are assumed to be invariable (i.e. rate = 0.0)



$$L_i = \Pr(D_i|r_1)p_{\text{invar}} + \Pr(D_i|r_2)(1 - p_{\text{invar}})$$

$$r_1 = 0.0$$

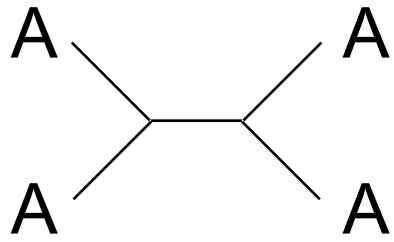
$$r_2 = \frac{1}{1 - p_{\text{invar}}}$$

Allows for the possibility that any given site could be variable or invariable

Reeves, J. H. 1992. Heterogeneity in the substitution process of amino acid sites of proteins coded for by mitochondrial DNA. Journal of Molecular Evolution 35:17-31.

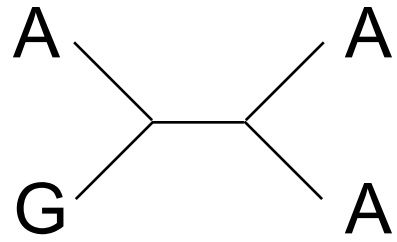
Invariable sites model

If site *i* is a *constant* site, both terms will contribute to the site likelihood:



$$L_i = \Pr(D_i|0.0)p_{\text{invar}} + \Pr(D_i|r_2)(1-p_{\text{invar}})$$

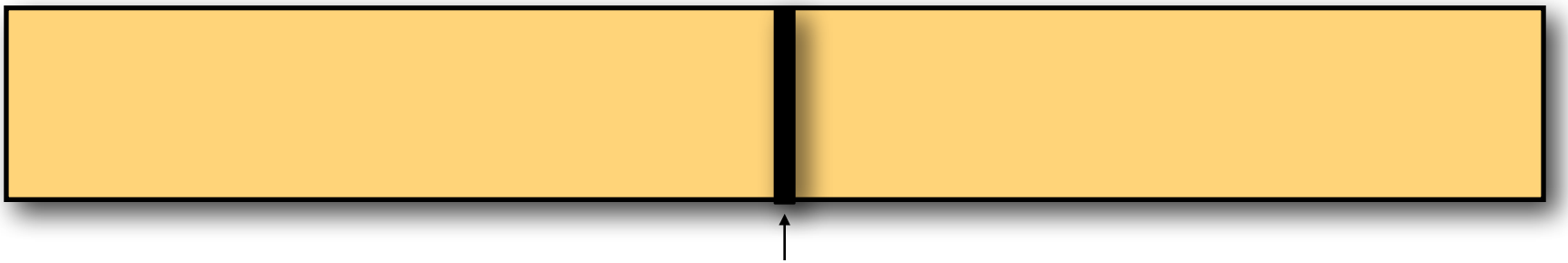
If site *i* is a *variable* site, there is no way to explain the data with a zero rate, so the first term is zero:



$$L_i = \cancel{\Pr(D_i|0.0)p_{\text{invar}}} + \Pr(D_i|r_2)(1-p_{\text{invar}})$$

Discrete Gamma Model

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



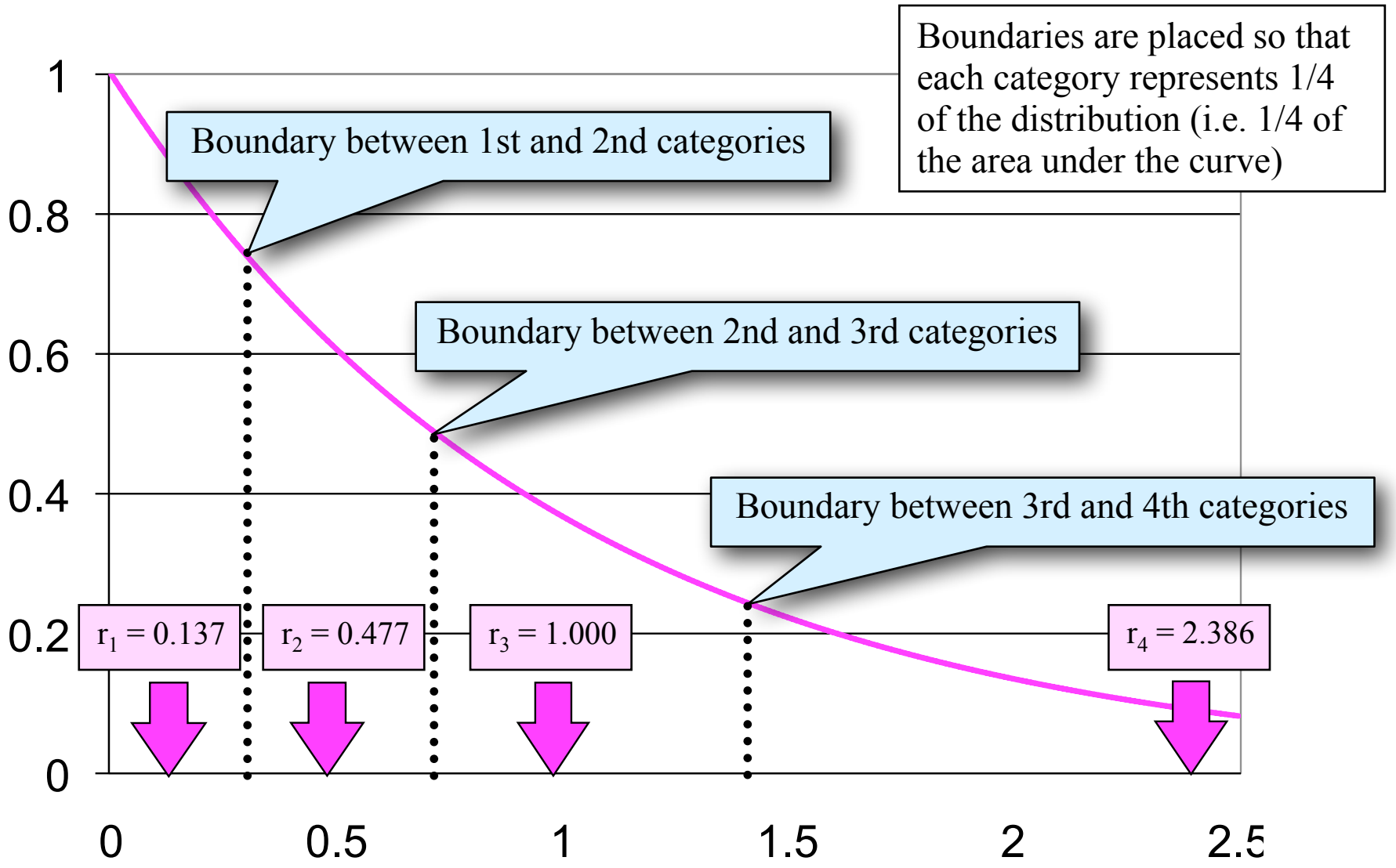
$$L = (\tfrac{1}{4})\Pr(D_i|r_1) + (\tfrac{1}{4})\Pr(D_i|r_2) + (\tfrac{1}{4})\Pr(D_i|r_3) + (\tfrac{1}{4})\Pr(D_i|r_4)$$

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

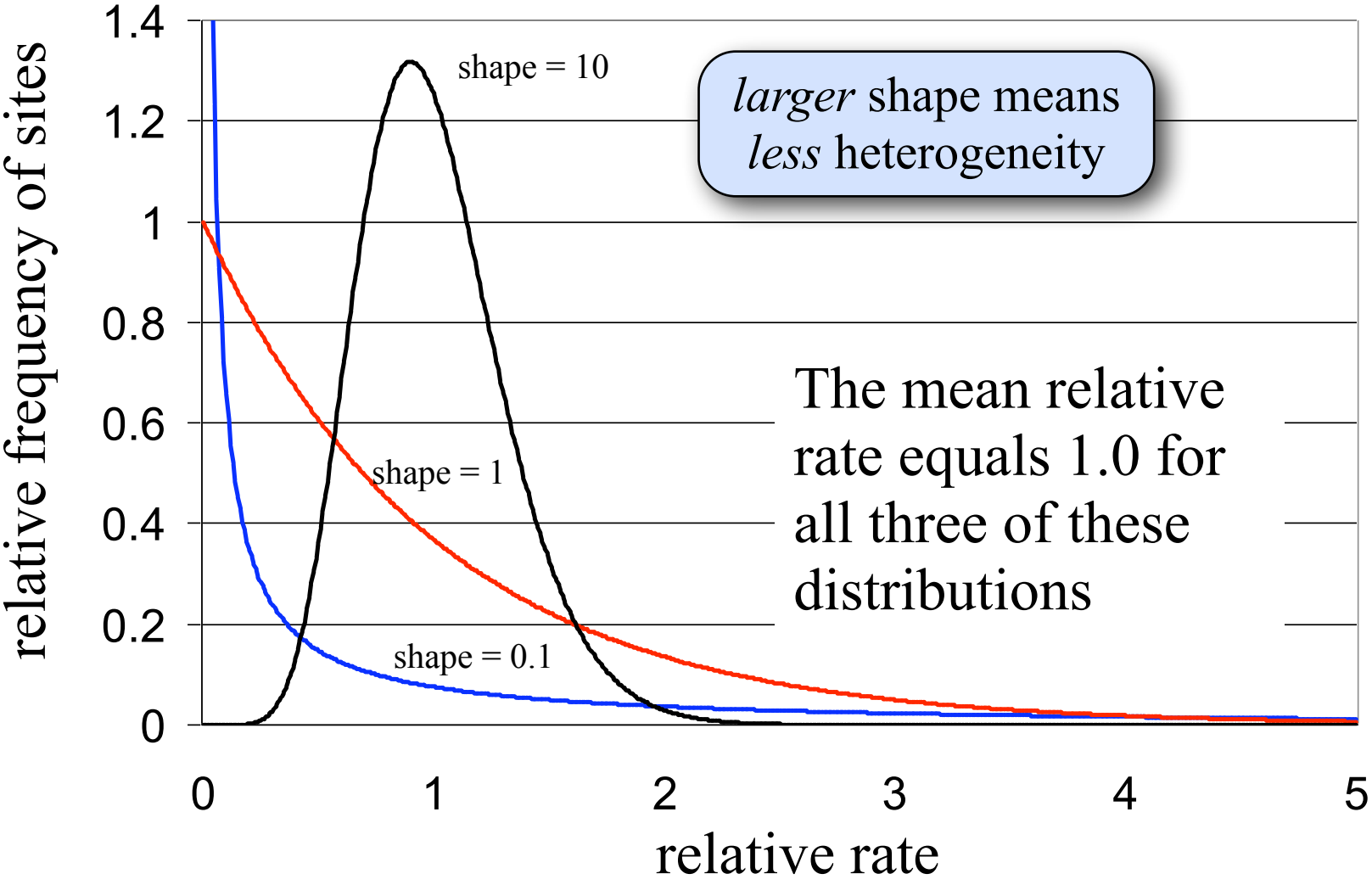
Yang, Z. 1993. Maximum-likelihood estimation of phylogeny from DNA sequences when substitution rates differ over sites. Molecular Biology and Evolution 10:1396-1401.

Yang, Z. 1994. Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. Journal of Molecular Evolution 39:306-314.

Relative rates in 4-category case



Gamma distributions



Codon models

Joe Bielawski will discuss codon models in *much* greater detail tomorrow.

The Genetic Code

First 12 nucleotides at the 5' end of the *rbc*L gene in corn:

```
5'-ATG|TCA|CCA|CAA-3'   coding strand
3'-TAC|AGT|GGT|GTT-5'   template strand
```

} DNA double helix

transcription

```
5'-AUG|UCA|CCA|CAA-3'   mRNA
```

translation

```
N-Met|Ser|Pro|Gln-C   polypeptide
```

Codon models treat codons as the independent units, not individual nucleotide sites.

Genetic Code

	U	C	A	G	
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA Stop	UGA Stop	A
	UUG Leu	UCG Ser	UAG Stop	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

http://www.langara.bc.ca/biology/mario/Assets/Geneticode.jpg

First codon models

- Muse and Gaut model (MG94) is simplest

  α = synonymous substitution rate

  β = nonsynonymous substitution rate

  π_A, π_C, π_G, π_T = base frequencies

- Goldman and Yang model (GY94) similar
  - accounts for synon./nonsynon. *and* trs/trv bias *and* amino acid properties (later simplified, see Yang et al. 1998)

Muse, S. V., and B. S. Gaut. 1994. A likelihood approach for comparing synonymous and nonsynonymous substitution rates, with application to the chloroplast genome. Molecular Biology and Evolution 11:715-724.

Goldman, N., and Z. Yang. 1994. A codon-based model of nucleotide substitution for protein-coding DNA sequences. Molecular Biology and Evolution 11:725-736.

Yang, Z., Nielsen, R., and Hasegawa, M. 1998. Models of amino acid substitution and applications to mitochondrial protein evolution. Molecular Biology and Evolution 15:1600-1611.

Table I. Part of Muse and Gaut's 61 × 61 instantaneous rate matrix[a]

Codon before substitution (the 'from' state)	Codon after substitution (the 'to' state)							
	TTT (Phe)	TTC (Phe)	TTA (Leu)	TTG (Leu)	CTT (Leu)	CTC (Leu)	…	GGG (Gly)
TTT (Phe)	– – –	$\alpha\pi_C$	$\beta\pi_A$	$\beta\pi_G$	$\beta\pi_C$	0	…	0
TTC (Phe)	$\alpha\pi_T$	– – –	$\beta\pi_A$	$\beta\pi_G$	0	$\beta\pi_C$	…	0
TTA (Leu)	$\beta\pi_T$	$\beta\pi_C$	– – –	$\alpha\pi_G$	0	0	…	0
TTG (Leu)	$\beta\pi_T$	$\beta\pi_C$	$\alpha\pi_A$	– – –	0	0	…	0
CTT (Leu)	$\beta\pi_T$	0	0	0	– – –	$\alpha\pi_C$	…	0
CTC (Leu)	0	$\beta\pi_T$	0	0	$\alpha\pi_T$	– – –	…	0
⋮	⋮	⋮	⋮		⋮	⋮	⋱	⋮
GGG (Gly)	0	0	0		0	0	…	– – –

Note that it is still easy for the change CTT → TTA to occur, it just requires more than one instant of time

Instantaneous rate is 0.0 if two or more nucleotides must change during the codon transition

Table 1 from: Lewis, P. O. 2001. Phylogenetic systematics turns over a new leaf. Trends in Ecology and Evolution 16:30-37.

Interpreting codon model results

$\omega = \beta/\alpha$ is the nonsynonymous/synonymous rate ratio

omega	mode of selection	example(s)
$\omega < 1$	stabilizing selection (nucleotide substitutions rarely change the amino acid)	functional protein coding genes
$\omega = 1$	neutral evolution (synonymous and nonsynonymous substitutions occur at the same rate)	pseudogenes
$\omega > 1$	positive selection (nucleotide substitutions often change the amino acid)	envelope proteins in viruses under active positive selection

Amino acid models

JC69 Flashback

$$
\begin{array}{c|cccc}
 & \text{A} & \text{C} & \text{G} & \text{T} \\
\text{A} & -3\alpha & \alpha & \alpha & \alpha \\
\text{C} & \alpha & -3\alpha & \alpha & \alpha \\
\text{G} & \alpha & \alpha & -3\alpha & \alpha \\
\text{T} & \alpha & \alpha & \alpha & -3\alpha
\end{array}
$$

← Q matrix
(instantaneous rates)

P matrix
(transition probabilities)
↓

$$
\begin{bmatrix}
\frac{1}{4}+\frac{3}{4}e^{-4\alpha t} & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) \\
\frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}+\frac{3}{4}e^{-4\alpha t} & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) \\
\frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}+\frac{3}{4}e^{-4\alpha t} & \frac{1}{4}\left(1-e^{-4\alpha t}\right) \\
\frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}\left(1-e^{-4\alpha t}\right) & \frac{1}{4}+\frac{3}{4}e^{-4\alpha t}
\end{bmatrix}
$$

A different path from Q to P

For many interesting models, it is not possible to obtain a *formula* for the transition probability.

We can, however, obtain transition probabilities *numerically* (i.e. obtain the value of the transition probability without plugging values into a formula)

$$\mathbf{P}(t) = e^{\mathbf{Q}t}$$

λ_1, λ_2, λ_3, and λ_4 are the eigenvalues of $\mathbf{Q}$

$$\mathbf{P}(t) = \mathbf{U} \begin{pmatrix} e^{\lambda_1 t} & 0 & 0 & 0 \\ 0 & e^{\lambda_2 t} & 0 & 0 \\ 0 & 0 & e^{\lambda_3 t} & 0 \\ 0 & 0 & 0 & e^{\lambda_4 t} \end{pmatrix} \mathbf{U}^{-1}$$

Matrix of eigenvectors of $\mathbf{Q}$

Inverse of $\mathbf{U}$

Separation of $\mathbf{Q}$ into eigenvectors and a diagonal matrix of eigenvalues is known as *diagonalization*

A different path from Q to P

Once freed from having to derive formulas for transition probabilities, we can use a great variety of Q matrices.

Dayhoff, Schwartz and Orcutt (1978; DSO78) identified 1572 accepted point mutations using closely-related sequences (<15% pairwise divergence), producing this matrix.

Kosiol and Goldman (2005) discussed ways of estimating a Q matrix from these numbers.

		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y
A	Ala																			
R	Arg	30																		
N	Asn	109	17																	
D	Asp	154	0	532																
C	Cys	33	10	0	0															
Q	Gln	93	120	50	76	0														
E	Glu	266	0	94	831	0	422													
G	Gly	579	10	156	162	10	30	112												
H	His	21	103	226	43	10	243	23	10											
I	Ile	66	30	36	13	17	8	35	0	3										
L	Leu	95	17	37	0	0	75	15	17	40	253									
K	Lys	57	477	322	85	0	147	104	60	23	43	39								
M	Met	29	17	0	0	0	20	7	7	0	57	207	90							
F	Phe	20	7	7	0	0	0	0	17	20	90	167	0	17						
P	Pro	345	67	27	10	10	93	40	49	50	7	43	43	4	7					
S	Ser	772	137	432	98	117	47	86	450	26	20	32	168	20	40	269				
T	Thr	590	20	169	57	10	37	31	50	14	129	52	200	28	10	73	696			
W	Trp	0	27	3	0	0	0	0	0	3	0	13	0	0	10	0	17	0		
Y	Tyr	20	3	36	0	30	0	10	0	40	13	23	10	0	260	0	22	23	6	
V	Val	365	20	13	17	33	27	37	97	30	661	303	17	77	10	50	43	186	0	17
		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y
		Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val

Figure 80. Numbers of accepted point mutations (X 10) accumulated from closely related sequences. Fifteen hundred and seventy-two exchanges are shown. Fractional exchanges result when ancestral sequences are ambiguous.

Dayhoff, M.O., Schwartz, R.M. and Orcutt, B.C. 1978. A model of evolutionary change in proteins. Chapter 22 in *Atlas of protein sequence and structure*, vol. 5, suppl. 3. M.O. Dayhoff (ed.), pp. 345-352, Natl. Biomed. Res. Found., Washington, DC

Kosiol C., and Goldman N. 2005. Different versions of the Dayhoff rate matrix. Molecular Biology and Evolution. 22:193–199.

The elements of Q

Once the elements of the Q matrix are estimated, the Q matrix can be separated into a symmetric matrix R of exchangeabilities and a set of state frequencies.

Ala								
Arg	0.267828							
Asn	0.984474	0.327059						
Asp	1.199805	0.000000	8.931515					
Cys	0.360016	0.232374	0.000000	0.000000				
Gln	0.887753	2.439939	1.028509	1.348551	0.000000			
Glu	1.961167	0.000000	1.493409	11.388659	0.000000	7.086022		
Gly	2.386111	0.087791	1.385352	1.240981	0.107278	0.281581	0.811907	
His	0.228116	2.383148	5.290024	0.868241	0.282729	6.011613	0.439469	...
Ile	0.653416	0.632629	0.768024	0.239248	0.438074	0.180393	0.609526	...
Leu	0.406431	0.154924	0.341113	0.000000	0.000000	0.730772	0.112880	...
Lys	0.258635	4.610124	3.148371	0.716913	0.000000	1.519078	0.830078	...
Met	0.717840	0.896321	0.000000	0.000000	0.000000	1.127499	0.304803	...
Phe	0.183641	0.136906	0.138503	0.000000	0.000000	0.000000	0.000000	...
Pro	2.485920	1.028313	0.419244	0.133940	0.187550	1.526188	0.507003	...
Ser	4.051870	1.531590	4.885892	0.956097	1.598356	0.561828	0.793999	...
Thr	3.680365	0.265745	2.271697	0.660930	0.162366	0.525651	0.340156	...
Trp	0.000000	2.001375	0.224968	0.000000	0.000000	0.000000	0.000000	...
Tyr	0.244139	0.078012	0.946940	0.000000	0.953164	0.000000	0.214717	...
Val	2.059564	0.240368	0.158067	0.178316	0.484678	0.346983	0.367250	...
	Ala	Arg	Asn	Asp	Cys	Gln	Glu	...

R matrix
(only values below diagonal shown)

Freq	0.087127	0.040904	0.040432	0.046872	0.033474	0.038255	0.049530	...

Frequencies

GTR Flashback

	A	C	G	T
A	$-$	$\pi_C a\mu$	$\pi_G b\mu$	$\pi_T c\mu$
C	$\pi_A a\mu$	$-$	$\pi_G d\mu$	$\pi_T e\mu$
G	$\pi_A b\mu$	$\pi_C d\mu$	$-$	$\pi_T f\mu$
T	$\pi_A c\mu$	$\pi_C e\mu$	$\pi_G f\mu$	$-$

Similarly, the GTR matrix can be separated into a symmetric R matrix and a diagonal matrix of frequencies.

$$\begin{pmatrix} - & a & b & c \\ a & - & d & e \\ b & d & - & f \\ c & e & f & - \end{pmatrix} \begin{pmatrix} \pi_A & 0 & 0 & 0 \\ 0 & \pi_C & 0 & 0 \\ 0 & 0 & \pi_G & 0 \\ 0 & 0 & 0 & \pi_T \end{pmatrix}$$

R matrix Frequencies

What does all this accomplish?

- Empirical Q matrix derived from many closely-related pairwise comparisons
- Fixed Q matrix can be extrapolated using diagonalization to generate a P matrix for any desired value of *t*
- This model has 0 parameters!
- Models generic features of protein evolution; does not necessarily reflect your particular sequences
- Fixed frequencies can be swapped with more appropriate set (locally estimated)

Ways to improve

- Base everything on a much larger protein database (JTT model)
- Avoid need to use closely-related sequence pairs by obtaining ML estimate of Q matrix (WAG model)
- Add rate heterogeneity to ML estimation of Q matrix (LG model)

JTT: Jones, D.T., Taylor, W.R., and Thornton, J.M. 1992. The rapid generation of mutation data matrices from protein sequences. Comput. Appl. Biosci. 8:275–282.

WAG: Whelan, S., and Goldman, N. 2001. A general empirical model of protein evolution derived from multiple protein families using a maximum-likelihood approach. Molecular Biology and Evolution. 18:691–699.

LG: Le, S.Q., and Gascuel, O. 2008. An improved general amino acid replacement matrix. Molecular Biology and Evolution. 25:1307–1320.

The End