

Introduction to Bioinformatics for Computer Scientists

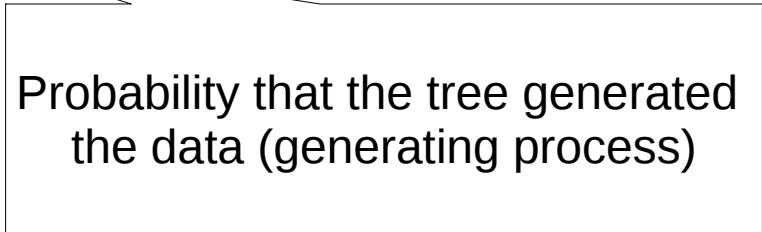
Lecture 9b

Likelihood

- Given:
 - MSA
 - Tree topology with branch lengths
 - Model
 - We can calculate $P_{x \rightarrow z}(b)$ for a branch length (or time) b

Likelihood

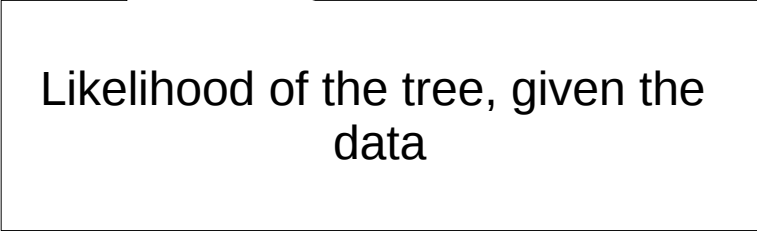
- $L(T|D) = P(D|T)$



Probability that the tree generated the data (generating process)

Likelihood

- $L(T|D) = P(D|T)$



Likelihood of the tree, given the data


Likelihood

- $L(T|D) = P(D|T)$

Likelihood: 10 coin flips → 10 heads
What's the likelihood that the coin is fair?

Probability: Probability of landing heads up
10 times

Likelihood

- $L(T|D) = P(D|T)$
 - $L(T|D) = \prod P(s_i|T)$
- Alignment site *i*
- 

Likelihood

- $L(T|D) = P(D|T)$

Alignment site i

- $L(T|D) = \prod P(s_i|T)$

What is problematic about this term?

Likelihood

- $L(T|D) = P(D|T)$
- $L(T|D) = \prod P(s_i|T)$
- $\log(L(T|D)) = \sum \log(P(s_i|T))$

Likelihood

- $L(T|D) = P(D|T)$
- $L(T|D) = \prod P(s_i|T)$
- $\log(L(\mathbf{T}|D)) = \sum \log(P(s_i|T))$



This is the model

1. Tree topology
 2. Branch lengths
 3. Model of nucleotide substitution
- generally lumped into parameter vector Θ : $L(\Theta|D)$

Likelihood

- $L(T|D) = P(D|T)$
- $L(T|D) = \prod P(s_i|T)$
- $\log(L(\mathbf{T}|D)) = \sum \log(\underline{P(s_i|T)})$

This is the model

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2. Branch lengths
3. Model of nucleotide substitution

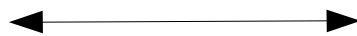
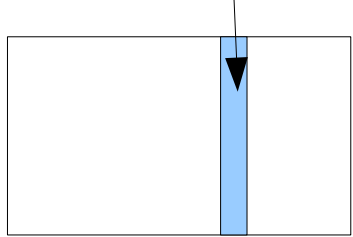
→ generally lumped into parameter vector Θ : $L(\Theta|D)$

How do we compute this?

Likelihood of a Tree

- We assume that sites evolve independently

Likelihood of site i

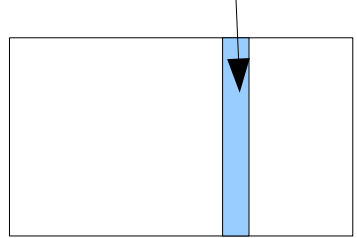


MSA length n

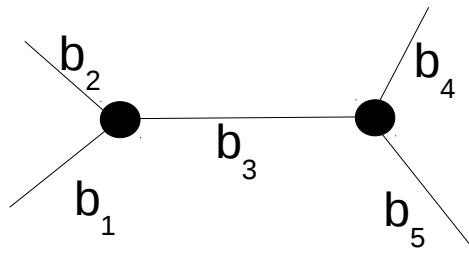
Likelihood of a Tree

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Likelihood of site i



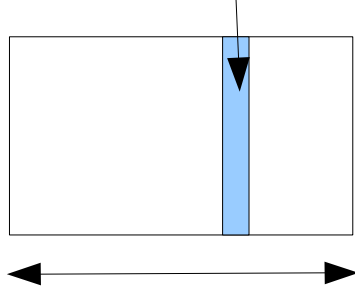
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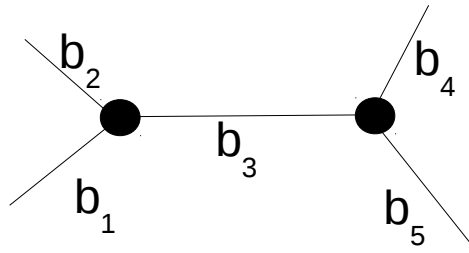
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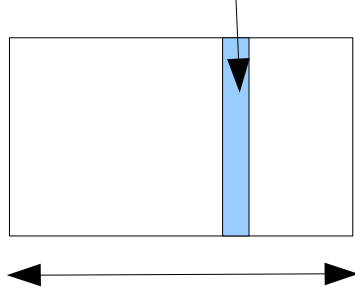


Model M
 $P_{ij}(t)$

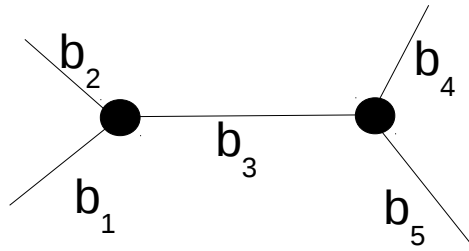
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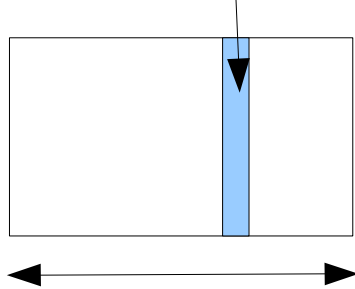
Model M
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- Overall likelihood: $L := \prod L_i$

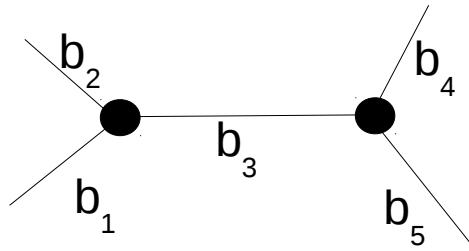
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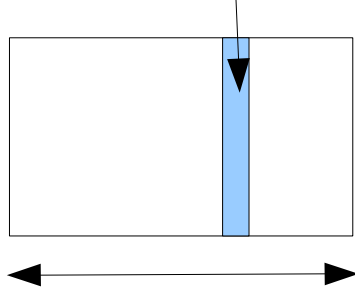
- Overall likelihood: $L := \prod L_i$
- $P_{ij}(t)$ i, j in $\{A, C, G, T\}$

Branch length/time

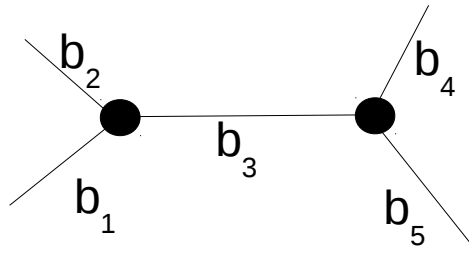
Likelihood of a Tree

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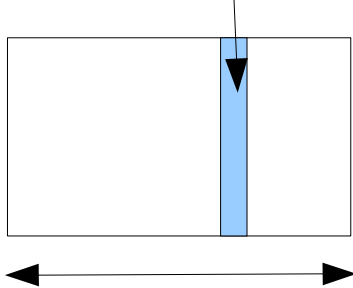
Model M
 $P_{ij}(t)$

- Overall likelihood: $L := \prod L_i$
- $P_{ij}(t)$ i, j in $\{A, C, G, T\}$
 - Probability of being in state j after time t
 - We assume that $P_{ij}(t)$ is a Markov Process

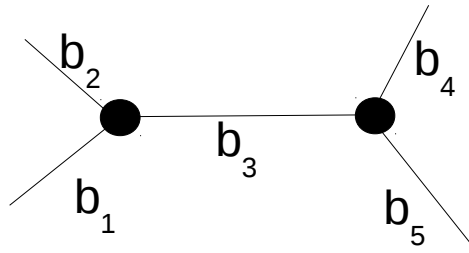
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Likelihood of site i



MSA length n



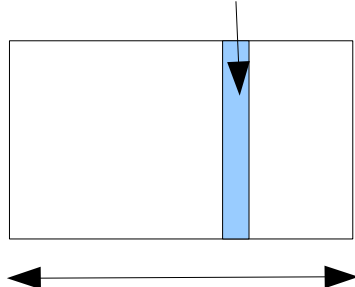
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- Equilibrium frequency vector $\pi = (\pi_A, \pi_C, \pi_G, \pi_T)$

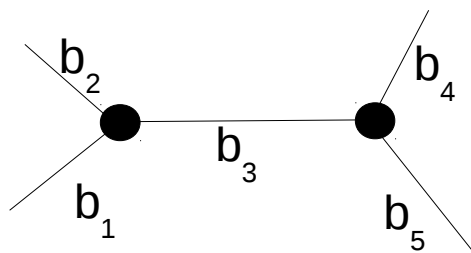
Likelihood of a Tree

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Likelihood of site i



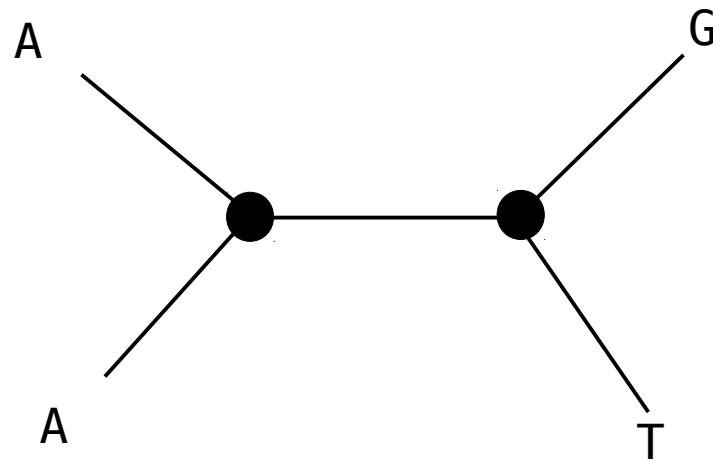
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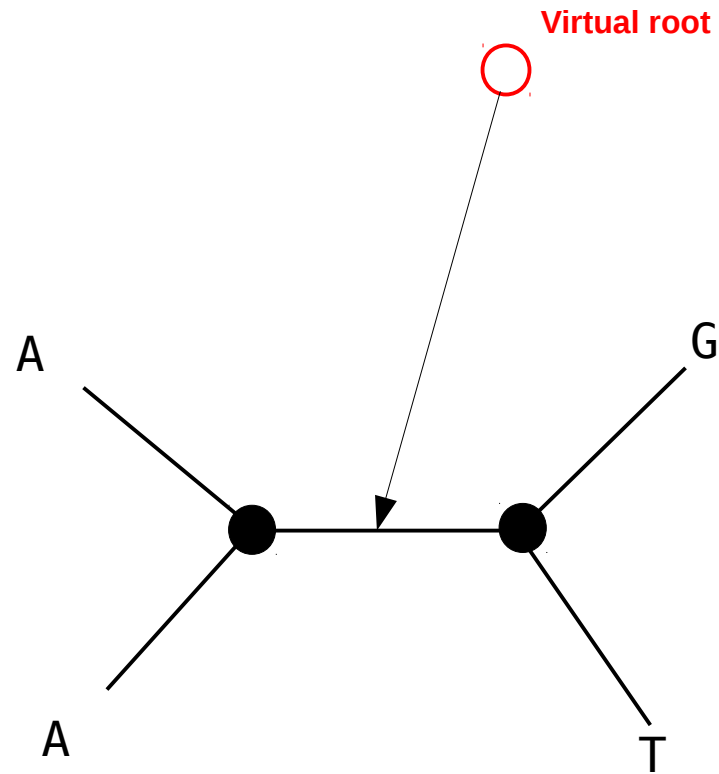
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 - We assume that $P_{ij}(t)$ is a Markov Process
- Equilibrium frequency vector $\pi = (\pi_A, \pi_C, \pi_G, \pi_T)$
- **Time reversibility:** $\pi_i P_{ij}(t) = \pi_j P_{ji}(t)$

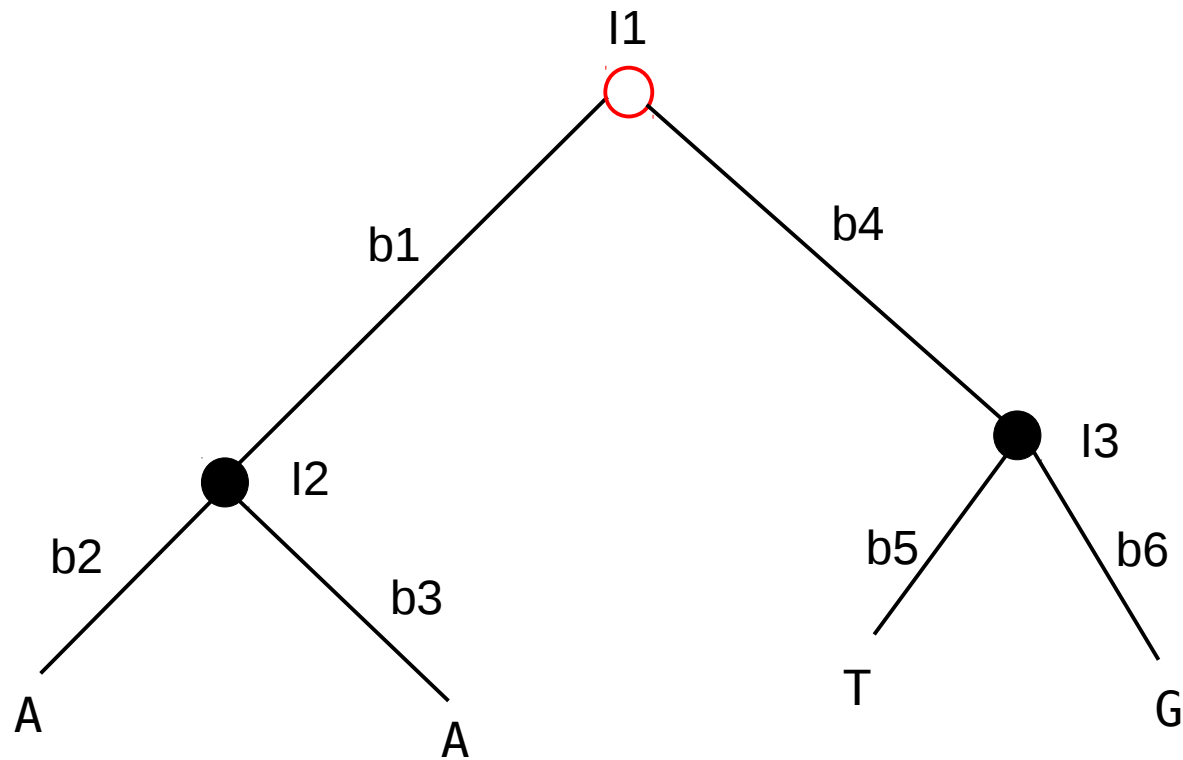
What's the likelihood of this tree?



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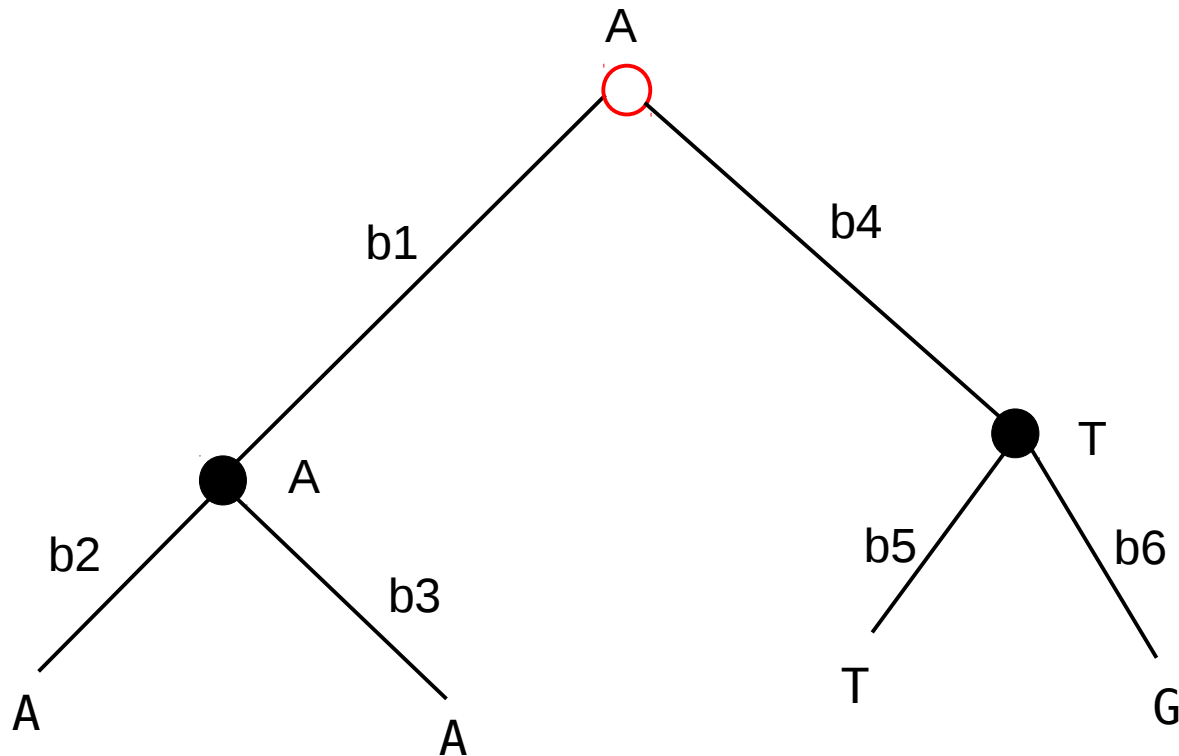


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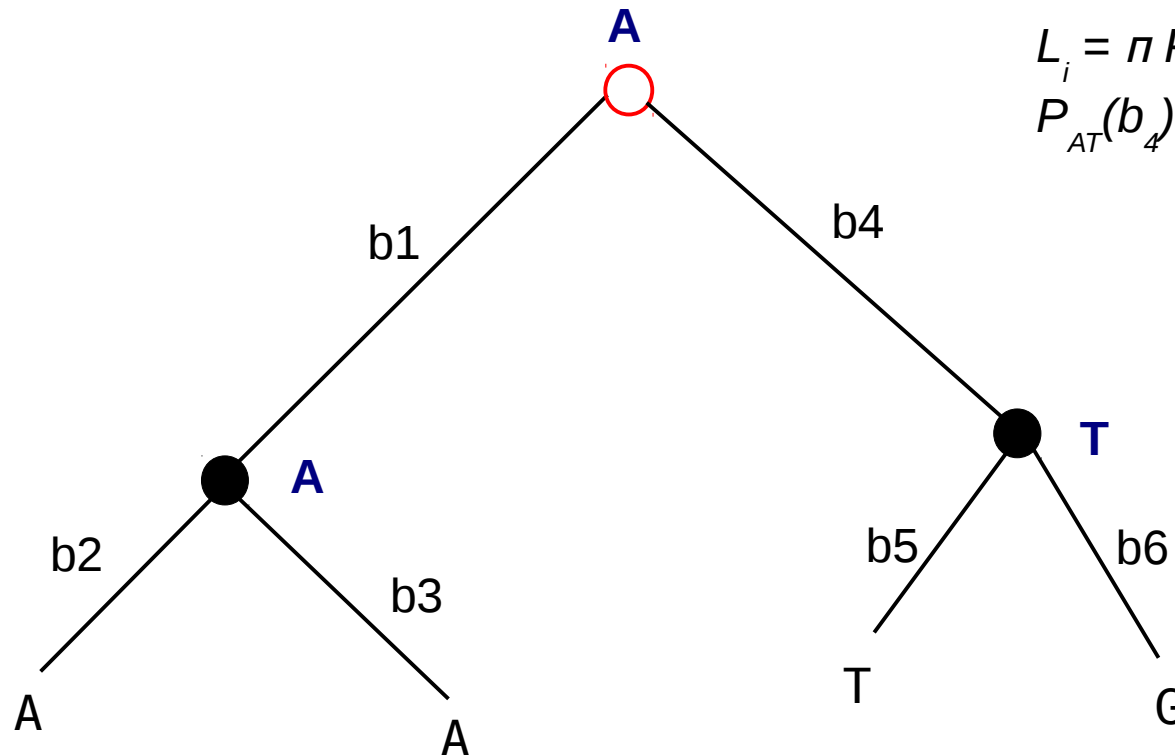
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Assume the inner states are given!
What is the likelihood of the tree if we
Interpret it as **Markov** diagram?



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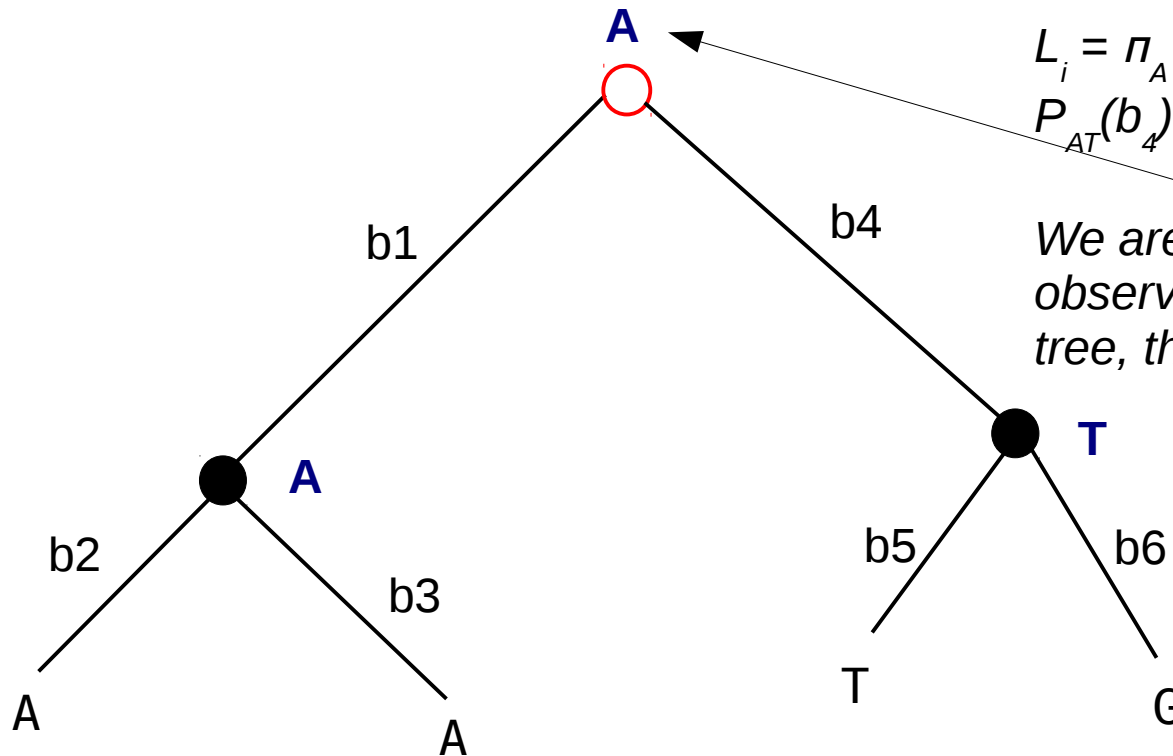
$$L_i = \pi P_{AA}(b_1) P_{AA}(b_2) P_{AA}(b_3) \\ P_{AT}(b_4) P_{TT}(b_5) P_{TG}(b_6)$$

What's the likelihood of this tree?

Assume the inner states are given!
What is the likelihood of the tree if we interpret it as **Markov** diagram?

$$L_i = \pi_A P_{AA}(b_1) P_{AA}(b_2) P_{AA}(b_3) P_{AT}(b_4) P_{TT}(b_5) P_{TG}(b_6)$$

We are multiplying here, because to observe the data at the tips, given the tree, the initial state must be **A** π_A



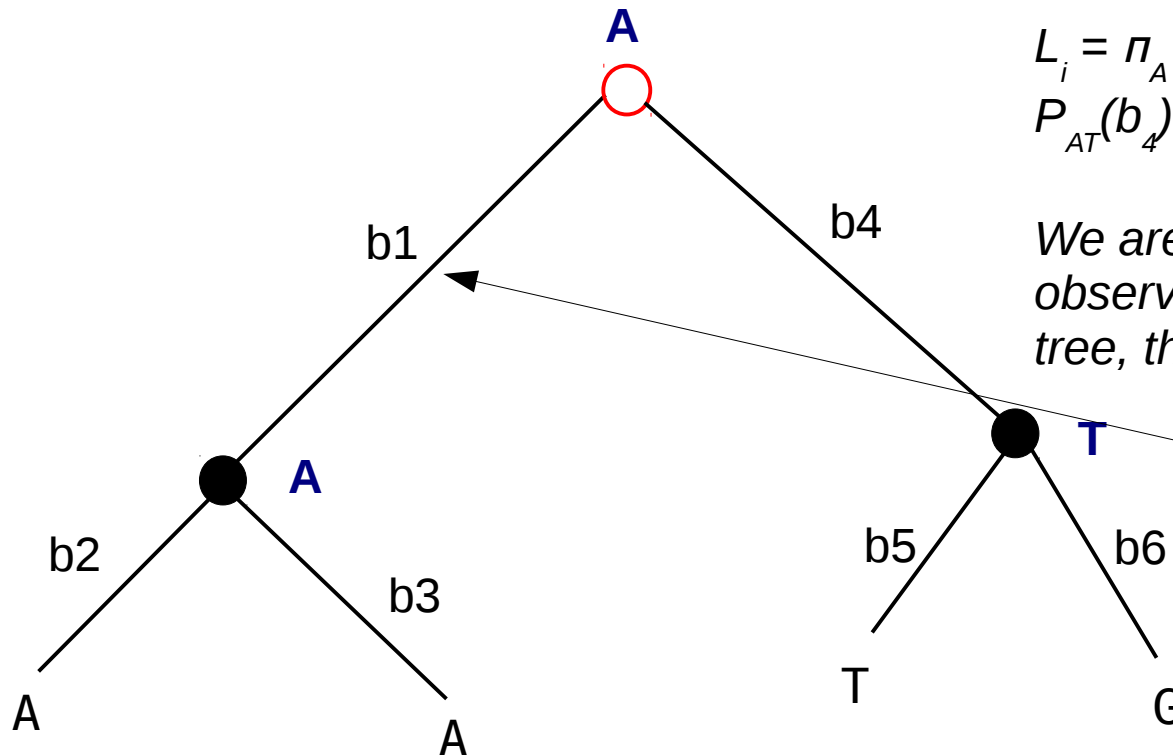
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AND then this happened



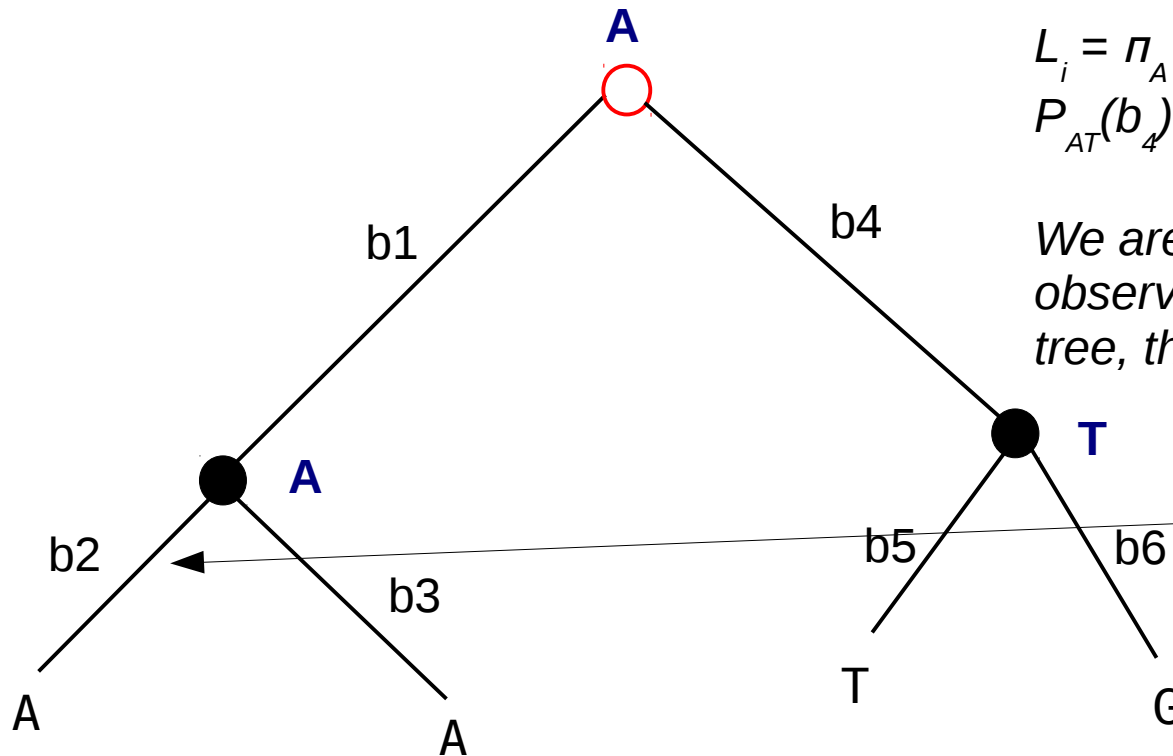
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AND this



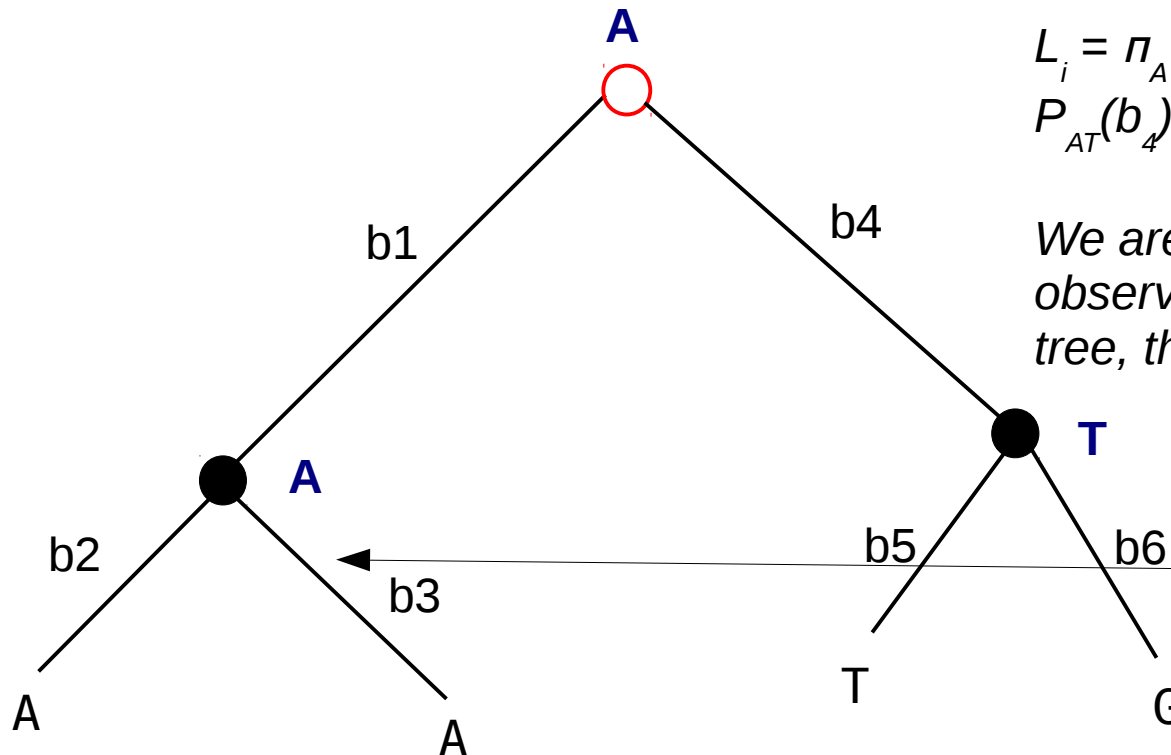
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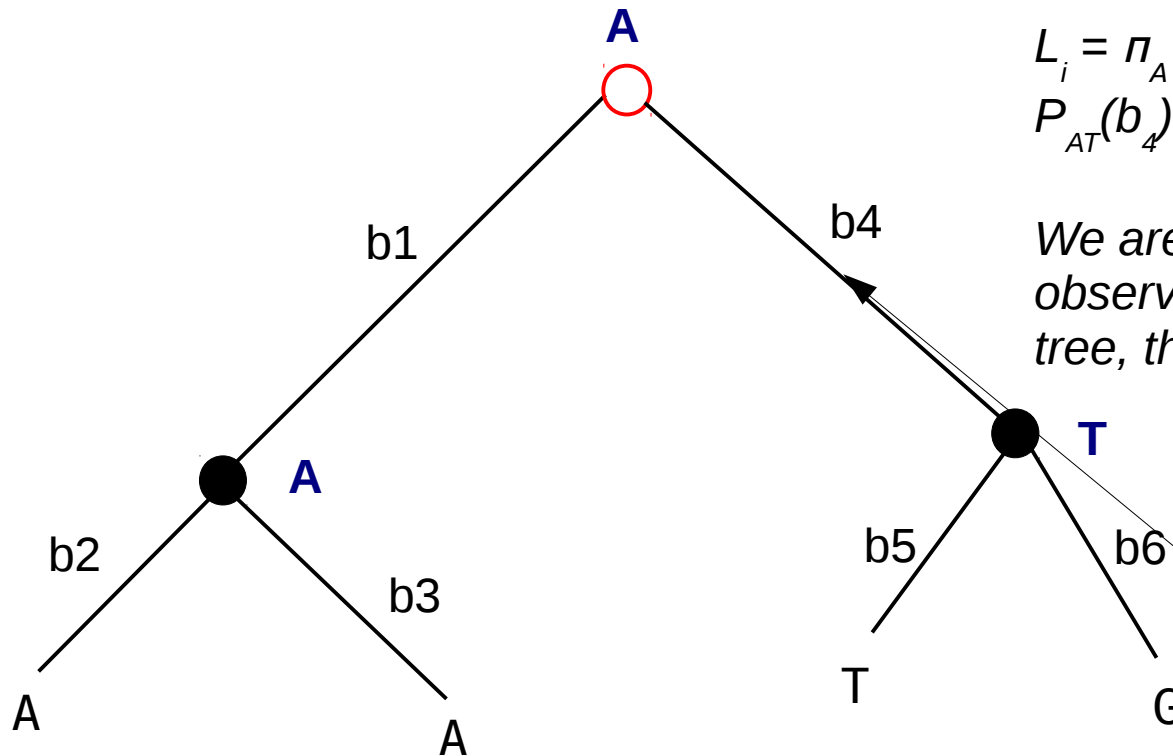
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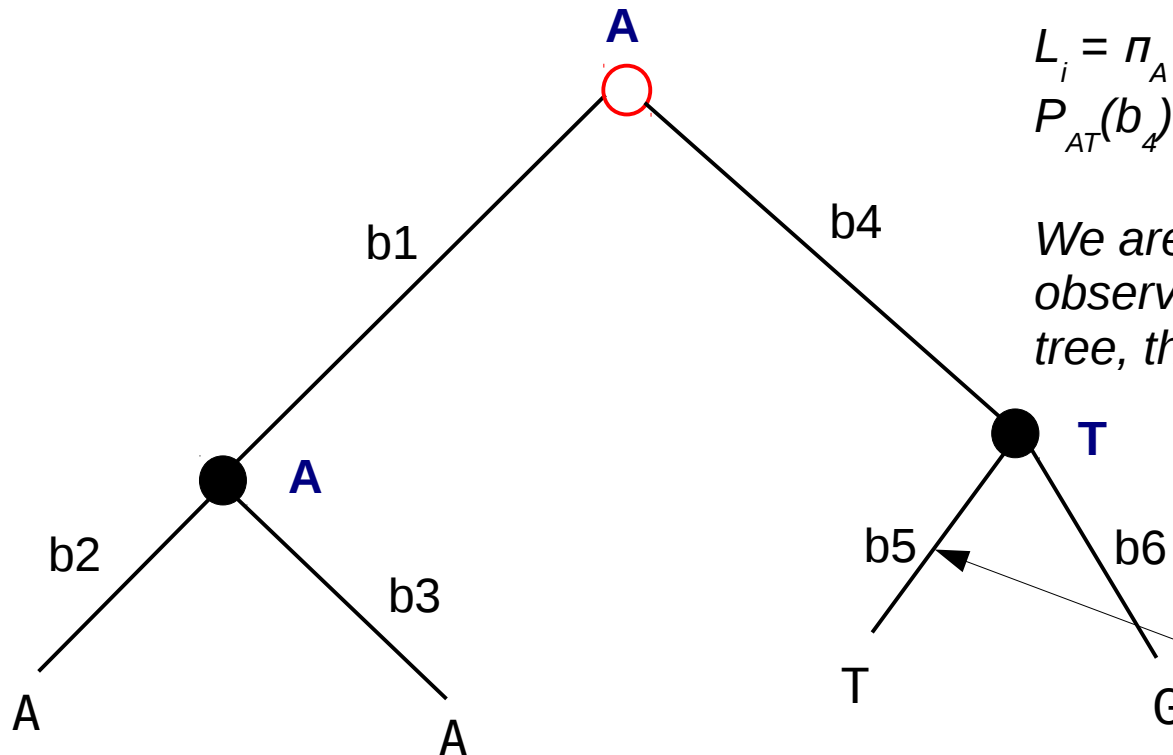
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AND this
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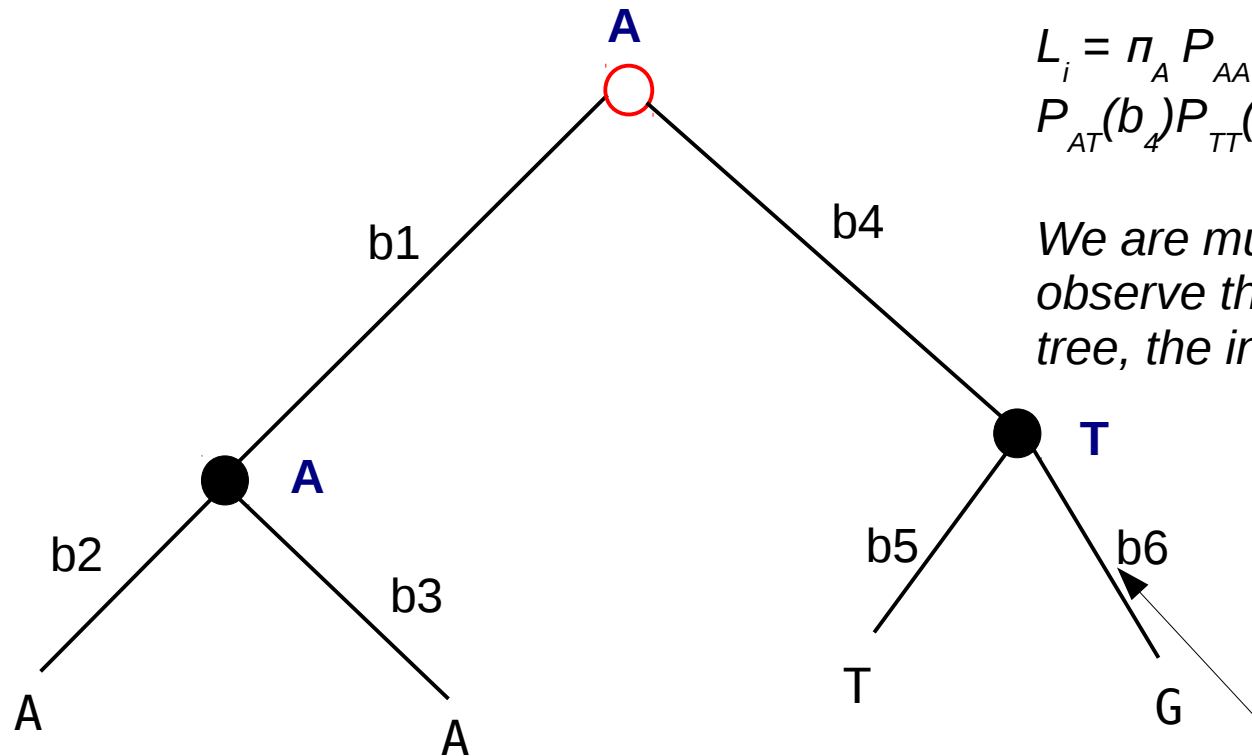


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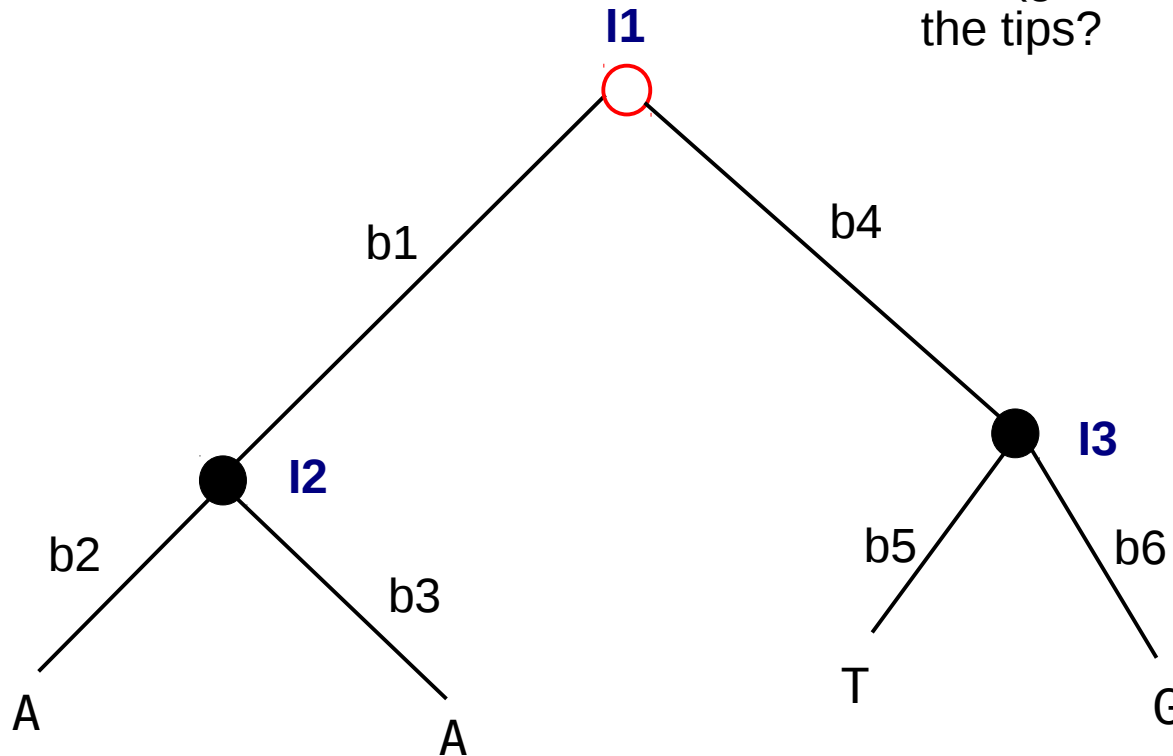
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AND then this happened
AND this
AND this
AND this
AND this
AND this

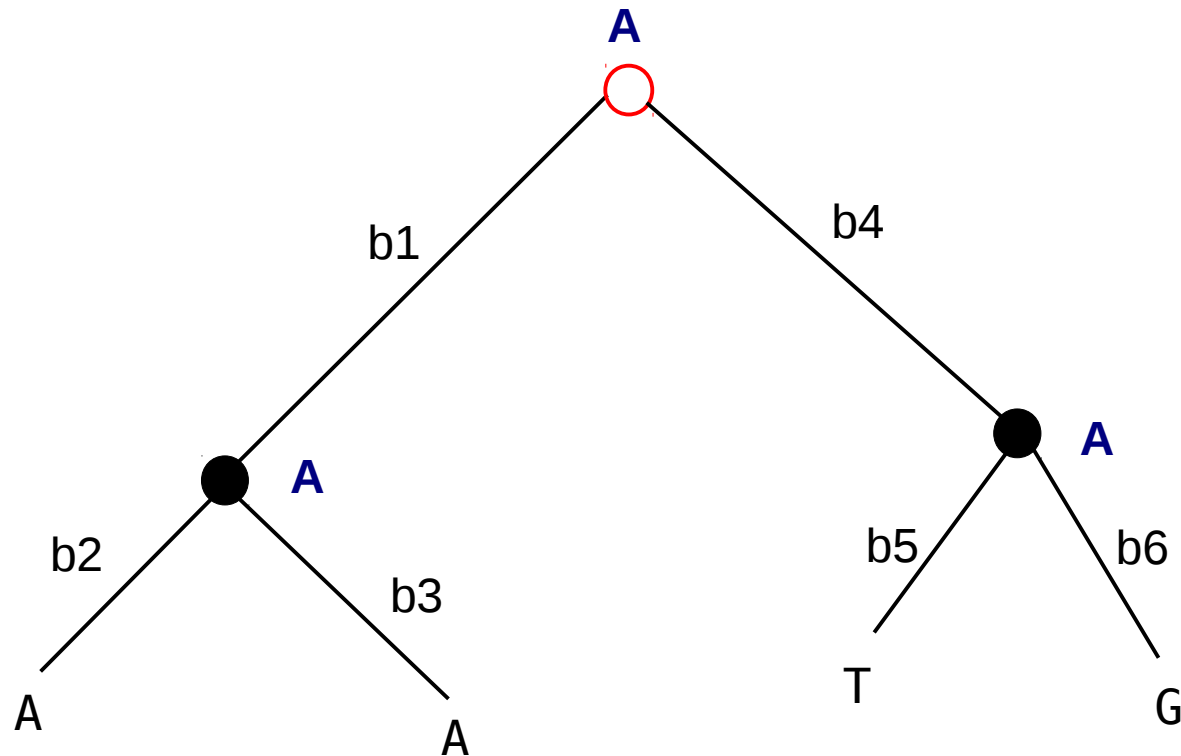
What's the likelihood of this tree?

However, we don't know the inner states :-(
So the question is: What are the possible evolutionary histories that could have given rise (generated) to the data we observe at the tips?



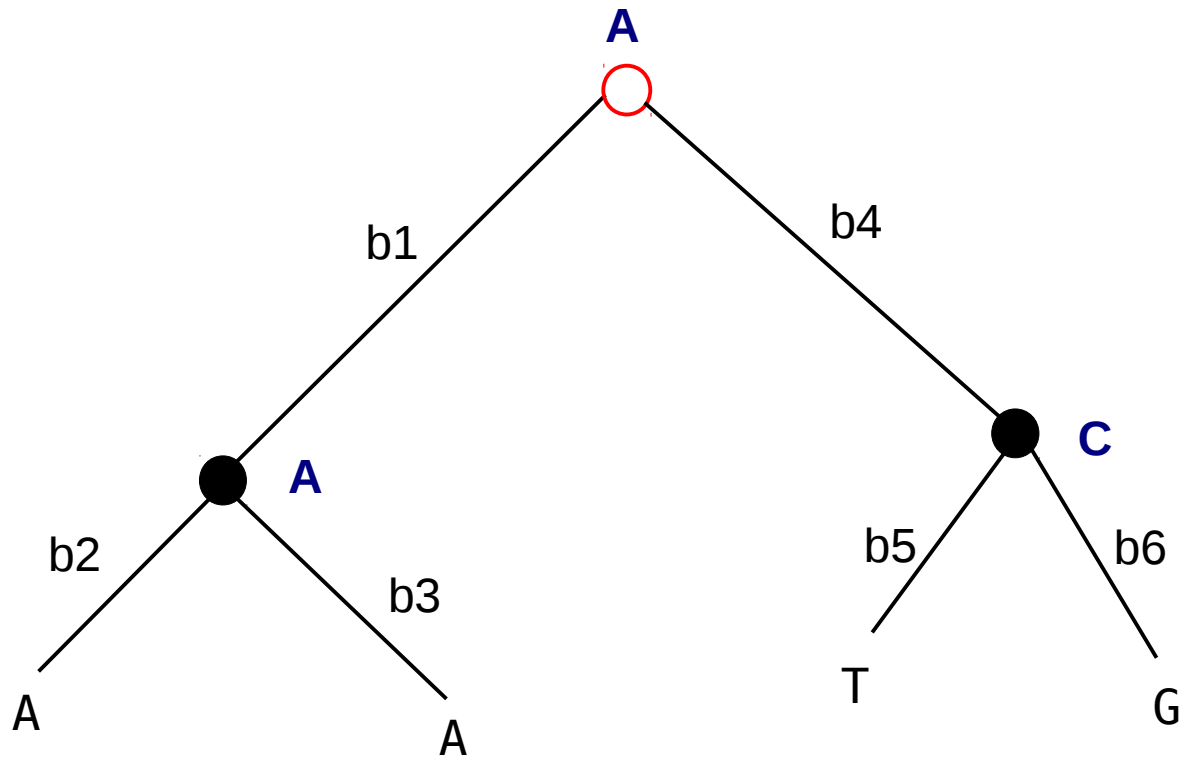
What's the likelihood of this tree?

It could be this



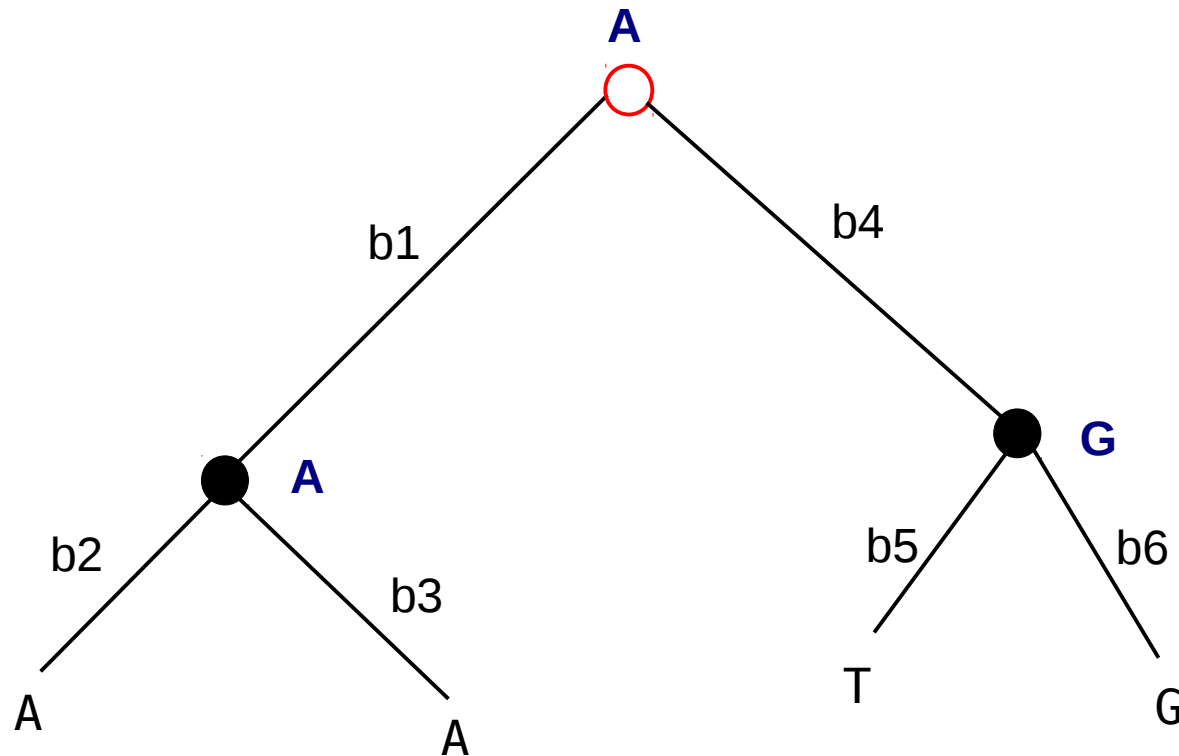
What's the likelihood of this tree?

It could be this
OR this



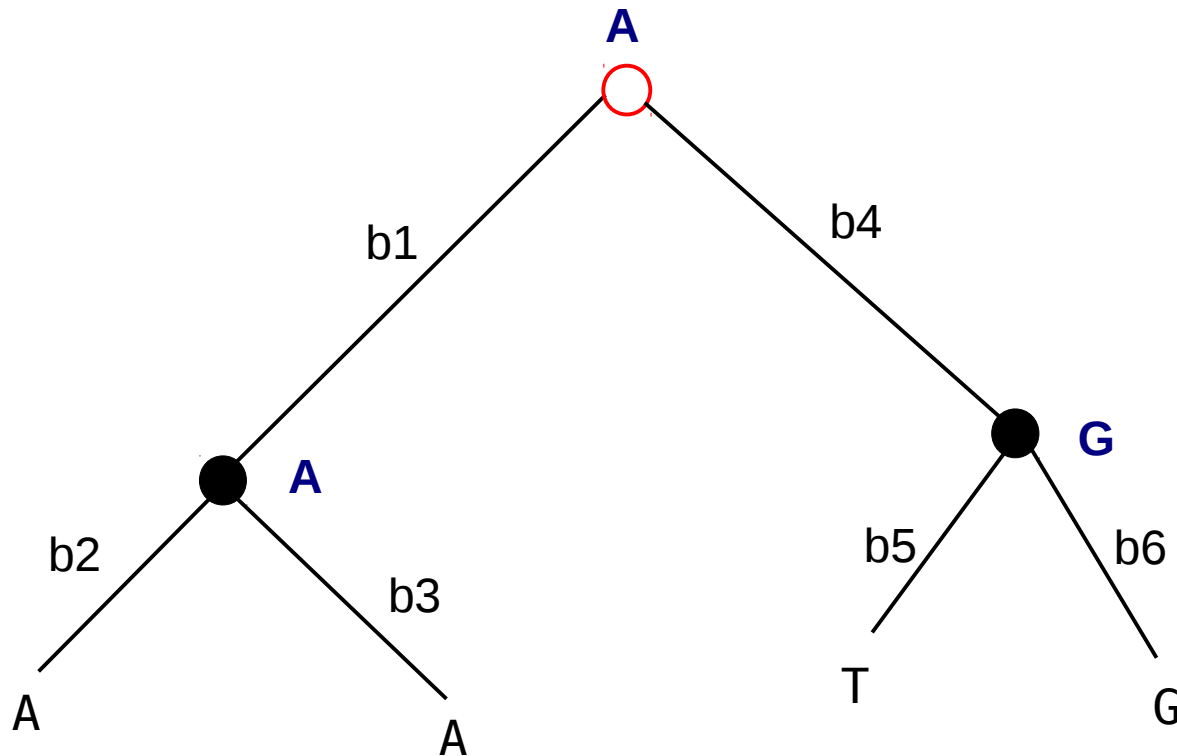
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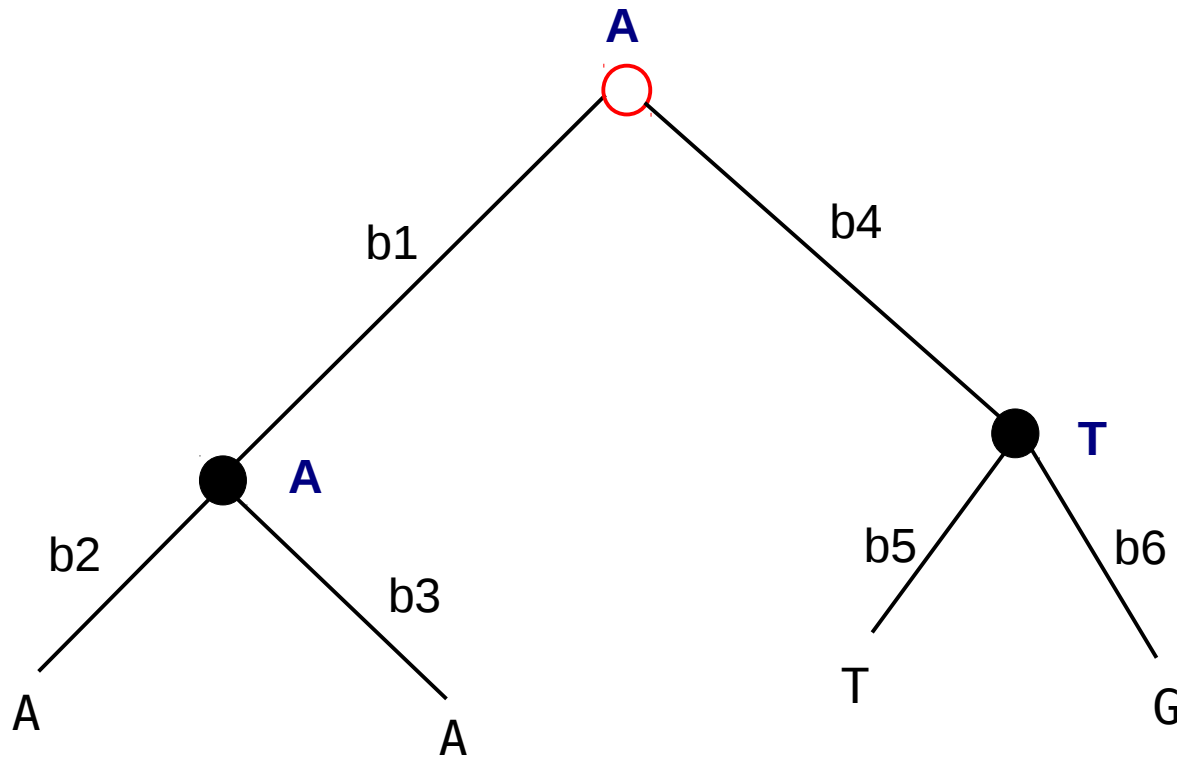
What's the likelihood of this tree?

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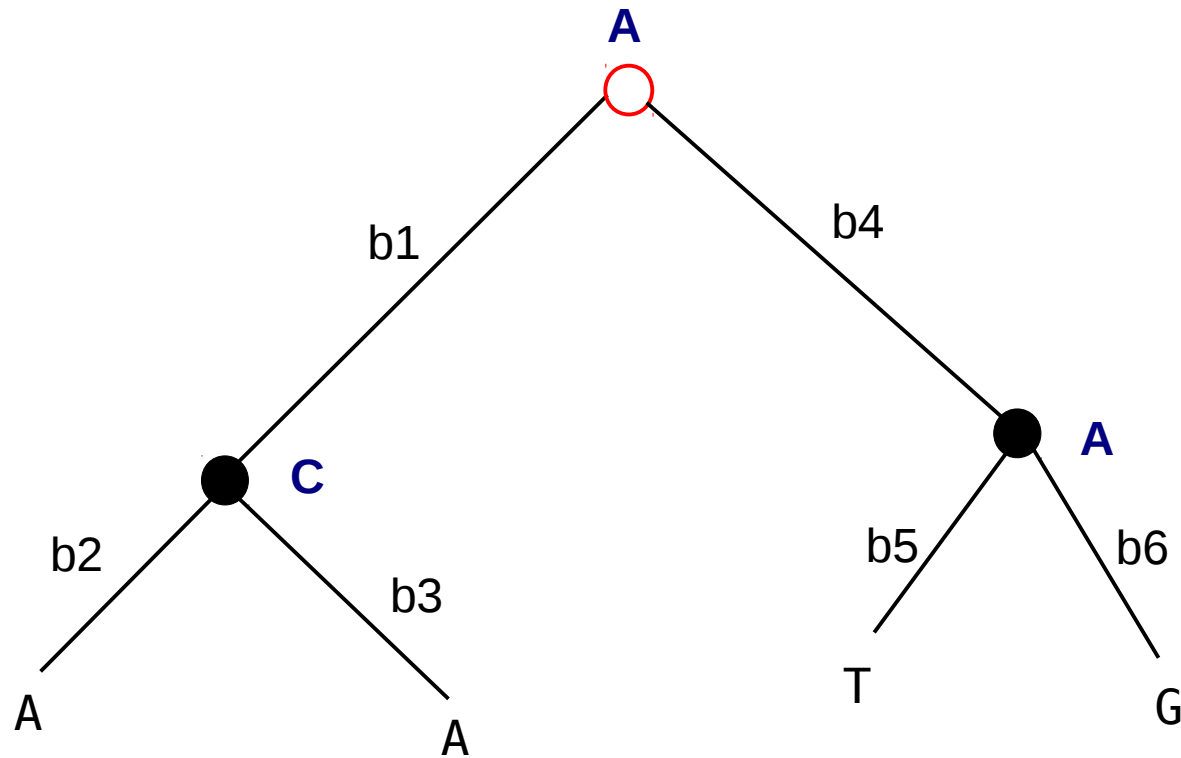


What's the likelihood of this tree?

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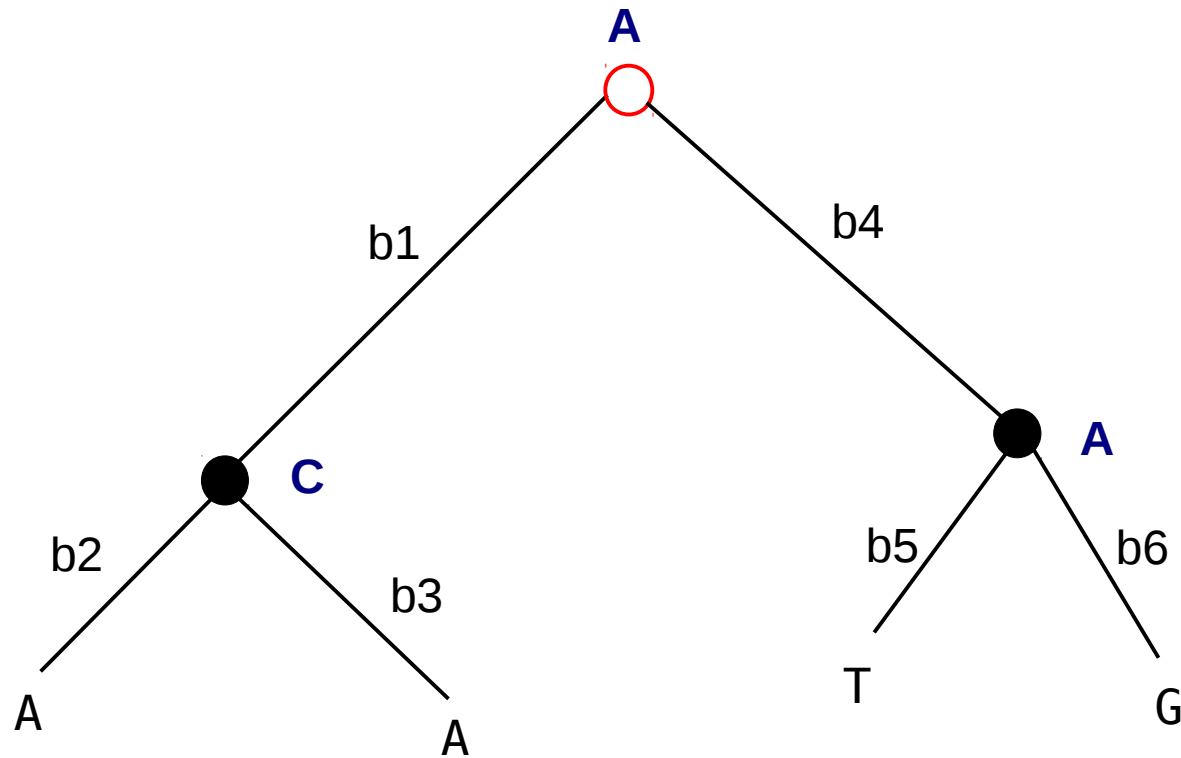


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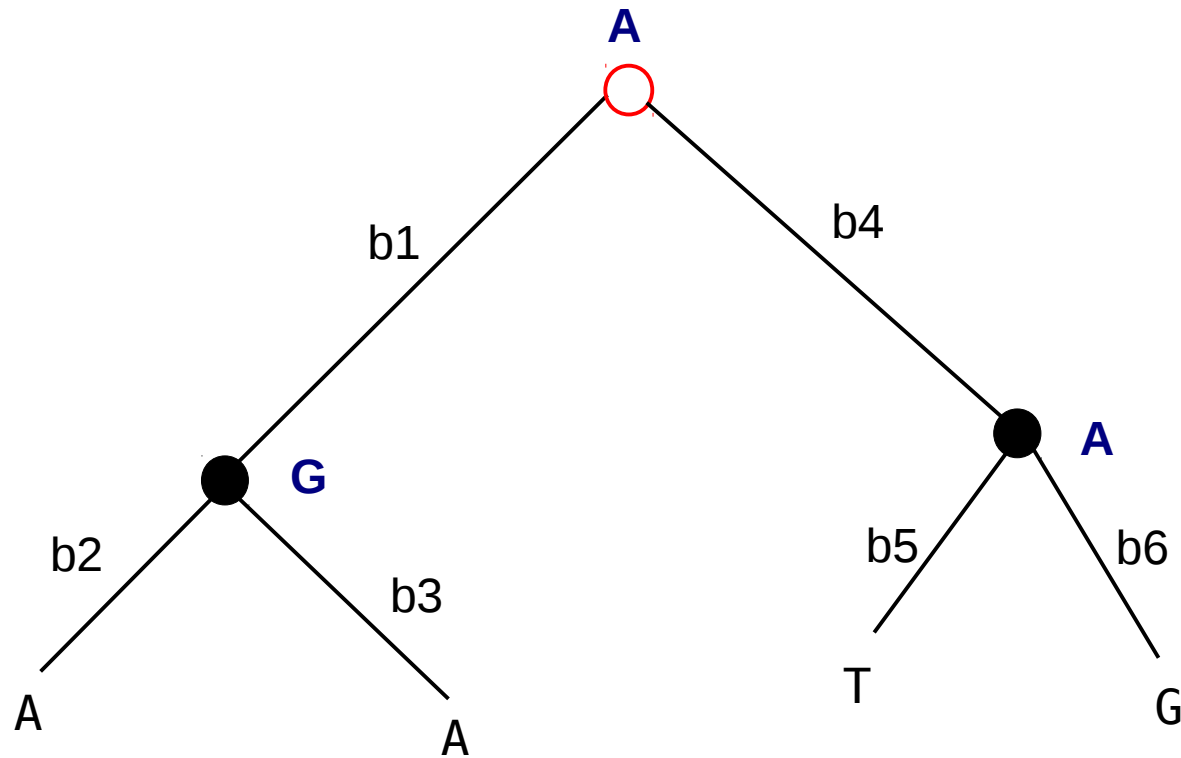
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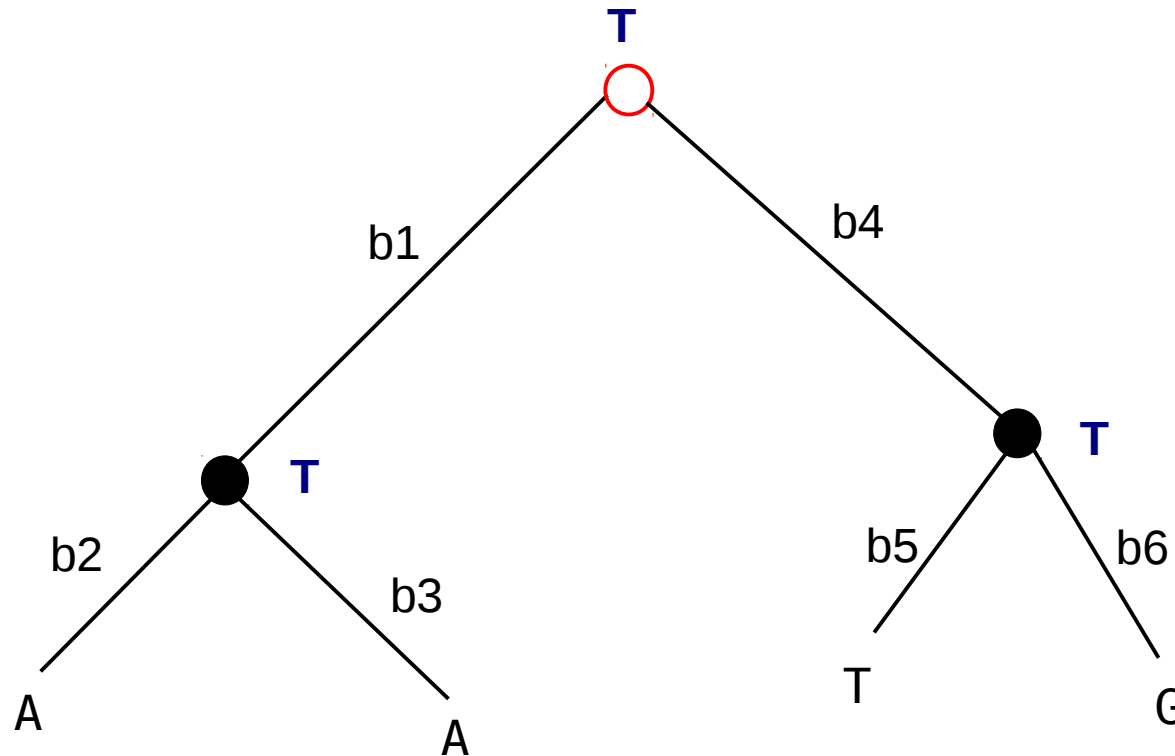
It could be this
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What's the likelihood of this tree?



It could be this
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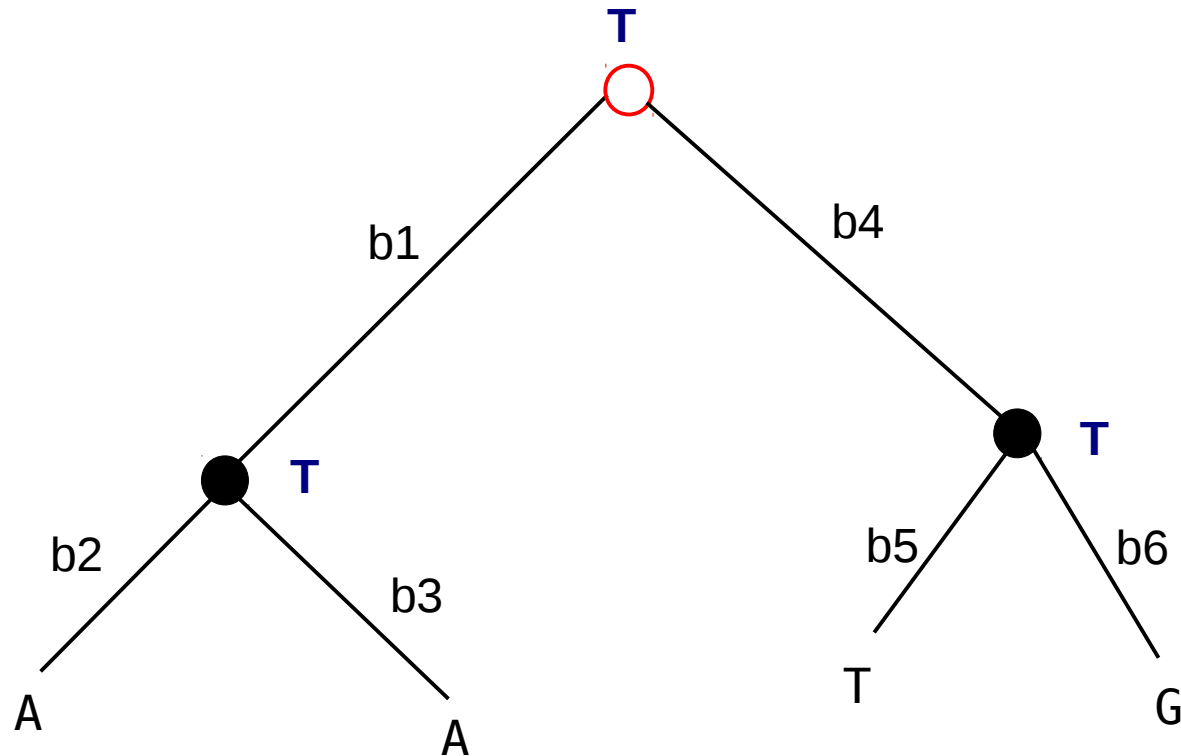
What's the likelihood of this tree?



It could be this
OR this
OR this
OR this
OR this
OR this
OR this
...
OR this

What's the likelihood of this tree?

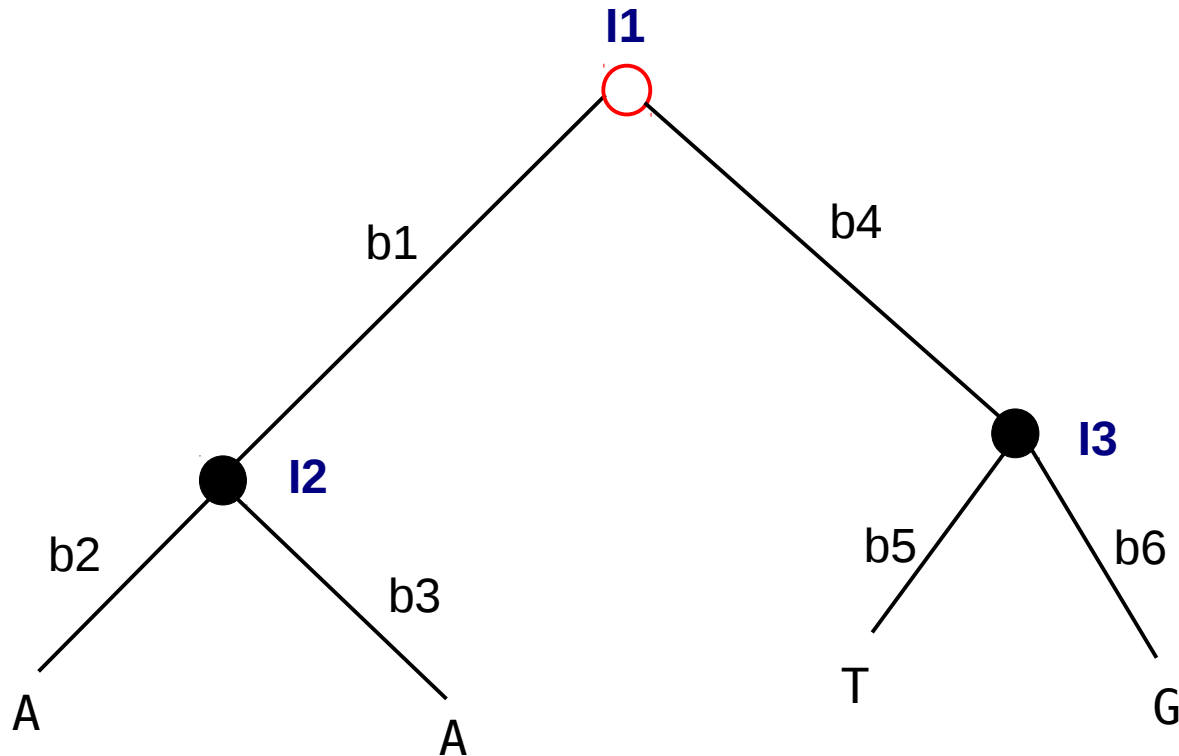
So the likelihood of the tree is the sum (**OR!**) over the likelihoods of all possible assignments of A, C, G, and T (all possible evolutionary histories) to the inner nodes *I1*, *I2*, *I3* of the tree.



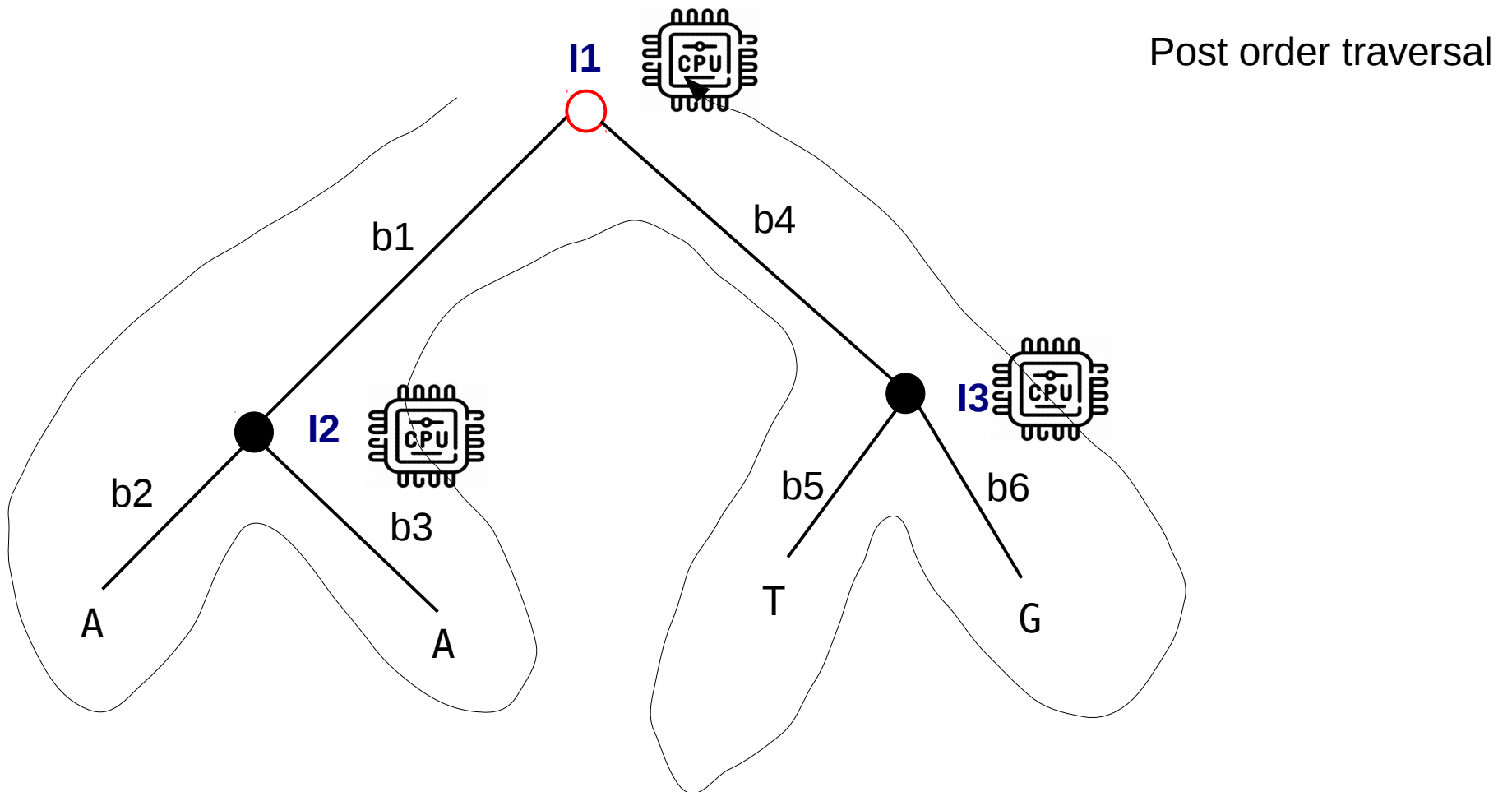
What's the likelihood of this tree?

So the likelihood of the tree is the sum (**OR!**) over the likelihoods of all possible assignments of A, C, G, and T (all possible evolutionary histories) to the inner nodes *I1*, *I2*, *I3* of the tree.

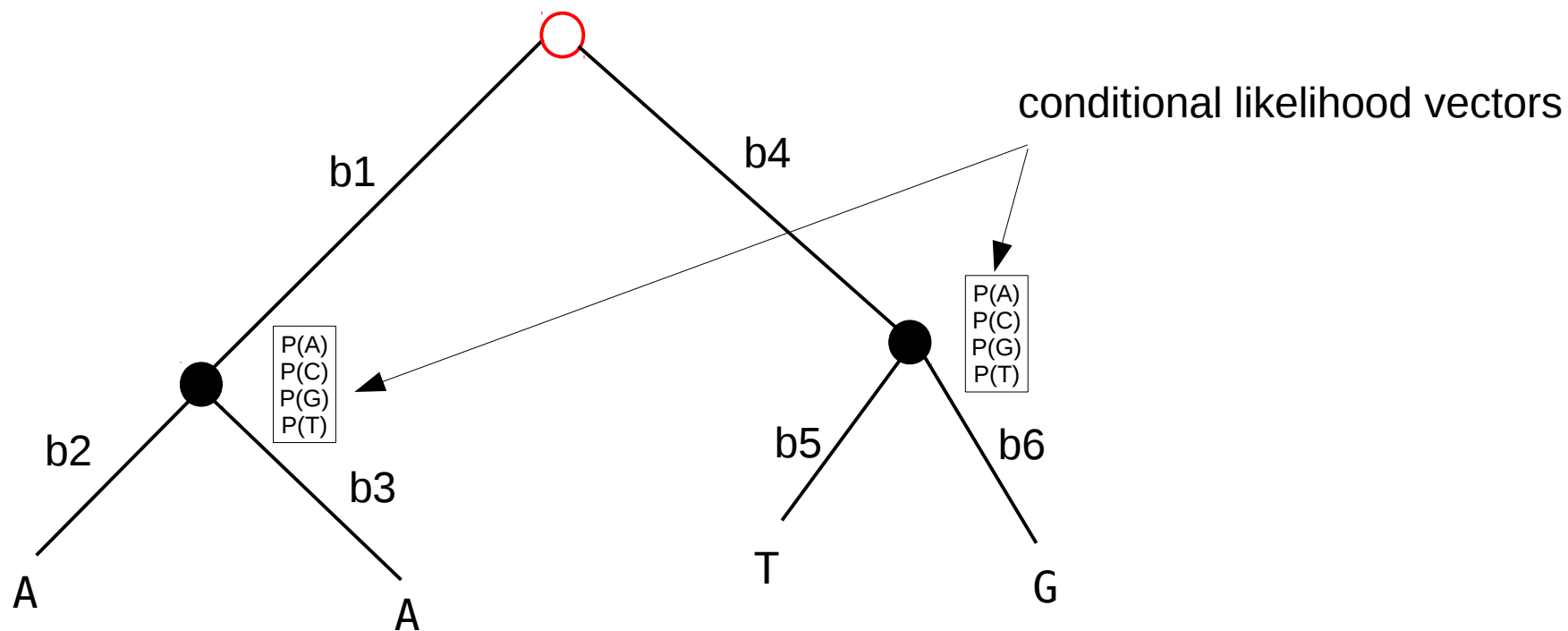
There are $4 \times 4 \times 4$ possible assignments in our example
→ this sounds very compute-intensive :-)



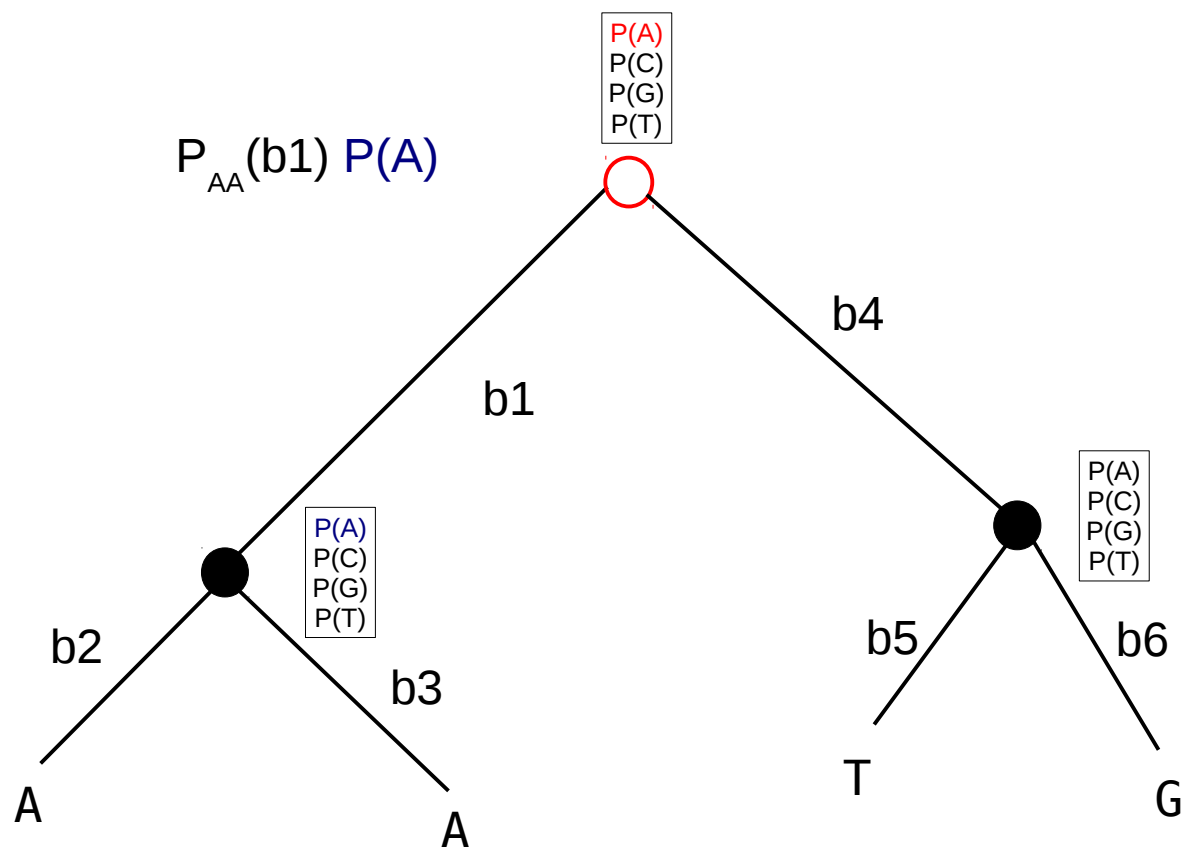
The Felsenstein Pruning Algorithm



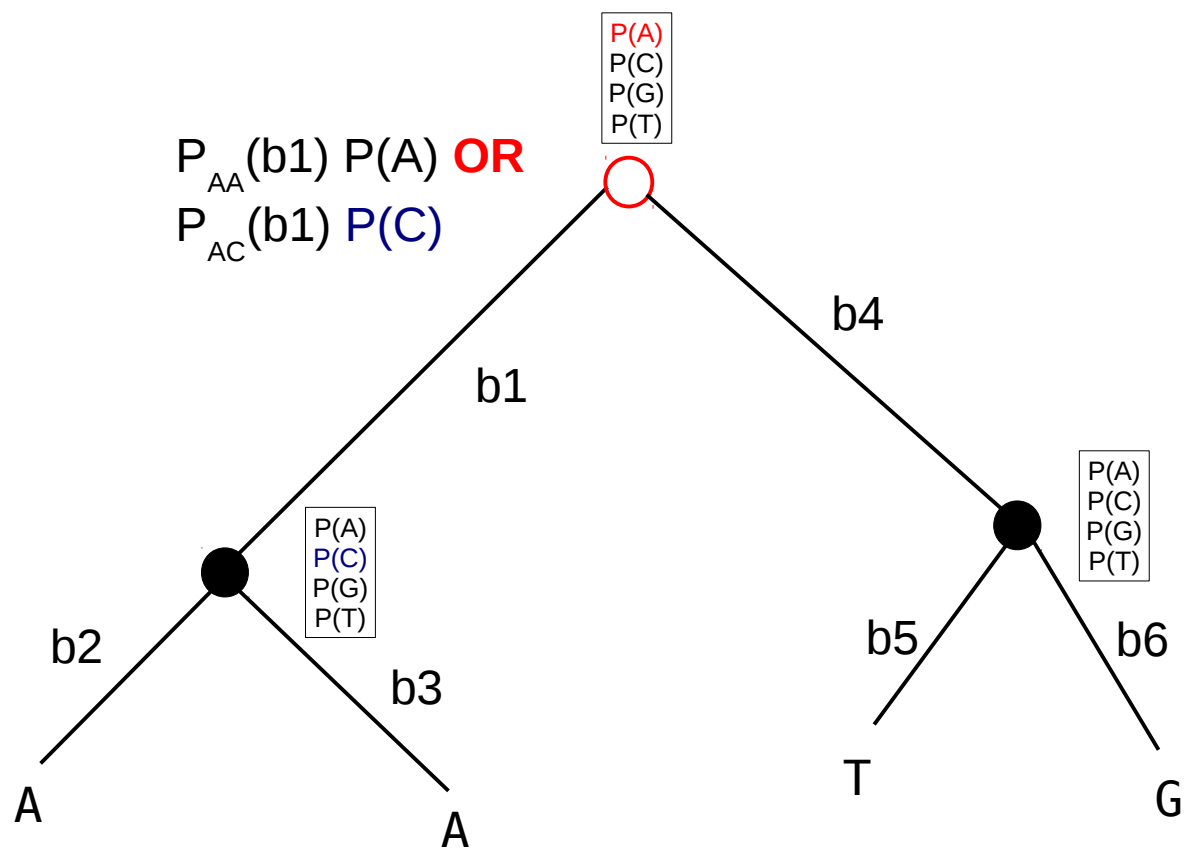
Felsenstein Pruning



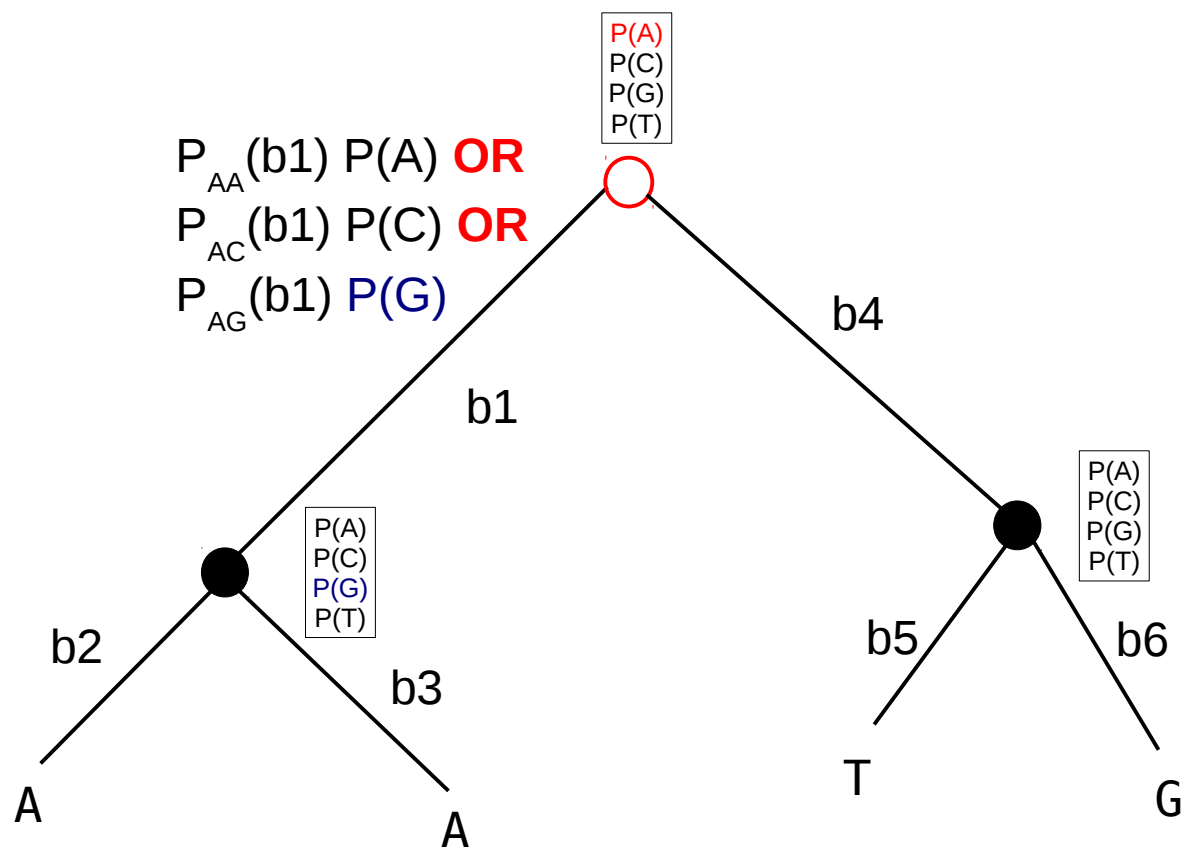
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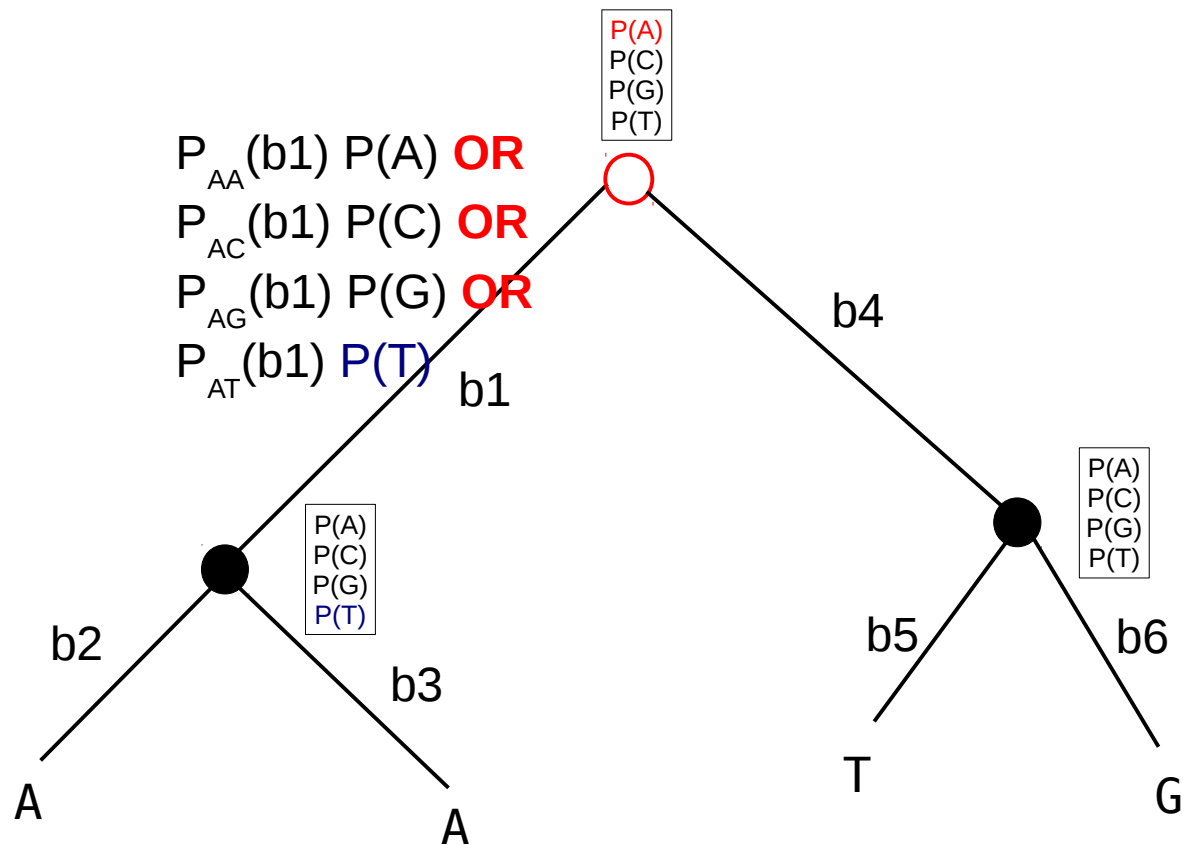
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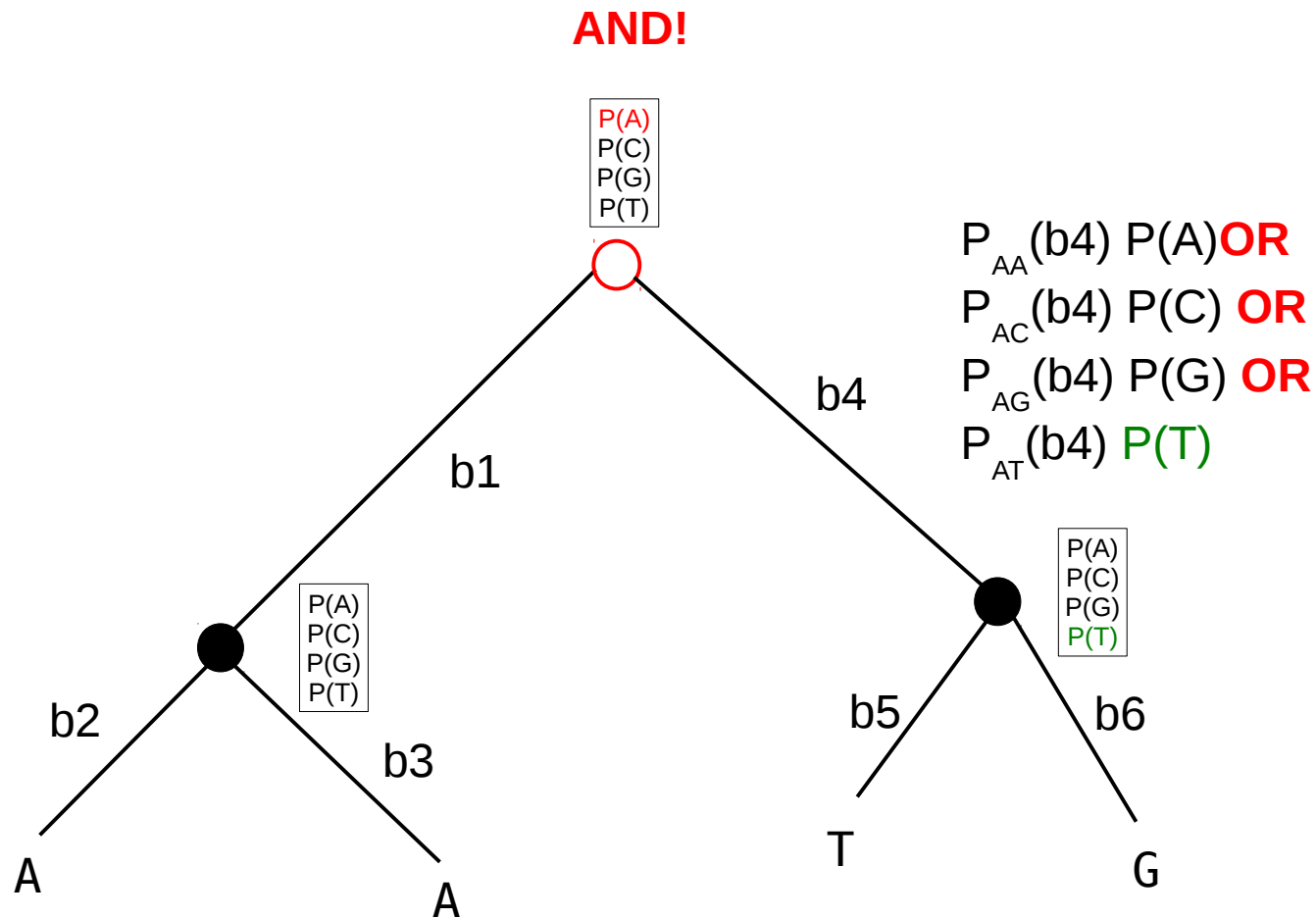
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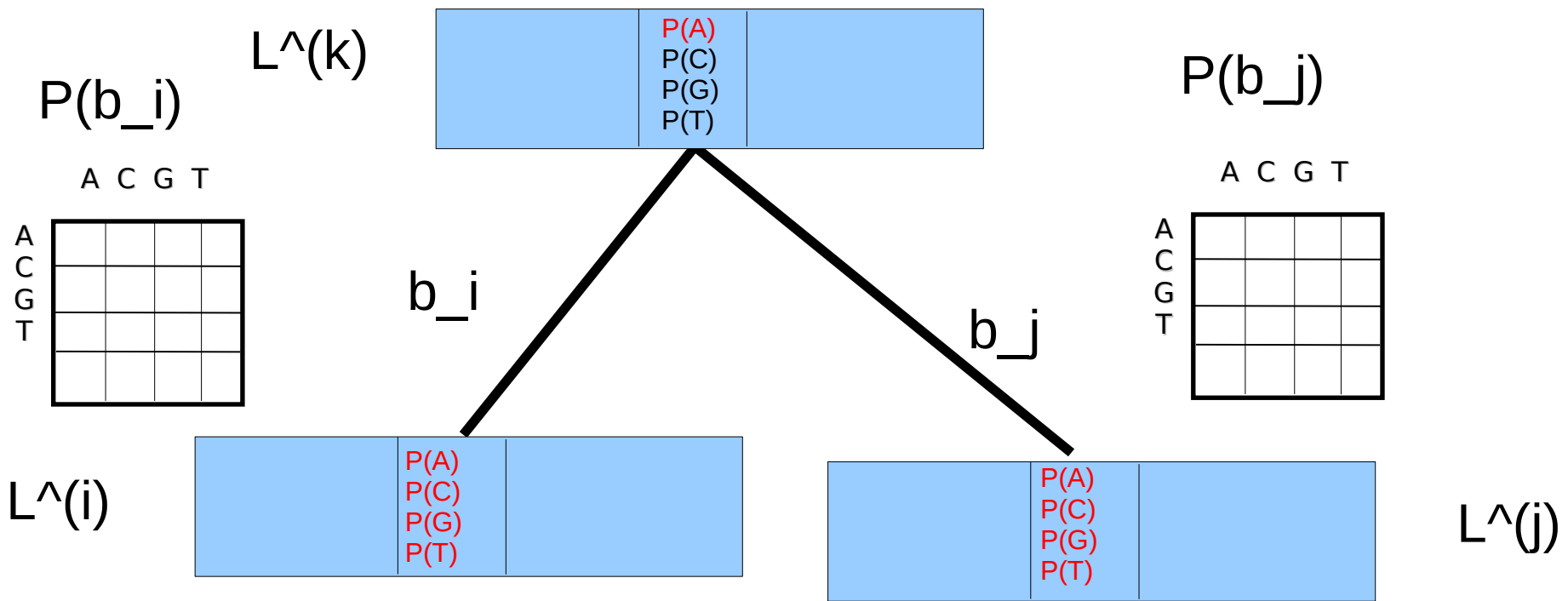
Felsenstein Pruning



Felsenstein Pruning

AND (left branch/right branch)

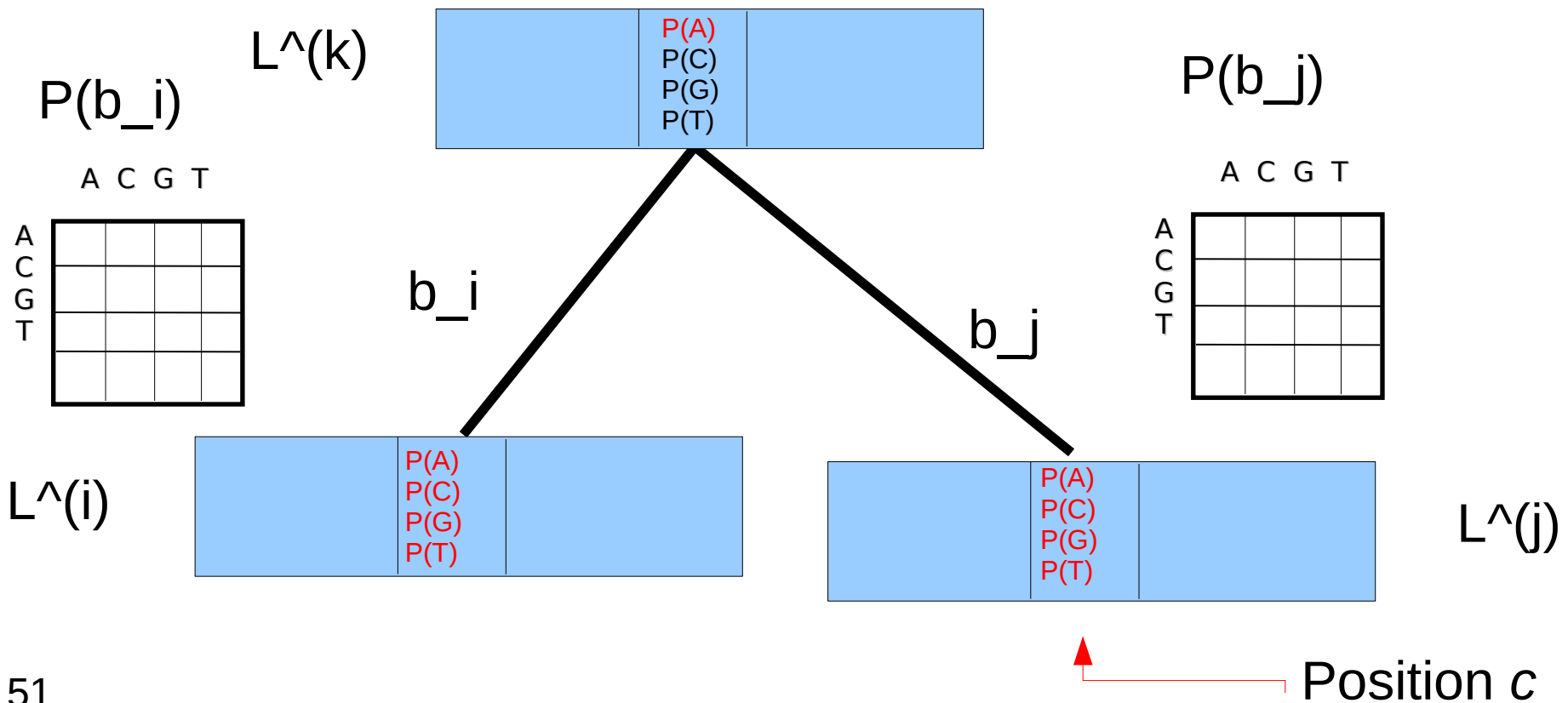
$$\vec{L}_A^{(k)}(c) = \left(\sum_{S=A}^T P_{AS}(b_i) \vec{L}_S^{(i)}(c) \right) \left(\sum_{S=A}^T P_{AS}(b_j) \vec{L}_S^{(j)}(c) \right)$$



Felsenstein Pruning

OR (along left branch)

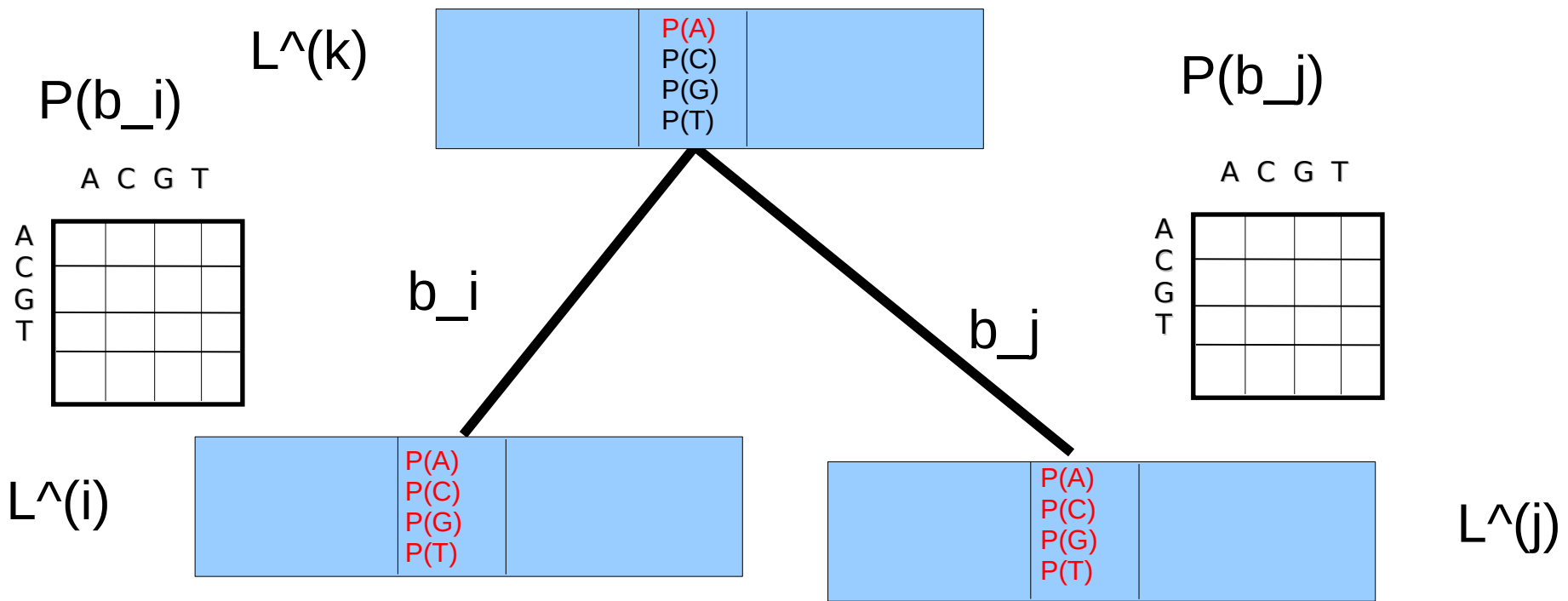
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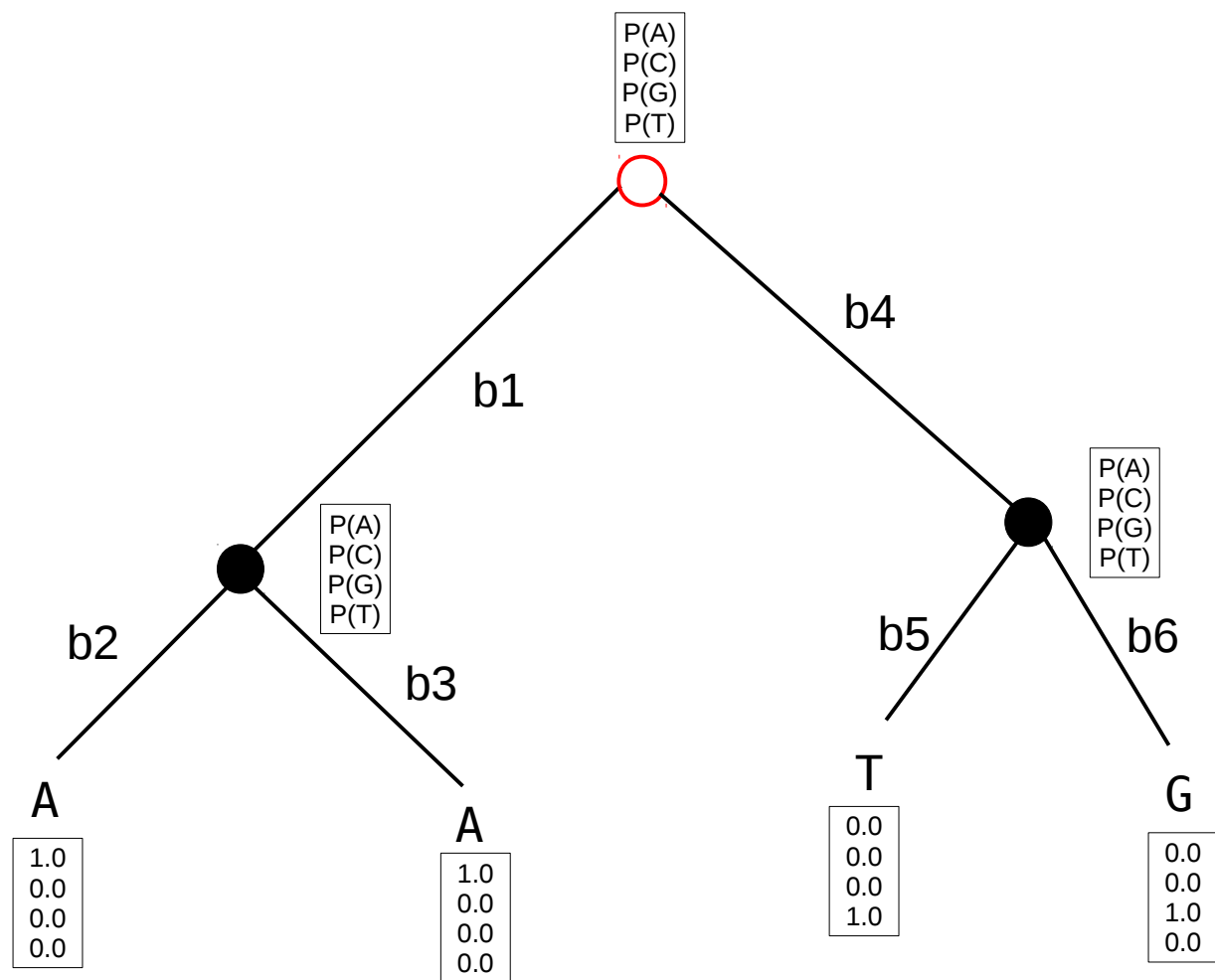
Felsenstein Pruning

OR (along right branch)

$$\vec{L}_A^{(k)}(c) = \left(\sum_{S=A}^T P_{AS}(b_i) \vec{L}_S^{(i)}(c) \right) \left(\sum_{S=A}^T P_{AS}(b_j) \vec{L}_S^{(j)}(c) \right)$$

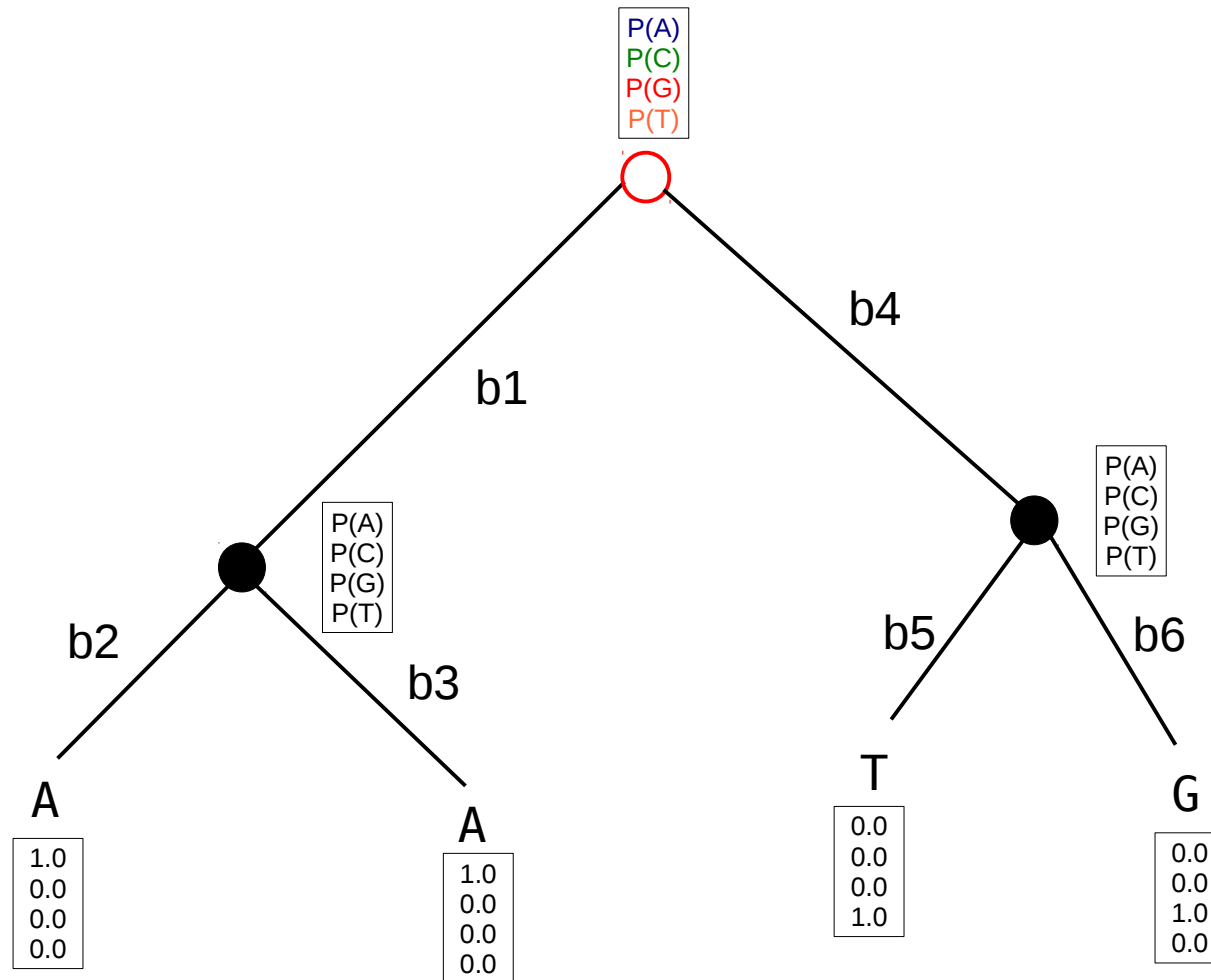


Felsenstein Pruning



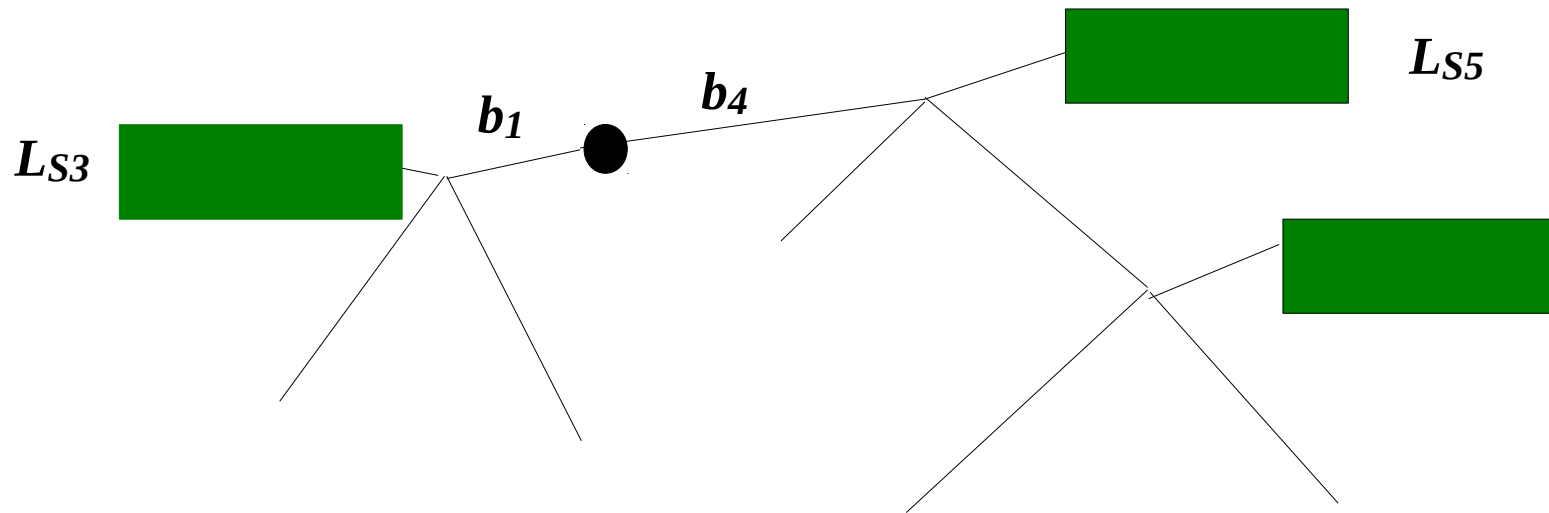
Felsenstein Pruning

Likelihood at the root: $L_i = \pi_A P(A) + \pi_C P(C) + \pi_G P(G) + \pi_T P(T)$



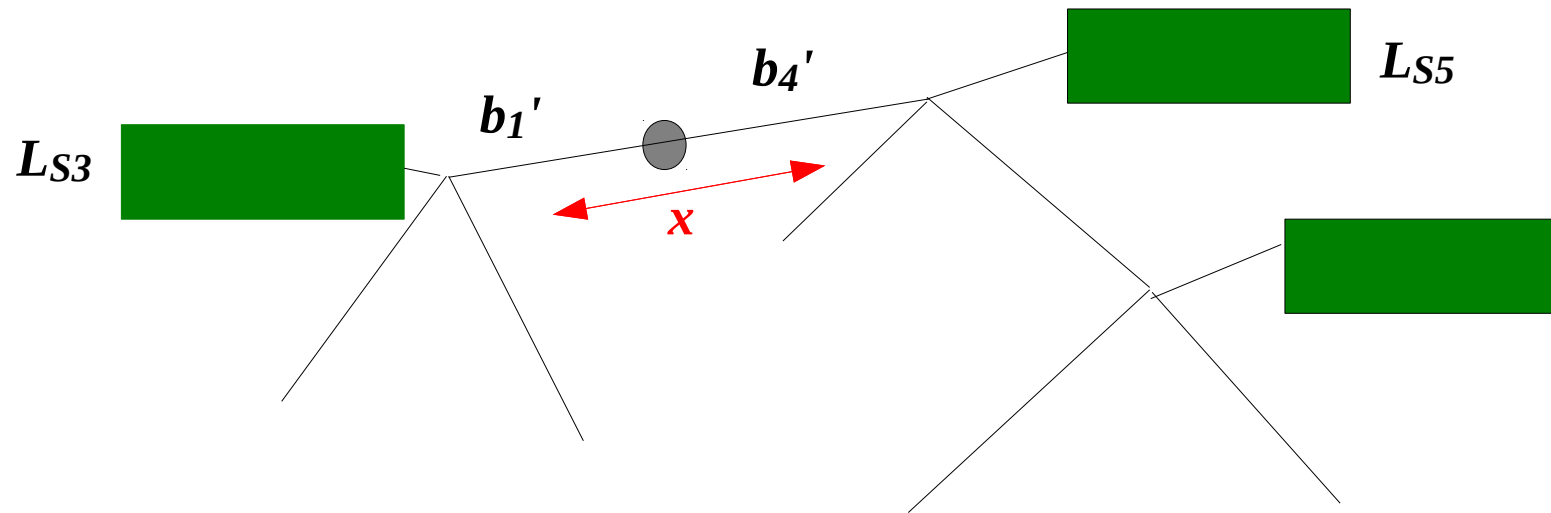
Why is time-reversibility important?

$$L = \sum_{S_4=A}^T \pi_{S_4} \sum_{S_3=A}^T P_{S_4 S_3}(b_1) L_{S_3}^{(3)} \sum_{S_5=A}^T P_{S_4 S_5}(b_4) L_{S_5}^{(5)}$$



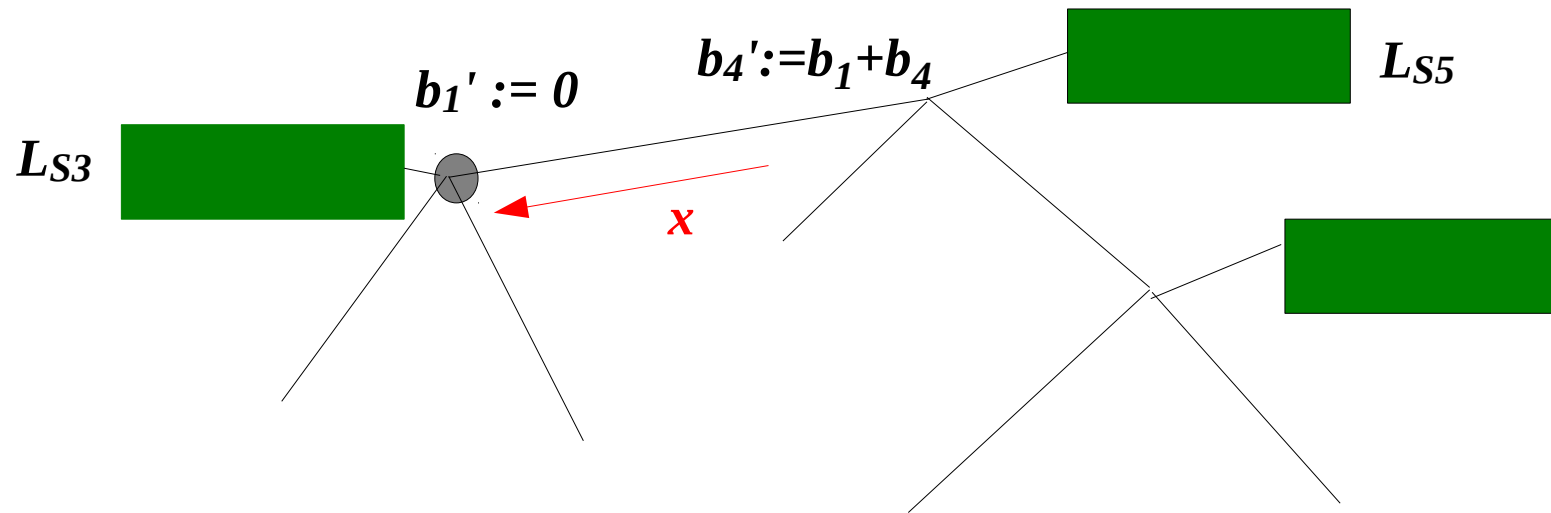
Why is time-reversibility important?

$$L = L' = \sum_{S_4=A}^T \pi_{S_4} \sum_{S_3=A}^T P_{S_4 S_3} (b_1 + x) L_{S_3}^{(3)} \sum_{S_5=A}^T P_{S_4 S_5} (b_4 - x) L_{S_5}^{(5)}$$



Why is time-reversibility important?

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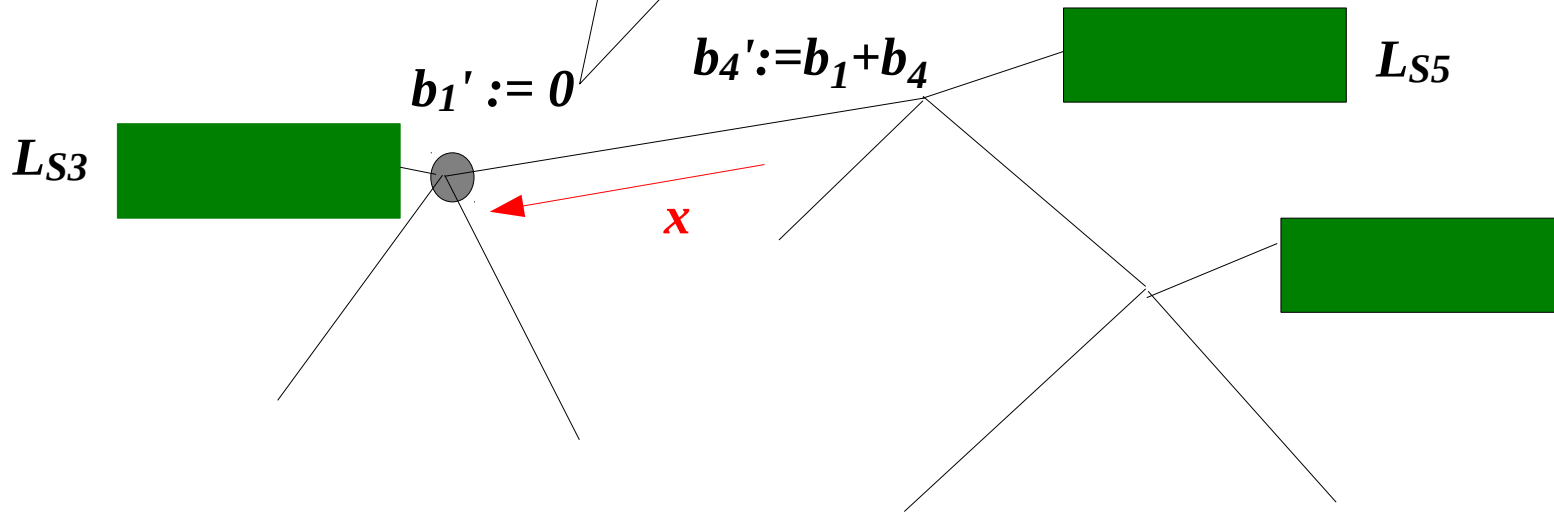


Why is time-reversibility important?

This observation can be applied recursively to the tree
 →
 It does not matter at all where we place the root!

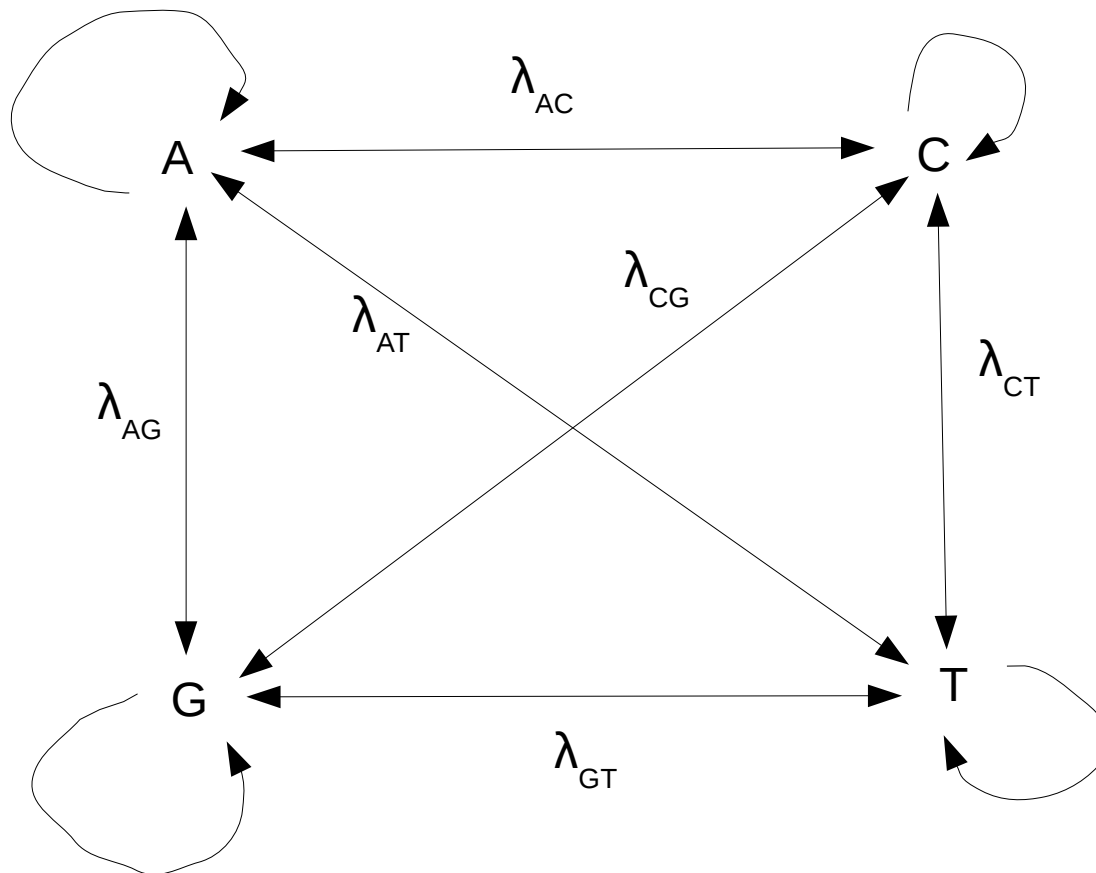
$$L = L' = \sum_{S_4=A}^T$$

$$\sum_{S_5=A}^T P_{S_4 S_5} (b_4 - x) L_{S_5}^{(5)}$$



What's in the black box $P_{ij}(t)$?

Instantaneous rate matrix R !

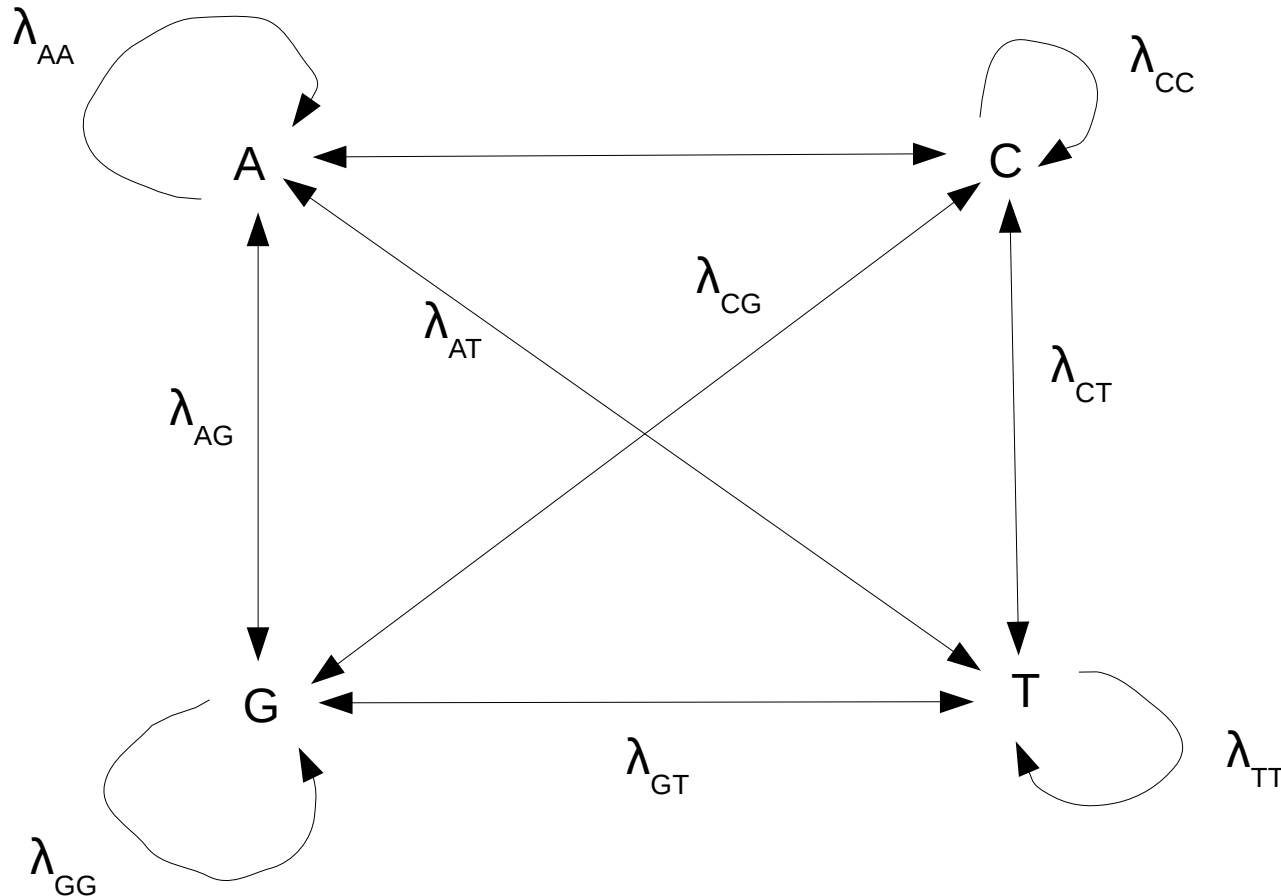


What's in the black box $P_{ij}(t)$?

What about the probabilities of staying in the current state?

→ they are given by the properties of continuous Markov chains!

e.g., $\lambda_{AA} = -(\lambda_{AC} + \lambda_{AG} + \lambda_{AT})$ rows in the R matrix need to sum to **0**



What's in the black box $P_{ij}(t)$?

$$\begin{array}{c} \text{A} \\ \text{C} \\ \text{G} \\ \text{T} \end{array} \left(\begin{array}{cccc} \text{A} & \text{C} & \text{G} & \text{T} \\ * & \lambda_{AC} & \lambda_{AG} & \lambda_{AT} \\ & * & \lambda_{CG} & \lambda_{CT} \\ & & * & \lambda_{GT} \\ & \text{Symmetric} & & * \end{array} \right)$$

What's in the black box $P_{ij}(t)$?

Diagonal values are given by the off-diagonal values (R matrix property)

$$\lambda_{AA} = -(\lambda_{AC} + \lambda_{AG} + \lambda_{AT})$$

	A	C	G	T
A	*	λ_{AC}	λ_{AG}	λ_{AT}
C		*	λ_{CG}	λ_{CT}
G			*	λ_{GT}
T				*

Symmetric

What's in the black box $P_{ij}(t)$?

$$\begin{array}{c} \text{A} \\ \text{C} \\ \text{G} \\ \text{T} \end{array} \begin{pmatrix} \text{A} & \text{C} & \text{G} & \text{T} \\ * & \lambda_{AC} & \lambda_{AG} & \lambda_{AT} \\ & * & \lambda_{CG} & \lambda_{CT} \\ & & * & \lambda_{GT} \\ \text{Symmetric} & & & * \end{pmatrix}$$

Equilibrium frequency vector $n = (n_A, n_C, n_G, n_T)$ where $n_A + n_C + n_G + n_T = 1$

The Jukes-Cantor model

$$\begin{array}{c} \text{A} \\ \text{C} \\ \text{G} \\ \text{T} \end{array} \begin{pmatrix} \text{A} & \text{C} & \text{G} & \text{T} \\ * & \lambda & \lambda & \lambda \\ & * & \lambda & \lambda \\ & & * & \lambda \\ & & & * \end{pmatrix}$$

$$\Pi = (1/4, 1/4, 1/4, 1/4)$$

Felsenstein 81

	A	C	G	T
A	*	λ	λ	λ
C		*	λ	λ
G			*	λ
T				*

$$\Pi_i \neq \Pi_j$$

Kimura 2-parameter model 1980

$$\begin{array}{c} \text{A} \\ \text{C} \\ \text{G} \\ \text{T} \end{array} \begin{pmatrix} \text{A} & \text{C} & \text{G} & \text{T} \\ * & \lambda & \zeta & \lambda \\ & * & \zeta & \lambda \\ & & * & \zeta \\ & & & * \end{pmatrix}$$

$$\Pi = (1/4, 1/4, 1/4, 1/4)$$

HKY85

$$\begin{array}{c} \text{A} \\ \text{C} \\ \text{G} \\ \text{T} \end{array} \begin{pmatrix} \text{A} & \text{C} & \text{G} & \text{T} \\ * & \lambda & \zeta & \lambda \\ & * & \zeta & \lambda \\ & & * & \zeta \\ & & & * \end{pmatrix}$$

$$\pi_i \neq \pi_j$$

GTR 1986

	A	C	G	T
A	*	α	β	γ
C		*	δ	ϵ
G			*	ζ
T				*

$$\Pi_i \neq \Pi_j$$

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A	*	α	β	γ
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Note that these are **relative** rates, their values only matter relative to each other, so we can set $\zeta := 1.0$ by default

$$\Pi_i \neq \Pi_j$$

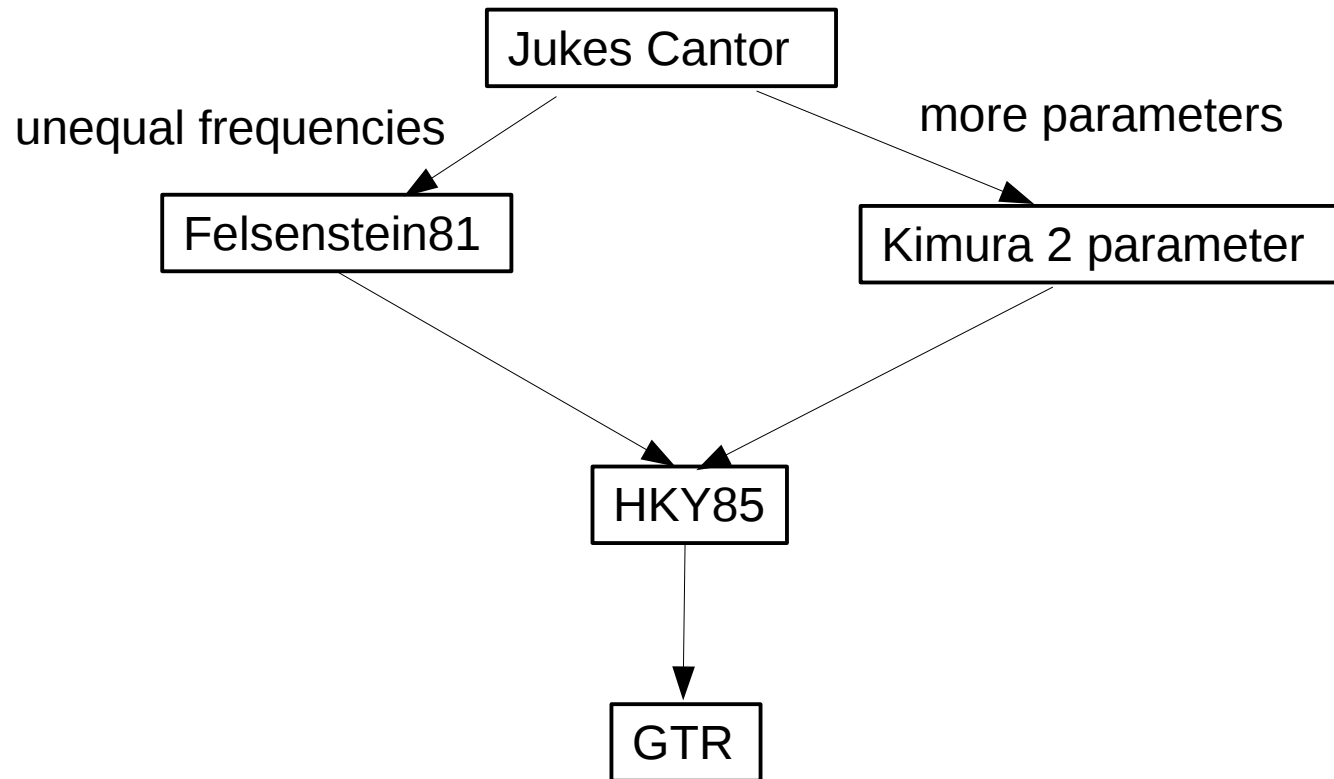
GTR 1986

	A	C	G	T
A	*	α	β	γ
C		*	δ	ϵ
G			*	1.0
T				*

Note that these are **relative** rates, their values only matter relative to each other, so we can set $\zeta := 1.0$ by default. Although the GTR model has **6 rates**, it **only** has **5 free parameters!**

$$\Pi_i \neq \Pi_j$$

Model Hierarchy



GTR 1986

	A	C	G	T
A	*	α	β	γ
C		*	δ	ϵ
G			*	1.0
T				*

This is a rate matrix,
time reversibility would
Require $\pi_i r_{ij} = \pi_j r_{ji}$

$$\pi_i \neq \pi_j$$

GTR 1986

$$\begin{array}{c}
 A \\
 C \\
 G \\
 T
 \end{array}
 \begin{pmatrix}
 & A & C & G & T \\
 & * & \alpha & \beta & \gamma \\
 & & * & \delta & \epsilon \\
 & & & * & 1.0 \\
 & & & & *
 \end{pmatrix}$$

$$\pi_i \neq \pi_j$$

This is a rate matrix,
time reversibility would
Require $\pi_i r_{ij} = \pi_j r_{ji}$
Solution: introduce a
Q matrix $Q := \text{diag}(\pi) R$

$$\begin{pmatrix}
 \pi_A & & & & \\
 & \pi_C & & & \\
 & & \pi_G & & \\
 & & & \pi_T & \\
 & & & &
 \end{pmatrix}$$

GTR 1986

$$\begin{array}{c}
 A \\
 C \\
 G \\
 T
 \end{array}
 \begin{pmatrix}
 & A & C & G & T \\
 * & & \alpha & \beta & \gamma \\
 & * & & \delta & \epsilon \\
 & & & * & 1.0 \\
 & & & & *
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$$\begin{pmatrix}
 \pi_A & & & \\
 & \pi_C & & \\
 & & \pi_G & \\
 & & & \pi_T
 \end{pmatrix}$$

Then, $\pi_i r_{ij} = \pi_j r_{ji}$ holds

So how do we compute $P(t)$ from Q ?

- As we have seen in the lecture on Markov chains:

$$P(t) = e^{Qt} = I + Qt + \frac{1}{2!} (Qt)^2 + \frac{1}{3!} (Qt)^3 + \dots$$

- but this is unfortunately a matrix exponential :-)
- I will spare you the details, but in general, e.g., for GTR we need to apply an eigenvector/eigenvalue decomposition of Q to calculate:

$$P(t) = U \exp(\text{diag}(\lambda_i)t) U^{-1}$$



Matrix and inverse matrix of eigenvectors of Q

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Diagonal matrix of eigenvalues of Q , here the exponential function $\exp()$ is invoked on scalar values!

Likelihood Calculations

- So far, we have only seen how to calculate **a** likelihood on a
 - given, fixed tree topology
 - with given fixed branch lengths
 - and given, fixed remaining model parameters
- Computing the **maximum** likelihood score, is much more complicated as it requires functions for optimizing continuous parameters and functions for searching the discrete space of trees !