# Substitution models 

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## Modelling the evolution of genomes

- The ultimate goal: to model the evolutionary distance between two genomes
- Input: sequences $S_{1}, S_{2} \in\{A, C, G, T\}^{*}=\Sigma^{*}$, evolutionary time $t$
- Output: $\operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2}\right]$ (formal way to denote: $\operatorname{Pr}\left[S_{2} \mid S_{1}, t\right]$ )
* Probability of sequence $S_{1}$ to mutate into sequence $S_{2}$ in evolutionary time $t$
« Formally: Probability of observing sequence $S_{2}$, given that its evolutionary ancestor in time $t$ is sequence $S_{1}$
- Requirements:
- $\operatorname{Pr}[S \xrightarrow{t=0} S]=1$ (no evolution in zero time)
- $\forall S^{\prime} \in \Sigma^{*}: \operatorname{Pr}\left[S^{\prime} \xrightarrow{t=\infty} S\right]=\pi_{S}$ (with enough time, the starting point is irrelevant)
- $\operatorname{Pr}\left[S_{1} \xrightarrow{t_{1}} S_{2} \wedge S_{2} \xrightarrow{t_{2}} S_{3}\right]=\operatorname{Pr}\left[S_{1} \xrightarrow{t_{1}} S_{2}\right] \cdot \operatorname{Pr}\left[S_{2} \xrightarrow{t_{2}} S_{3}\right]$ (no memory)
- $\operatorname{Pr}\left[S_{1} \xrightarrow{t=t_{1}+t_{2}} S_{3}\right]=\sum_{S_{2} \in \Sigma^{*}} \operatorname{Pr}\left[S_{1} \xrightarrow{t_{1}} S_{2}\right] \cdot \operatorname{Pr}\left[S_{2} \xrightarrow{t_{2}} S_{3}\right]$ (multiplicativity)
* we can break time $t$ into two parts $t_{1}$ and $t_{2}$, and sum over all possible intermediate states


## What can we do with such a model (in the near future)

- Given a phylogenetic tree (phylogeny) $T=\left(\mathbf{S} \subset \Sigma^{*}, E \subset \mathbf{S}^{2}, t: E \rightarrow \mathbf{R}\right)$ of sequences $\mathbf{S}$ with times $\mathbf{t}(\cdot, \cdot)$ on the edges, we can compute its total probability by multiplying probabilities of each edge:

$$
\operatorname{Pr}[\mathbf{S} \mid E, \mathbf{t}]=\operatorname{Pr}\left[S_{\text {root }}\right] \cdot \prod_{e:\left(S_{a}, S_{s}\right) \in E} \operatorname{Pr}\left[S_{a} \xrightarrow{\mathbf{t}\left(S_{a}, S_{s}\right)} S_{s}\right]
$$

- This allows us to compute the likelihood $\mathcal{L}(E, \mathbf{t} ; \mathbf{S})$ of a potential phylogeny $T$ structure $E$ and times $\mathbf{t}$ w.r.t. sequences $\mathbf{S}$ in the nodes
- We can choose the best phylogeny structure by maximizing the total likelihood
- We can even maximize the likelihood using only sequences in the leaves (present species) by using the Felsenstein algorithm (next week)


## Simplifying assumptions

- No indels, only substitutions

$$
\bullet \Longrightarrow\left|S_{1}\right|=\left|S_{2}\right|=n
$$

- All bases mutate independently
- Compute mutation prob. for each base, and then multiply:

$$
\begin{array}{r}
\operatorname{Pr}\left[S_{1}=\left(a_{1}, \ldots, a_{n}\right) \xrightarrow{t} S_{2}=\left(b_{1}, \ldots, b_{n}\right)\right]= \\
=\operatorname{Pr}\left[a_{1} \xrightarrow{t} b_{1}\right] \cdot \operatorname{Pr}\left[a_{2} \xrightarrow{t} b_{2}\right] \cdot \ldots \cdot \operatorname{Pr}\left[a_{n} \xrightarrow{t} b_{n}\right]= \\
=\prod_{i=1}^{n} \operatorname{Pr}\left[a_{i} \xrightarrow{t} b_{i}\right] .
\end{array}
$$

- Now, we only need to model the evolution of a single base $\operatorname{Pr}[a \xrightarrow{t} b]$


## Substitution model for one base

- $\operatorname{Pr}[a \xrightarrow{t} b]$ for a fixed time $t$ has only 16 possible input combinations $\{A, C, G, T\}^{2}$
- Written as a matrix: $S(t)=\left(\begin{array}{lllll}\operatorname{Pr}[A \xrightarrow{t} A] & \operatorname{Pr}[A \xrightarrow{t} C] & \operatorname{Pr}[A \xrightarrow{t} G] & \operatorname{Pr}[A \xrightarrow{t} T] \\ \operatorname{Pr}[C \xrightarrow{t} A] & \operatorname{Pr}[C \xrightarrow{t} C] & \operatorname{Pr}[C \xrightarrow{t} G] & \operatorname{Pr}[C \xrightarrow{t} T] \\ \operatorname{Pr}[G \xrightarrow{t} A] & \operatorname{Pr}[G \xrightarrow{t} C] & \operatorname{Pr}[G \xrightarrow{t} G] & \operatorname{Pr}[G \xrightarrow{t} T] \\ \operatorname{Pr}[T \xrightarrow{t} A] & \operatorname{Pr}[T \xrightarrow{t} C] & \operatorname{Pr}[T \xrightarrow{t} G] & \operatorname{Pr}[T \xrightarrow{t} T]\end{array}\right)$
- General properties of matrix $S(t)$ :
- $\operatorname{Pr}[C \xrightarrow{t} G]=$


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- General properties of matrix $S(t)$ :
- $\operatorname{Pr}[C \xrightarrow{t} G]=\left(\begin{array}{llll}0 & 1 & 0 & 0\end{array}\right) \cdot S(t) \cdot\left(\begin{array}{llll}0 & 0 & 1 & 0\end{array}\right)^{T}$
- $S(0)=$


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- $S(0)=I_{4}$
- $S\left(t_{1}\right) \cdot S\left(t_{2}\right)=$


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- $S(0)=I_{4}$
- $S\left(t_{1}\right) \cdot S\left(t_{2}\right)=\left(\sum_{x \in \Sigma} \operatorname{Pr}\left[i \xrightarrow{t_{4}} x\right] \cdot \operatorname{Pr}\left[x \xrightarrow{t_{2}} j\right]\right)_{i, j \in \Sigma} \stackrel{\text { multiplicativity }}{=}\left(\operatorname{Pr}\left[i^{t_{1}+t_{2}} j\right]\right)_{i, j \in \Sigma}=S\left(t_{1}+t_{2}\right)$ $\star S(k \cdot t)=S^{k}(t)$


## Model with discrete time

- Assume that evolutionary time $t$ is discrete
- at most one mutation occurs in time 1
- A base now has 4 possible states, and has a chance to transit between them in each time step, or stay the same $\Longrightarrow$ Markov chain
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- Stationary distribution (equilibrium)

$$
S(\infty)=\lim _{t \rightarrow \infty} S(t)=\lim _{t \rightarrow \infty} S^{t}(1)=\left(\begin{array}{cccc}
\pi_{A} & \pi_{C} & \pi_{G} & \pi_{T} \\
\pi_{A} & \pi_{C} & \pi_{G} & \pi_{T} \\
\pi_{A} & \pi_{C} & \pi_{G} & \pi_{T} \\
\pi_{A} & \pi_{C} & \pi_{G} & \pi_{T}
\end{array}\right)
$$



## Quick summary so far

- Evolution model $=$ prob. $\operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2}\right]=\operatorname{Pr}\left[S_{2} \mid S_{1}, t\right]$ of observing $S_{2}$ given that its ancestor in evolutionary time $t$ is $S_{1}$
- Assuming only substitutions
- $\left|S_{1}\right|=\left|S_{2}\right|=n$
- Assuming independent evolution for each base
- $\operatorname{Pr}\left[S_{1}=\left(a_{1}, \ldots, a_{n}\right) \xrightarrow{t} S_{2}=\left(b_{1}, \ldots, b_{n}\right)\right]=\prod_{i=1}^{n} \operatorname{Pr}\left[a_{i} \xrightarrow{t} b_{i}\right]$
- Only need to define a (substitution) model for a single base
$-\operatorname{Pr}[a \xrightarrow{t} b]=S(t)=\left(\begin{array}{lllll}\operatorname{Pr}[A \xrightarrow[\rightarrow]{t} A] & \operatorname{Pr}[A \xrightarrow{t} C] & \operatorname{Pr}[A \xrightarrow{t} G] & \operatorname{Pr}[A \xrightarrow{t} T] \\ \operatorname{Pr}[C \xrightarrow{t} A] & \operatorname{Pr}[C \xrightarrow{t} C] & \operatorname{Pr}[C \xrightarrow{t} G] & \operatorname{Pr}[C \xrightarrow{t} T] \\ \operatorname{Pr}[G \xrightarrow[\rightarrow]{t} A] & \operatorname{Pr}[G \xrightarrow{t} C] & \operatorname{Pr}[G \xrightarrow{t} G] & \operatorname{Pr}[G \xrightarrow{t} T] \\ \operatorname{Pr}[T \xrightarrow{t} A] & \operatorname{Pr}[T \xrightarrow{t} C] & \operatorname{Pr}[T \xrightarrow{t} G] & \operatorname{Pr}[T \xrightarrow{t} T]\end{array}\right)$
- $S\left(t_{1}+t_{2}\right)=S\left(t_{1}\right) \cdot S\left(t_{2}\right)$
- For discrete time, only need to define $S(1)$
- Classic Markov chain with states $\{A, C, G, T\}, S(1)=$ matrix of transition probabilities


## Jukes-Cantor JC69 model

- The plan: define Markov chains with continuous time (CTMC), where all substitutions are equally likely
- $S(t)=$


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$$
\text { - } S(t)=\left(\begin{array}{cccc}
1-3 s(t) & s(t) & s(t) & s(t) \\
s(t) & 1-3 s(t) & s(t) & s(t) \\
s(t) & s(t) & 1-3 s(t) & s(t) \\
s(t) & s(t) & s(t) & 1-3 s(t)
\end{array}\right)=I+\left(\begin{array}{cccc}
-3 & 1 & 1 & 1 \\
1 & -3 & 1 & 1 \\
1 & 1 & -3 & 1 \\
1 & 1 & 1 & -3
\end{array}\right) \cdot s(t)
$$

## Jukes-Cantor JC69 model

- The plan: define Markov chains with continuous time (CTMC), where all substitutions are equally likely
- $S(t)=\left(\begin{array}{cccc}1-3 s(t) & s(t) & s(t) & s(t) \\ s(t) & 1-3 s(t) & s(t) & s(t) \\ s(t) & s(t) & 1-3 s(t) & s(t) \\ s(t) & s(t) & s(t) & 1-3 s(t)\end{array}\right)=I+\left(\begin{array}{cccc}-3 & 1 & 1 & 1 \\ 1 & -3 & 1 & 1 \\ 1 & 1 & -3 & 1 \\ 1 & 1 & 1 & -3\end{array}\right) \cdot s(t)$
- Let's look at $s(t)$ closely
- $s(0)=0$
- Let's denote the first derivative of $s(t)$ at zero as $\alpha$ :
$\star$ Formally, $\alpha:=s^{\prime}(0) \stackrel{\text { def. }}{=} \lim _{\varepsilon \rightarrow 0} \frac{s(0+\varepsilon)-s(0)}{\varepsilon}=\lim _{\varepsilon \rightarrow 0} \frac{s(\varepsilon)}{\varepsilon}$
$\star \alpha=\left.\frac{\partial \operatorname{Pr}[a \xrightarrow{t} b]}{\partial t}\right|_{t=0}$


## Derivative of $S(t)$

$$
\begin{aligned}
& S^{\prime}(t) \stackrel{\text { def. }}{=} \lim _{\varepsilon \rightarrow 0} \frac{S(t+\varepsilon)-S(t)}{\varepsilon}=\lim _{\varepsilon \rightarrow 0} \frac{S(t) S(\varepsilon)-S(t)}{\varepsilon}= \\
&=\lim _{\varepsilon \rightarrow 0} \frac{S(t)(S(\varepsilon)-I)}{\varepsilon}=\lim _{\varepsilon \rightarrow 0} \frac{S(t) \cdot\left(\begin{array}{cccc}
-3 & 1 & 1 & 1 \\
1 & -3 & 1 & 1 \\
1 & 1 & -3 & 1 \\
1 & 1 & 1 & -3
\end{array}\right) \cdot s(\varepsilon)}{}= \\
&=S(t) \cdot\left(\begin{array}{cccc}
-3 & 1 & 1 & 1 \\
1 & -3 & 1 & 1 \\
1 & 1 & -3 & 1 \\
1 & 1 & 1 & -3
\end{array}\right) \cdot \lim _{\varepsilon \rightarrow 0} \frac{s(\varepsilon)}{\varepsilon}= \\
&=S(t) \cdot\left(\begin{array}{cccc}
-3 \alpha & \alpha & \alpha & \alpha \\
\alpha & -3 \alpha & \alpha & \alpha \\
\alpha & \alpha & -3 \alpha & \alpha \\
\alpha & \alpha & \alpha & -3 \alpha
\end{array}\right)
\end{aligned}
$$

## Differential equation

- We've got diff. equation $S^{\prime}(t)=S(t) \cdot R$, where $R=\left(\begin{array}{cccc}-3 \alpha & \alpha & \alpha & \alpha \\ \alpha & -3 \alpha & \alpha & \alpha \\ \alpha & \alpha & -3 \alpha & \alpha \\ \alpha & \alpha & \alpha & -3 \alpha\end{array}\right)$
- $R$ is called transition rate matrix
- It is really a system of 16 ordinary differential equations $S^{\prime}(t)_{a, b}=(S(t) \cdot R)_{a, b}$
- for $(A, A):-3 s^{\prime}(t)=(1-3 s(t))(-3 \alpha)+3 s(t) \alpha=-3 \alpha+12 \alpha s(t)$

$$
\star s^{\prime}(t)=\alpha-4 \alpha s(t)
$$

- for $(A, C): s^{\prime}(t)=(1-3 s(t)) \alpha+s(t)(-3 \alpha)+2 s(t) \alpha=\alpha-4 \alpha s(t)$
- which reduces to a single ordinary differential equation $s^{\prime}(t)=\alpha-4 \alpha s(t)$ with start condition $s(0)=0$
- Solution: $s(t)=\frac{1}{4}-\frac{1}{4} e^{-4 \alpha t} ; \quad 1-3 s(t)=\frac{1}{4}+\frac{3}{4} e^{-4 \alpha t}$

$$
\left.\begin{array}{r}
\frac{d s}{d t}=\alpha-4 \alpha s \\
\frac{d s}{\alpha-4 \alpha s}=d t \\
\frac{1}{\alpha} \int \frac{d s}{1-4 s}=\int 1 d t \\
|(1-4 s)=x,-4 d s=d x| \\
\frac{1}{-4 \alpha} \int \frac{d x}{x}=\int 1 d t \\
\frac{1}{-4 \alpha} \ln (1-4 s)=t+C \\
1-4 s=e^{-4 \alpha t+C}
\end{array}\right\} \begin{array}{r}
s=\frac{1-e^{-4 \alpha t+C}}{4} \\
\text { Solution: } s(t)=\frac{1-e^{-4 \alpha t}}{4} ; 1-3 s(t)=\frac{1}{4}+\frac{3}{4} e^{-4 \alpha t}
\end{array}
$$

## Equilibrium for Jukes-Cantor model

$$
\begin{gathered}
\lim _{t \rightarrow \infty} \operatorname{Pr}[A \xrightarrow{t} A]=\lim _{t \rightarrow \infty} \frac{1}{4}+\frac{3}{4} e^{-4 \alpha t}=\frac{1}{4} \\
\lim _{t \rightarrow \infty} \operatorname{Pr}[A \xrightarrow{t} C]=\lim _{t \rightarrow \infty} \frac{1}{4}-\frac{1}{4} e^{-4 \alpha t}=\frac{1}{4} \\
S(\infty)=\left(\begin{array}{llll}
1 / 4 & 1 / 4 & 1 / 4 & 1 / 4 \\
1 / 4 & 1 / 4 & 1 / 4 & 1 / 4 \\
1 / 4 & 1 / 4 & 1 / 4 & 1 / 4 \\
1 / 4 & 1 / 4 & 1 / 4 & 1 / 4
\end{array}\right)
\end{gathered}
$$

## Quick summary so far

- Jukes-Cantor substitution model:
- Continuous time $t$
- Equal probability of substitution $\forall a \neq b: \operatorname{Pr}[a \xrightarrow{t} b]=s(t)$
- Matrix form

$$
S(t)=\left(\begin{array}{cccc}
1-3 s(t) & s(t) & s(t) & s(t) \\
s(t) & 1-3 s(t) & s(t) & s(t) \\
s(t) & s(t) & 1-3 s(t) & s(t) \\
s(t) & s(t) & s(t) & 1-3 s(t)
\end{array}\right)
$$



- Diff. equation $s^{\prime}(t)=1-3 s(t), s(0)=0$
- $\operatorname{Pr}[a \xrightarrow{t} b]=S_{J C}(t)_{a, b}= \begin{cases}\frac{1}{4}+\frac{3}{4} e^{-4 \alpha t} & a=b \\ \frac{1}{4}-\frac{1}{4} e^{-4 \alpha t} & a \neq b\end{cases}$
- Equilibrium for JC: $\pi_{A}=\pi_{C}=\pi_{G}=\pi_{T}=\frac{1}{4}$



## Example for Jukes-Cantor

- Input: $S_{1}=\operatorname{TAACCGT}, S_{2}=$ AATGCGT, evolutionary time $t=0.5, \alpha=3$
- Result:

$$
\begin{aligned}
\operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2}\right] & =\prod_{i=1}^{n} \operatorname{Pr}\left[a_{i} \xrightarrow{t} b_{i}\right]=\left(\frac{1}{4}+\frac{3}{4} e^{-4 \alpha t}\right)^{\#\left(a_{i}=b_{i}\right)} \cdot\left(\frac{1}{4}-\frac{1}{4} e^{-4 \alpha t}\right)^{\#\left(a_{i} \neq b_{i}\right)}= \\
& =\left(\frac{1}{4}+\frac{3}{4} e^{-6}\right)^{4} \cdot\left(\frac{1}{4}-\frac{1}{4} e^{-6}\right)^{3} \approx(0.2519)^{4} \cdot(0.2493)^{3} \approx 0.0000624
\end{aligned}
$$

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& =\left(\frac{1}{4}+\frac{3}{4} e^{-6}\right)^{4} \cdot\left(\frac{1}{4}-\frac{1}{4} e^{-6}\right)^{3} \approx(0.2519)^{4} \cdot(0.2493)^{3} \approx 0.0000624
\end{aligned}
$$

- Notice that parameters $t=30, \alpha=1 / 20$ would give the same result
- Because $t$ and $\alpha$ are always in a product
- Standard practice is to select $\alpha$ such that $E[\#$ mutations in time $t=1]=1$
* \# mutations in time $t=1 \sim \operatorname{Poisson}(\lambda=3 \alpha), E=3 \alpha, E[\#]=1$ when $\alpha=1 / 3$


## Estimation of evolutionary time in JC model

- Input: $S_{1}=$ TAACCGT, $S_{2}=$ AATGCGT, $\alpha=1 / 3$ (standard)
- Goal: find the best evolutionary time $t^{*}$
- Best $=$ with highest likelihood
- likelihood $\mathcal{L}\left(t ; S_{1}, S_{2}, \alpha\right)=\operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2} \mid \alpha\right]=\left(\frac{1}{4}+\frac{3}{4} e^{-4 \alpha t}\right)^{\#\left(a_{i}=b_{i}\right)} \cdot\left(\frac{1}{4}-\frac{1}{4} e^{-4 \alpha t}\right)^{\#\left(a_{i} \neq b_{i}\right)}$.
- $t^{*}=\underset{t>0}{\arg \max } \mathcal{L}\left(t ; S_{1}, S_{2}, \alpha\right)=-\frac{1}{4 \alpha} \ln \left(1-\frac{4}{3} d\right)$, where $d:=$ proportion of different positions



## Exact estimator of evolutionary time in JC model

$$
\begin{array}{r}
t^{*}=\underset{t \geq 0}{\arg \max } \mathcal{L}\left(t ; S_{1}, S_{2}, \alpha\right)=\underset{t \geq 0}{\arg \max } \log \mathcal{L}\left(t ; S_{1}, S_{2}, \alpha\right)= \\
=\underset{t \geq 0}{\arg \max } \#\left(a_{i}=b_{i}\right) \log (1-3 s(t))+\#\left(a_{i} \neq b_{i}\right) \log s(t) . \\
\frac{d f}{d s}=-\frac{3 \#\left(a_{i}=b_{i}\right)}{1-3 s}+\frac{\#\left(a_{i} \neq b_{i}\right)}{s}=\frac{(1-3 s) \#(\neq)-3 s \#(=)}{s(1-3 s)} . \\
\frac{d s}{d t}=\alpha \cdot e^{-4 \alpha t} \\
\frac{d f}{d t}=0 \Longrightarrow \frac{d f}{d s} \frac{d s}{d t}=0 \Longrightarrow \frac{d f}{d s}=0 \Longrightarrow \frac{(1-3 s) \#(\neq)-3 s \#(=)}{s(1-3 s)}=0 \Longrightarrow \\
\Longrightarrow(1-3 s) \#(\neq)-3 s \#(=)=0 \Longrightarrow s=\frac{\#(\neq)}{3 \cdot(\#(\neq)+\#(=))}=\frac{\#(\neq)}{3 n} . \\
\frac{1}{4}-\frac{1}{4} e^{-4 \alpha t}=\frac{\#(\neq)}{3 n} \Longrightarrow-4 \alpha t=\ln \left(1-\frac{4 \#(\neq)}{3 n}\right) \Longrightarrow \\
\Longrightarrow t=\frac{-\ln \left(1-\frac{4}{3} \frac{\#(\neq)}{n}\right)}{4 \alpha}=\frac{-\ln \left(1-\frac{4}{3} d\right)}{4 \alpha} .
\end{array}
$$

## Behaviour of the time estimator

$$
t^{*}=-\frac{1}{4 \alpha} \ln \left(1-\frac{4}{3} \cdot d\right)
$$



## More general models

- JC69 model: rate matrix $R_{J C 69}=\left(\begin{array}{cccc}-3 \alpha & \alpha & \alpha & \alpha \\ \alpha & -3 \alpha & \alpha & \alpha \\ \alpha & \alpha & -3 \alpha & \alpha \\ \alpha & \alpha & \alpha & -3 \alpha\end{array}\right)$
- Sum in a row must equal to 0
- $R_{a, b}:=\frac{\partial \operatorname{Pr}[a \stackrel{t}{\rightarrow} b]}{\partial t}$ speed of change from $a$ to $b$
- In general: $R=\left(\begin{array}{cccc}* & \mu_{A, C} & \mu_{A, G} & \mu_{A, T} \\ \mu_{C, A} & * & \mu_{C, G} & \mu_{C, T} \\ \mu_{G, A} & \mu_{G, C} & * & \mu_{G, T} \\ \mu_{T, A} & \mu_{T, C} & \mu_{T, G} & *\end{array}\right)$
- Diagonal is set to make row sum up to 0
- Some regularity conditions apply


## Solution to a general model

- The differential equation $S^{\prime}(t)=S(t) \cdot R$ holds for any rate matrix $R$
- The general solution is $S(t)=e^{R t}$
- How to compute $e^{R t}$ ?
- diagonalization of matrix $R=Q \cdot \Lambda \cdot Q^{-1}$, where
$\star Q=$ orthogonal matrix (of eigenvectors)
$\star \Lambda=\operatorname{diag}\left(\lambda_{1}, \ldots, \lambda_{4}\right)$ is a diagonal matrix (of eigenvalues)
- $R^{n}=\left(Q \cdot \wedge \cdot Q^{-1}\right)^{n}=Q \wedge Q^{-1} Q \wedge Q^{-1} Q \ldots Q^{-1} Q \wedge Q^{-1}=Q \wedge^{n} Q^{-1}=$ $Q \cdot \operatorname{diag}\left(\lambda_{1}^{n}, \ldots, \lambda_{4}^{n}\right) \cdot Q^{-1}$

$$
e^{R t}=\sum_{i=0}^{\infty} \frac{(R t)^{n}}{n!}=\sum_{i=0}^{n} \frac{Q \cdot \operatorname{diag}\left(\left(\lambda_{1} t\right)^{n}, \ldots,\left(\lambda_{4} t\right)^{n}\right) \cdot Q^{-1}}{n!}=
$$

$=Q \cdot \operatorname{diag}\left(\sum_{i=0}^{\infty} \frac{\left(\lambda_{1} t\right)^{n}}{n!}, \ldots, \sum_{i=0}^{\infty} \frac{\left(\lambda_{1} t\right)^{n}}{n!}\right) \cdot Q^{-1}=Q \cdot \operatorname{diag}\left(e^{\lambda_{1} t}, \ldots, e^{\lambda_{4} t}\right) \cdot Q^{-1}$

## Solution in general form

$$
\begin{aligned}
& \frac{d S}{d t}=S R \Longrightarrow \int \frac{d S}{S}=\int R d t \Longrightarrow \ln S=R t+C \Longrightarrow S=e^{R t+C} ; S(0)=I \Longrightarrow S(t)=e^{R t} \\
& R_{J C 69}=\left(\begin{array}{cccc}
-1 & -1 & -1 & 1 \\
0 & 0 & 1 & 1 \\
0 & 1 & 0 & 1 \\
1 & 0 & 0 & 1
\end{array}\right) \cdot \operatorname{diag}(-4 \alpha,-4 \alpha,-4 \alpha, 0) \cdot\left(\begin{array}{cccc}
-0.25 & -0.25 & -0.25 & 0.75 \\
-0.25 & -0.25 & 0.75 & 0.25 \\
-0.25 & 0.75 & -0.25 & -0.25 \\
0.25 & 0.25 & 0.25 & 0.25
\end{array}\right) \\
& S_{J C 69}(t)=\left(\begin{array}{cccc}
-1 & -1 & -1 & 1 \\
0 & 0 & 1 & 1 \\
0 & 1 & 0 & 1 \\
1 & 0 & 0 & 1
\end{array}\right) \cdot \operatorname{diag}\left(e^{-4 \alpha t}, e^{-4 \alpha t}, e^{-4 \alpha t}, 1\right) \cdot\left(\begin{array}{cccc}
-0.25 & -0.25 & -0.25 & 0.75 \\
-0.25 & -0.25 & 0.75 & 0.25 \\
-0.25 & 0.75 & -0.25 & -0.25 \\
0.25 & 0.25 & 0.25 & 0.25
\end{array}\right) \\
& \text { PARENTA I } \\
& \text { ADV|SORY } \\
& \text { WARDMIII }
\end{aligned}
$$

## Kimura's K80 model

- Also called Kimura's 2 parameter model (K2P)
- $A$ and $G$ are purines, $C$ and $T$ are pyrimidines
- Transitions: within the same group $A \longleftrightarrow G, C \longleftrightarrow T$
- Transversions: between the groups
- Transitions are more frequent than transversions
- $\kappa:=\frac{\text { rate of transitions }}{\text { rate of transversions }}$, set rate of transversions to 1
- $R_{K 80}=\left(\begin{array}{cccc}* & 1 & \kappa & 1 \\ 1 & * & 1 & \kappa \\ \kappa & 1 & * & 1 \\ 1 & \kappa & 1 & *\end{array}\right)$

- Equilibrium is still $\pi_{A}=\pi_{C}=\pi_{G}=\pi_{T}=25 \%$


## Hasewaga-Kishino-Yano HKY85 model

- Transition/transversion ratio $\kappa$ \& arbitrary equilibrium $\left(\pi_{A}, \pi_{C}, \pi_{G}, \pi_{T}\right)$
- $R_{H K Y 85}=\left(\begin{array}{cccc}* & \pi_{C} & \kappa \cdot \pi_{G} & \pi_{T} \\ \pi_{A} & * & \pi_{G} & \kappa \cdot \pi_{T} \\ \kappa \cdot \pi_{A} & \pi_{C} & * & \pi_{T} \\ \pi_{A} & \kappa \cdot \pi_{C} & \pi_{G} & *\end{array}\right)$


## Other models

- Kimura's 3 parameter model (K3P, K81)
- 1 transition rate +2 transversion rates
- admits Hadamard transformation (generalized Fourier)
- Felsenstein F81 model
- JC69 + arbitrary equilibrium

- Tamura T92 model
- K80 + GC content
- Tamura and Nay TN93 model
- 2 transition rates +1 transversion rate
- Tavaré GTR86 model (General Time Reversible)
- everything from the above: arbitrary equilibrium +6 rate parameters



## Summary

- Evolution model: $\operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2}\right]$
- Independent base evolution $\Longrightarrow \operatorname{Pr}\left[S_{1} \xrightarrow{t} S_{2}\right]=\prod_{i=1}^{n} \operatorname{Pr}\left[a_{i} \xrightarrow{t} b_{i}\right]$
- Continuous time $t+$ Only substitutions $\Longrightarrow$ Continuous time Markov chains (CTMC)
- Substitution model for one base (CTMC)
- substitution rate matrix $R=\left(\begin{array}{cccc}* & \mu_{A, C} & \mu_{A, G} & \mu_{A, T} \\ \mu_{C, A} & * & \mu_{C, G} & \mu_{C, T} \\ \mu_{G, A} & \mu_{G, C} & * & \mu_{G, T} \\ \mu_{T, A} & \mu_{T, C} & \mu_{T, G} & *\end{array}\right)$, rows sum up to zero
- $S_{a, b}(t)=\operatorname{Pr}[a \xrightarrow{t} b]$ from $S(t)=e^{R t}$ using diagonalization trick
- Different rate matrices $R$ give different models:
- JC69 model: all substitutions are equally likely, equilibrium $25 \%$
- K80 model: transition/transversion ratio $\kappa$, equlibrium 25\%
- HKY85 model: K80 + arbitrary equilibrium

