last lecture: from Review

All we observe is differences between sequences:

ATG GAA ... ATG GTA ...

we want to infer evolutionary distance to we do this in of p the probability of a difference given x:

Juhes-Cantor: p= = = = = = = + = =

General: P= Po e mt w

Equilibrium Regeneies!

方= ☆W

## Likelihood:

Pr (dedal model)

sequence 1 sequence 2

Simple example AC ut AA

In this rase, the model is just the value of mt plus any free parameters is substitution mater For instance, for Htey, the substitution model would have 4 parameters: ), Tr, Tr, Tr.

Here we will just use Julies - Counter, so the model is just

Pr(Ac | AA, mt) = Pr(A|A, mt) · Pr(C|A, mt) e what does this line assume?  $= \rho \cdot \left(\frac{1-\rho}{3}\right)$  $= \left(\frac{3}{4}e^{\frac{1}{3}mt} + \frac{1}{4}\right) \left(\frac{1 - \left[\frac{3}{4}e^{\frac{1}{3}mt} + \frac{1}{4}\right]}{2}\right)$ 

	nt 1	Pr(Ac) AA, and)	
	0	0	For not much data (2 n/s)
modimum liholihud rshimde	0.1	0.028	likelihood is not sharply
	0.5	0,077	preahed. Would be more preaked
	0.824	6.083	with more data
	1.6	0,082	Even for 60st model, likelihood Kli, why?
	2.0	0,070	
	4.0	0.063	

Than 2 seguences:

Alignmond of 1 nt sequences: A

Here is one tree topology T.

Model is no.

Esubstitution model, T, E, ta, E, Eu)

Given this topology T:

Pr(dala | model) = ZZPr(A, A, C, x, y 1 t, t2, t3, 64)

 $= \sum_{x} \sum_{y} \Pr(x) \cdot \Pr(y|x,t_1) \cdot \Pr(A|y,t_2) \cdot \Pr(A|y,t_3) \cdot \Pr(C|x,t_n)$ (this can will got very large for large trees, Felsentoin Pruning algorithm, or dyromic programming)  $= \sum_{x} P_{c}(x) \cdot P_{c}(c(x, t_{4}) \cdot \sum_{y} P_{c}(y(x, t_{4}) \cdot P_{c}(A|y, t_{2}) \cdot P_{c}(A|y, t_{3}) \cdot P_{c}(A|y, t_{3})$ 

For Jules-Cantor, what is Pr(x)? Pr(x)= TT = 1/4

Johns Cambon, what is Pro(C/x, Lu)?  $Pr(C|x,t_{n}) = \begin{cases} p = \frac{3}{4}e^{-\frac{1}{3}mt} + \frac{1}{4} & \text{if } \text{ only } C = x \\ 1 - p = \frac{3}{4}e^{-\frac{3}{3}mt} & \text{if } C \neq x \end{cases}$ 

To find maximum likelihood, must optimize parameters (branch lengths, madel parameters) for each topology <u>Plus</u> smith over tree topologies.

Model comprison:

Should we use a more complex model? For intune Kimura 2- parameter vs. Julies- Cantor?

Libelihood ratio lost (most od models)

Aikoko Information Criterion (AIC): AIC = -2. In (L) +2. parametro

Advantage! Tolls us what was racelly want, Pr(model Idata). No over sitting problem given appropriate priors.

Disadvantages: 1) Hard to compute (less of a problem now)
2) what is prior, Pr(model)?

How to compete?

Marhou Chain Monle Carlo (MCMC)

- 1) start ut model m,
- 2) pick a new model Mz. If using Modropolis mothod, choose Mz such that proposal rate M, > mz = mz > m,.

  Typically local steps (mz similar to M.)
- 3) Compute R= Pr(m2 Idala) Pr (dala Im2). Pr (m2)
  Pr (m. Idala) Pr (dala Im). Pr (m2)
  Pr (dala Im). Pr (m,)
- H) If R≥1, move to model me otherwise move to me ul probability R.
  - 5) Reput stop (z)

If Mone is idented repeatedly, the Guetien (; of semples when the chain is of model m; of is (; » Pr(m; I data).

to see this, consider models mi and my with Pr(mildula) 2 Pr(mildula)

At equilibrium,

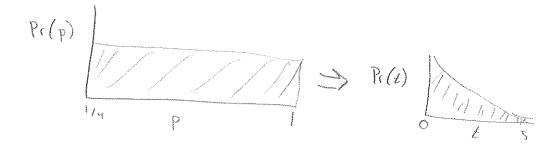
Pr  $(m_i \rightarrow m_j) = f_j \cdot Pr (m_j \rightarrow m_i)$ Now  $Pr (m_i \rightarrow m_j) = R = \frac{Pr (m_j | data)}{Pr (m_j | data)}$ 

 $\begin{cases} Pr(m_j \rightarrow m_i) = 1 \\ Fr(m_i) data \end{cases} = \begin{cases} f_i & Pr(m_i) data \end{cases}$   $\begin{cases} Fr(m_i) data \end{cases} = \begin{cases} f_i & Pr(m_i) data \end{cases}$   $\begin{cases} Pr(m_i) data \end{cases} = \begin{cases} f_i & Pr(m_i) data \end{cases}$ 

In MCMC, how do we know when we have run chair "long renough"?

Julies-Cantor:  $p = \frac{3}{4}e^{-\frac{1}{3}-nt} + \frac{1}{4}$ Choosing a "Flat" prior over parameters can be dangerous...

Flat prior on P



on to Pill)