In Statistics, there are two frameworks for inference:

Maximum LIKELIHOOD

Bayesian Analysis

"frequentiets"

"Bayes ans"

p(H)= p unknown

get a POSTERIOR DIST.

HTHTTH ---> W

or your parameter of interest

β = prepartion of H → P

In n tricus

P=P(H)

• P=P(H)

We begin with the Likelihood francwork. Warning: Need to review optimization

Easy example: Show that the Maximum Likelihood Estimator (MLE) pr

for n coin flips is  $\hat{p} = \frac{\# \text{ of } H}{n} = \text{propertion of } H \text{ in n tosses}$ 

Setup: 1) p= p(H) is unknown and with be estimated

2) there are in coin figs and my are H, my are T, nut + m=n.

The data are not = data,

With p unknown, define the likelihood function

(Assumes i.i.d.)

 $L(p) = Prob \left( data \mid p \right) = p^{n_H} \left( i - p \right)^{n_T}$ 

then the MAXIMUM LIKELIHOOD ESTIMATOR P = PME IS the value

of p that maximizes L(p). [The value of p That maker the

data you observed most probable.

Quice CALC I optimization:

$$L'(p) = P^{30} \left[ \frac{1}{4} \alpha (1-p)^{69} (-1) \right] + \frac{30p^{29}}{10p^{29}} (1-p)^{40}$$

$$= P^{29} \left( 1-p \right)^{69} \left[ \frac{30}{10p^{29}} (1-p) - \frac{1}{10p^{29}} \right]$$

$$p^{29}$$
  $(i-p)^{69}$   $\left[30-100p\right] = 0$  (i.e.  $p=0,1,\frac{30}{100}=.3$ 

Using your favorite test, it is clear 7 = .3 is a global max.

$$\hat{p} = \hat{p}_{MLE} = .3 = \frac{n_{H}}{n}$$

Redo: Since ML will require set derivetives to zero (and typically iid. assumption) in practice, we the Log-likelihood function.

Since  $\log(x)$  is an increasing function, the log-likelihood and likelihood function are maximized at the same value of P.

Easy to differentate ...

Thes critical points at P=0,1, =3

Caution: MLEs may fall to exist or not be unique.

Maximum Likelihood Trees in phylogenetics

God Fix a six substitution model JC, K2P, GTR

and find the parameters T, (p, Q, Etc) that maximize The likelihood

Example: Model Jukes - Canter on 1-edge tree

P = (,21 ,21 ,25 ,21) Known

Q= (-1 1/3 1/3 1/3 ) Known

Unknown parameter t = branch length

Data: Fab = pattern frequencies counts of pattern (under ild assumption) = ( nAA nAG nAC NAT )

16 bits of data

not

Under JG the expected pattern frequency array is (1-alt) alt alt alt alt) Where a(t) is a function of the unknown parameter t

alt) = a = \frac{3}{4} (1-e^{-\frac{3}{3}t})

Thus, the log-likelihood is

In L(a) = In L(a | data) = In (Prob(data (a))

= In PAA PAG ... PAT ] = In ( TT Pij )

= In Pii Enij

$$\ln L(\alpha) = \ln \left[ \left( \frac{1-\alpha}{3} \right)^{\frac{2}{1+\beta}} \left( \frac{\alpha}{12} \right)^{\frac{2}{1+\beta}} \right] = \left( \frac{2}{3} n_{ii} \right) \ln \left( \frac{1-\alpha}{3} \right) + \left( \frac{2}{3} n_{ij} \right) \ln \left( \frac{\alpha}{12} \right)$$

-Differentiating . . .

$$\frac{d}{dt} \ln L(\alpha(t)) = \sum_{n \in \mathbb{N}} \left(\frac{3}{1-\alpha}\right) \frac{(-1)}{3} \cdot \alpha'(t) + \sum_{n \in \mathbb{N}} \frac{12}{\alpha} \left(\frac{1}{2}\right) \alpha'(t)$$

Assume a'(t)=0 (i.e. there is change!) and require equal to 300

$$\Rightarrow (\Xi n_{ii}) a = (\Xi n_{ij}) - (\Xi n_{ij}) a \Rightarrow \alpha = \frac{\Xi n_{ij}}{\Xi n_{ii} + \Xi n_{ij}}$$

I.e. 
$$a(t) = \frac{\sum n_{ij}}{n} = proportion of sites that doffer!$$

and 
$$\hat{t} = \hat{t}_{ME} = -\frac{3}{4} \ln (1 - \frac{4}{3} \hat{a}) = d_{JC}(a, 5)$$

I.e. The JC distance is the Maximum Likelihood estimate for to