

Likelihood general approach

- 1) process model function
 - the biology
 - > `biomod(parameters)`
- 2) nll function (error distribution)
 - the stochasticity or error
 - > `-sum(ddist(data, dpar=biomod, error_parameters, log=T))`
- 3) optimize
 - find biology parameters and error parameters
 - > `optim(parameters, nllfunc, data)`
- This recipe is the same no matter how complicated the process model or what the error distribution is

Notation (equivalent variants)

$$L(\theta) = \mathcal{L} = P(y | \theta) \leftarrow \text{Probability of the data given the model parameters}$$

“The likelihood of the model is the probability of the data given the model”

The following is equivalent:

$$L(y; \theta) = P(y | \theta)$$

Notice that we use a semicolon or comma here rather than a vertical bar

“The likelihood function is the probability of the data given the model”

Sometimes you may see it this way (e.g. Edwards 1992. "Likelihood".):

$$L(\theta | y) = P(y | \theta)$$

The vertical bar is the conditional operator.

“The likelihood of the model given the data ...”

Hilborn and Mangel (1997) and some other places in ecology/evolution:

$$L(y | \theta) = P(y | \theta)$$

This is probably not technically correct.

But **DON'T** read it thus “The likelihood of the data given the model ...”

Today

- Coding likelihood intervals
- McElreath problem set