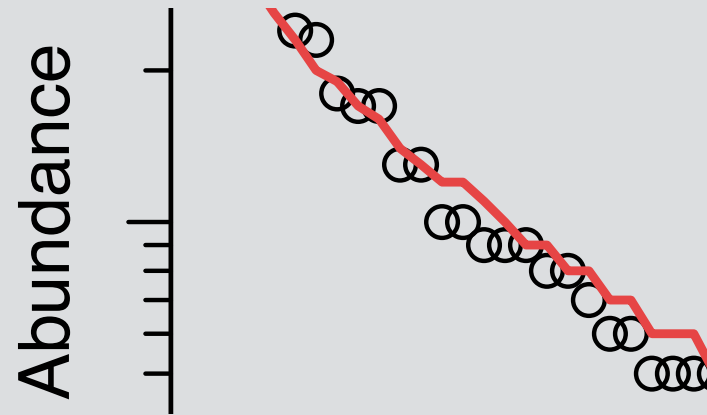


Get happy with your SAD

$$\int_{\theta} p(n \mid \theta) f(\theta) d\theta$$

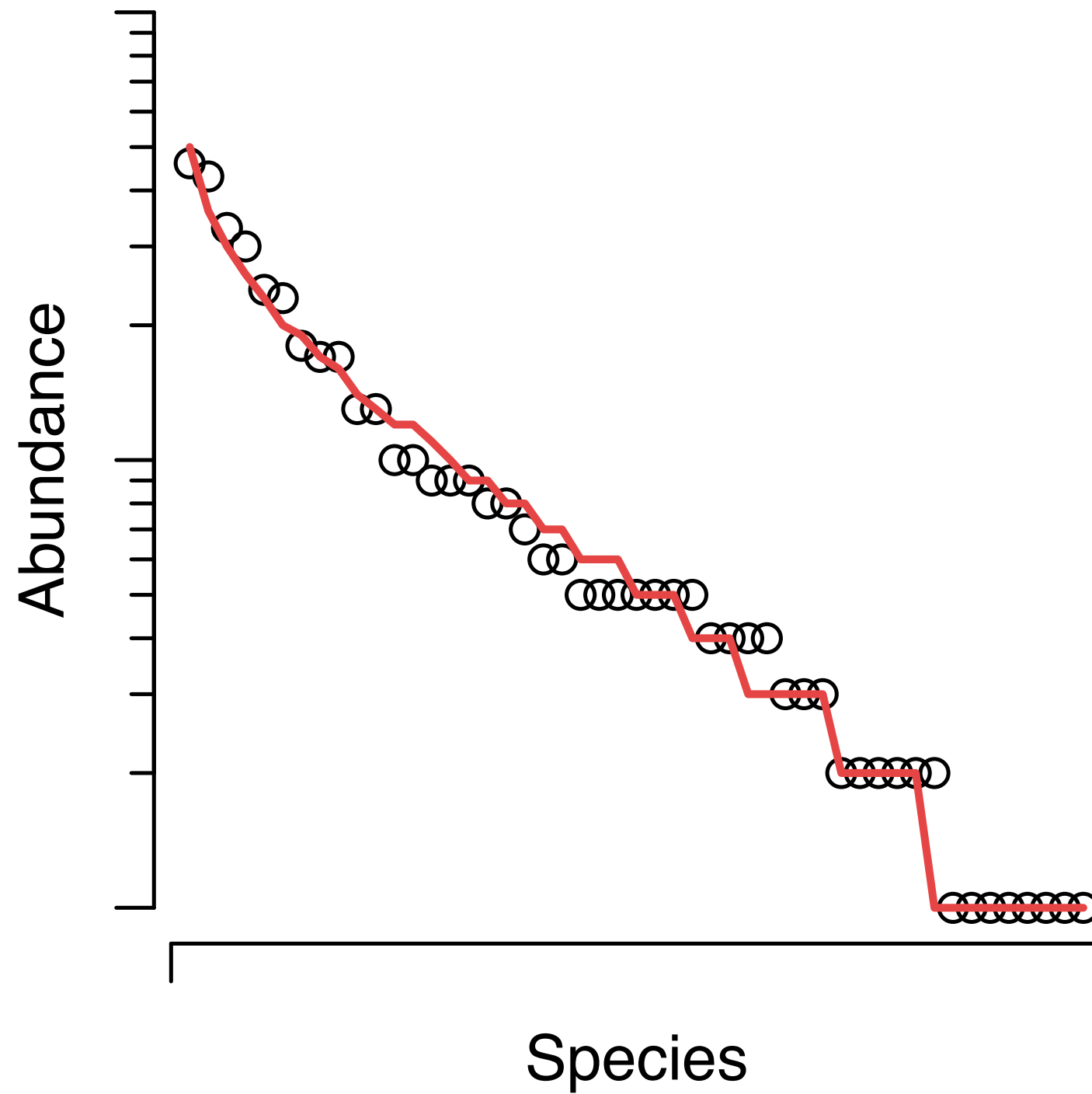


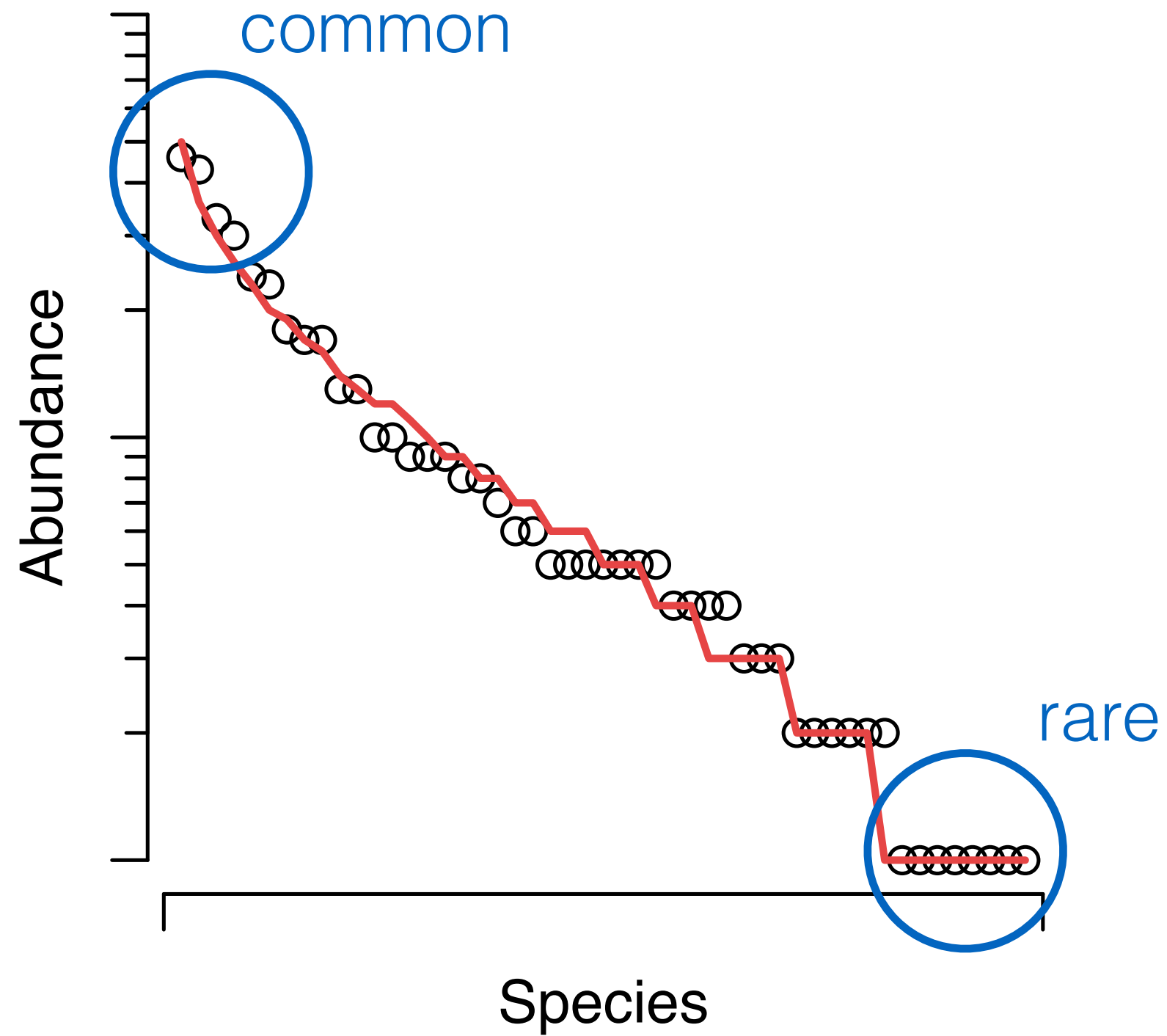
:]

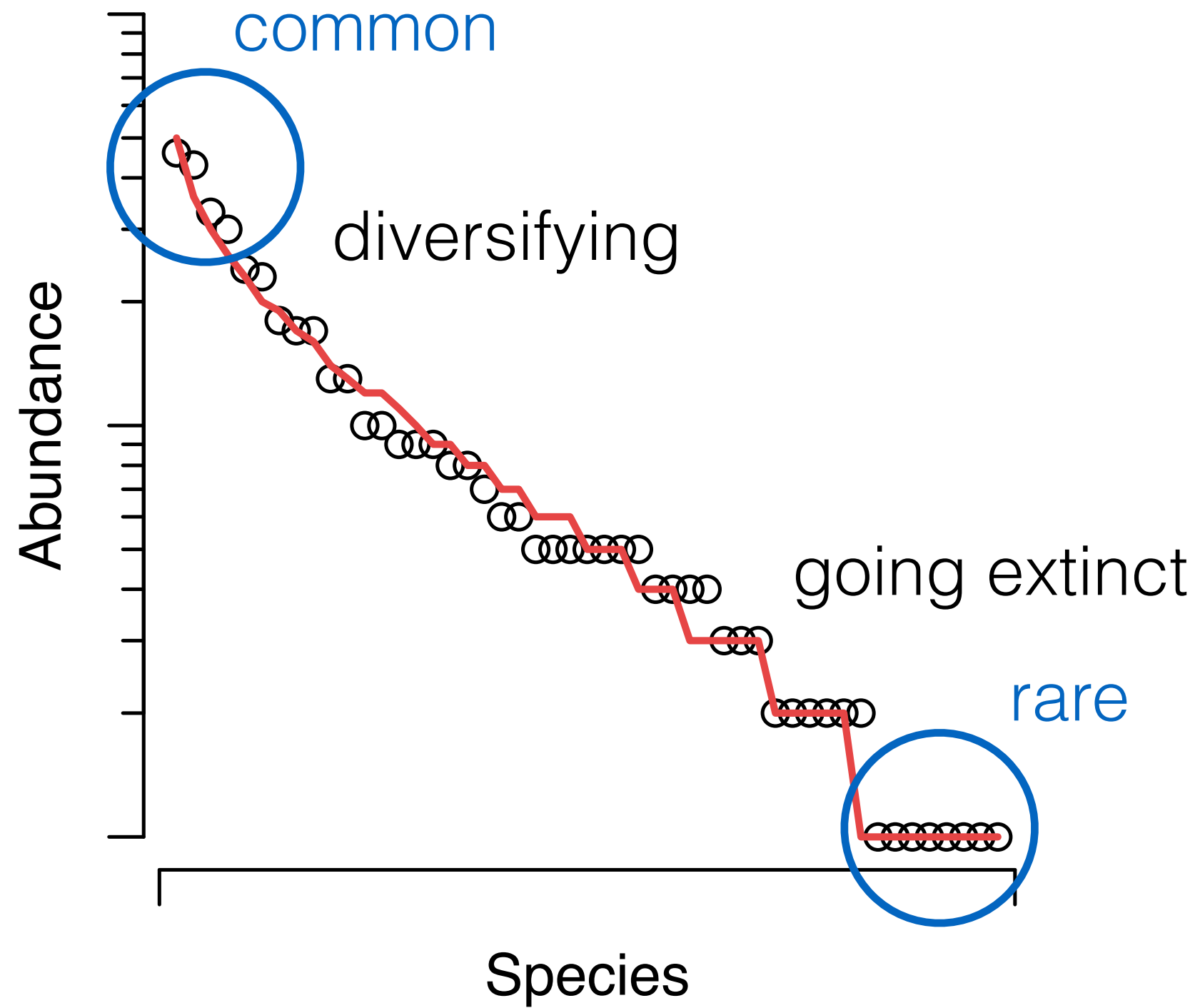
Andy Rominger

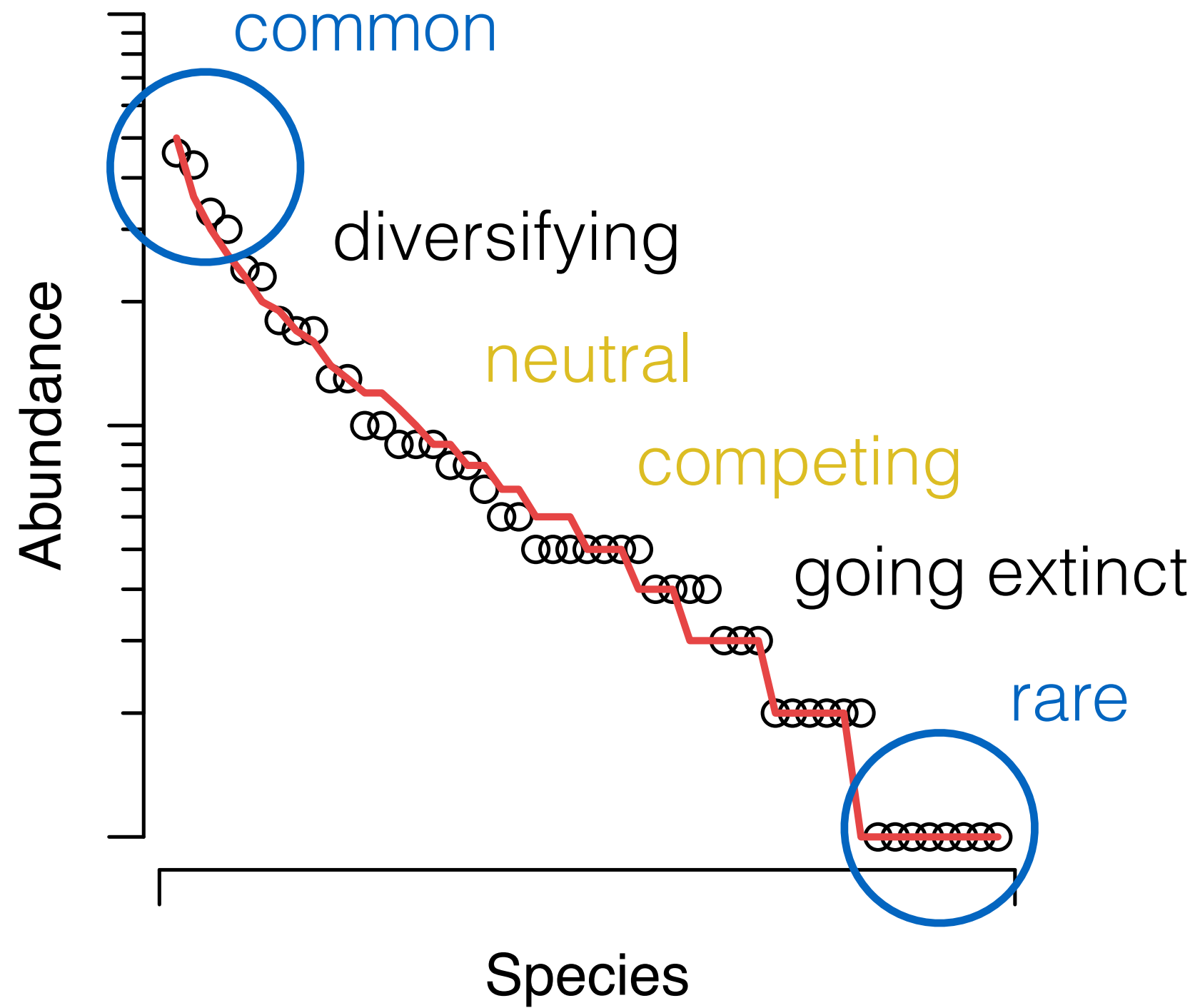
nature.berkeley.edu/~rominger

11 August 2016 • ESA, Ft. Lauderdale







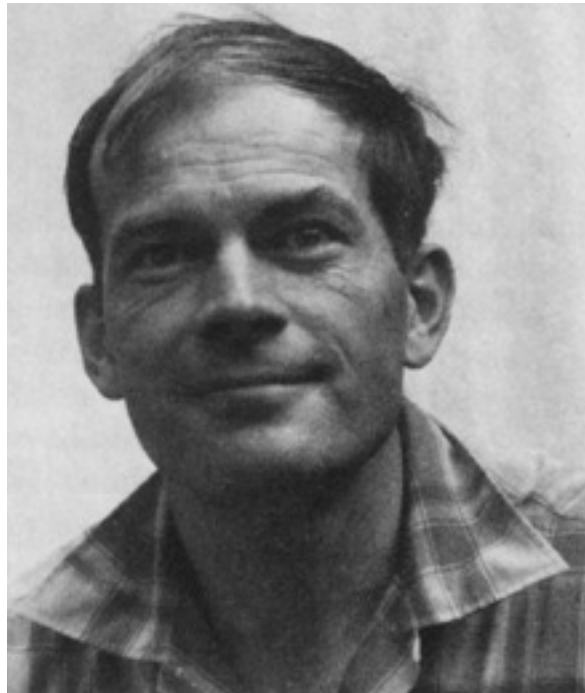


log-series



R. A. Fisher

broken stick



R. H. MacArthur

neutral

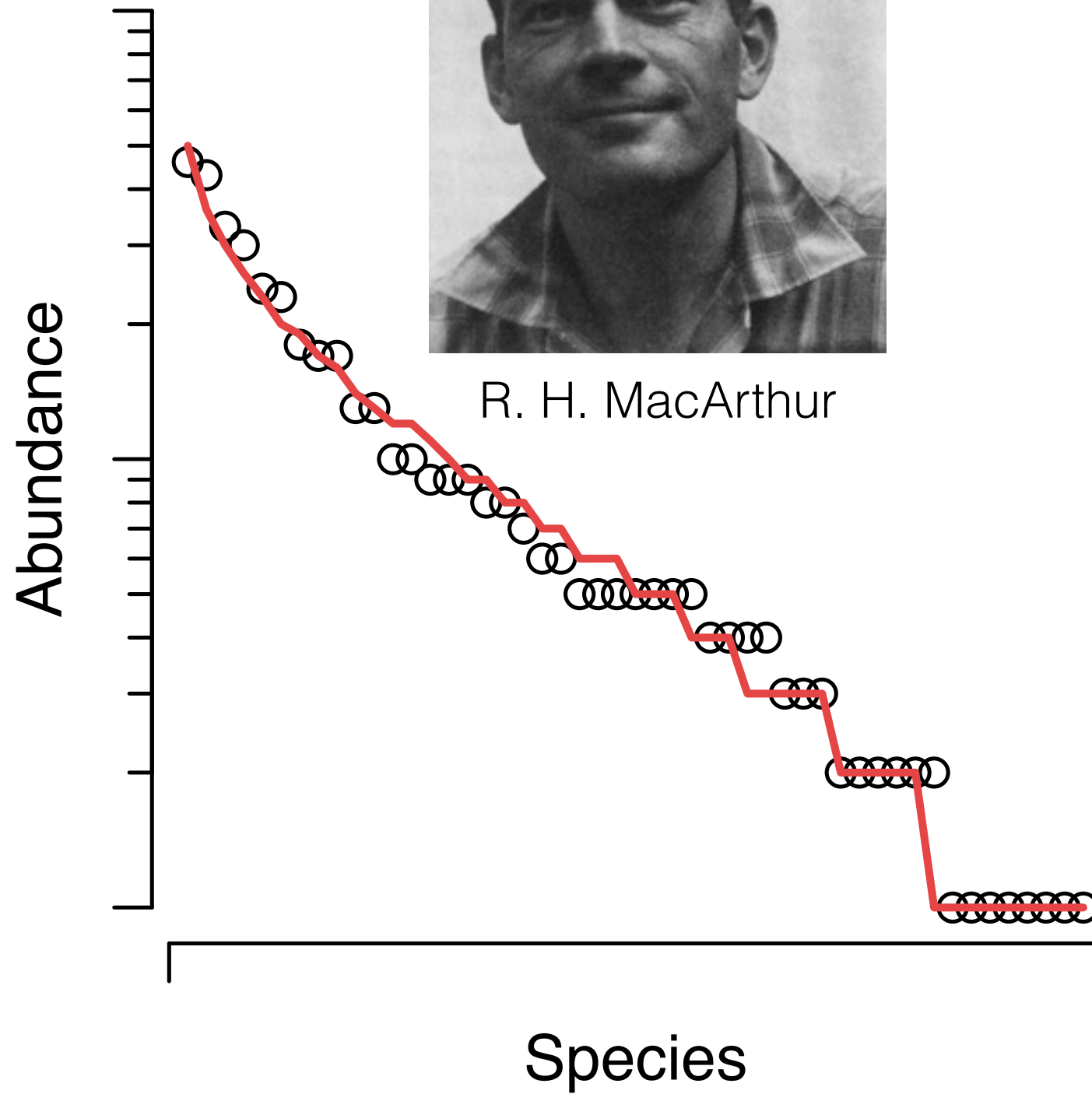


S. P. Hubbell

lognormal



F. W. Preston

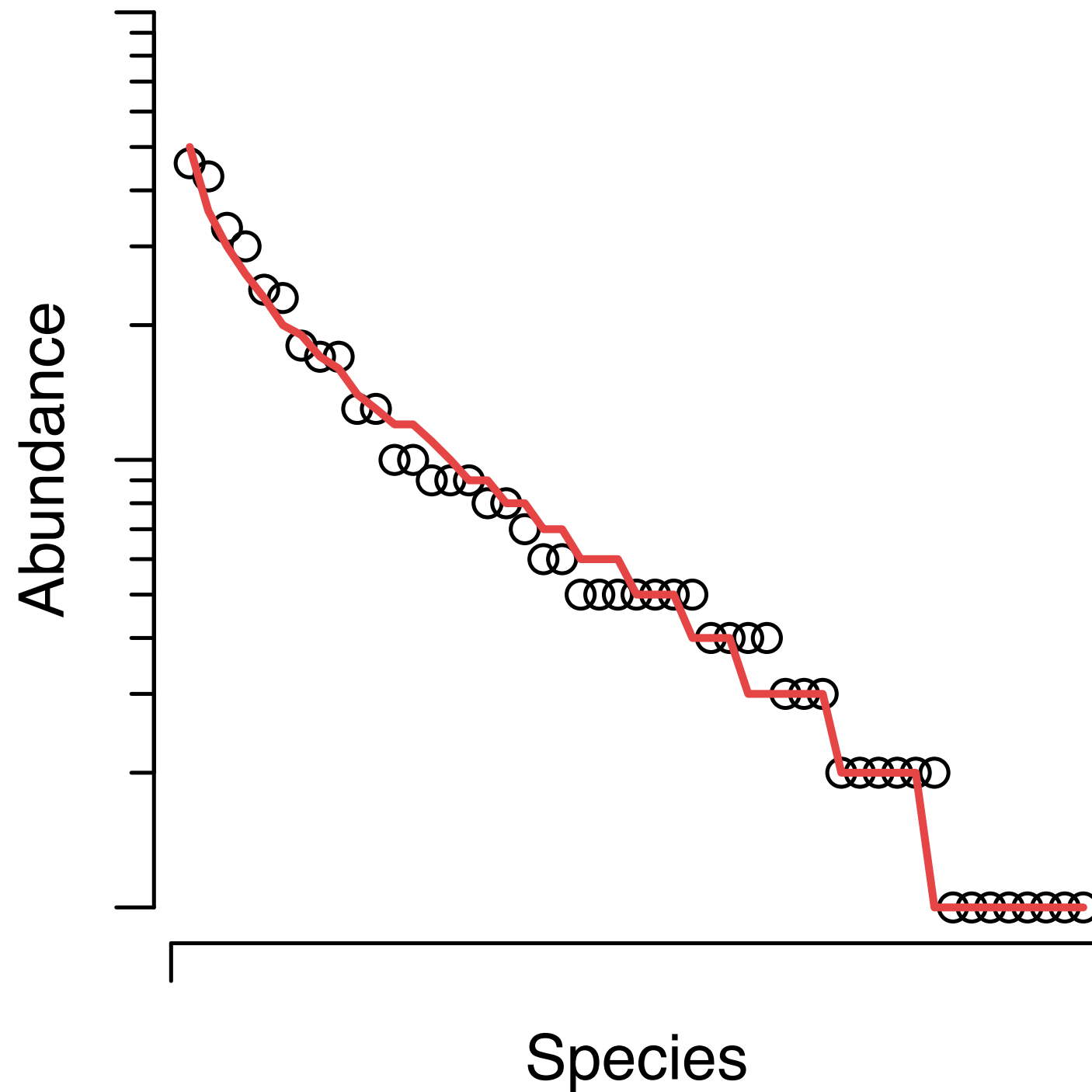


max ent



J. Harte

Need for best practices



Need for best practices

Misconceptions/dos-don'ts

But whys

Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

- Yes

Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

- Yes
- SAD still pervasive and unexplained

Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

- Yes
- SAD still pervasive and unexplained
- Disillusion from poor methods

Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

- Yes
- SAD still pervasive and unexplained
- Disillusion from poor methods
- Best practices are universal

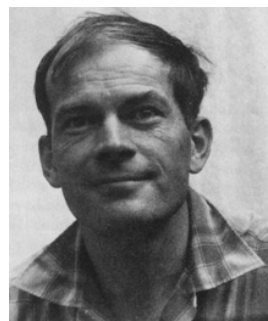
Need for best practices

Misconceptions/dos-don'ts

But whys

Why not traits?

- Yes
- SAD still pervasive and unexplained
- Disillusion from poor methods
- Best practices are universal
- Need better trait theory



Need for best practices

Misconceptions/dos-don'ts

- Relationships of SADs
- Subsampling
- Binning is bad
- Likelihood is good

But whys

Need for best practices

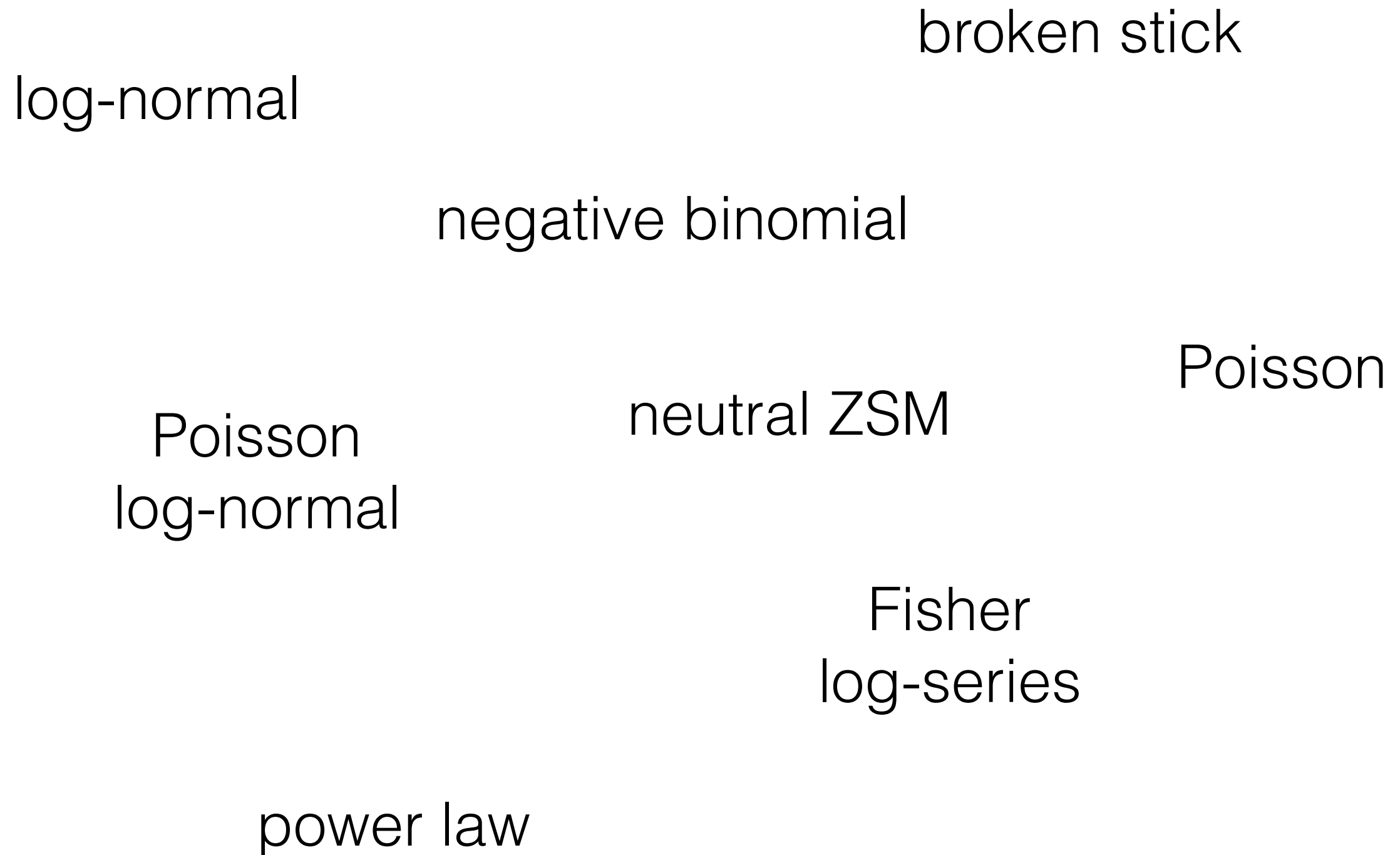
Misconceptions/dos-don'ts

- Relationships of SADs
- Subsampling
- Binning is bad
- Likelihood is good

But whys

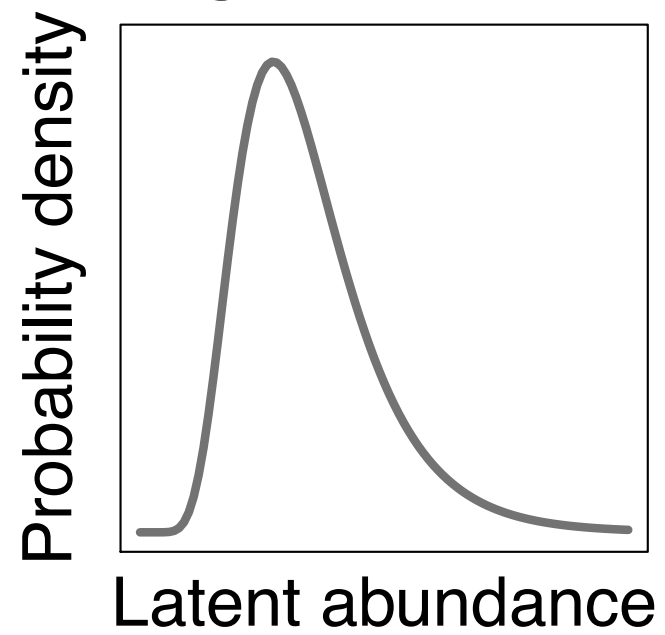
- Seeking generality

Relationships of SADs

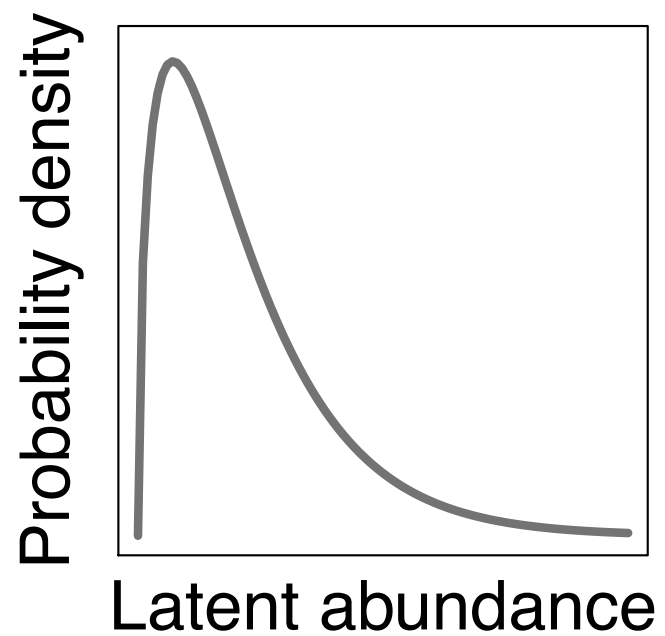


Latent distribution

log-normal



gamma

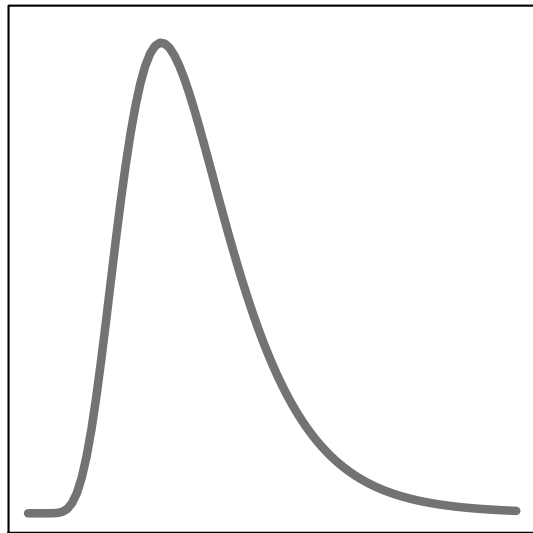


Latent distribution

Poisson sampling

log-normal

Probability density

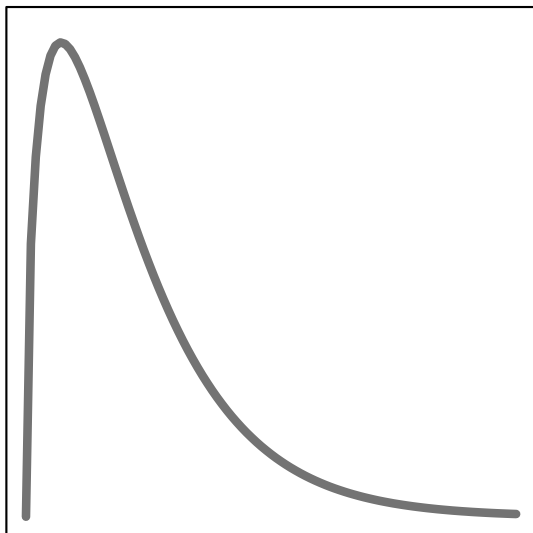


Latent abundance

Poisson
log-normal

gamma

Probability density



Latent abundance

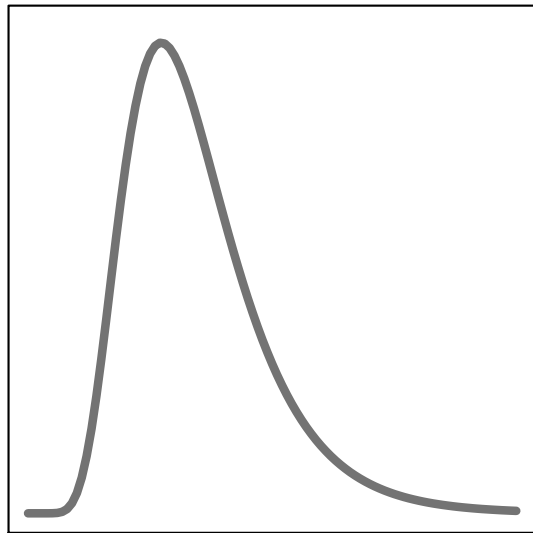
negative binomial

Latent distribution

Poisson sampling

log-normal

Probability density

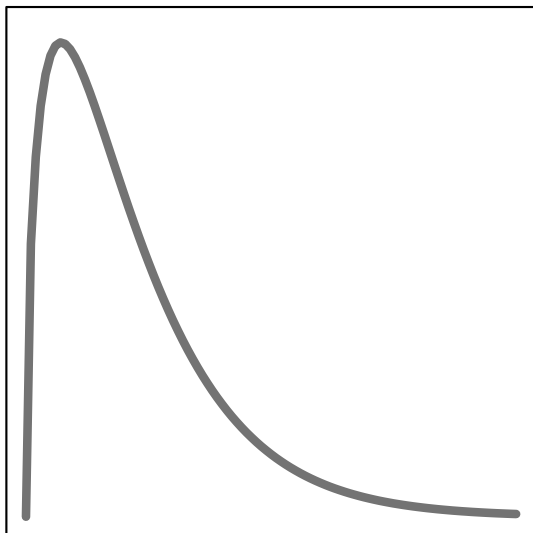


Latent abundance

Poisson
log-normal

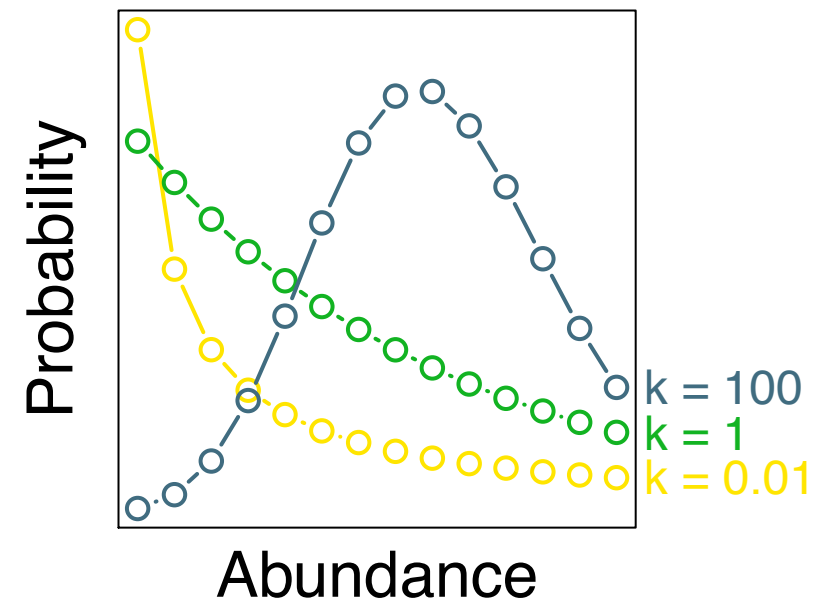
gamma

Probability density



Latent abundance

negative binomial



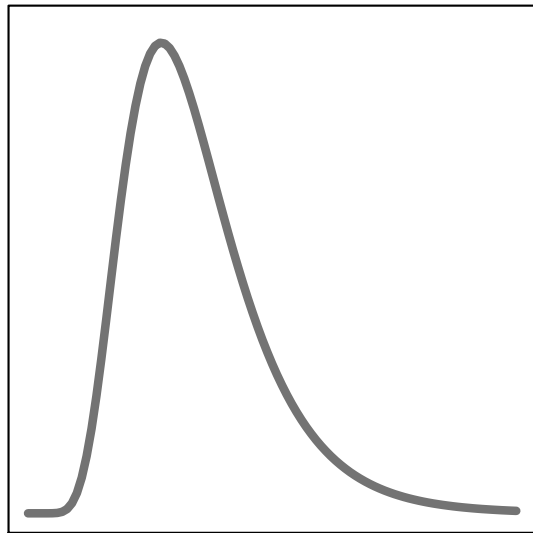
Latent distribution

Poisson sampling

Limits

log-normal

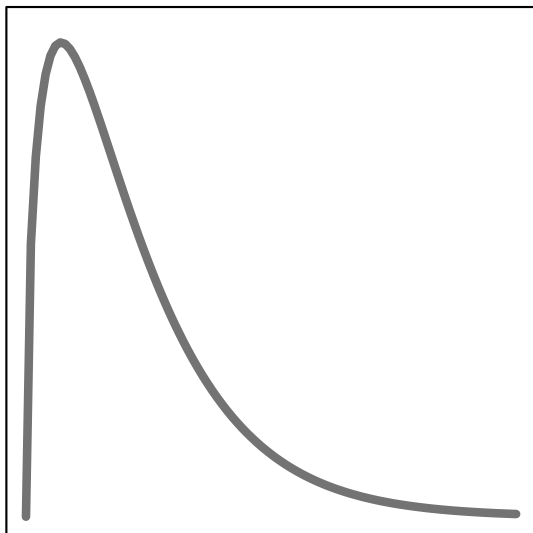
Probability density



Latent abundance

gamma

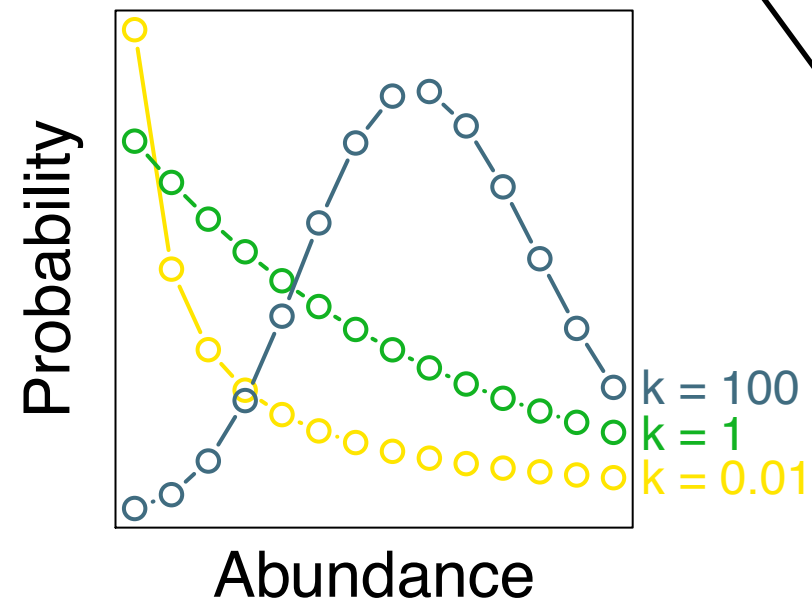
Probability density



Latent abundance

Poisson
log-normal

negative binomial



Poisson
 $k \rightarrow \infty$

geometric
(broken stick)
 $k = 1$

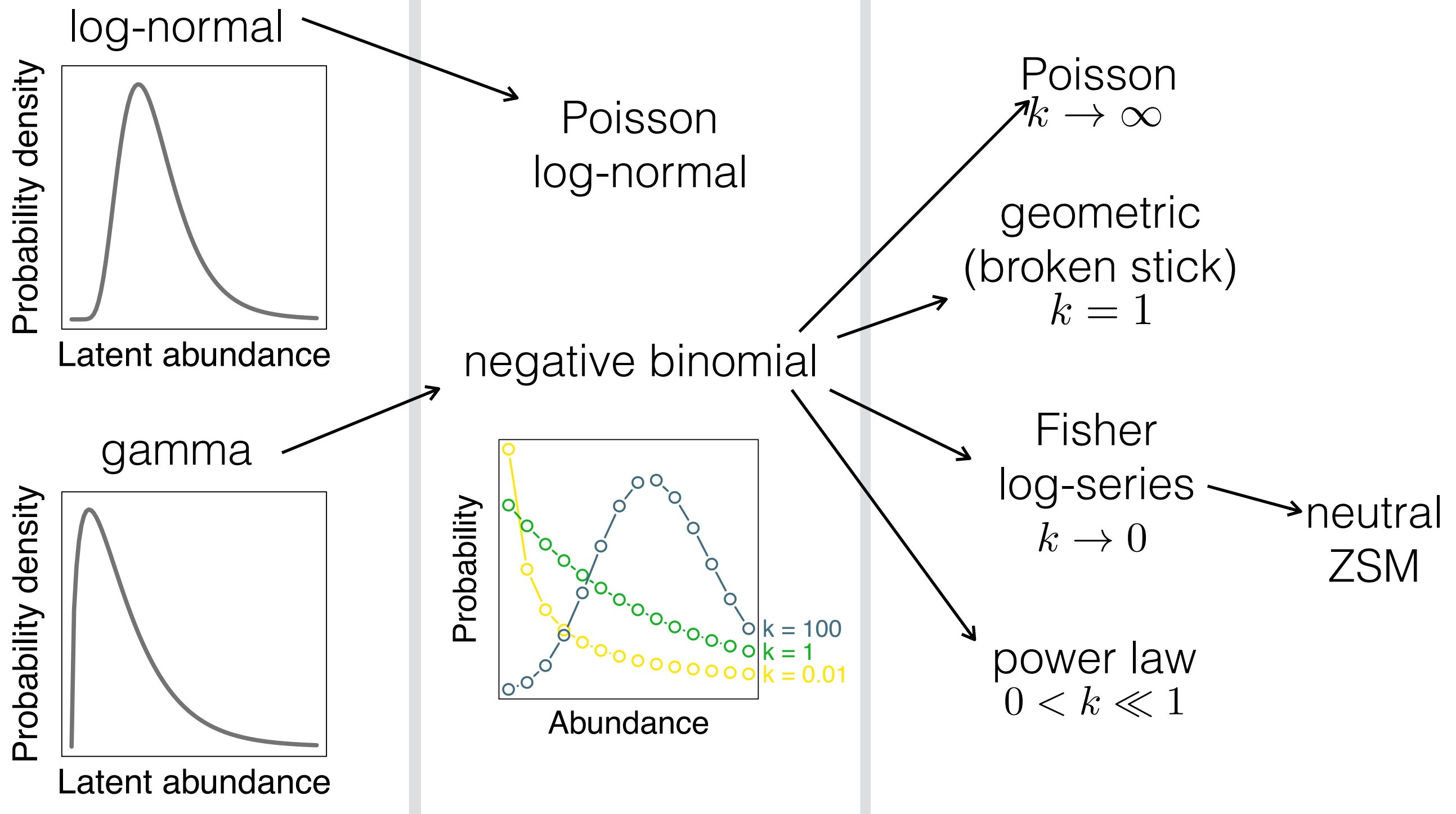
Fisher
log-series
 $k \rightarrow 0$

power law
 $0 < k \ll 1$

Latent distribution

Poisson sampling

Limits

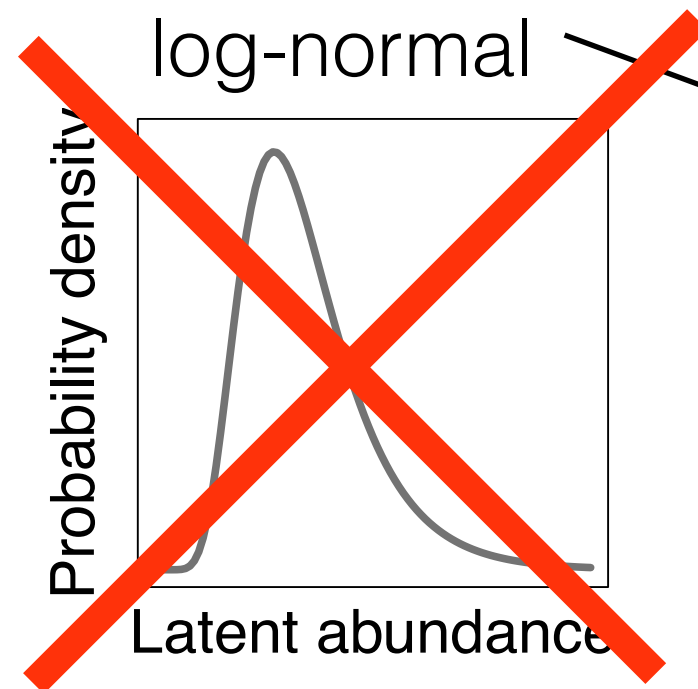


More sampling theories: Green & Plotkin (2007) *Ecol. Lett.*; Conlisk *et al.* (2010) *Oikos*

Latent distribution

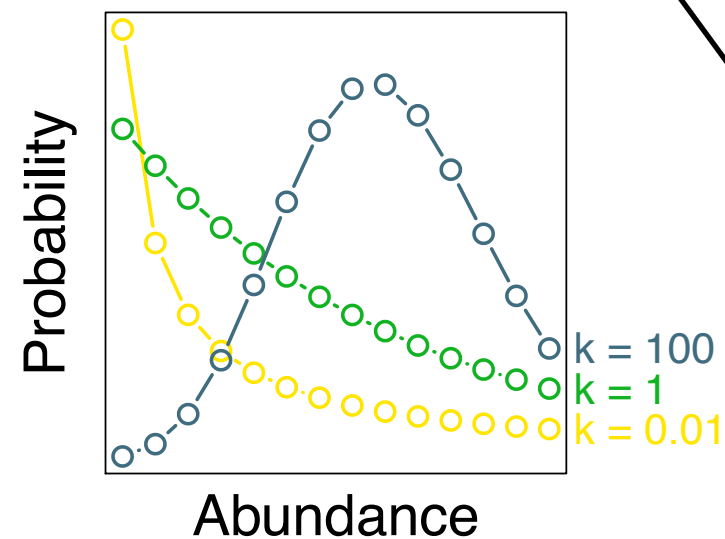
Poisson sampling

Limits



Poisson
log-normal

negative binomial



Poisson
 $k \rightarrow \infty$

geometric
(broken stick)
 $k = 1$

Fisher
log-series
 $k \rightarrow 0$

neutral
ZSM

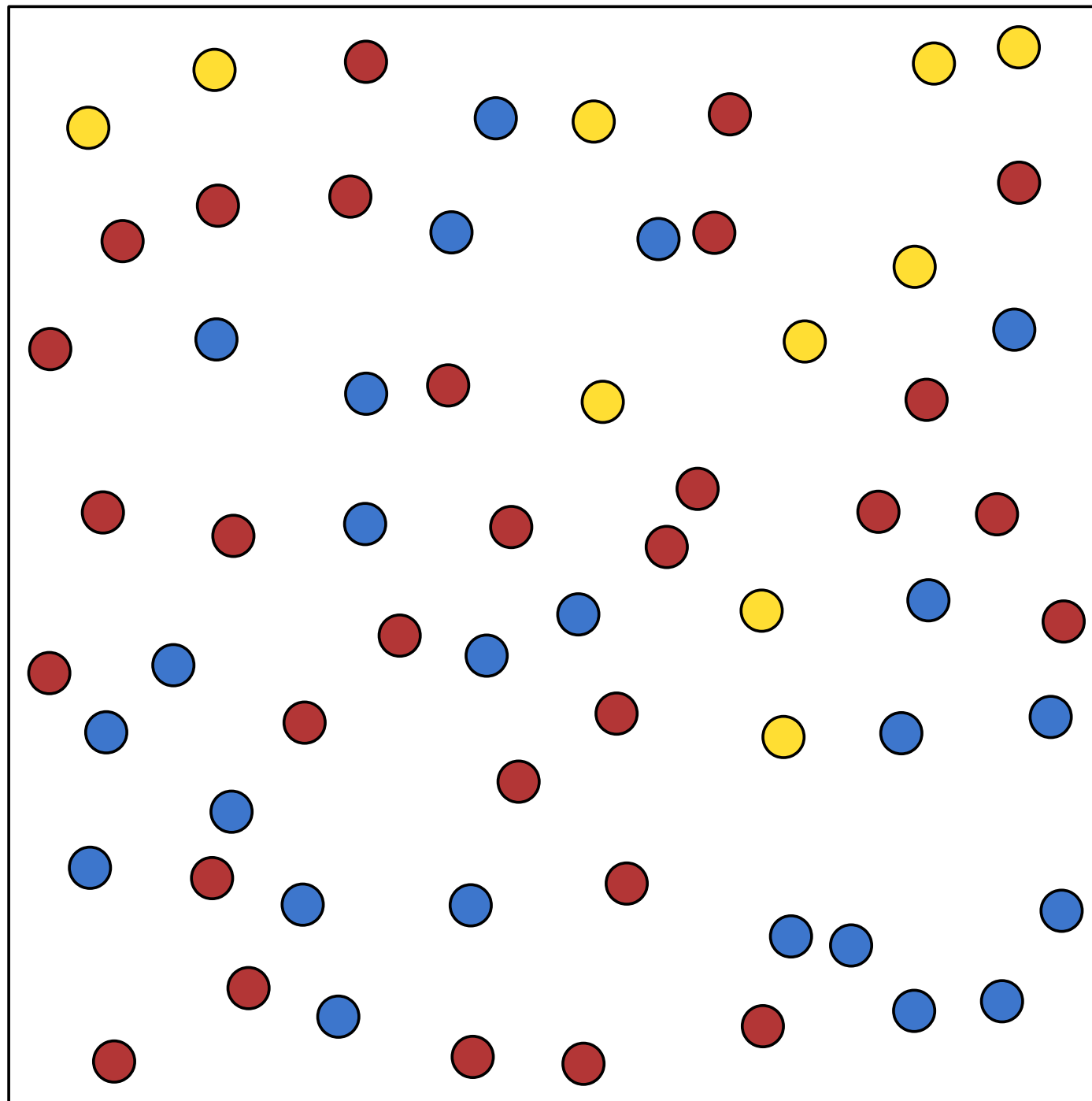
power law
 $0 < k \ll 1$

More sampling theories: Green & Plotkin (2007) *Ecol. Lett.*; Conlisk *et al.* (2010) *Oikos*

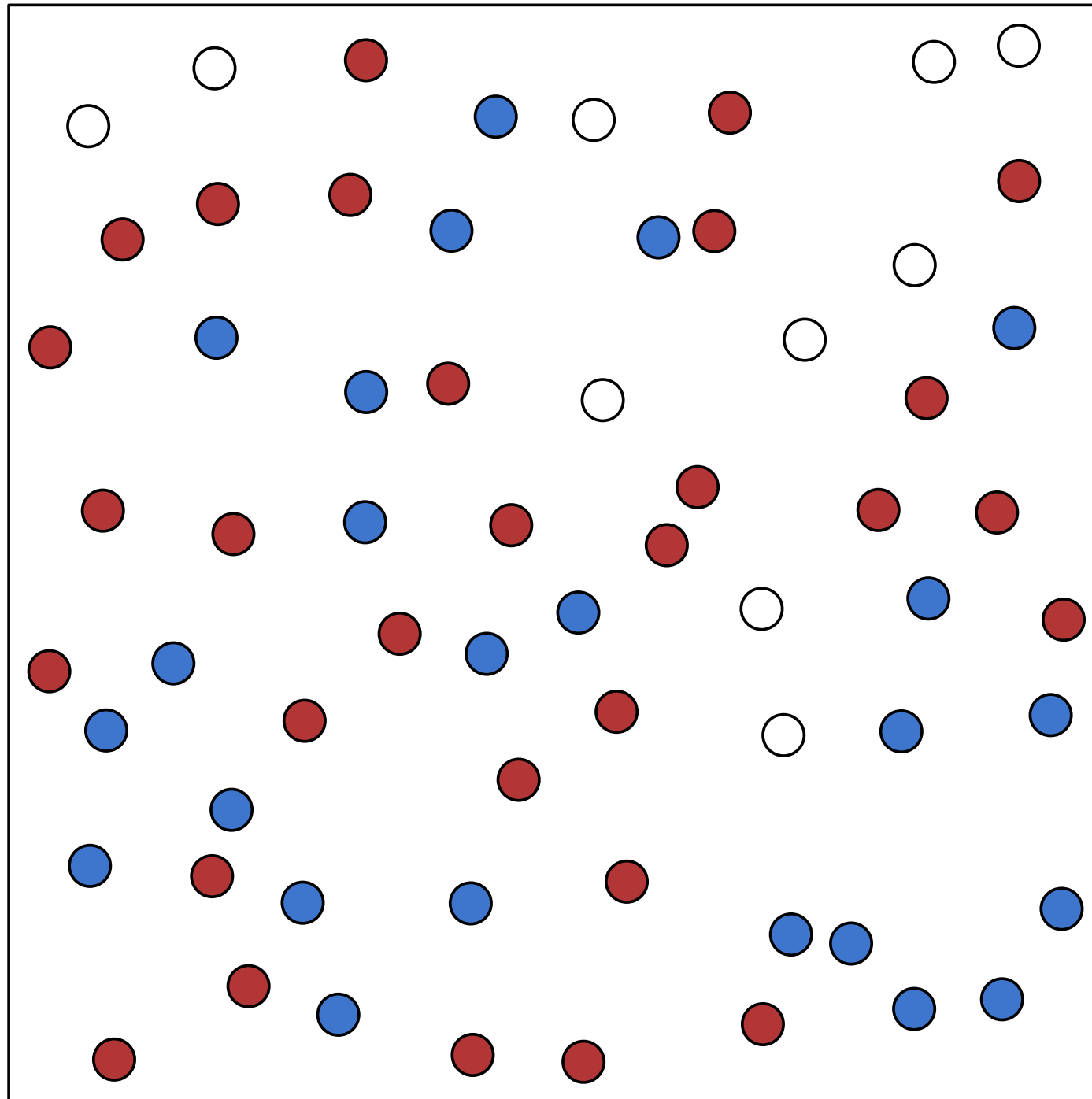
Subsampling

The veil-line is a fallacy

Subsampling

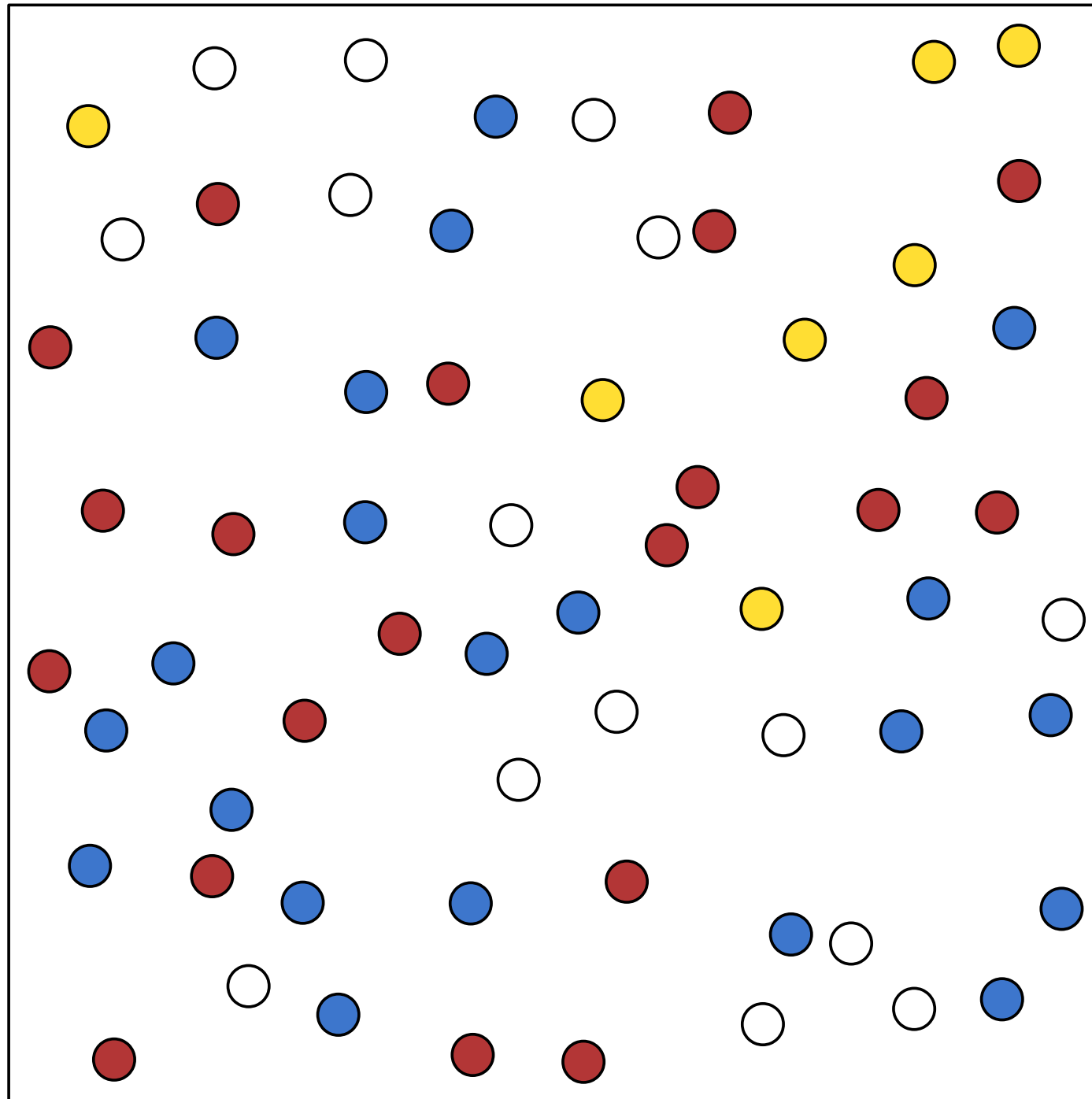


Subsampling



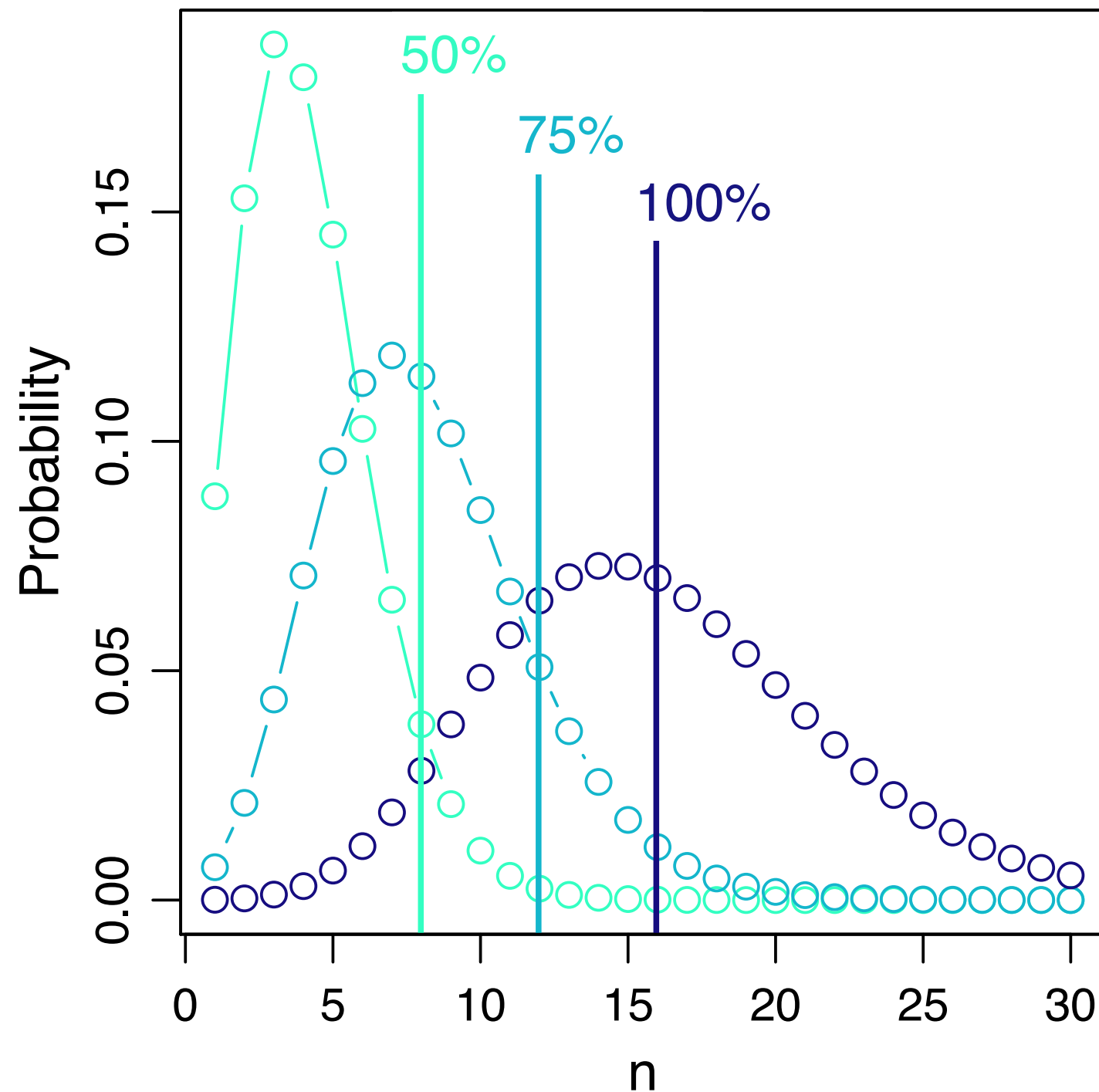
we don't sample species

Subsampling



we sample individuals

Subsampling

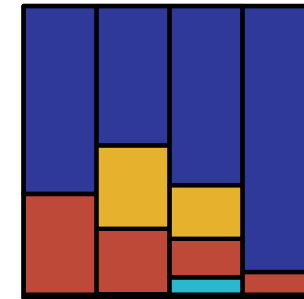
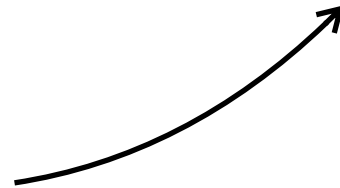


Poisson sampling changes mean but not parametric form

Subsampling

Logseries PoisLogNorm BrokenStick TruncNegBin

simulate true
distribution



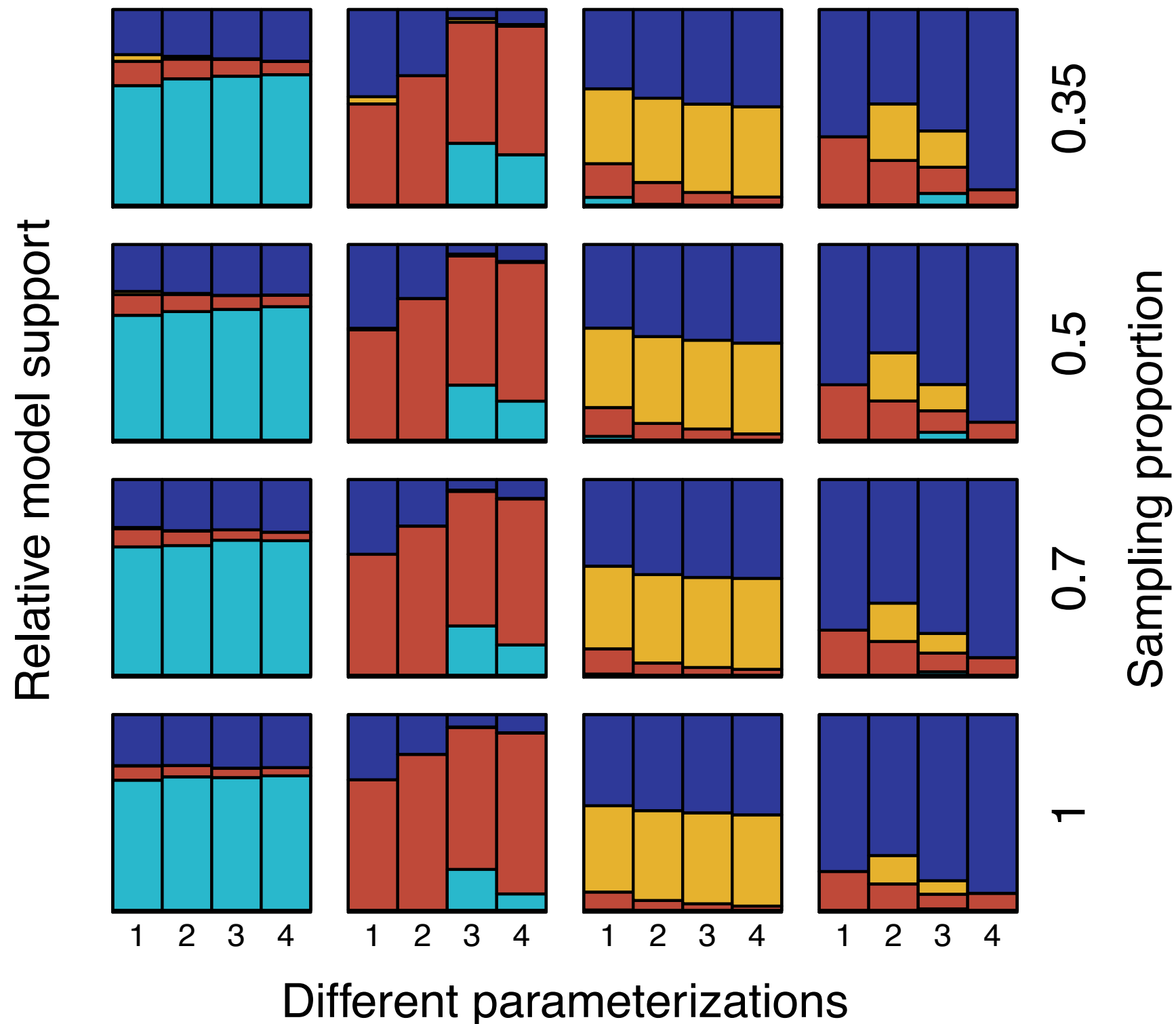
for each, fit all models

1 0.7 0.5 0.35
Sampling proportion

Different parameterizations

Subsampling

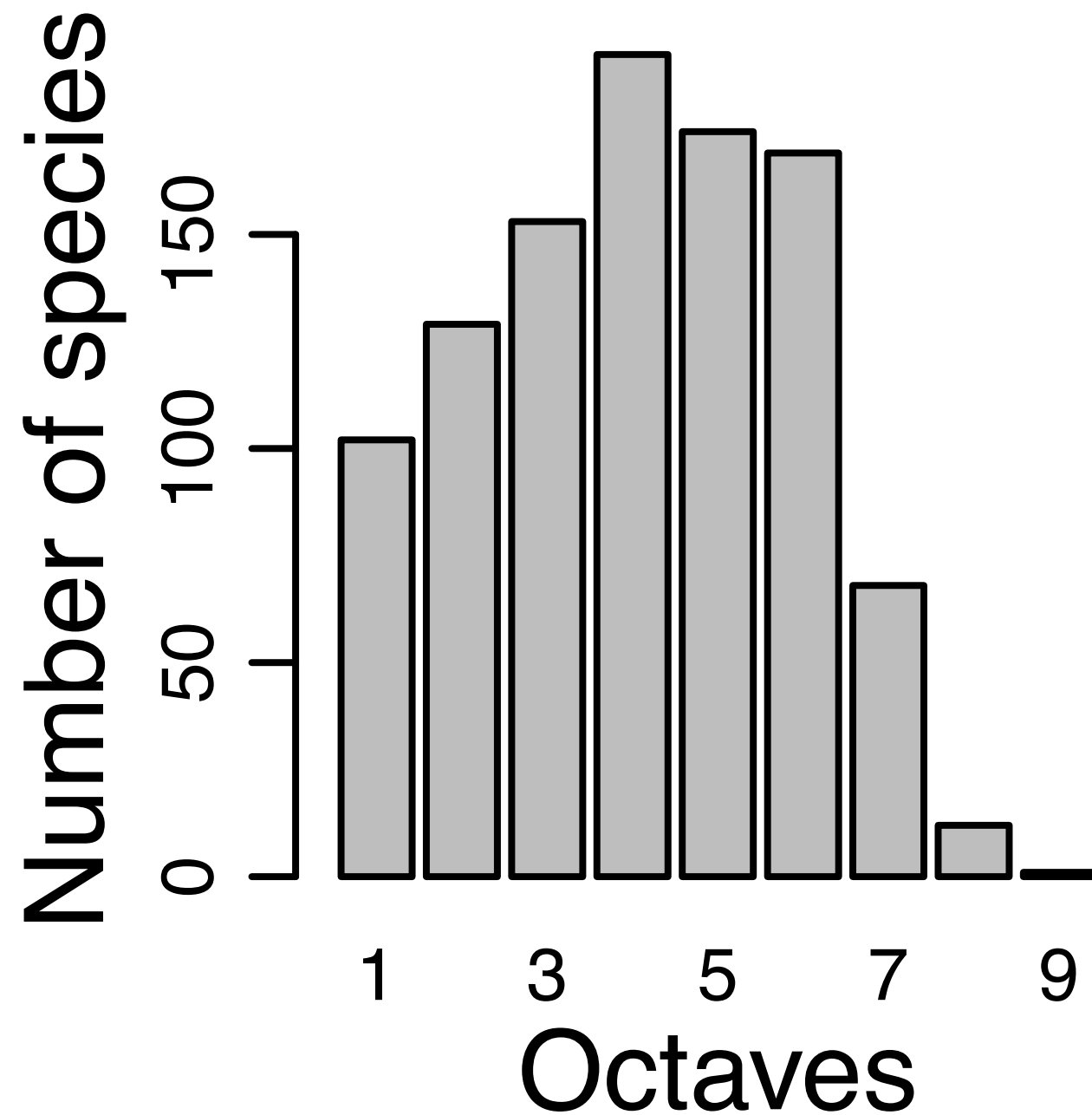
Logseries PoisLogNorm BrokenStick TruncNegBin



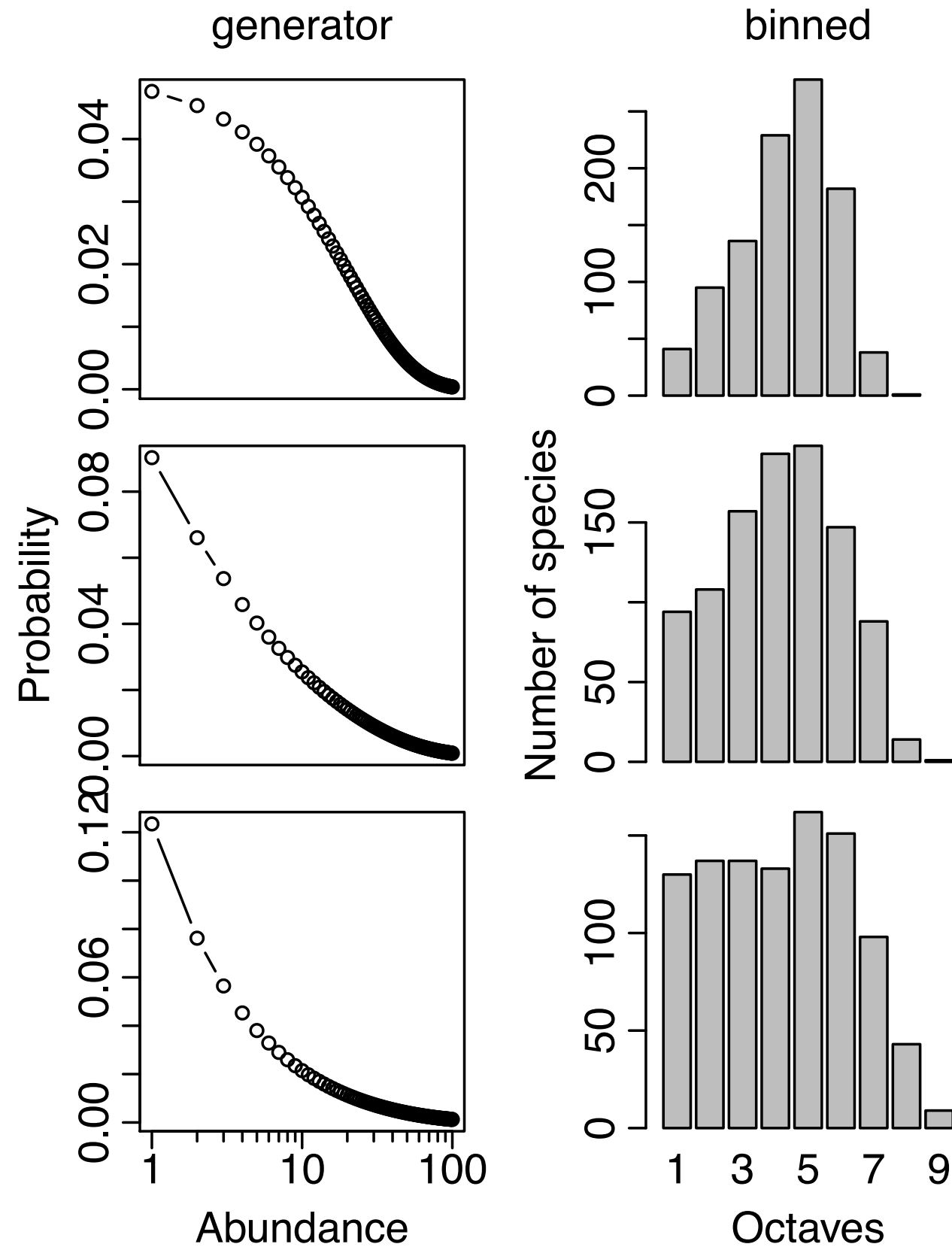
Evaluating model fit

Giving one model wins, *how good* is it really?

Evaluating model fit

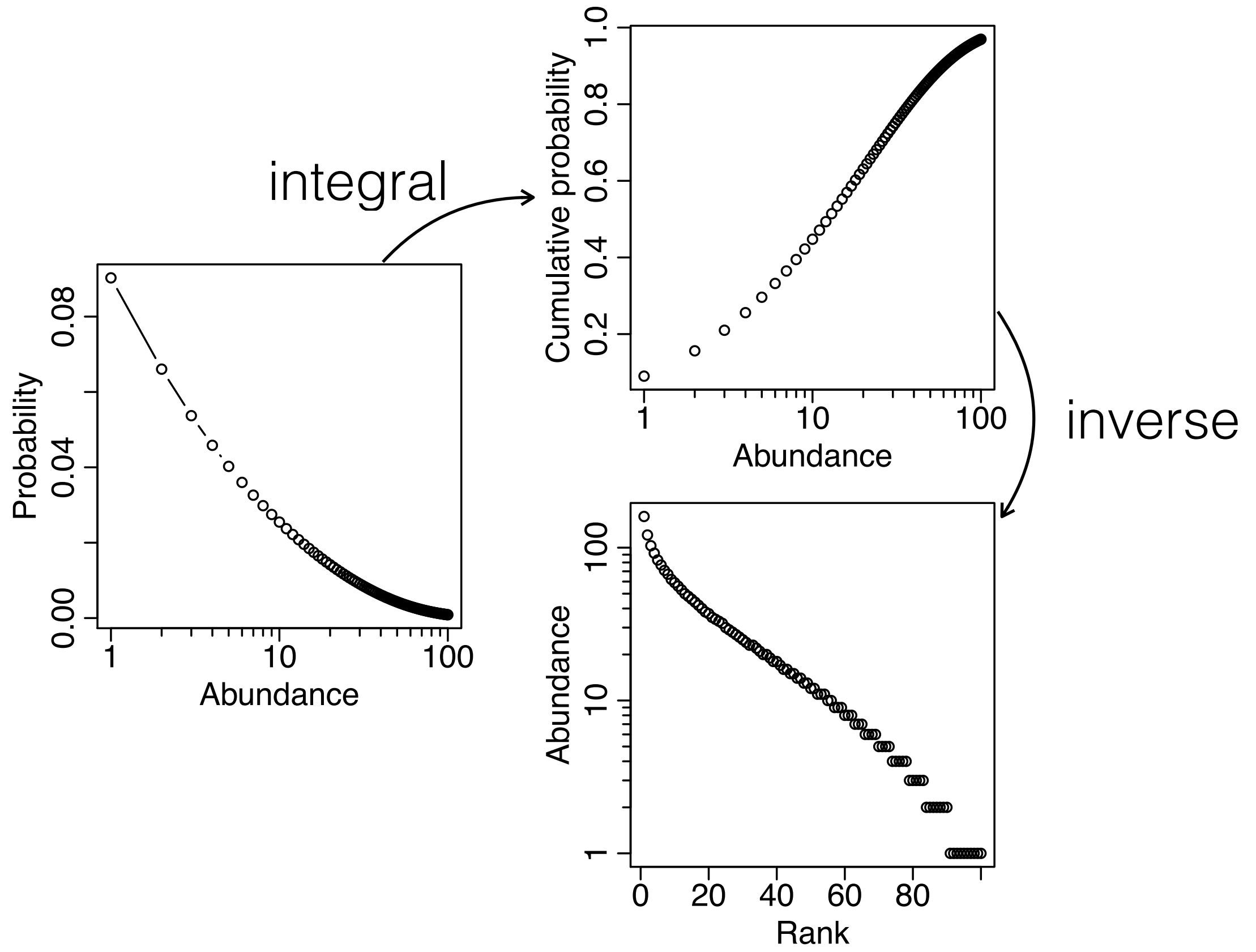


Binning is bad

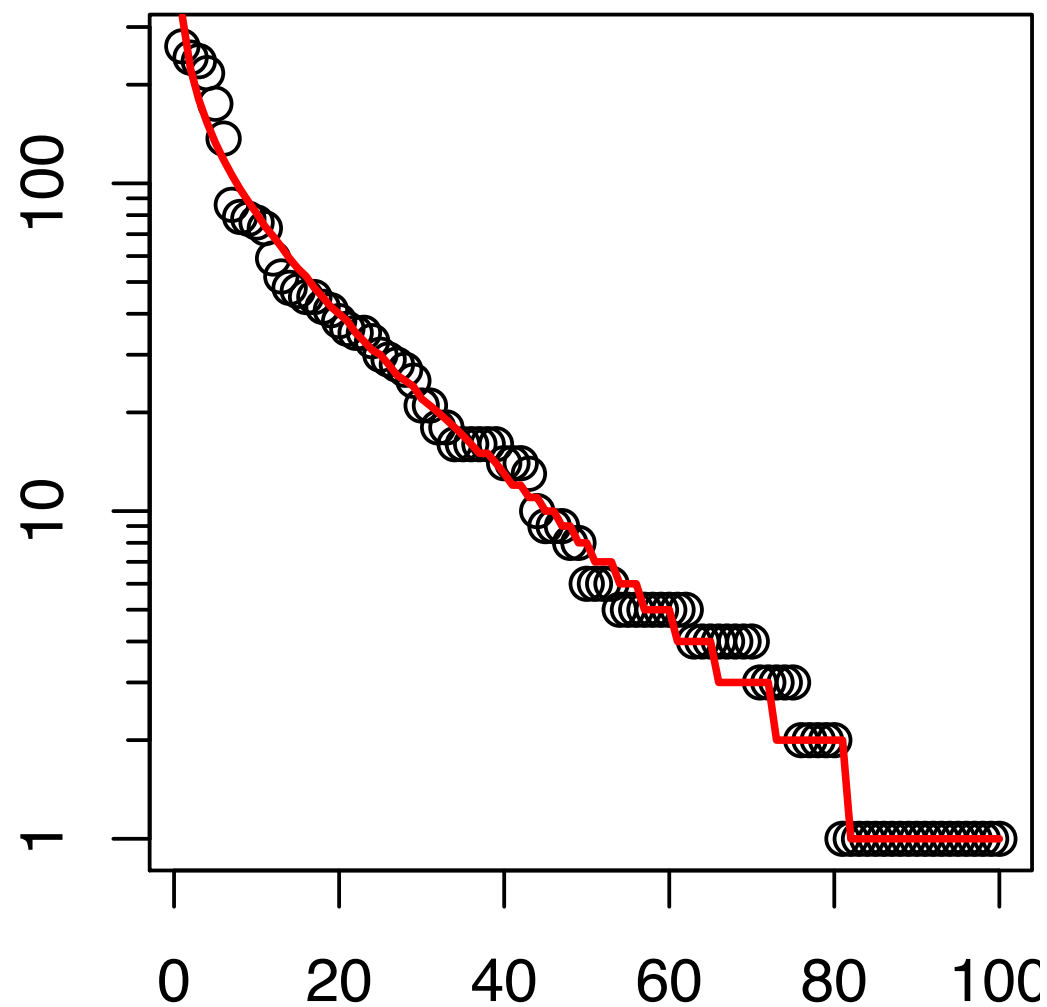
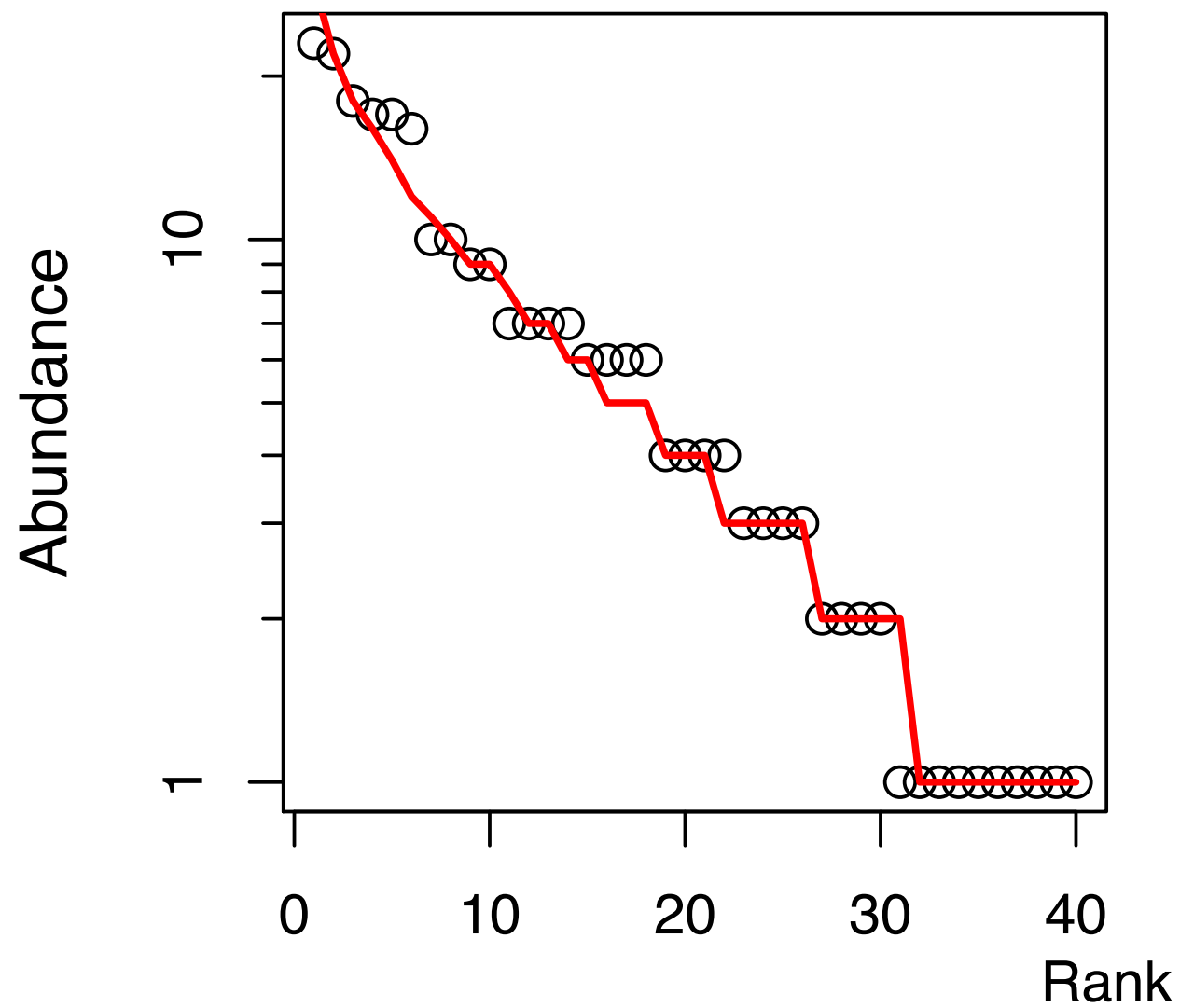


Nekola, et al. (2008)
Folia Geobotanica

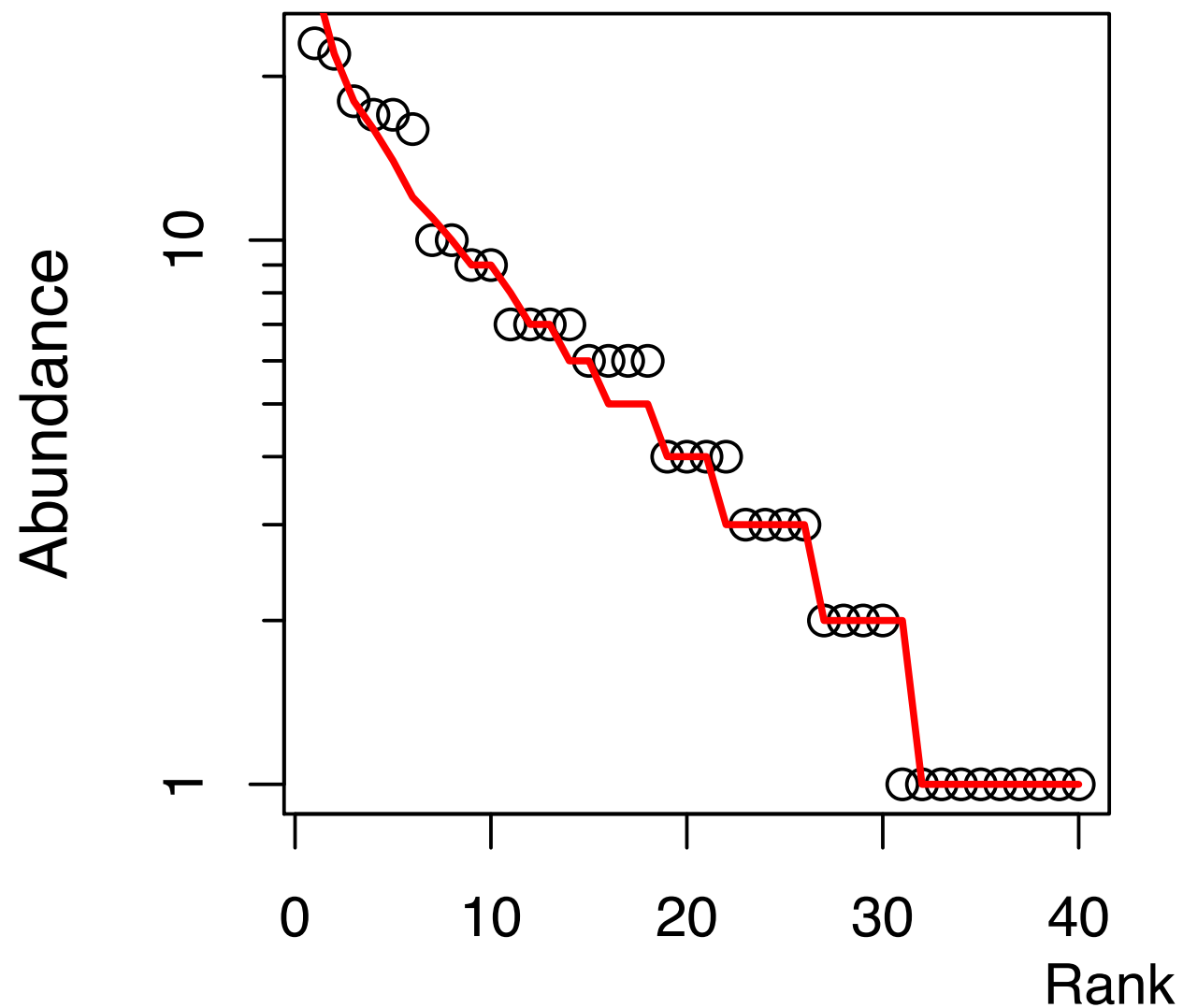
Don't bin!



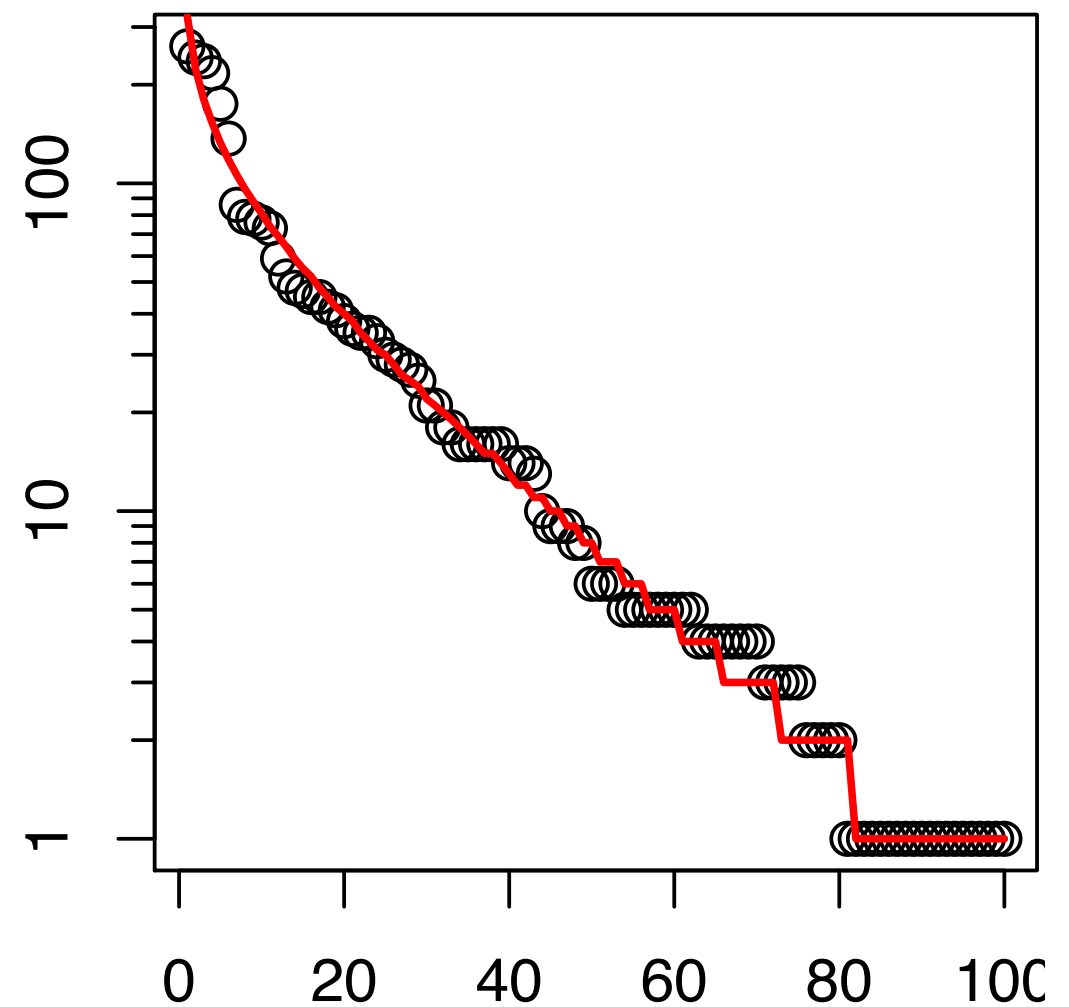
Evaluating model fit



Evaluating model fit

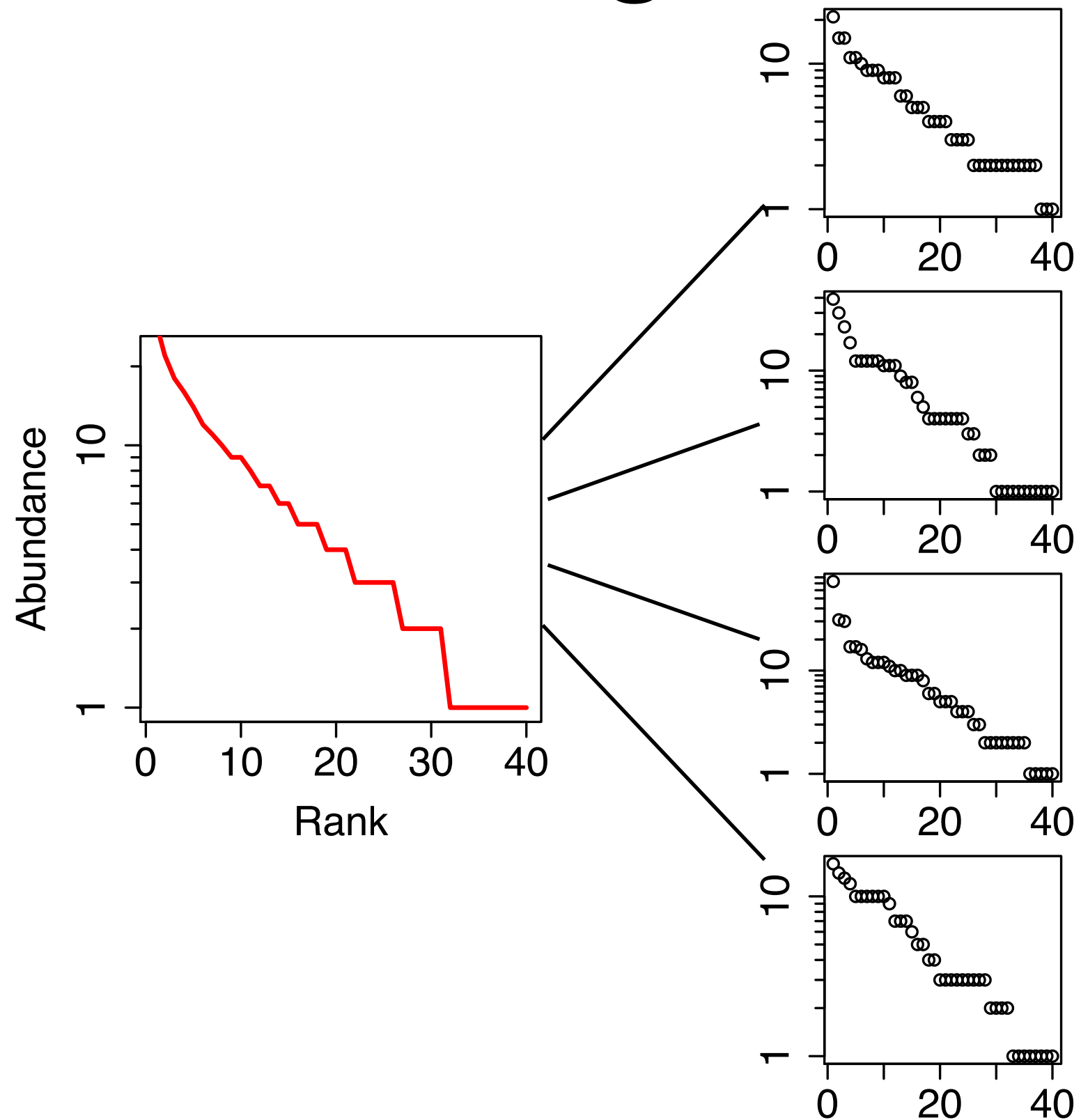


$\log\text{Lik} = -109.0252$

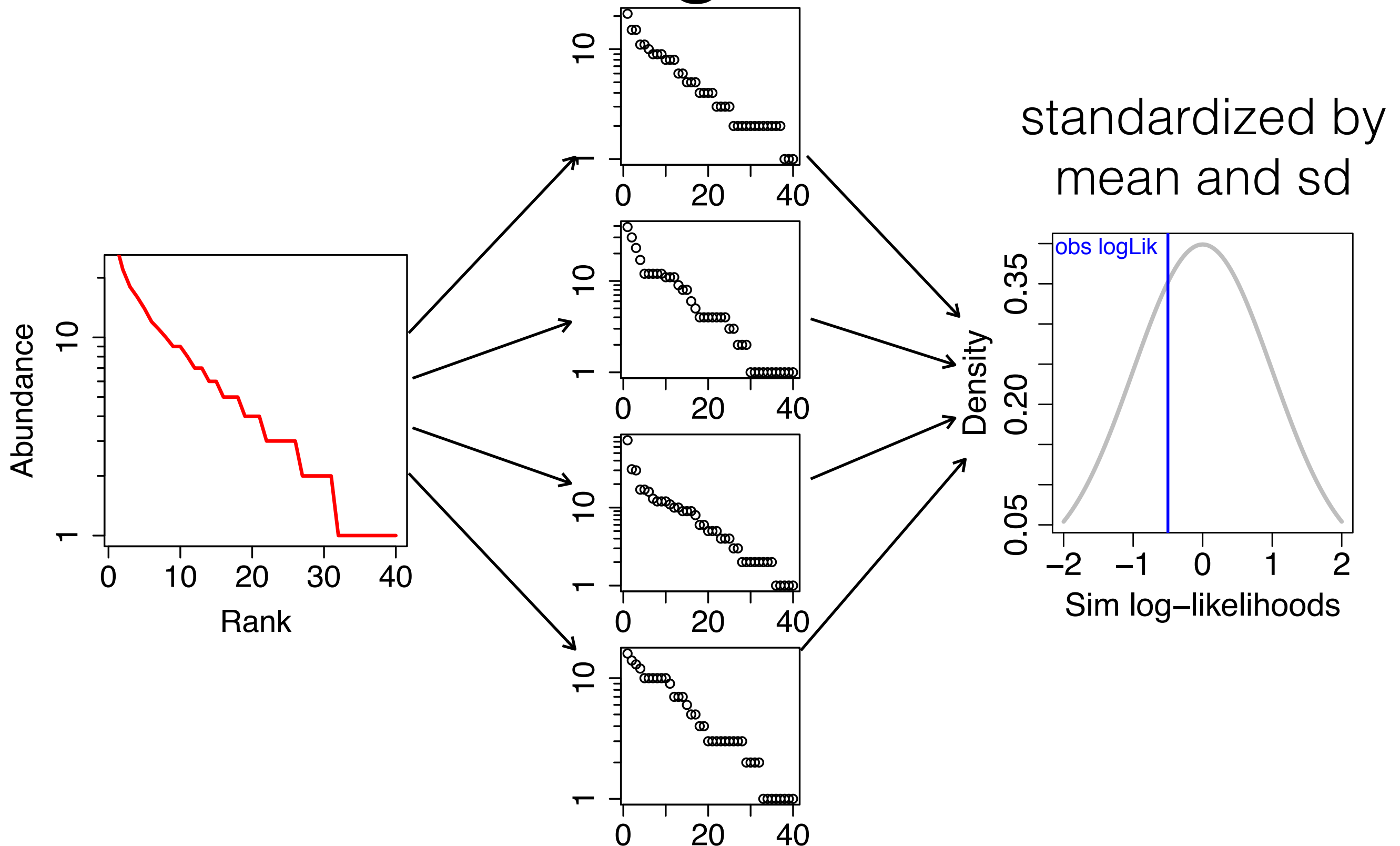


$\log\text{Lik} = -392.3673$

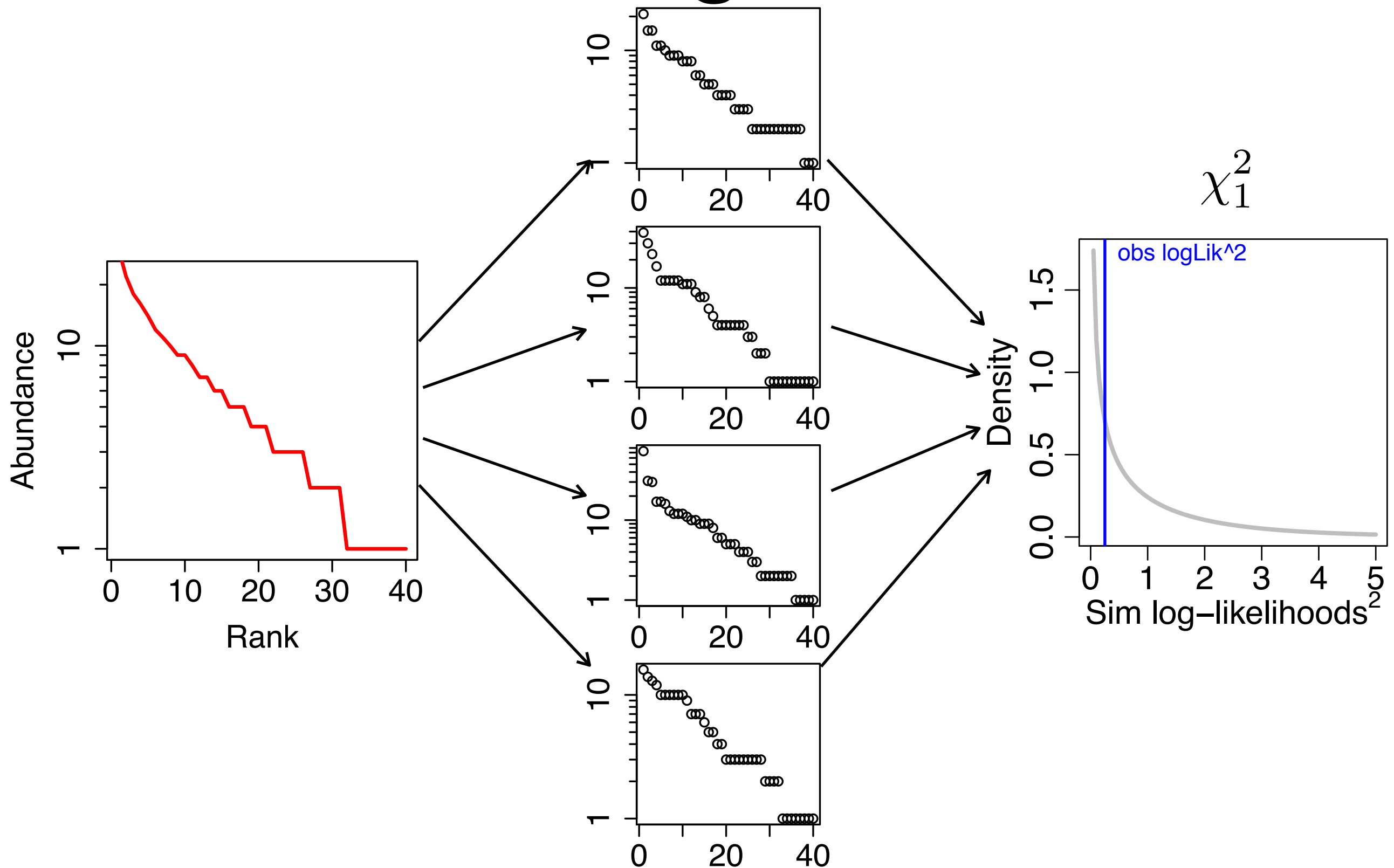
Evaluating model fit



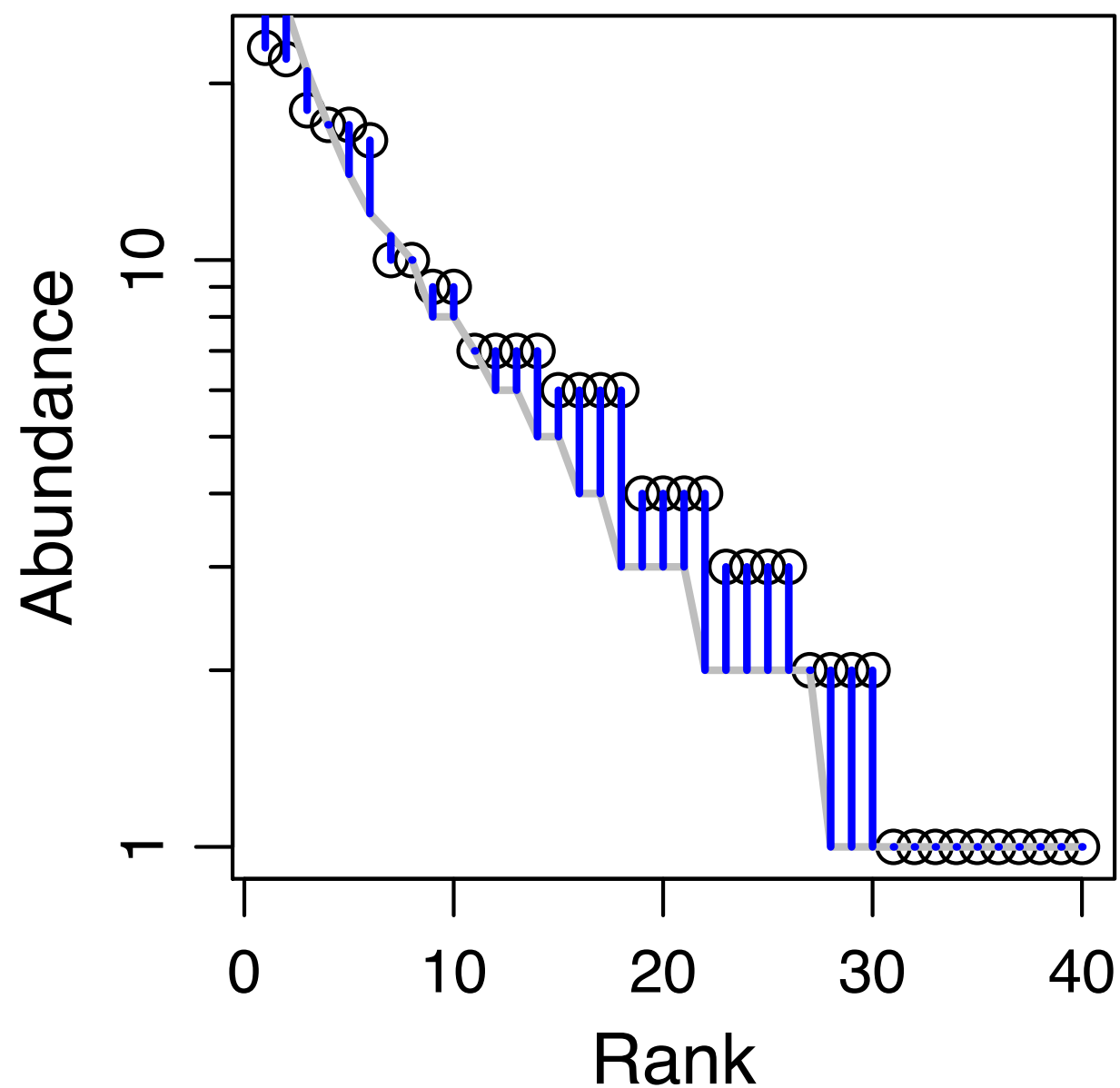
Evaluating model fit



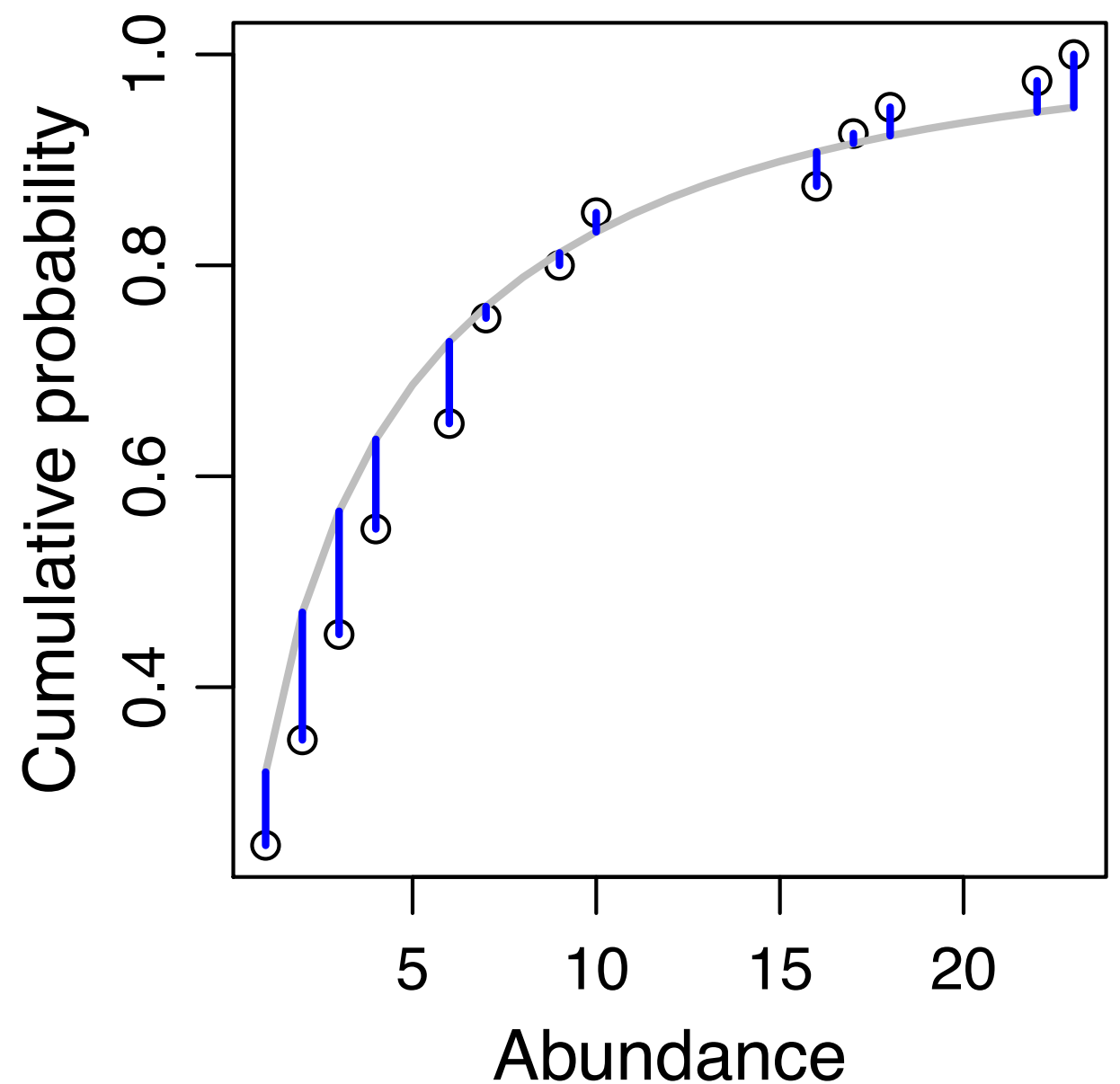
Evaluating model fit



Evaluating model fit

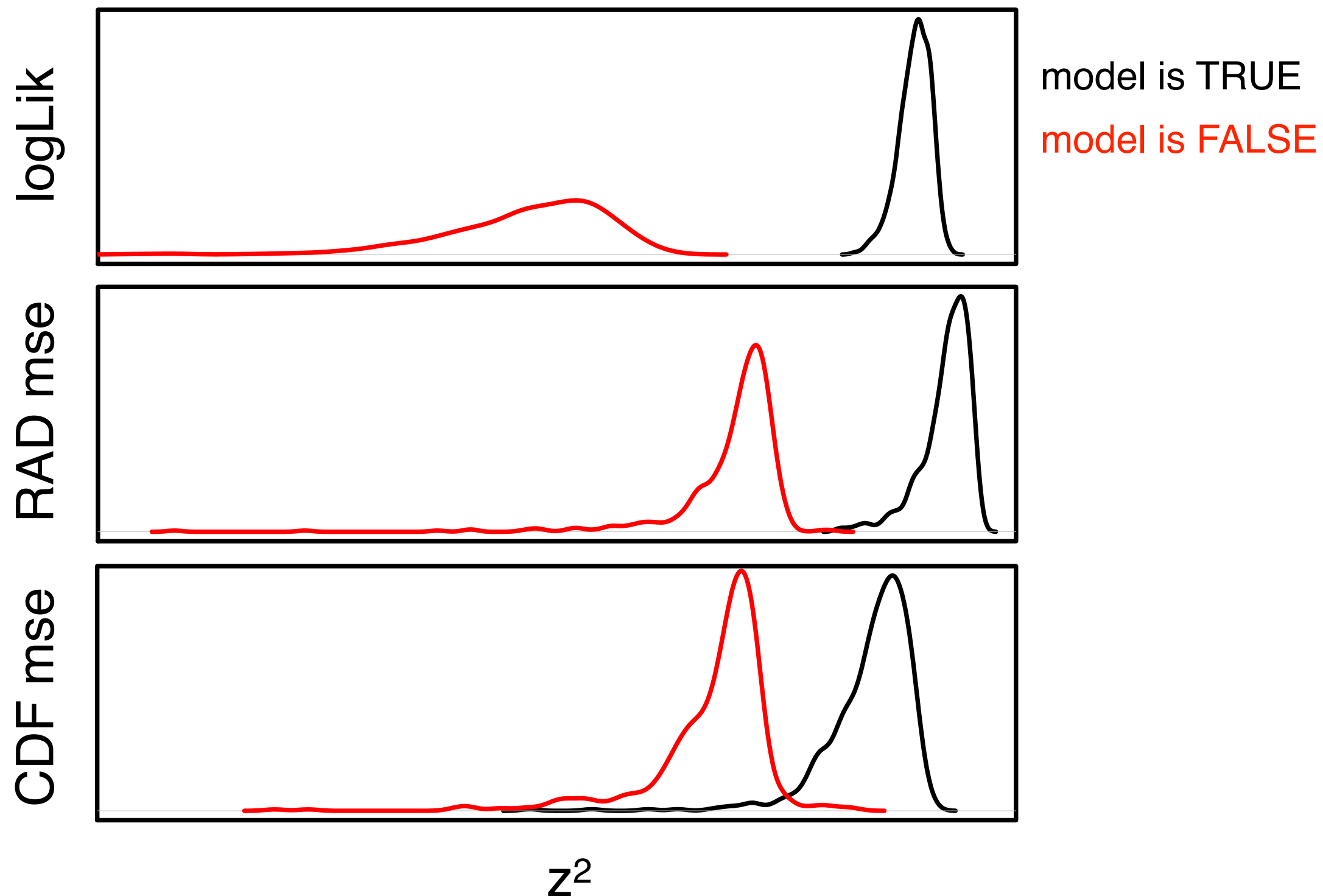


RAD mean squared error

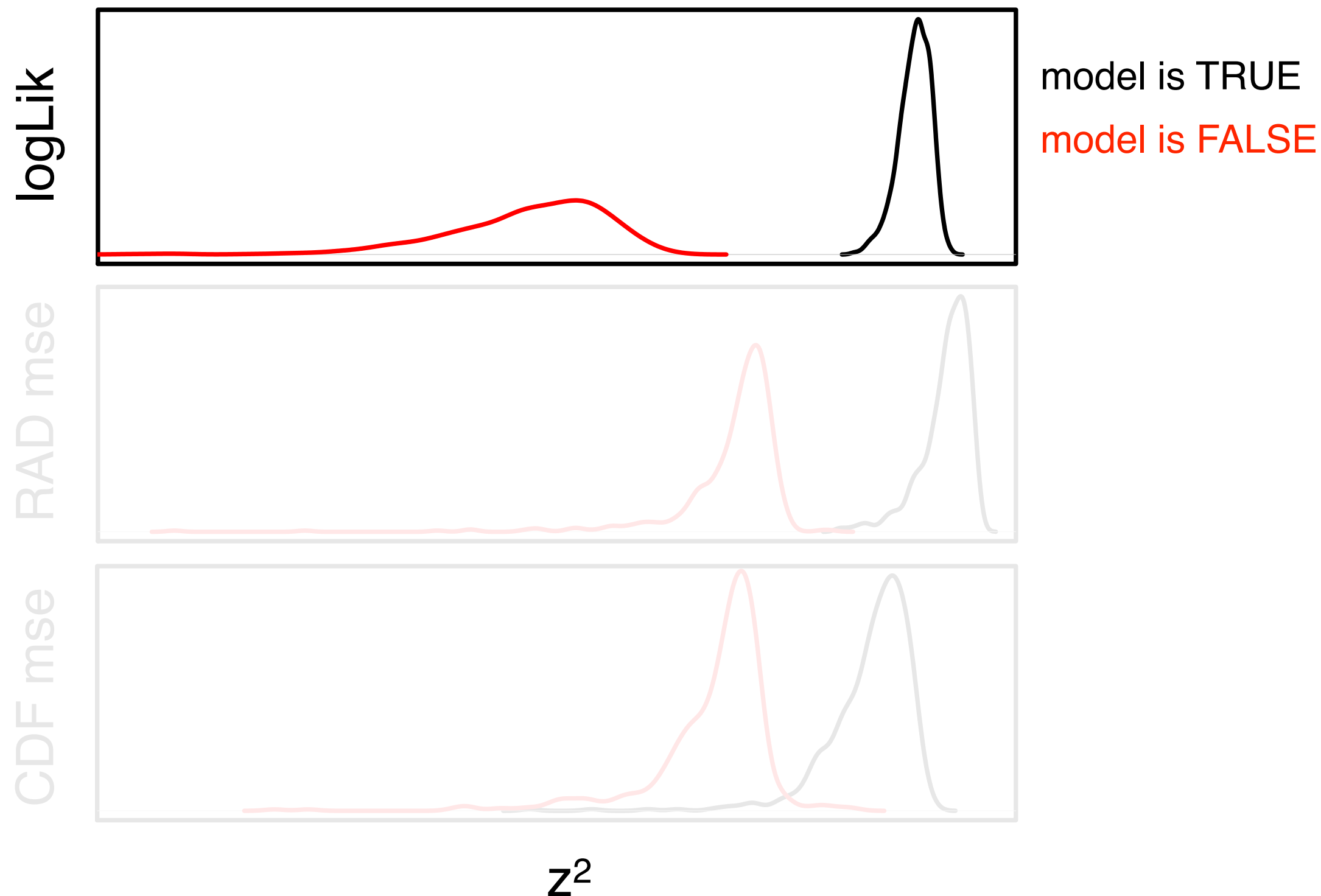


CDF mean squared error

Evaluating model fit



Likelihood is good



Seeking generality

Latent distribution

Poisson sampling

Limits

negative binomial

Poisson
 $k \rightarrow \infty$

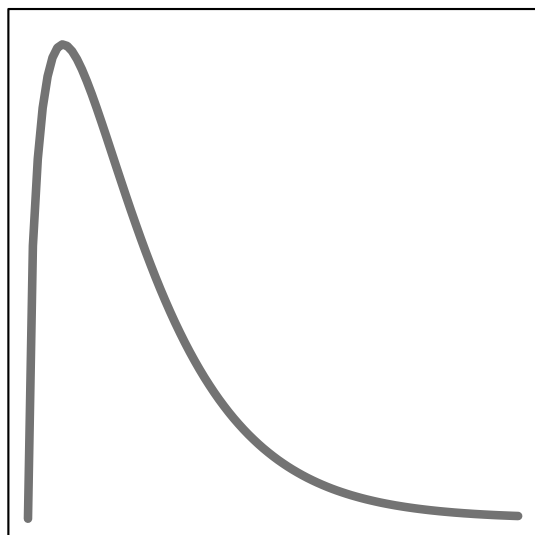
geometric
(broken stick)
 $k = 1$

Fisher
log-series
 $k \rightarrow 0$

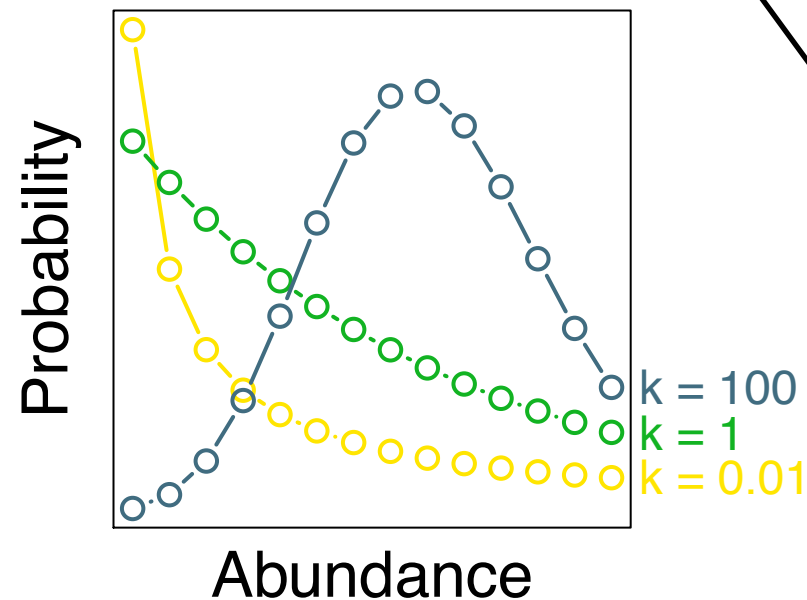
power law
 $0 < k \ll 1$

gamma

Probability density



Latent abundance



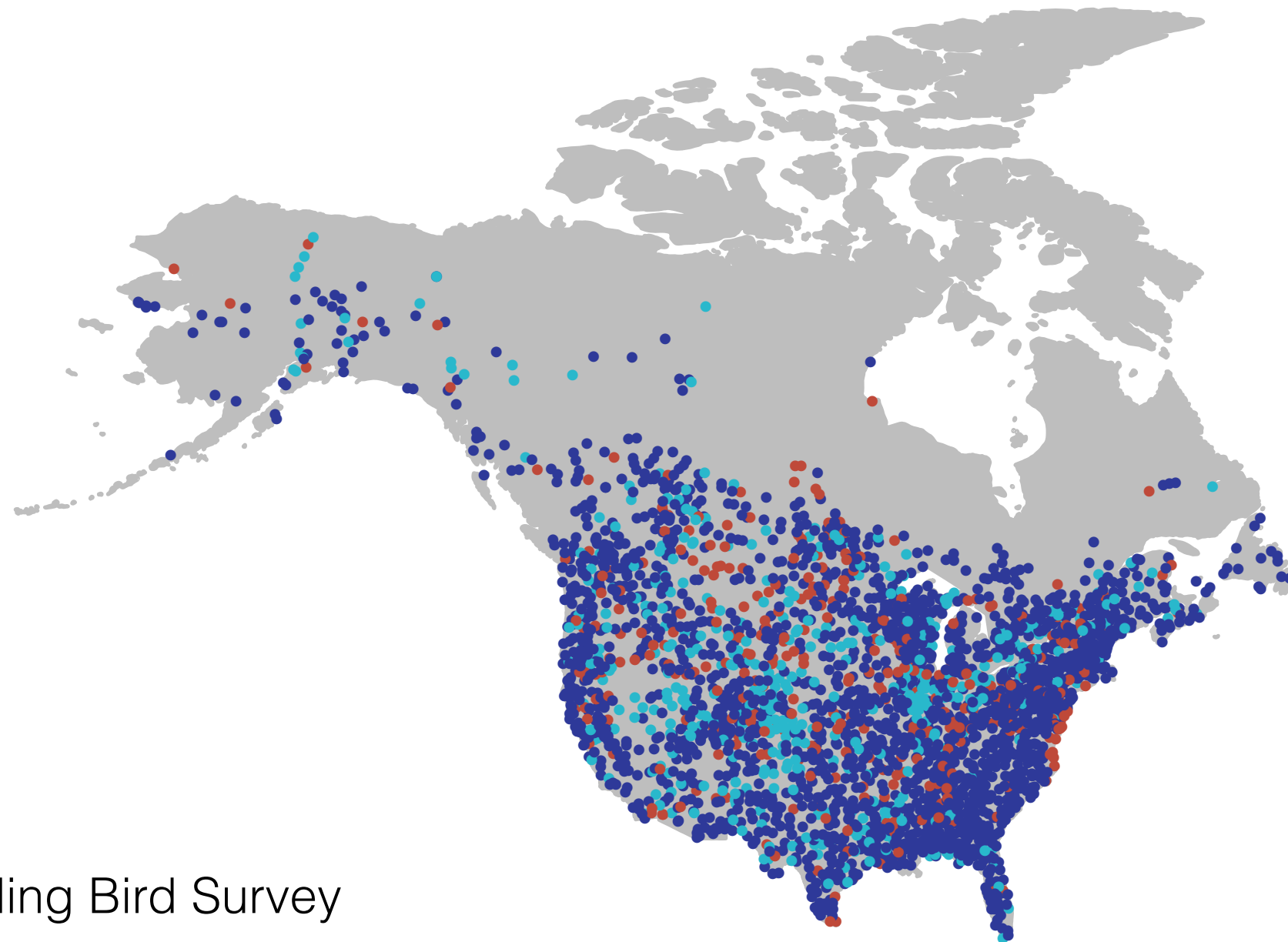
Pois log-
lognorm series

neg binom

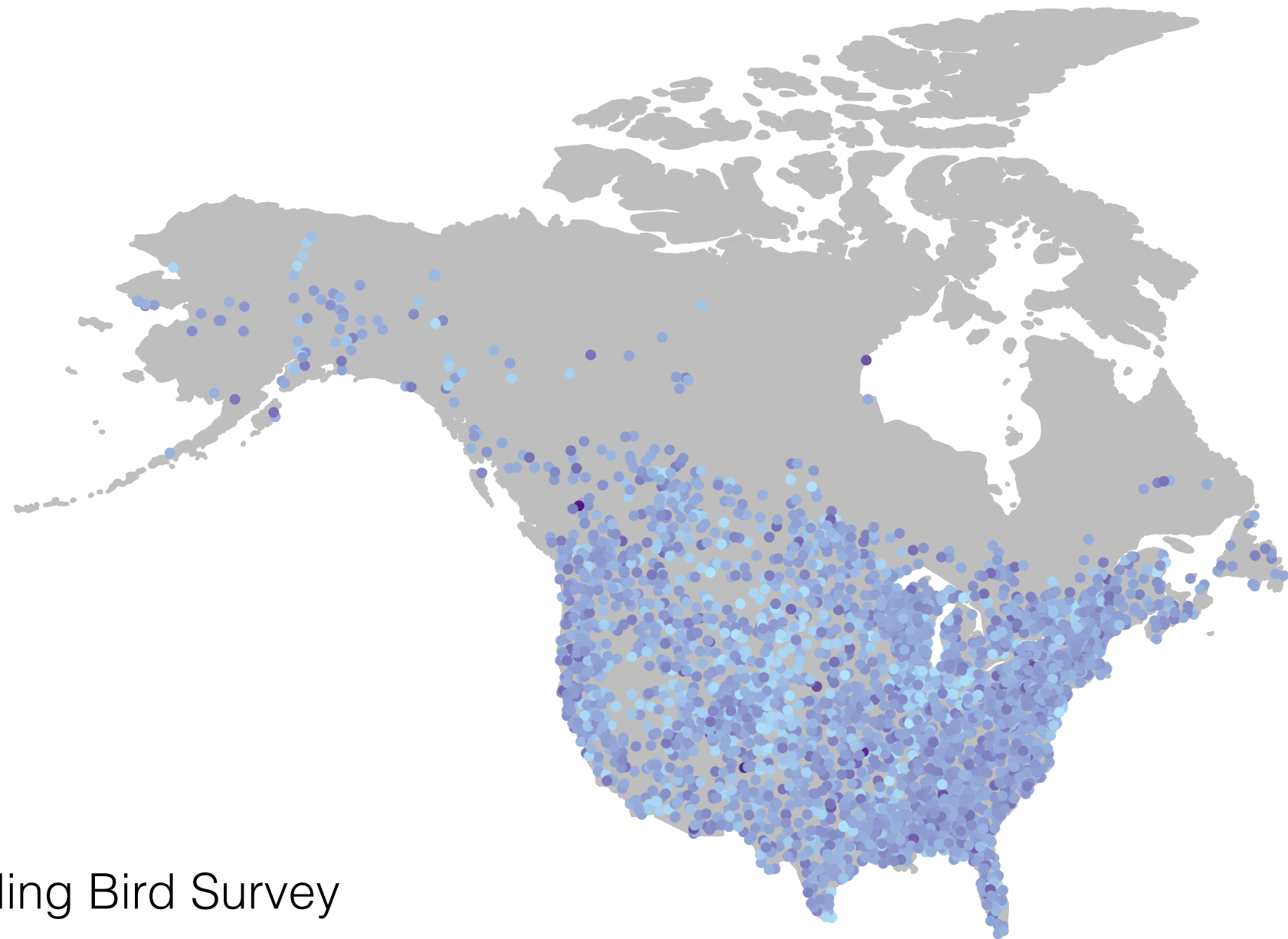
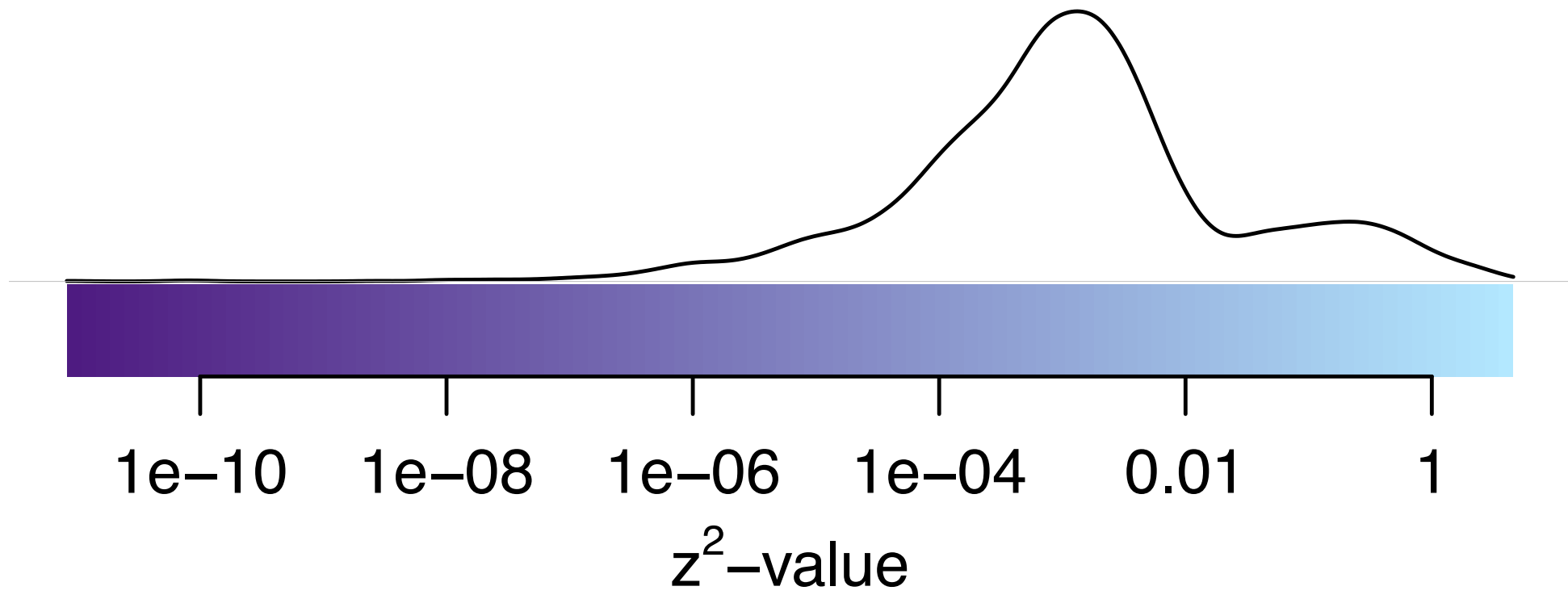
343

439

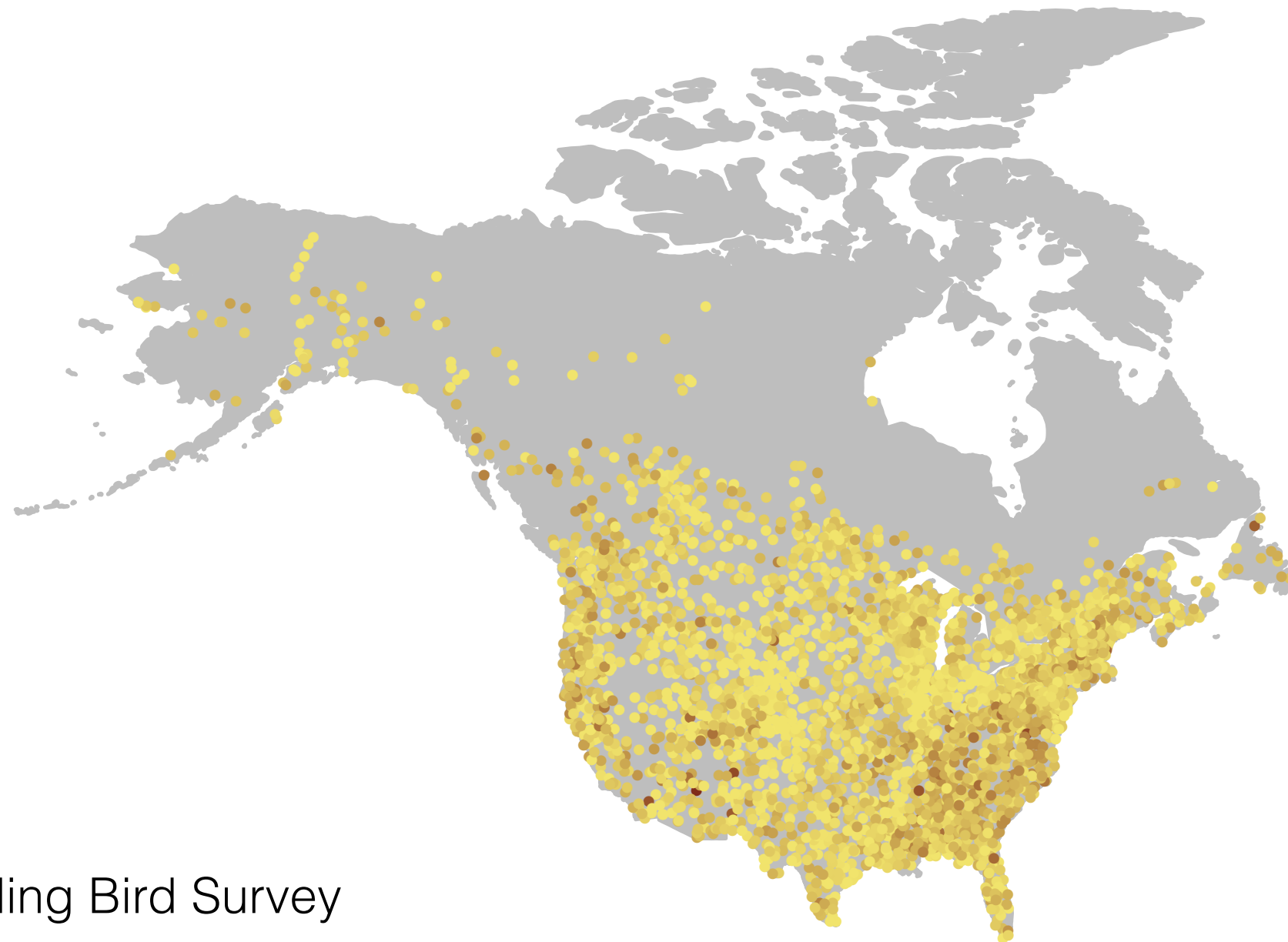
2176



data from Breeding Bird Survey

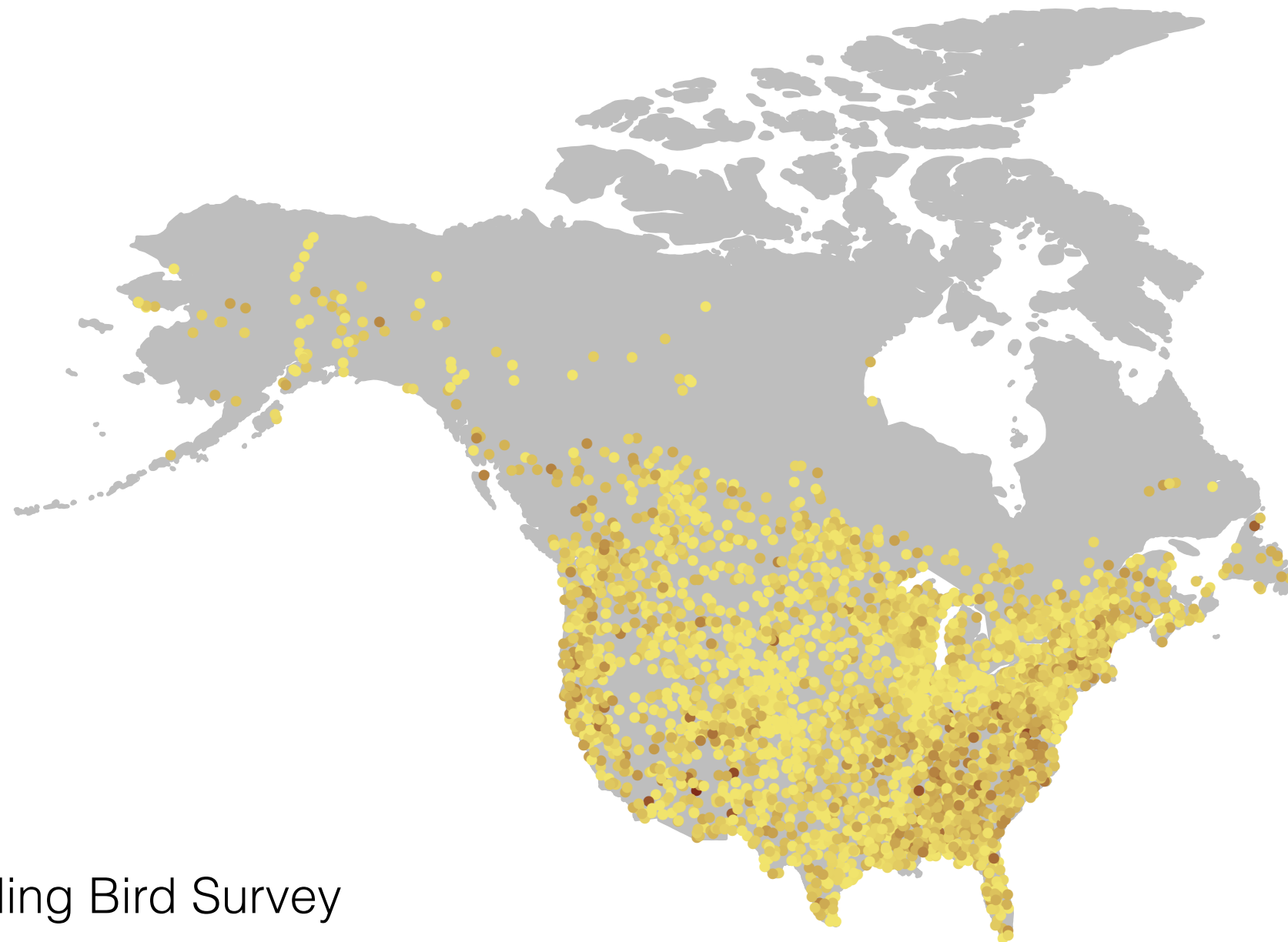


data from Breeding Bird Survey



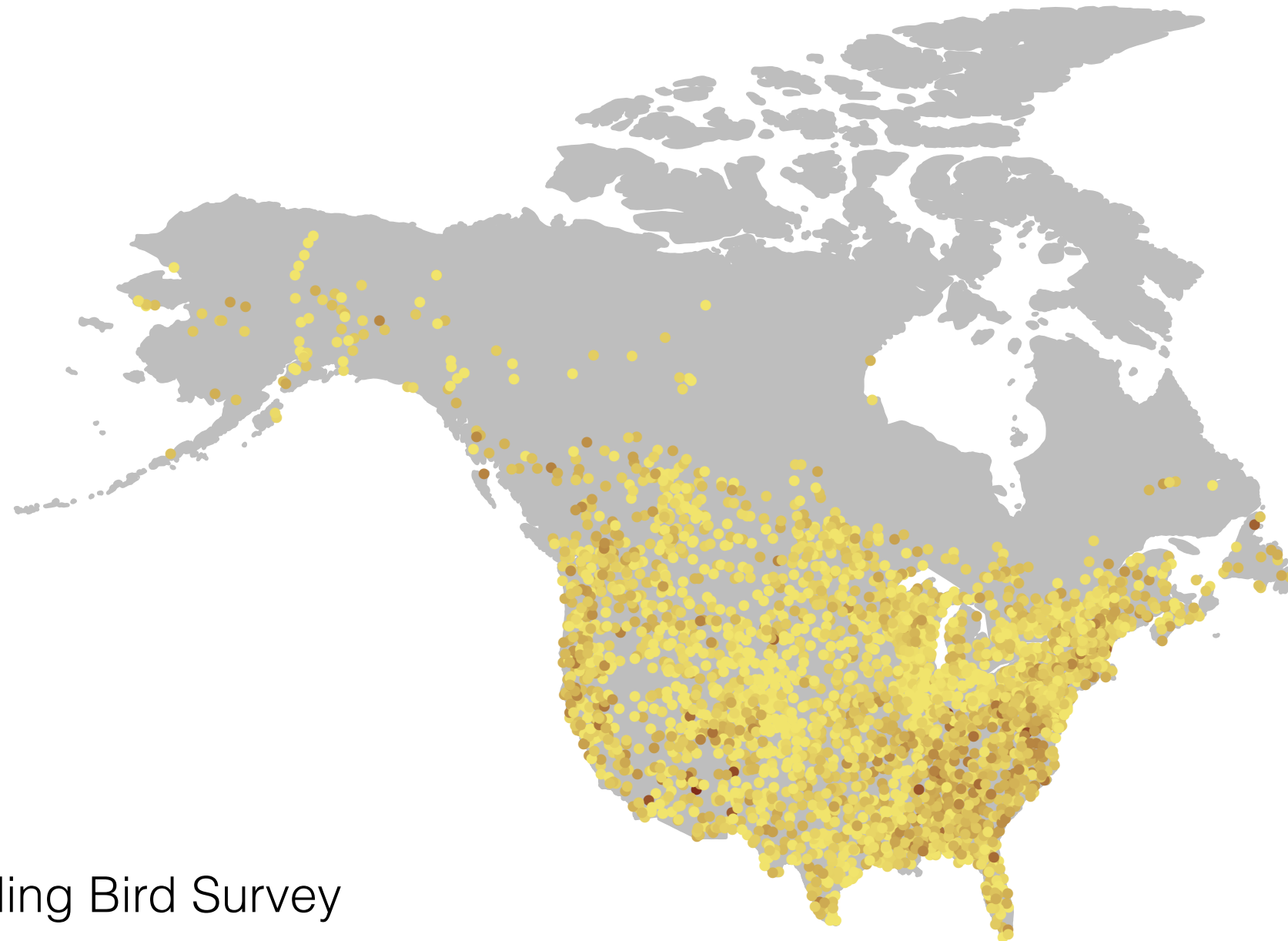
data from Breeding Bird Survey

Predicted by: environment? landuse? evolutionary history?



data from Breeding Bird Survey

Predicted by: environment? landuse? evolutionary history?
Why Gamma?



data from Breeding Bird Survey

Thanks!



J. Harte

y'all



C. Merow

Berkeley
UNIVERSITY OF CALIFORNIA

Global Change Biology



Thanks!



J. Harte

y'all



C. Merow

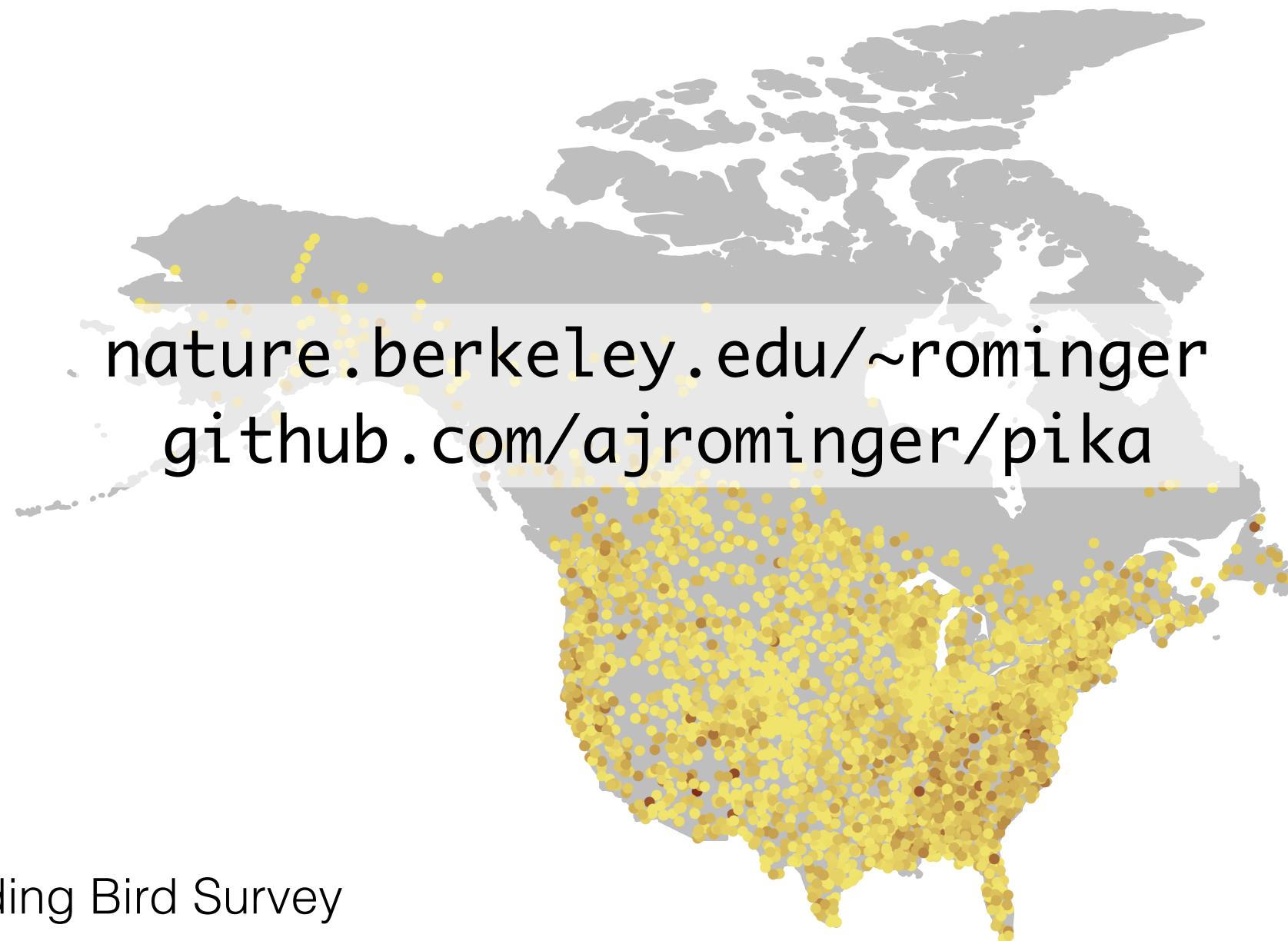
github.com/ajrominger/pika

Berkeley
UNIVERSITY OF CALIFORNIA

Global Change Biology



Questions?



data from Breeding Bird Survey