Model comparison: Confirmatory and Exploratory analysis

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Outline


ALWAYS HOPE, THERE IS

Principles for statistical ecology

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Methods in Ecology and Evolution

REVIEW

Four principles for improved statistical ecology

Gordana Popovic[1] | Tanya Jane Mason[2,3] | Szymon Marian Drobniak[4,5] | Tiago André Marques[6,7] | Joanne Potts[8] | Rocío Joo[9] | Res Altwegg[10] | Carolyn Claire Isabelle Burns[11] | Michael Andrew McCarthy[12] | Alison Johnston[13] | Shinichi Nakagawa[4] | Louise McMillan[14] | Kadambari Devarajan[15,16] | Patrick Leo Taggart[17] | Alison Wunderlich[18] | Magdalena M. Mair[19,20] | Juan Andrés Martínez-Lanfranco[21] | Malgorzata Lagisz[4] | Patrice Pottier[4]

Poor practice

- Hypothesising after results are known (HARKing)
- Not reporting non-significant results
- Misinterpreting non-significant results
- Providing insufficient detail on methods and analysis
- P-hacking

Four principles

1. Define a focused research question
   - Plan sampling
   - Plan analysis
2. Develop a model
   - Think about the distribution
   - Generally consider data properties (e.g., dependence)
3. Report methods in detail
   - Report findings in detail
   - Ensure reproducibility

A protocol for data exploration

Methods in Ecology and Evolution

British Ecological Society

Methods in Ecology and Evolution 2010, **1**, 3–14 doi: 10.1111/j.2041-210X.2009.00001.x

A protocol for data exploration to avoid common statistical problems

Alain F. Zuur*[1,2], Elena N. Ieno[1,2] and Chris S. Elphick[3]

Highly cited. Perhaps because this is a difficult subject?

A protocol: steps

1) Look for outliers
2) Check constant variance
3) Check normality
4) Consider excess zeros
5) Explore collinearity of covariates
6) What shape does $y = f(x)$ take?
7) Interactions
8) Account for study design

Typical steps in a real analysis

Before analysis

1. Determine research question
2. Collect data
3. *Plan analysis*

Analysis

1) Explore the data
2) Fit a model
3) Fit another model
4) **Determine which model is better**
5) Check model assumptions, if violated return to 3)
6) Report all results

What makes a good statistical model?

https://www.menti.com/alrfxf8u5y9i

What makes a good statistical model?

For prediction or for inference?

- A model is usually only good at one thing
- Prediction
- Inference

In my experience, most Biologists are interested in inference.

What makes a good statistical model?

One that helps to answer your research question.

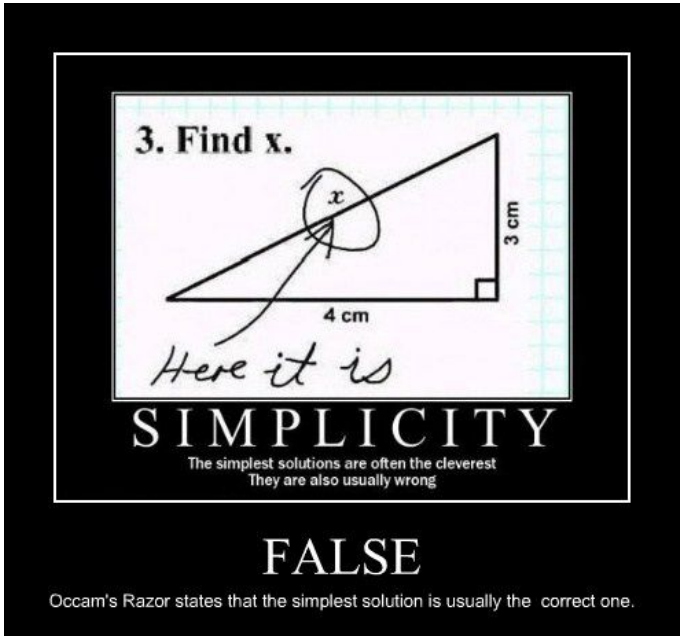
- Accurately represents the data generating process
- Not too difficult to interpret
- Is robust

Principle of Parsimony

The simplest explanation is often the correct one.

A simpler model might

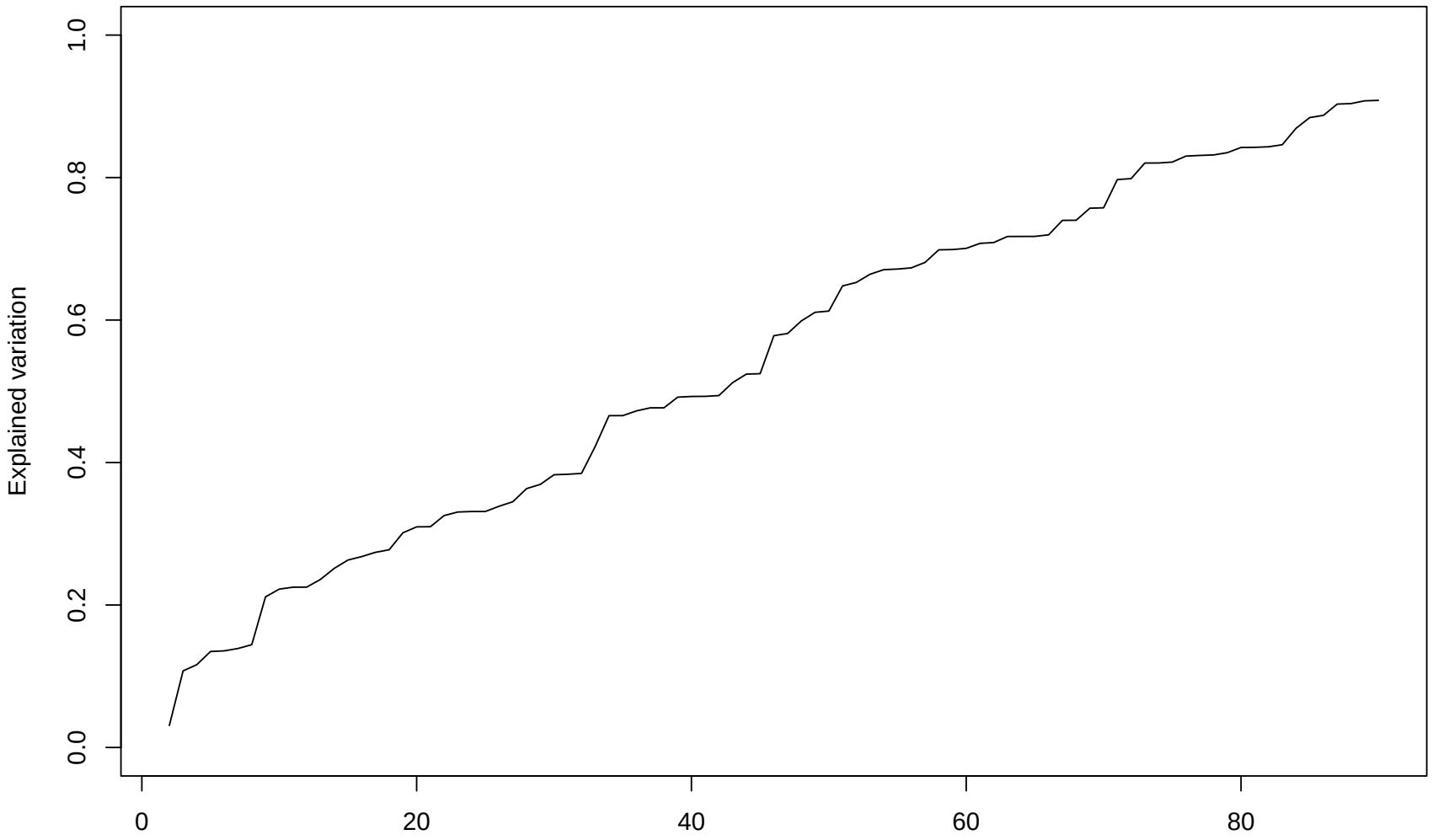
- Make fewer assumptions
- Be easier to interpret
- Be less prone to overfitting
- **Inadequatley accommodate properties of data**



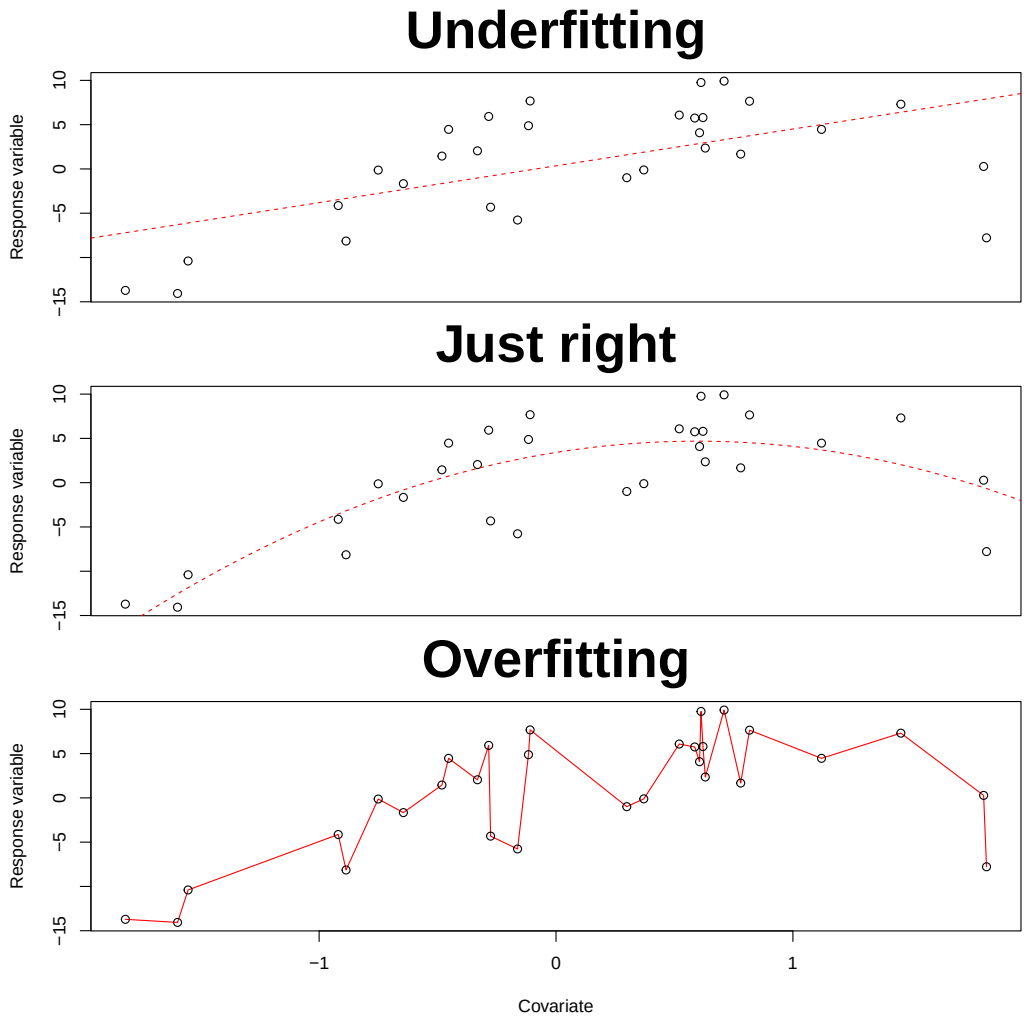
If two competing models fit the data equally well, we continue with the simpler model.

The problem of model complexity

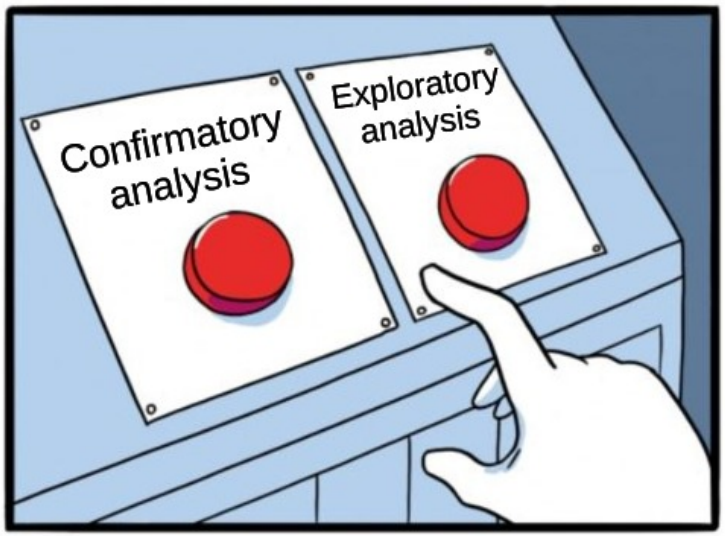
A model with always fit better if you add a parameter



Model complexity



Confirmatory vs. Exploratory analysis



Confirmatory: test hypothesis
Exploratory: find a good model

Usually indicated by the research question.

Hypothesis testing

1) Define null hypothesis
2) Define alternative hypothesis
3) Choose a test statistic (e.g., deviance in GLMs)
4) Calculate its distribution under the null hypothesis
5) Check if the observed test statistic falls within the null distribution
6) Accept/Reject

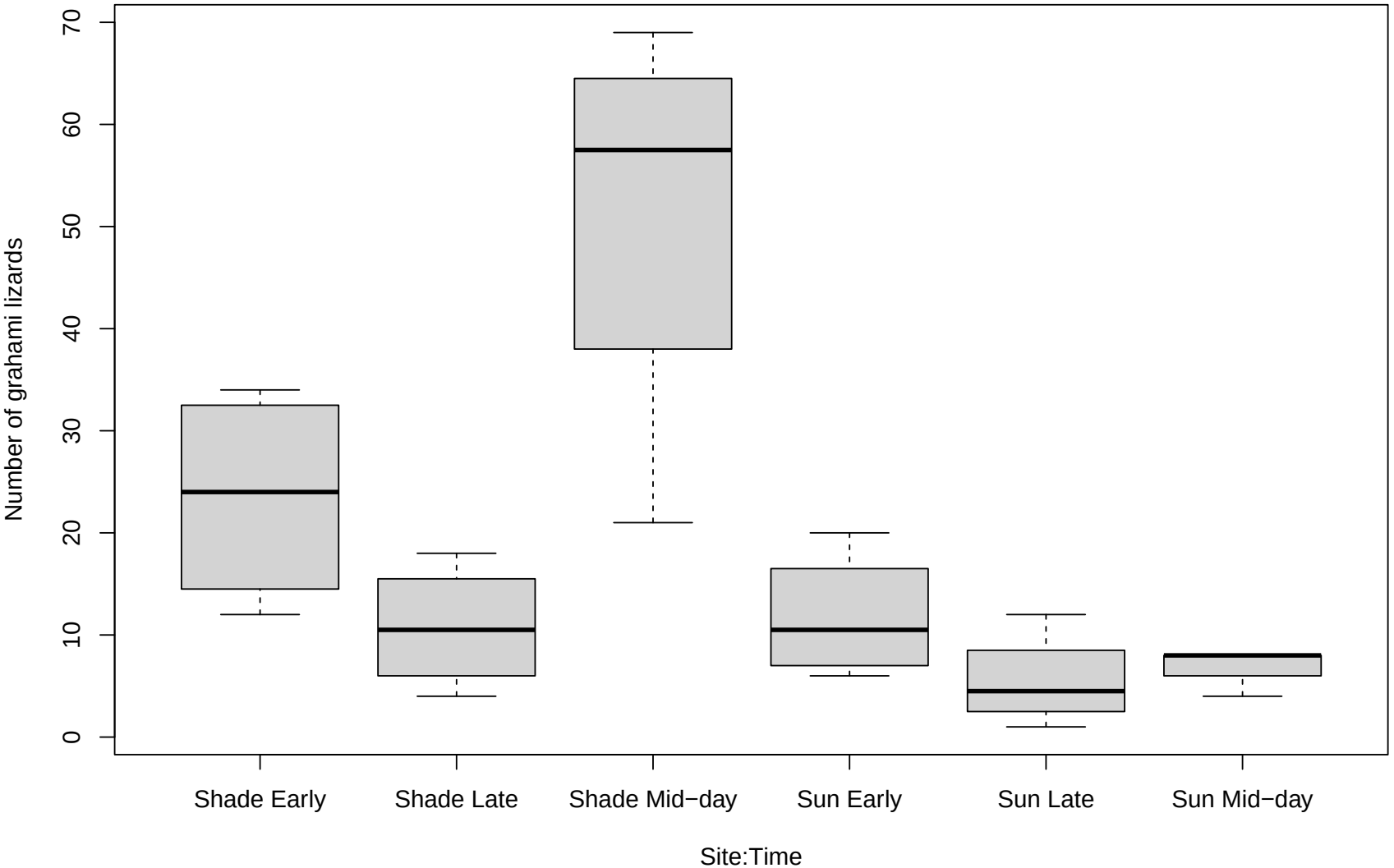
Likelihood ratio test

Is improved fit due to noise or is the alternative model actually better?

Procedure

- Fit two models: M_0 with k parameters and M_1 with r
- Calculate likelihood ratio $\Lambda = \log\left(\frac{\mathcal{L}(\mathbf{y};\Theta_0)_{M_0}}{\mathcal{L}(\mathbf{y};\Theta_1)_{M_1}}\right)$
- $\mathcal{L}(\mathbf{y};\Theta_0)_{M_0} \leq \mathcal{L}(\mathbf{y};\Theta_1)_{M_1}$
- $-2\Lambda \sim \chi^2(k_1 - k_0)$ under the null
- $p \geq 0.05$ difference in likelihood is due to sampling

Example: Lizards



Lizards: interaction

Null hypothesis: There is no interaction of Time and Site

Fit M_0:

```
nmodel <- glm(cbind(grahami, opalinus)~Time+Site,
              data = lizards, family="binomial")
```

Alternative hypothesis: There is an interaction of Time and Site

Fit M_1:

```
amodel <- update(nmodel, formula = . ~ Time*Site)
```

Lizards: interaction

```
##
## Call:
## glm(formula = cbind(grahami, opalinus) ~ Time + Site + Time:Site,
##     family = "binomial", data = lizards)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            2.24071    0.47037   4.764  1.9e-06 ***
## TimeMid-day            0.06188    0.87818   0.070   0.9438
## TimeLate              -1.22911    0.62585  -1.964   0.0495 *
## SiteShade             -1.16315    0.51296  -2.268   0.0234 *
## TimeMid-day:SiteShade  0.07270    0.91343   0.080   0.9366
## TimeLate:SiteShade     0.69387    0.70486   0.984   0.3249
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
```

Lizards: LRT

```
(Lambda <- 2*(logLik(amodel)-logLik(nmodel)))
```

```
## 'log Lik.' 1.098943 (df=6)
```

```
k <- attr(logLik(amodel),"df")-attr(logLik(nmodel),"df")
pchisq(Lambda, k,lower.tail=FALSE)
```

```
## 'log Lik.' 0.5772548 (df=6)
```

We reject the alternative hypothesis.

LRT approximation assumptions

- $n \to \infty$
- Θ_0 contained in Θ_1: nested models
- The true parameter is in the interior of the parameter space
- Model is "identifiable"
- Hessian matrix is sufficiently close to the Fisher information
- y_i are independent

These assumptions may fail, especially in models more complex than GLMs

Alternatively: LRT by simulation.

LRT and deviance

$$\Lambda = \frac{D(\mathbf{y}; \hat{\boldsymbol{\mu}}_{M0}) - D(\mathbf{y}; \hat{\boldsymbol{\mu}}_{M1})}{\phi} \tag{1}$$

LRT by simulation

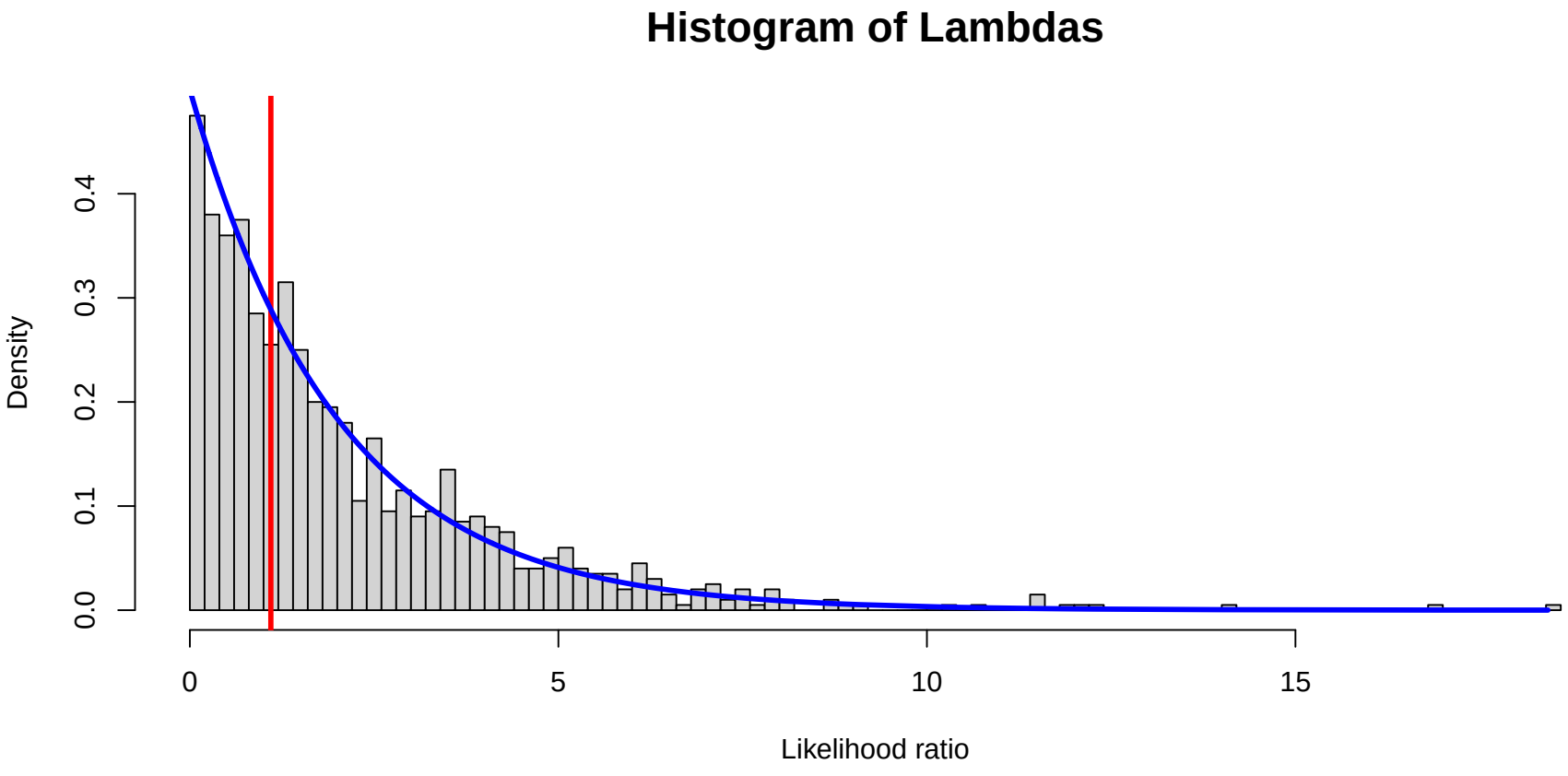
```
Lambdas <- NULL
for(i in 1:1000){
ynew <- as.matrix(stats::simulate(nmodel))
nmodel2 <- glm(ynew~Time+Site,
               data = lizards, family="binomial")
amodel2 <- update(nmodel2, formula = .~Time*Site)
# Store test statistic
Lambdas <- c(Lambdas,
               2*(logLik(amodel2)-logLik(nmodel2)))
}
# if <0.05 our test statistic in the tail.
sum(Lambdas>Lambda)/1000
```

```
## [1] 0.598
```

LRT by simulation

Red: Observed statistic

Blue: $\chi^2(2)$



Information criteria

A different paradigm:
Find the best model amongst a set of models.

Best:

- Penalise complexity (# parameters)
- By fit (likelihood)

Most commonly:

1) AIC: Akaike's Information Criterion (Akaike 1974)
2) BIC: Bayesian Information Criterion (Schwarz 1978)

Lower = better

Akaike's Information Criterion

$$\text{AIC} = -2\mathcal{L}(\mathbf{y}; \Theta) + 2k \tag{2}$$

- Penalizes model complexity
- (approximately) Measures information loss to the true data generating process
- Asymptotically

AIC tends to select too complex models with little data. Finite sample correction (Sugiura 1978):

$$\text{AIC}_\text{c} = \text{AIC} + \frac{2k(k+1)}{n-k-1} \tag{3}$$

Find the model that predicts best

Bayesian Information Criterion

$$\text{BIC} = -2\mathcal{L}(\mathbf{y}; \Theta) + k \log(n) \tag{4}$$

So the penalty is different.

Find the model closest to the "true" model

Lizards: interaction selection

```
##         df      AIC
## nmodel   4 119.7237
## amodel   6 122.6248
```

```
##         df     AICc
## nmodel   4 121.9460
## amodel   6 127.8748
```

```
##         df      BIC
## nmodel   4 124.2657
## amodel   6 129.4378
```

Connection of AIC and LRT

Rule of thumb: difference of 2 points means a model is better

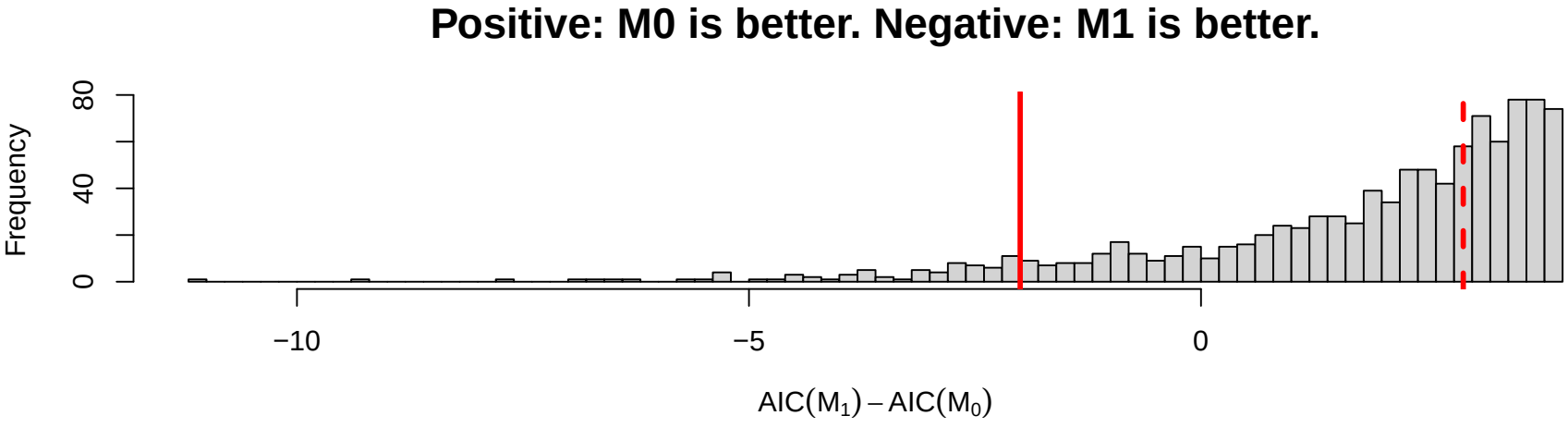
$$\begin{aligned}\Delta\text{AIC} =& \text{AIC}_{M_1} - \text{AIC}_{M_0} \\ &= 2\mathcal{L}(\mathbf{y};\Theta_0) - 2\mathcal{L}(\mathbf{y};\Theta_1) + 2k_1 - 2k_0 \\ &= -2\Lambda + 2(k_1 - k_0)\end{aligned} \tag{5}$$

So AIC with a rule of $= 2$ can be seen as a more liberal LRT (Sutherland et al. 2023)

ΔAIC by simulation under the better model

Solid: observed ΔAIC

Dashed: -2 ΔAIC



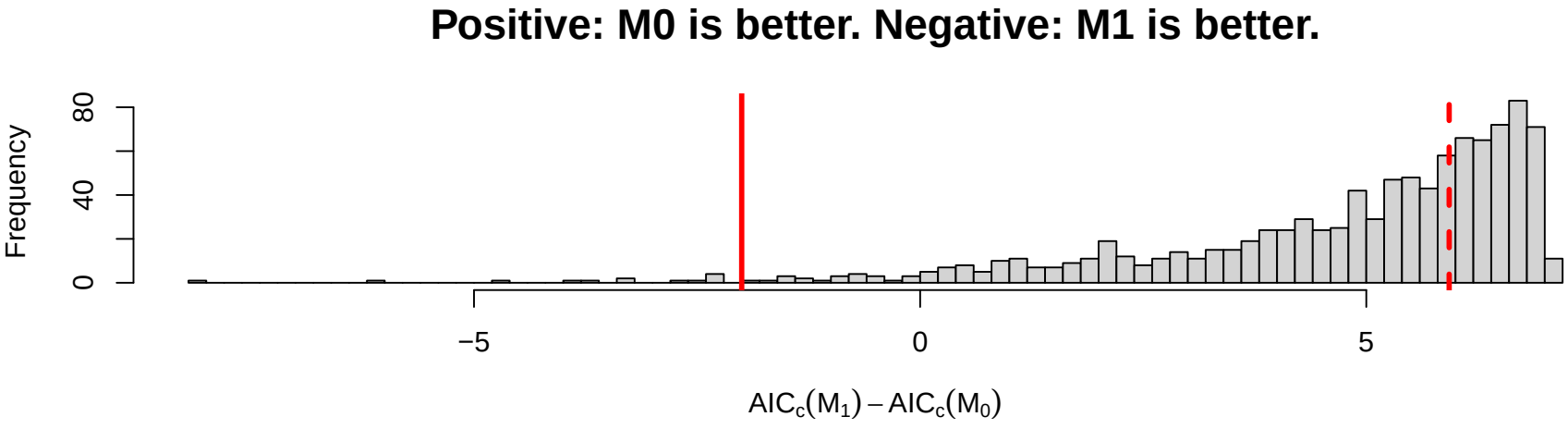

```
## Models with a more extreme test statistic: 0.607
```

```
## Models with more than 2 AIC difference: 0.591
```

ΔAICc by simulation under the better model

Solid: observed ΔAICc

Dashed: -2 ΔAICc




```
## Models with more than 2 AIC difference: 0.591
```

```
## Models with more than 2 AICc difference: 0.885
```

The cult of (A)IC

Presentation by Mark Brewer

"Always use (A)IC for model comparison"

- Use common sense
- Do not blindly test all models ("dredging")
- Use model comparison techniques in moderation

Don't take "best" model paradigm too seriously

Freedman's paradox

Just by chance, predictors with no relationship to the response will be selected.

Omitted variable bias

Occurs if we omit a variable, i.e., we have the model:

$$\mathrm{g}\{\mathbb{E}(y_i|x_{i1}, x_{i2})\} = \alpha + x_{i1}\beta_1 + x_{i2}\beta_2 \tag{6}$$

but we fit without x_{i2}. The consequence is especially clear for linear models:

$$y_i = \alpha + x_{i1}\beta_1 + \epsilon_i, \qquad \text{with } \epsilon_i = x_{i2}\beta_2 + \epsilon_i^\star \tag{7}$$

- ϵ_i may be correlated with x_{i1}
- Residual variance changes with x_{i1}
- Causes bias in parameter estimates and incorrect standard errors

Multimodel inference

What to do when you have multiple models that are equally good?

- The simpler model
- Do not "model average" for inference a rant
- Report multiple models

Summary

- Hypothesis testing and information criteria: two different paradigms
- Do not mix them
- Do not fall for "the best model"
- The full model is often a good model
- Keep things simple
- See also Murtaugh (2014) and Burnham and Anderson, and a lot of others