



EVROPSKÁ UNIE



MINISTERSTVO ŠKOLSTVÍ,  
MLÁDEŽE A TĚLOVÝCHOVY



OP Vzdělávání  
pro konkurenceschopnost

## INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tento projekt je spolufinancován Evropským sociálním fondem a Státním rozpočtem ČR  
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INVESTMENTS IN EDUCATION DEVELOPMENT

# Model Selection

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# Recap

- Linear Models (lm) assume:
  - Independence
  - Normality
  - Homogeneity
- Generalized Linear Models (glm) allow:
  - Linear predictor ( $Y \sim a + b \cdot X_1 + c \cdot X_2 \dots$ )
  - Family distribution (variance)
  - Link function (mean)
- GLMs work with:
  - Continuous but positive (skewed) data (Gamma)
  - Count data (Poisson)
  - Proportion data or presence/absence data (binomial)

# Model Selection

- Compare GLMs on the same data, with the same distributions, but with different link functions
- Compare GLMs with different predictors, to see which one(s) explain the data better

# P Value Model Selection

- Run a nested sequence of models to successively compare and test terms in the models
- Omit non-significant terms in a process of model simplification
- Aim for a parsimonious Minimal Adequate (simplest) Model

# Critique of Model Selection by hypothesis testing

- Subjective P-level
- Problem of multiple comparisons
- Problematic for non-nested models

# Friedman's Paradox

- Even when the response is independent of the explanatory variables...
- When there are many explanatory variables ( $\sim 50$ ) variable selection methods will give high  $R^2$ s and many significant F and t values with coefficients biased away from zero.
- Partial resolution: Keep the number of candidate models small relative to the number of parameters to be estimated.

# Model-selection uncertainty

- Remember that a given dataset is always a special case which may contain some unique (not general) effects that would not be present in replicated datasets of the same type.
- Avoid tailoring a model too much to a given dataset (over-fitting)



# Maximum Likelihood

- **Given a set of data and a chosen a model** (we could try and compare several)...
- Maximum likelihood is a method for determining **which parameters of the model** produce the best model fit, as measured by **deviance**, and **make the data most likely to be observed**.
- No exact solutions but iterative approximations.
- The formula for the deviance changes for different types of data/error distributions
- However, for normal data the maximum likelihood estimate is the least squares estimate.

# AIC

Decreases as more terms are added

$$\text{AIC} = -2 \ln[\mathcal{L}(\hat{\theta} | \mathbf{Y})] + 2K$$

Increases as more terms are added

- Trade-off between bias and variance ( $\sim$ complexity), or, under fitting and over fitting, that is fundamental to the principle of parsimony (Occam's razor)
- Usually positive but can be negative, smaller values indicate better models
- Absolute value is of no interest due to relative scale that is also strongly dependent on sample size
- Recommended to report and compare AIC differences

# Comparing models by AIC differences

## Models Within Two Units of the Best Model

Models having  $\Delta_i$  within about 0–2 units of the best model should be examined to see whether they differ from the best model by 1 parameter *and* have essentially the same values of the maximized log-likelihood as the best model.

In this case, the larger model is not really supported or competitive, but rather is “close” only because it adds 1 parameter and therefore will be within 2  $\Delta_i$  units, even though the fit, as measured by the log-likelihood value, is not improved.

# Advantages of AIC

- AIC can be used to compare non-nested models while likelihood ratio tests cannot.
- Allows ranking of models
- Allows ratio of evidence for different models
- Allows multimodel inference using parameter weighted averages
- Order of calculating AICs for different models does not matter

# Limits on Model Comparison

- AIC can only be used to compare different models applied to **exactly** the same dataset.
- Different transformations cannot be used when comparing models using AIC.
- Instead use GLMs to compare models with different link functions.
- But, is only straight-forward when using the same error distribution in the GLM (see B&A p.318; Faraway 2006 p. 138).
- Cannot know how close to the 'true' model candidate models are (even if truth is assumed to exist), only their relative rankings

# Pitfalls

- Large numbers of models for small datasets
- Bad candidate models and subset models
- Models within 2 IT units are approximately equally good but may contain 1 useless parameter (since the penalty term is  $2p$ )
- Use of AIC with small samples
- AIC 'best' models may contain parameters with little support (estimates close to zero etc.).

# Important things to keep in mind

- Models have to make sense
- Choosing the best model between two bad models is still bad
- Don't try to fit all possible models. Select a few that correspond to the hypotheses you want to test.

# Model selection in R: P value

```
> mod1 <- glm(Y ~ X1 + X2, data)
> mod2 <- glm(Y ~ X1 + X2 + X1:X2, data)
> anova(mod1, mod2)
# gives a p-value for how different the two models are
# if the difference is significant, take the model with the
smallest deviance (or the residual SS in case of lm)
# if there is no difference, take the simpler model
# mod1 is “nested” within mod2
```



# Model selection in R: AIC

```
> mod1 <- glm(Y ~ X1 + X2, data)
> mod2 <- glm(Y ~ X1 + X3 + X4 + X1:X3, data)
> AIC(mod1, mod2)
# the lower the AIC, the better model
# mod1 and mod2 don't have to be nested
# mod1 and mod2 should still be working with the same
dataset, and the same Y
```

# Example in R: the forest dataset

```
> mod1 <- lm(Prod ~ SpDiv, data=forest)
> mod2 <- lm(Prod ~ SpDiv + ForType, data=forest)
> anova(mod1, mod2)
```

Analysis of Variance Table

Model 1: Prod ~ SpDiv

Model 2: Prod ~ SpDiv + ForType

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	103	6.3835				
2	101	<b>2.0374</b>	2	4.346	107.72	< <b>2.2e-16 ***</b>

# the two models are significantly different, so take the one with the smallest Residual SS: it means that it has less unexplained variance.

# Example in R: the forest dataset

```
> mod1 <- lm(Prod ~ SpDiv, data=forest)
> mod2 <- lm(Prod ~ SpDiv + ForType, data=forest)
> mod3 <- lm(Prod ~ SpDiv * ForType, data=forest)
> mod4 <- lm(Prod ~ SpDiv, data=forest)
> AIC(mod1, mod2, mod3, mod4)
      df      AIC
mod1  3    9.950882
mod2  5 -105.961317
mod3  7 -133.809405
mod4  3    9.950882
# same result with the AIC criterion: mod3 has a better AIC (lower)
# here all models don't have to be nested (mod4 is not nested in mod1)
```

# Exercises in R

- For every dataset you've been working on this week (GLMs), use the `AIC()` to compare the different models.
- Does the result of the AIC make sense? Compare with the diagnostic plots, i.e. `plot(model)`, and with what you see graphically, i.e. `qplot(X,Y, geom=c("point","smooth"), method(link))`