

Module 12: Summing up and some cautionary notes

TMA4268 Statistical Learning V2020

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Overview

- Course content and learning outcome
- Overview of modules and core course topics (with exam type questions)
- Some cautionary notes

Some of the figures and slides in this presentation are taken (or are inspired) from G. James et al. (2013).

Learning outcomes of TMA4268

1. **Knowledge.** The student has knowledge about the most popular statistical learning models and methods that are used for *prediction* and *inference* in science and technology. Emphasis is on regression- and classification-type statistical models.
2. **Skills.** The student can, based on an existing data set, choose a suitable statistical model, apply sound statistical methods, and perform the analyses using statistical software. The student can present, interpret and communicate the results from the statistical analyses, and knows which conclusions can be drawn from the analyses, and what are the caveats.

And: you got to be an expert in using the R language and writing R Markdown reports.

Core of the course

Supervised and unsupervised learning:

- *Supervised*: regression and classification
 - examples of regression and classification type problems
 - how complex a model to get the best fit?
flexibility/overfitting/underfitting.
 - the bias-variance trade-off
 - how to find the perfect fit - validation and cross-validation (or AIC-type solutions)
 - how to compare different solutions
 - how to evaluate the fit - on new unseen data
- *Unsupervised*: how to find structure or groupings in data?

and of course all **the methods** (with underlying models) to perform regression, classification and unsupervised learning. We have gained some theoretical understanding, but in some cases deeper theoretical background and understanding of the models is provided in other statistics courses.

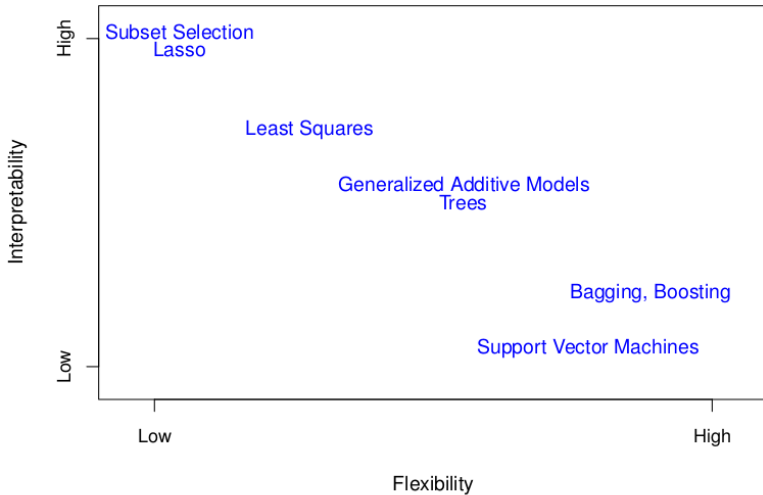


Figure 2.7 from Gareth James et al. (2013)

The modules

1. Introduction

- Examples, the modules, required background in statistics and
- Introduction to R

2. Statistical learning

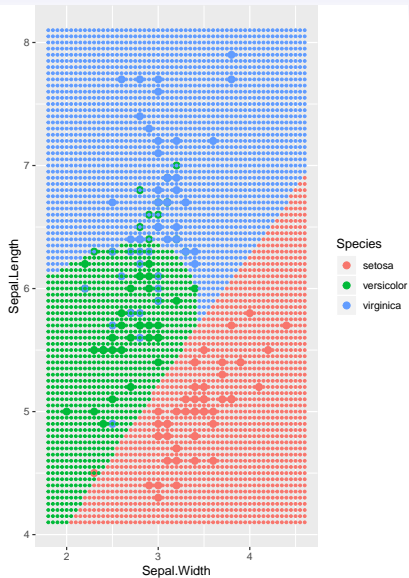
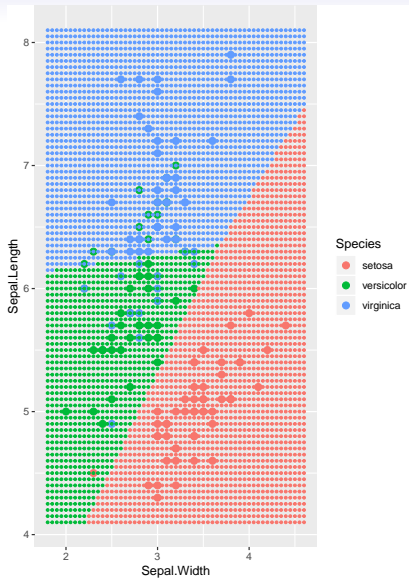
- Model complexity
 - Prediction vs. interpretation.
 - Parametric vs. nonparametric.
 - Inflexible vs. flexible.
 - Overfitting vs. underfitting
- Supervised vs. unsupervised.
- Regression and classification.
- Loss functions: quadratic and 0/1 loss.
- Bias-variance trade-off (polynomial example): mean squared error, training and test set.
- Vectors and matrices, rules for mean and covariances, the multivariate normal distribution.
- Model complexity and the bias-variance trade-off is important in “all” subsequent modules.

3. Linear regression

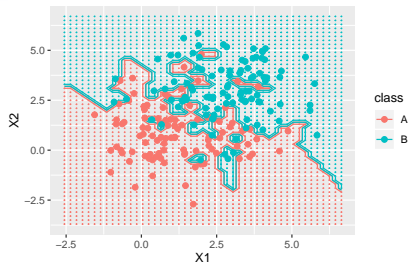
- The classical normal linear regression model on vector/matrix form.
- Parameter estimators and distribution thereof. Model fit.
- Confidence intervals, hypothesis tests, and interpreting R-output from regression.
- Qualitative covariates, interactions.
- This module is a stepping stone for all subsequent uses of regression in Modules 6, 7, 8, and 11.

4. Classification (Mainly two-class problems)

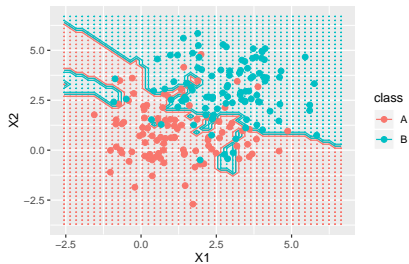
- Bayes classifier: classify to the most probable class gives the minimize the expected 0/1 loss. We usually do not know the probability of each class for each input. The Bayes optimal boundary is the boundary for the Bayes classifier and the error rate (on a test set) for the Bayes classifier is the Bayes error rate.
- Two paradigms (not in textbook):
 - *Diagnostic* (directly estimating the posterior distribution for the classes). Example: KNN classifier, logistic regression.
 - *Sampling* (estimating class prior probabilities and class conditional distribution and then putting together with Bayes rule). Examples: LDA, QDA with linear or quadratic class boundaries.
- ROC curves, AUC, sensitivity and specificity of classification methods.



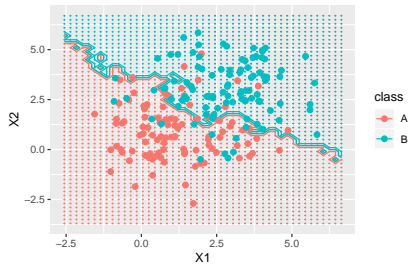
k = 1



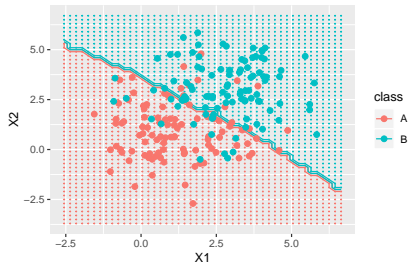
k = 3



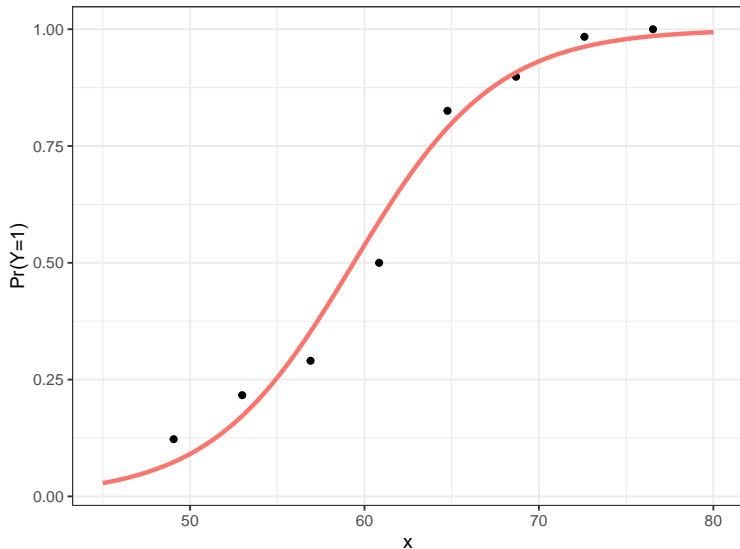
k = 10



k = 150



Logistic regression gives a probability, given a certain value of the covariats $P(Y = 1 | x)$.



5. Resampling methods

Cross-validation

- Data rich situation: Training-validation and test set.
- Validation set approach
- Cross-validation for regression and for classification.
- LOOCV, 5 and 10 fold CV
- good and bad issues with validation set, LOOCV, 10-fold CV
- bias and variance for k -fold cross-validation.
- Selection bias – the right and wrong way to do cross-validation

The Bootstrap

- Idea: Re-use the same data to estimate a statistic of interest by *sampling with replacement*.

6. Linear model selection and regularization:

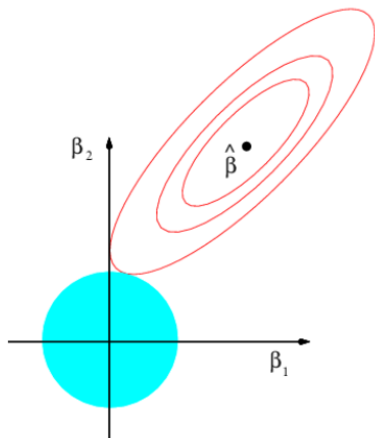
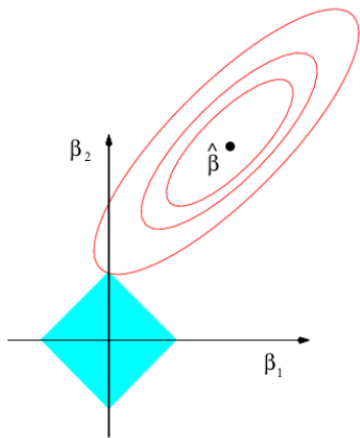
Subset-selection. Discriminate:

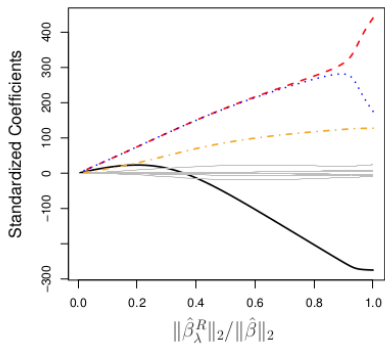
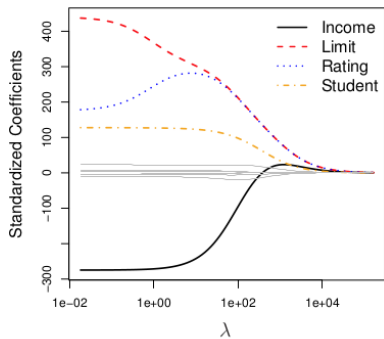
- *Model selection*: estimate performance of different models to choose the best one.
- *Model assessment*: having chosen a final model, estimate its performance on new data.

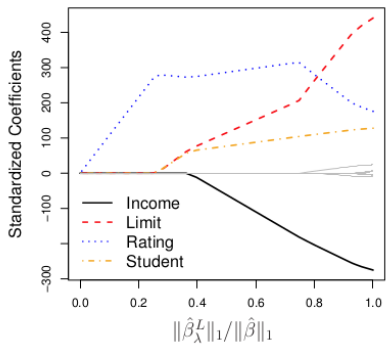
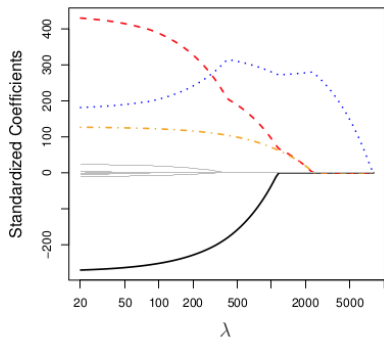
How?

- Model selection by
 - Subset selection (best subset selection or stepwise model selection)
 - Penalizing the training error: AIC, BIC, C_p , Adjusted R^2 .
 - Cross-validation.
- Model assessment by
 - Cross-validation.

- Shrinkage methods
 - ridge regression: quadratic L2 penalty added to RSS
 - lasso regression: absolute L1 penalty added to RSS
 - no penalty on intercept, not scale invariant: center and scale covariates
- Dimension reduction methods:
 - principal component analysis: eigenvectors, proportion of variance explained, scree plot
 - principal component regression
 - partial least squares
- High dimensionality issues: multicollinearity, interpretation.





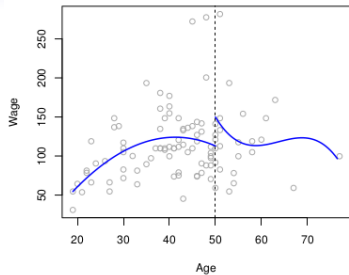


7. Moving beyond linearity

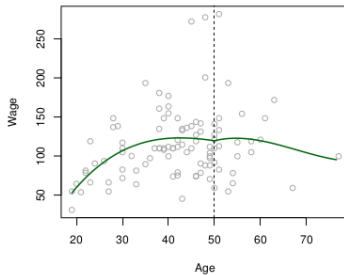
- Modifications to the multiple linear regression model - when a linear model is not the best choice. First look at one covariate, combine in “additive model”.
- Basis functions: fixed functions of the covariates (no parameters to estimate).
- Polynomial regression: multiple linear regression with polynomials as basis functions.
- Step functions - piece-wise constants. Like our dummy variable coding of factors.
- Regression splines: regional polynomials joined smoothly - neat use of basis functions. Cubic splines very popular.

- Smoothing splines: smooth functions - minimizing the RSS with an additional penalty on the second derivative of the curve. Results in a natural cubic spline with knots in the unique values of the covariate.
- Local regressions: smoothed K -nearest neighbour with local regression and weighting. In applied areas **loess** is very popular.
- (Generalized) additive models (GAMs): combine the above. Sum of (possibly) non-linear instead of linear functions.

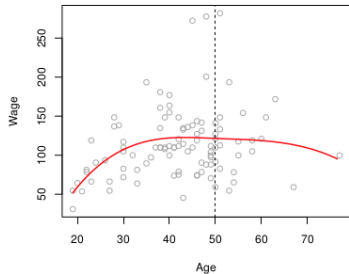
Piecewise Cubic



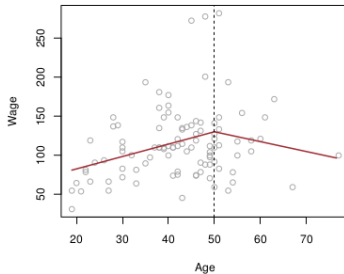
Continuous Piecewise Cubic



Cubic Spline



Linear Spline



8. Tree-based methods

- Method applicable both to regression and classification (K classes) and will give non-linear covariate effects and include interactions between covariates.
- A tree can also be seen as a division of the covariate space into non-overlapping regions.
- Binary splits using only at the current best split: *greedy strategy*.
- Minimization criterion: residual sums of squares (RSS), Gini index or cross-entropy.
- Stopping criterion: When to stop: decided stopping criterion - like minimal decrease in RSS or less than 10 observations in terminal node.
- Prediction:
 - Regression: Mean in box R_j
 - Classification: Majority vote or cut-off on probability.

- *Pruning*: Grow full tree, and then prune back using pruning strategy: cost complexity pruning.

To improve prediction (but worse interpretation):

- *Bagging* (bootstrap aggregation): draw B bootstrap samples and fit one full tree to each, used the average over all trees for prediction.
- *Random forest*: as bagging but only m (randomly) chosen covariates (out of the p) are available for selection at each possible split. Rule of thumb for m is \sqrt{p} for classification and $p/3$ for regression.
- Out-of-bag estimation can be used for model selection - no need for cross-validation.
- Variable importance plots: give the total amount of decrease in RSS or Gini index over splits of a predictor - averaged over all trees.
- *Boosting*: fit one tree with d splits, make residuals and fit a new tree, adjust residuals partly with new tree - repeat.

9. Support vector machines

- SVM can be used both classification and regression, but we have only studied two-class classification.
- Aim: find high dimensional hyperplane that separates two classes $f(x) = \beta_0 + x^T \beta = 0$. If $y_i f(x_i) > 0$ observation x_i is correctly classified.
- Central: maximizing the distance (on both sides) from the class boundary to the closes observations (the margin M). This was relaxed with slack variables (support vector classifiers), and to allow nonlinear functions of x by extending an inner product to kernels (support vector machine).
- Support vectors: observations that lie on the margin or on the wrong side of the margin.

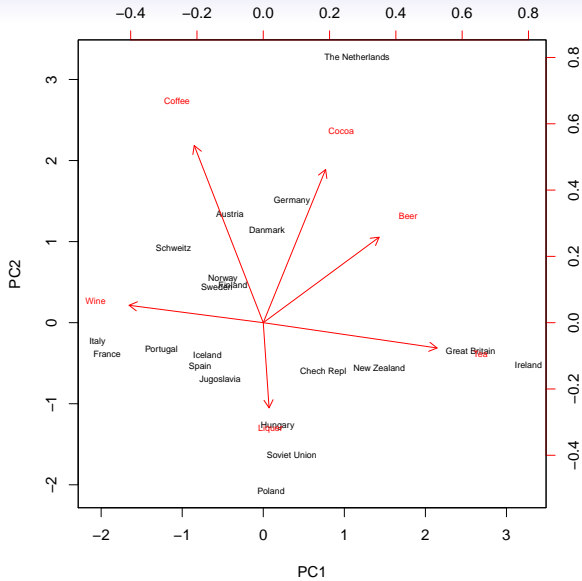
- Kernels: generalization of an inner product to allow for non-linear boundaries and to speed up calculations due to inner products only involve support vectors. Most popular kernel is radial

$$K(x_i, x'_i) = \exp(-\gamma \sum_{j=1}^p (x_{ij} - x'_{ij})^2) .$$

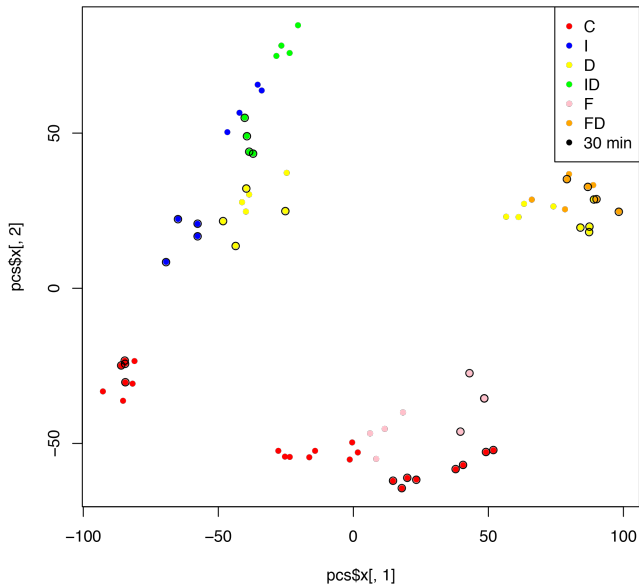
- Tuning parameters: cost and parameters in kernels - chosen by CV.
- Unfortunately not able to present details since then a course in optimization is needed.
- Nice connection to non-linear and ridged version of logistic regression - comparing hinge loss to logistic loss - but then without the computational advantages of the kernel method.

10. Unsupervised learning

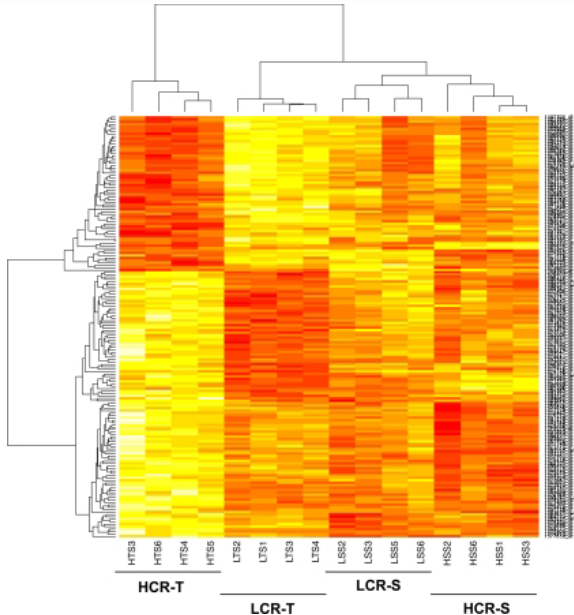
- Principal component analysis:
 - Mathematical details (eigenvectors corresponding to covariance or correlation matrix) also in TMA4267.
 - Understanding loadings, scores and the biplot, choosing the number of principal components from proportion of variance explained or scree-type plots (elbow).
- Clustering:
 - k -means: number of clusters given, iterative algorithm to classify to nearest centroid and recalculate centroid
 - hierarchical clustering: choice of distance measure, choice of linkage method (single, average, complete),



PCA for quality control



Hierarchical clustering for visualization



11. Neural networks

- Feedforward network architecture: mathematical formula - layers of multivariate transformed (**relu**, **linear**, **sigmoid**) inner products - sequentially connected.
- Loss function to minimize (on output layer): regression (mean squared), classification binary (binary crossentropy), classification multiple classes (categorical crossentropy)
- Remember the correct choice of output activation function: mean squared loss goes with linear activation, binary crossentropy with sigmoid, categorical crossentropy with softmax.
- Gradient based (chain rule) back-propagation - many variants.
- Technicalities: **nnet** in R
- **keras** in R. Use of tensors: Piping sequential layers, piping to estimation and then to evaluation (metrics).

Some cautionary words

- In most of the problems we looked at we could (or had to) choose a set of variables to explain or predict an outcome (y).
- Model selection was the topic of Module 6, but there is more to say about it, in particular in the regression context.
- Importantly, the approach to find a model **heavily depends on the aim** for which the model is built.

It is important to make the following distinction:

- The aim is to *predict* future values of y from known regressors.
- The aim is to *explain* y using known regressors. In this case, the ultimate aim is to find causal relationships.

→ Even among statisticians there is no real consensus about how, if, or when to select a model:

Methods in Ecology and Evolution



Methods in Ecology and Evolution 2016, 7, 679–692

doi: 10.1111/2041-210X.12541

SPECIAL FEATURE: 5TH ANNIVERSARY OF *METHODS IN ECOLOGY AND EVOLUTION*

The relative performance of AIC, AIC_C and BIC in the presence of unobserved heterogeneity

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Summary

1. Model selection is difficult. Even in the apparently straightforward case of choosing between standard linear regression models, there does not yet appear to be consensus in the statistical ecology literature as to the right approach.

Note: The first sentence of a paper in *Methods in Ecology and Evolution* from 2016 is: “Model selection is difficult.”

Why is finding a model so hard?

A model is an approximation of the reality. The aim of statistics and data analysis is to find connections (explanations or predictions) thanks to simplifications of the real world.

Box (1979): *“All models are wrong, but some are useful.”*

→ There is often not a “right” or a “wrong” model – but there are more and less useful ones.

→ Finding a model or the appropriate method with good properties is sometimes an art...

Predictive and explanatory models

When choosing a method or a model, you need to be clear about the scope:

- **Predictive models:** These are models that aim to predict the outcome of future subjects.
Example: In the bodyfat example (module 3) the aim is to predict people's bodyfat from factors that are easy to measure (age, BMI, weight,...).
- **Explanatory models:** These are models that aim at understanding the (causal) relationship between covariates and the response.
Example: The South African heart disease data aims to identify important risk factors for coronary heart disease.

→ **The model selection strategy depends on this distinction.**

Prediction vs explanation

When the aim is ***prediction***, the best model is the one that best predicts the fate of a future subject (smallest test error rate). This is a well defined task and “objective” variable selection strategies to find the model which is best in this sense are potentially useful.

However, when used for ***explanation*** the best model will depend on the scientific question being asked, **and automatic variable selection strategies have no place.**

Chapters 27.1 and 27.2 in Clayton and Hills (1993)

Model selection with AIC, BIC, C_p , adjusted R^2

Given m potential variables to be included in a model. Remember from Module 6:

- Subset selection using forward, backward or best subset selection method.
- Use an “objective” criterion to find the “best” model.

Cautionary Note:

The coefficients of such an optimized “best” model should *not be interpreted* in a causal sense! Why?

→ Subset selection may lead to **biased parameter estimates**, thus **do not draw (biological, medical,..) conclusions** from models that were optimized for prediction, for example by AIC/AICc/BIC minimization!

See, e.g., Freedman (1983), Copas (1983)

Your aim is prediction?

Then you are basically free to do what you want. Your only aim is to minimize some sort of prediction error.

Your aim is explanation?

Explanation means that you will want to interpret the regression coefficients, 95% CIs and p -values. It is then often assumed that some sort of causality ($x \rightarrow y$) exists.

In such a situation, you should formulate a *confirmatory model*:

- Start with a *clear hypothesis*.
- Select your covariates according to *a priori knowledge*.
- Ideally, formulate *only one* or a few model(s) *before you start analysing your data*.

Explanatory: Confirmatory vs exploratory

Any **additional analyses** that you potentially do with your data have the character of **exploratory models**.

→ Two sorts of *explanatory models/analyses*:

- **Confirmatory:**
 - Clear hypothesis and **a priori** selection of regressors for y .
 - **No subset selection!**
 - Allowed to interpret the results and draw quantitative conclusions.
- **Exploratory:**
 - Build whatever model you want, but the results should only be used to generate new hypotheses, a.k.a. “speculations”.
 - Clearly label the results as “exploratory”.

Explanatory models to confirm hypotheses (so-called confirmatory models) have a long tradition in medicine. In fact, the main conclusions in a study are only allowed to be drawn from the main model (which needs to be specified even before data are collected):

It will rarely be necessary to include a large number of variables in the analysis, because only a few exposures are of genuine scientific interest in any one study, and there are usually very few variables of sufficient *a priori* importance for their potential confounding effect to be controlled for. Most scientists are aware of the dangers of analyses which search a long list of potentially relevant exposures. These are known as *data dredging* or *blind fishing* and carry a considerable danger of false positive findings. Such analyses are as likely to impede scientific progress as to advance it. There are similar dangers if a long list of potential confounders is searched, either with a view to explaining the observed relationship between disease and exposure or to enhancing it.— findings will inevitably be biased. Confounders should be chosen *a priori* and not on the basis of statistical significance. In particular, variables which have been used in the design, such as matching variables, must be included in the analysis.

Clayton and Hills (1993)

Interpretation of exploratory models?

Results from exploratory models can be used to generate new hypotheses, but it is then *not allowed to draw causal conclusions from them*, or to over-interpret effect-sizes.

→ In biological publications it is (unfortunately) still common practice that exploratory models, which were optimized with model selection criteria (like AIC), are used to draw conclusions as if the models were confirmatory.

→ We illustrate why this is a problem on the next slides.

Illustration: Model selection bias

Aim of the example: To illustrate how model selection purely based on AIC can lead to biased parameters and overestimated effects.

Procedure:

1.) Randomly generate 100 data points for 50 covariables $x^{(1)}, \dots, x^{(50)}$ and a response y :

```
set.seed(1234)
data <- data.frame(matrix(rnorm(51 * 100), ncol = 51))
names(data)[51] <- "y"
```

`data` is a 100×51 matrix, where the last column is the response. The **data were generated completely independently**, the covariates do not have any explanatory power for the response!

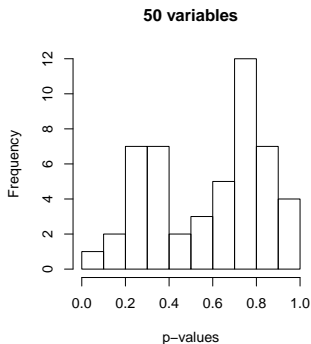
2.) Fit a linear regression model of y against all the 50 variables

$$y_i = \beta_0 + \beta_1 x_i^{(1)} + \dots + \beta_{50} x_i^{(50)} + \epsilon_i .$$

```
r.lm <- lm(Y ~ ., data)
```

As expected, the distribution of the p -values is (more or less) uniform between 0 and 1, with none below 0.05:

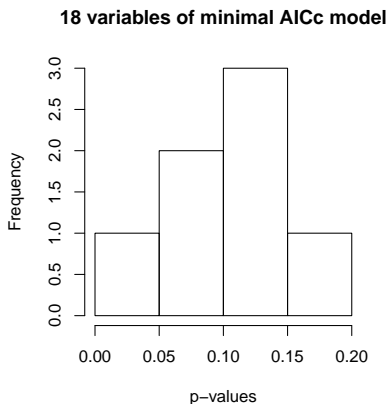
```
hist(summary(r.lm)$coef[-1, 4], freq = T, main = "50 variables", xlab = "p-values")
```



3.) Then use AICc minimization to obtain the objectively “best” model:

```
library(MASS)
r.AICmin <- stepAIC(r.lm, direction = c("both"), trace = FALSE, AICc = TRUE)

hist(summary(r.AICmin)$coef[-1, 4], freq = T, main = "18 variables of minimal AICc model",
      xlab = "p-values")
```



The distribution of the p -values is now skewed: many of them reach rather small values (1 have $p < 0.05$). This happened *although none*

After TMA4268 - what is next?

What are the statistical challenges we have not covered?

Do you want to learn more about the methods we have looked at in this course? And also methods that are more tailored towards specific types of data? Then we have many statistics courses that you may choose from.

An overview of statistics courses is kindly put together by Mette Langaas: <https://folk.ntnu.no/mettela/Talks/3klinfo20190325.html>

Final word

Thank you for attending this course - good luck for the compulsory exercise 3 and let's hope we are soon back into normal teaching mode in the post-Covid-19 era!

References

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