Nonlinear regression
Experimental design
Mediation vs. Confounding

Bo Markussen
bomar@math.ku.dk

Department of Mathematical Sciences

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Lecture outline

- Non-linear regression.
- Elements of experimental design:
  - Replication, Randomization, Blocking, Covariates, Multifactorial.
  - Generation of optimal designs.
- Causal diagrams:
  - Mediation and confounding.
  - Path analysis.

Summary (Day 1)

- Statistics answers four important questions:
  1. Is there an effect? (falsification of null hypothesis, p-value)
  2. Where is the effect? (p-values from post hoc analyses)
  3. What is the effect? (confidence and prediction intervals)
  4. Can the conclusions be trusted? (model validation)

- We do model based frequentist statistics: Interpretation of p-values and confidence intervals via the meta-experiment.

- Datasets consists of variables (columns) and observations (rows).

Summary (Day 4)

Can the conclusions be trusted? — Validation of linear normal models

- **Do residuals have mean=0?** Plot of residuals vs predicted values.
- **Do residuals have same variance?** Plot of standardized residuals vs predicted values.
  - Often seen is that variance increases with predicted values. May often be solved by log-transformation.
  - This is also seen as "trumpet shape" in the residual plot.
- **Are residuals normal distributed?** Normal quantile plot of standardized residuals.
  - Banana shape indicates need for log-transformation.
- **Are residuals independent?** Not validated formally. Use instead knowledge about design of experiment. See also course Day 5.
- **Are there any outliers?** Plot of standardized residuals vs leverages. Critical lines in terms of Cook's distances (D=0.5, D=1.0).
  - Generally it is not advisable to remove observations!
  - But robustness of the results excluding some observations may be tried.

Non-linear regression

A potential solution when the residuals don't have mean zero

- Continuous response y (the dependent variable).
- Continuous covariates $x_1, \ldots, x_K$ (the independent variables).
- Assume there exists a parameter θ and a function f_θ such that for every repetition i,

$$y_i = f_\theta(x_{1i}, \ldots, x_{Ki}) + \epsilon_i, \qquad \epsilon_i\text{'s independent } \mathcal{N}(0, \sigma^2)$$

- Parameter estimate $\hat{\theta}$ minimizes the sum of squared errors

$$\sum_{i=1}^{N} \left| y_i - f_\theta(x_{1i}, \ldots, x_{Ki}) \right|^2$$

- Parameter σ estimated by the Root-Mean-Squared-Error

$$\hat{\sigma} = \sqrt{\frac{1}{N-p} \sum_{i=1}^{N} \left| y_i - f_{\hat{\theta}}(x_{1i}, \ldots, x_{Ki}) \right|^2}, \qquad p = \dim \theta$$

Some examples of $y_i = f_\theta(x_{1i}, \ldots, x_{Ki})$

- One covariate x and two parameters α, β:

$$y = \alpha + \beta x \qquad \text{(the straight line)}$$

$$y = \frac{1}{\alpha + \beta x} \qquad \text{(an inverse line)}$$

$$y = \alpha \cdot e^{\beta x} \qquad \text{(exponential function)}$$

$$y = \alpha \cdot x^{\beta} \qquad \text{(power function)}$$

- One covariate x and four parameters α, β, γ, δ:

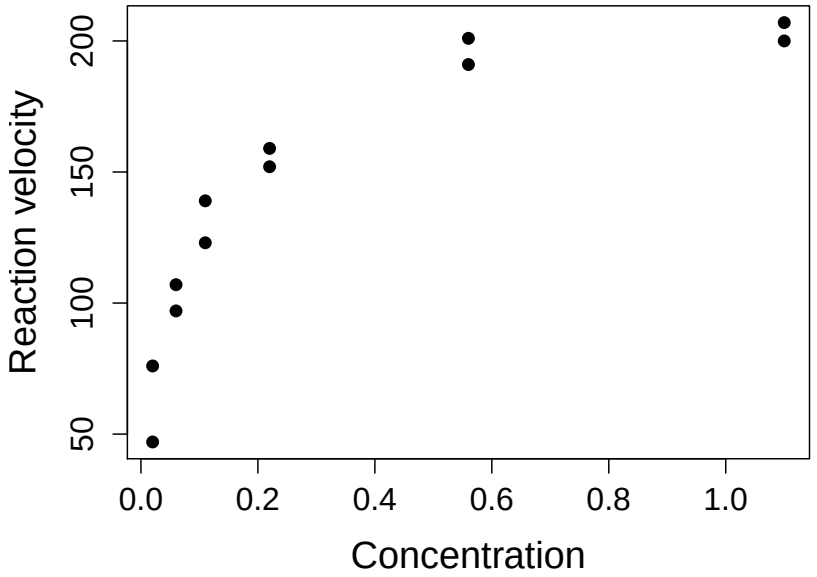
$$y = \alpha + \beta x + \gamma x^2 + \delta x^3 \qquad \text{(cubic regression)}$$

- The model is called linear if it is a linear function in the model parameters.
  - Quiz: Which of the above models are linear?
  - Quiz: Which of the above models can be made linear by using transformations?

Data example: Puromycin

Dataset `puromycin`: Reaction velocity (y) as a function of concentration (x)

concentration	reaction
0.02	76
0.02	47
0.06	97
0.06	107
0.11	123
0.11	139
0.22	159
0.22	152
0.56	191
0.56	201
1.10	207
1.10	200



Michaelis-Menten model with parameters α (max velocity) and β (concentration at max/2):

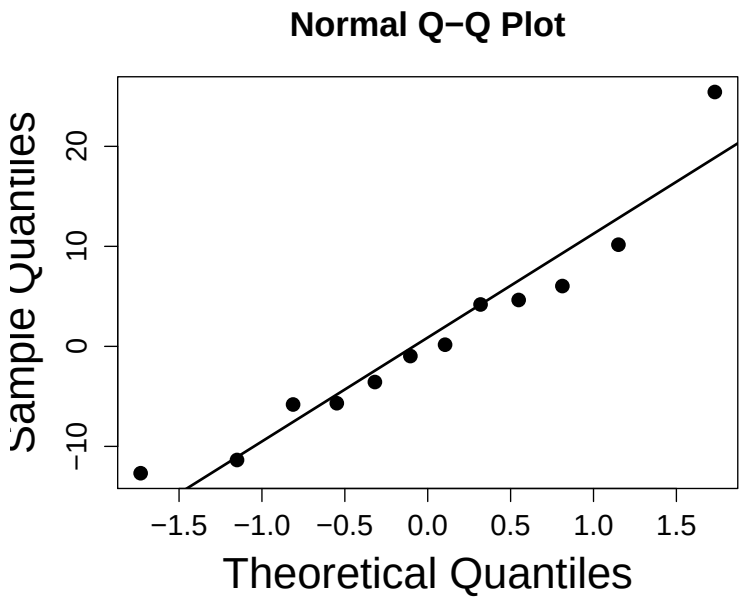
$$y = \frac{\alpha x}{\beta + x}$$

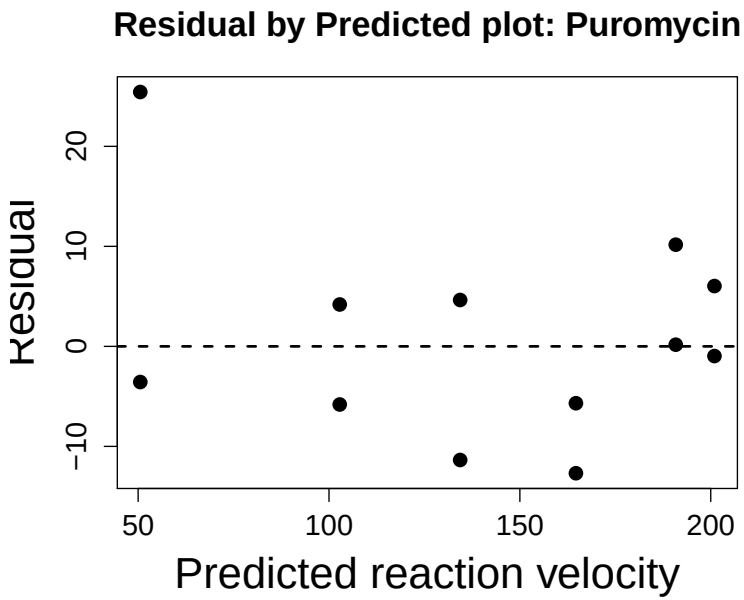
Puromycin: Non-linear regression (I)

```
# Read data from text file, and make plot
puromycin <- read.delim("puromycin.txt")
plot(reaction~concentration,data=puromycin)

# Make non-linear regression: Guesses taken from plot
m1 <- nls(reaction~a*concentration/(b+concentration),
          start=list(a=200,b=0.1),data=puromycin)

# Can the conclusions be trusted?
# Normal quantile plot:
qqnorm(residuals(m1))
abline(mean(residuals(m1)),sd(residuals(m1)))

# Residual plot:
plot(predict(m1),residuals(m1))
abline(0,0,lty=2)
```

Puromycin: Non-linear regression (II)

Neither the normal quantile plot nor the residual plot are too good (largely due to 1 observation at the lowest concentration):



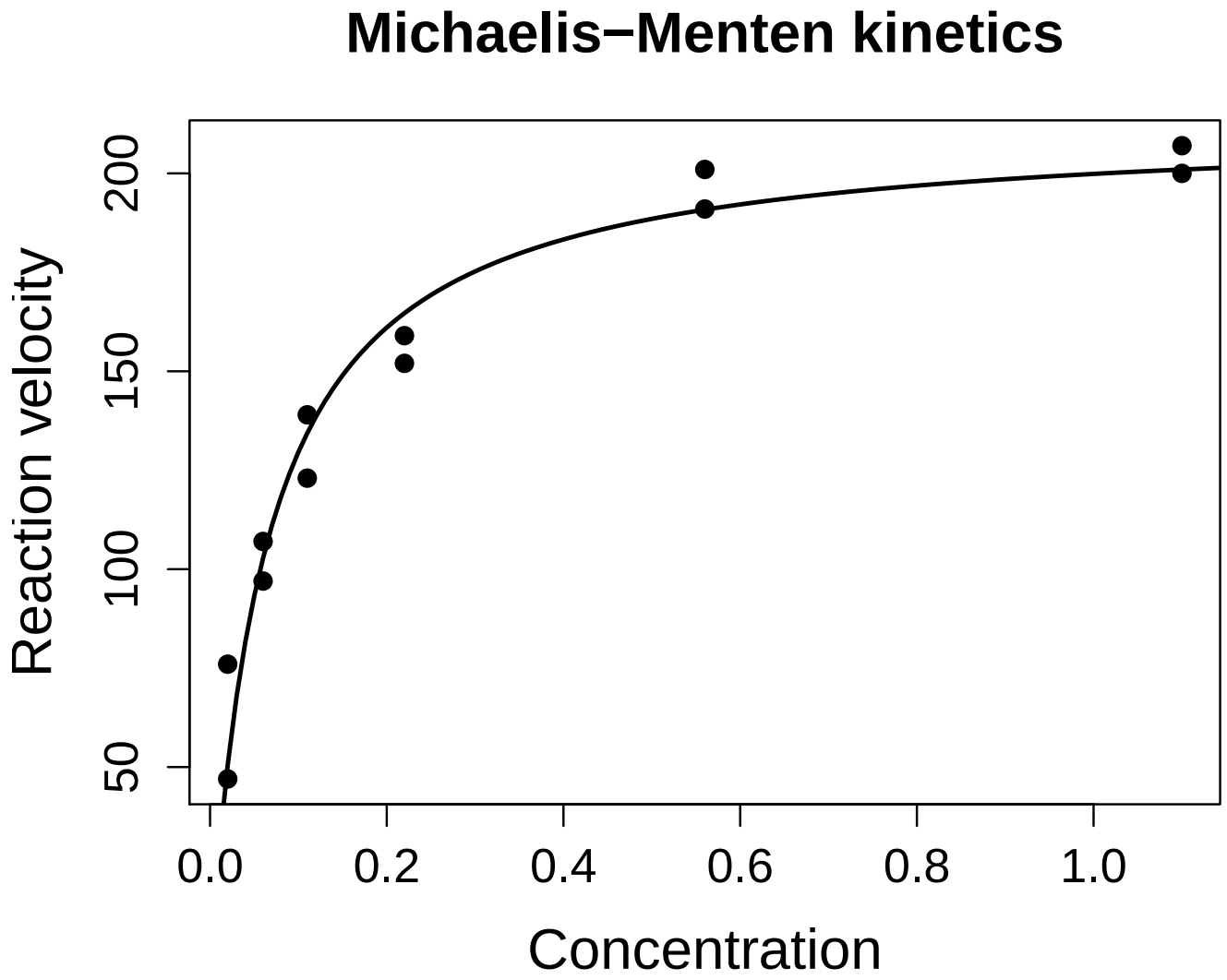


To be on the safe side we do a Lack-of-Fit test, which gives p=0.4468:

```
m0 <- lm(reaction~factor(concentration),data=puromycin)
plot(m0)
anova(m1,m0)
```

Puromycin: Fitted curve ($\hat{\alpha} = 212.68$, $\hat{\beta} = 0.0641$)

Presently neither confidence nor prediction intervals available in `predict.nls()`



Exercise 4.2 revisited: World running records

R code available in script "addendum_ex4_2.R"

- World running records are (rather) well modelled on the log vs. log scale if we allow for a change-point between short and long running distances:

$$\log(\text{time}) \approx \alpha(\text{sex}) + \beta * \log(\text{distance}) + \gamma * \log\left(\frac{\max(\delta, \text{distance})}{\delta}\right)$$

- This model is linear in the parameters $\alpha(\text{men}), \alpha(\text{women}), \beta, \gamma$ and non-linear in the parameter δ. Here δ encodes the change-point.

- Non-linear regression gives the estimates:

$$\hat{\alpha}(\text{men}) = -3.4480, \qquad \hat{\alpha}(\text{women}) = -3.3365,$$
$$\hat{\beta} = 1.2059, \qquad \hat{\gamma} = -0.1379,$$
$$\hat{\delta} = 1212.9478.$$

Please note that `nls()` not always finds the best model fit!

Questions?

- And then a break.
- After the break we discuss Design of Experiments.

Design of experiments

Important concepts

- Replications
- Randomization
- Blocking
- Covariates
- Multifactorial design

Replications

Design of experiments

- Necessary for statistical analysis.
- Needed to estimate size of random variation.
- The only way to know about reproducibility and hence to assess treatment effect.
- More replicates leads to higher precision. Needed sample size growths quadratic with required precision.

Randomization

Design of experiments

- Random allocation of experimental units to treatments.
- Ensures against systematic errors (bias), e.g. from confounding.
- Carry out by true randomness, e.g.
  - rolling dice, random numbers from computer.
- Balancing: Rearrangement making groups alike. May invalidate statistical analysis and should be avoided.
  - Example: Switch animals between groups to make groups similar according to initial weight. May invalidate an ANOVA since the variation within groups becomes too large.
  - However, see next slide on blocking.

Blocking

Design of experiments

- Grouping of experimental units into homogeneous groups (called **blocks**).
- Randomization: Units allocated randomly to treatments within block.
- Model should include main effects of used blocks (there might be more than one). Possibly as random effects (see Day 5).
- Reduces residual variation $\Longrightarrow$ Increases precision and power.
- Examples:
  - litters or herds
  - different areas in fields
  - replication, e.g. day of experiment
  - experimental unit in cross-over designs

Covariates

Design of experiments

- Continuous measure on each unit with possible relation to response.
- Reduces residual variation $\Longrightarrow$ Increases precision and power.
  - See exercise 6.3 for an example of this.
- Should (ideally) not be associated to the treatment
  - If influenced by the treatment: mediation!
  - If influencing the treatment: confounding!
- Several covariates may be used simultaneously in the model.

Multifatorial design

Design of experiments

- Use multifactorial designs — not one factor at a time.
- More information $\Longrightarrow$ more efficient.
- Interactions can be investigated.
  - Analysis done similar to the 2-way ANOVA. But now we may also have 3'rd or higher order interactions.
  - I, however, often prefer only to include 2-way interactions unless the application calls for more.

Construction of experimental designs

Example: Half-fraction factorial design

Suppose the following 5 factors are believed to influence the percentage of chemicals that respond in a reactor:

- The feed rate of chemicals (FeedRate), 10 or 15 liters per minute.
- The percentage of the catalyst (Catalyst), 1% or 2%.
- The agitation rate of the reactor (AgitRate), 100 or 120 revolutions per minute.
- The temperature (Temp), 140 or 180 degrees Celsius.
- The concentration (Conc), 3% or 6%.

A complete factorial design of 5 factors on 2 levels each requires $2^5 = 32$ experimental units. Suppose you only can afford 16 experimental units and want to estimate all main effects and all two-factor interactions.

Then you are looking for a so-called 2^{5-1}_V design (see *Fractional Factorial Design* on Wikipedia).

Design Of Experiments in R

- One of the general packages in R for DOE is called AlgDesign.
- From a larger collection of experimental units, e.g. the full factorial design, an optimal subset of a prespecified size is selected.
- An often used criterion is the so-called D-optimality.
- Apparently you have to do the randomization afterwards "by hand", e.g. using `sample()`.

```
# Full factorial design for 5 factors on 2 level
full.factorial <- gen.factorial(levels=2,nVars=5,
  varNames=c("FeedRate","Catalyst","AgitRate","Temp","Conc"))

# Design with 16 units for main effects + 2-way interactions
optFederov(~(FeedRate+Catalyst+AgitRate+Temp+Conc)^2,
           full.factorial,nTrials=16)$design
```

What is the power to detect differences?

- Designs generated by AlgDesign, say, are optimal in some mathematical sense. But how can we know if they actually have sufficient power to answer our scientific question?
- One possibility is to insert simulated data for the response variable and do the statistical analysis. Typically the response variable is simulated using one of the following two methods:
  1. Using the systematic differences and variances we believe (e.g. from the literature) to be present.
  2. Using the systematic differences we want to be able to detect. In this case it is often convenient to measure in scales of the standard deviation, which amounts to setting the variance to 1.
- This is repeated 10,000 times, say, in order to estimate the power by the fraction of times we observe a significant effect.

Classical sample size computations

Only available for the most simple situations

- For T-tests, 1-way ANOVA and comparisons of proportions the needed sample size may be computed without using simulations:
  - `power.t.test()`, `power.anova.test()`, `power.prop.test()`.
  - A few more things available in the `pwr`-package.
- The following numbers must be specified:
  - Used significance level, typically $\alpha = 0.05$. But remember the moral from Sterne & Smith, namely to consider a lower significance level.
  - The standard deviation in the population. This number must be known from previous experiments or from the literature.
  - The systematic difference between the treatment groups, possibly the least relevant difference to detect.
  - The wanted power, i.e. the chance that you will find a significant effect.
- Alternatively, you may get the power as a function of the sample size.

Questions?

- And then a break.
- After the break we discuss confounding and mediation. This is done using causal diagrams.
  - Causal inference is a hot topic in contemporary methodological research in statistics.

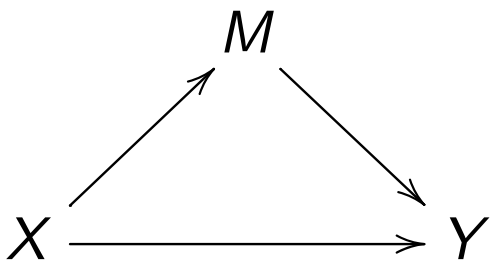
Causal diagrams

- Causal diagrams display the causal relations that the scientist (not the statistician) believes/knows to be present in advance.
  - It is very hard (although possible in some situations) to infer this from observational data. But relations can be established by randomized trials.
- In multilinear regressions (i.e. many explanatory variables) it is important to understand the role of the explanatory variables.
  - Mediators or Confounders?
- When the joint distribution is normal (as discussed today), many things can be done:
  - Correction by confounders allow for estimation of causal effects.
  - Instrumental variables to deal with non-observed confounders.
  - Path analysis to decompose mediation.
- Of course similar issues also arise for non-normal responses. But here the mathematics is much more difficult, and much of this is ongoing research.

Causal diagrams: Mediation vs. Confounding

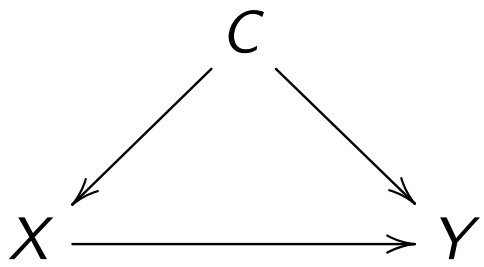
What variables should be included, and what is the interpretation?

Effect of X mediated through M



- Regression of Y on X gives the total effect.
- Regression of Y on (X, M) gives the direct effect (of X).
- total effect = direct effect + indirect effect.

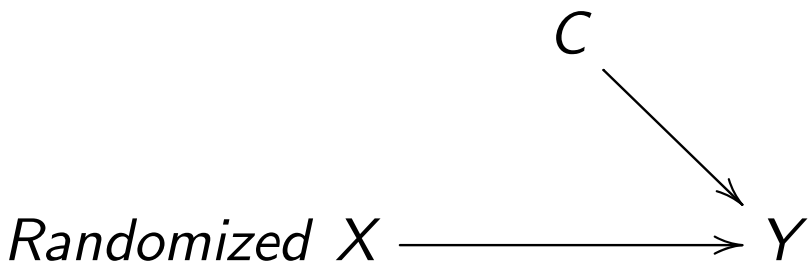
Effect of X confounded by C



- Spurious effects avoided by including the confounders.
- $\Longrightarrow$ effect of X quantified via coefficient on X in the regression of Y on (X, C).

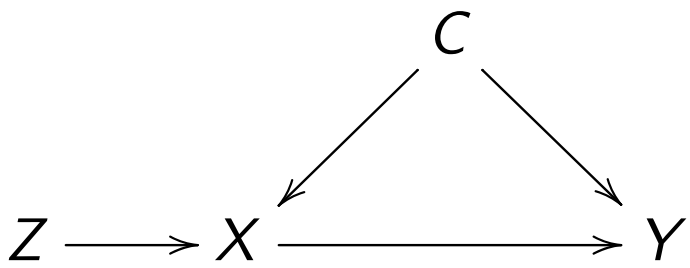
Causal effects with unobserved confounders

Randomized Controlled Trial



- Relation between confounder C and regressor X is broken by the randomization.
- Effect of X is now causal.
- If observed confounder C might be included to reduce variation.

Instrumental variable Z

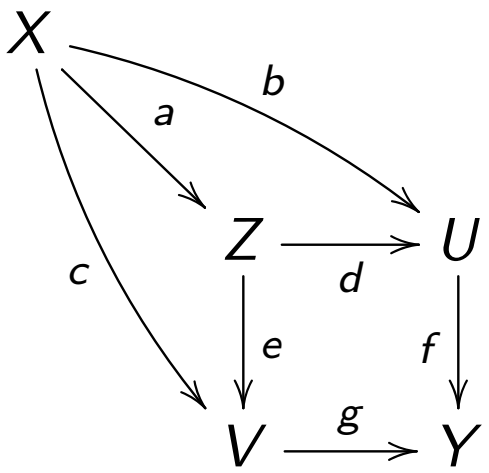


Two step procedure:

1. Regress X on Z to find predicted value $\hat{X} = E[X|Z]$.
2. Regress Y on $\hat{X}$. Coefficient gives causal effect of X.

Removes effect of confounder C.
But procedure can have low power!

Path analysis: An arbitrary example with 3 mediators



Solved by 4 regressions (from "right" to "left"):

$$Y - \mu_Y = f * (U - \mu_U) + g * (V - \mu_V) + \text{error}$$
$$V - \mu_V = c * (X - \mu_X) + e * (Z - \mu_Z) + \text{error}$$
$$U - \mu_U = b * (X - \mu_X) + d * (Z - \mu_Z) + \text{error}$$
$$Z - \mu_Z = a * (X - \mu_X) + \text{error}$$

Combined these gives a decomposition of the total effect of X on Y:

$$Y - \mu_Y = \big(f * (b + d * a) + g * (c + e * a)\big) * (X - \mu_X) + \text{error}$$

This concludes the lecture part of the course

- There is a final exercise session this afternoon.
- AS participants do an applied project, and SmB-participants may sign up for doing an applied project in block 3 (SmB-II):
  - Using statistical methodology in practice is (in my judgement) the best way really to learn doing statistics.
  - Doing statistics in practice may be surprisingly difficult. It involves biological and mathematical reasoning, as well as technical skills. Its wonderfully challenging — you may keep on learning all of your life.

Thank you!