

Questions

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Formating rules

- Questions That is how you format questions.
 - Answers That is how you format answers.

Questions / Answers

- Why do breeding values not have a unit? In this video they have a unit: https://www.youtube.com/watch?v=_JxcTELevoc.
 - They have a unit, when the trait has a unit. (But not always shown)
- How do you calculate the total breeding value at the moment?
 - The total breeding value is not existing yet.
- How big is the basis population at the moment. How could I find out myself?
 - Defined, should be stable and not influence differences of Breeding values. Like in geography you use the sea level for measuring altitudes (Problem bridge building in different countries). But has to be adapted, to not have too high numbers.
- How should I format the glossary so you could help me to get rid of my mistakes?
 - Tag “?” inside.
- How do you validate your data?
 - You make a frame where the values should fit to exclude outliers.
- Why do you do the breeding valuation separately for Calves (KV) and Heifers (MT) and separately for each breed?
 - Because you slaughter them at different ages where different genes are in action. It has political/economic reason that you either breed heifers or calves.
- At the moment you are breeding carcass conformation to C, carcass weight to maximum and carcass fat coverage to maximum, don't you?
 - Not actually breeding, but the maximum of breeding values also means the maximum of the trait.
- Should I call Fettabdeckung carcass fat or carcass fat coverage?
 - carcass fat
- The big disadvantage of the introduction of carcass fat as a breeding value is, that current animals can not be compared to past animals, isn't it?
 - No there is no disadvantage. You could calculate the new model also for the past breeding values.
- The big advantage of the introduction of carcass fat coverage as a breeding value is, that breeders can now breed organised towards more carcass fat coverage, which has generally declined over years, isn't it?
 - No, the big advantage is, that you have a predictor trait for early maturity. Fat is usually created after the building up of proteins in a body. And it is important for good payment. So it can be easily linked to early maturity.
- For Calves (KV) carcass fat coverage negativeley correlates with conformation, for beef it is the opposite, how can this be?
 - The correlations mentioned are that small that they are not worthy to interpret.
- Is the accuracy of breeding values the same as the certainty of breeding values?
 - The accuracy is defined by Bestimmtheitsmass. Certainty can mean the same but may be context dependent.
- What is ASR F&E? Found in notice of meeting 16.5.

- It is the umbrella association of all cattle breeding associations. It is superordinate to Mutterkuh Schweiz.
- Somehow I could never really understand what the degrees of freedom means. Could you please give me a simple explanation?
 - You either count the number of observations or the number of rest effects minus the possibilities of grouping in fixed effects? Could be clarified.
- Is it a good idea to look at breeding methods of other animal species to compare it to beef cattle?
 - Later it can be useful to look at the breeding program of growing pig, because they are ahead of the cattle breeders.
- Can you give an example for each why you choose a variable to be a random effect or a fixed effect?
 -
- At the Strickhof I heard that early maturity could also be linked to sexual maturity. Do you think it is worth to look for more informations in this topic?
 - Yes it could be interesting too look e.g. at the differences of steers (not much testosterone) and bulls.
- Could you say that conformation is important, because it gives you information about the proportion of meat and fat to bones and other slaughter by-products?
 - I would just say, it is the degree of meatiness.
- What are Schaufeln?
 - Schaufeln are Teeth of cattle to estimate their age. In English called incisors.
- What is the purpose of genetic groups?
 -
- What are variance components?
 - Variables that explain the variance over a population? E.G. genetics, farm.
- What is a selection path?
 - It is can be sire of sire, sire of dam, dam of sire or dam of dam.
- Can you recommend me a paper that highlights the importance of early maturity and carcass fat?
 - Hospenthal Thesis.
- How would you translate Rind to English. Is it heifer or young bull?
 - Heifer = young female, young bull = young male
- Are at the moment carcass weight and carcass conformation corrected for age at slaughter when calculated as Breeding value?
 - Yes and carcass fat too. Also they are all corrected by sex, category, farm, Proviande employee and ...
- In English I will call Frühreife not early maturity but rate of maturation, do you agree?
 - No, rate of maturation describes the process until an animal is mature. However we are not interested to breed for that. The only thing we are interested in is that the animals should be maturer as early as possible, no matter how. (Maybe we have to look at it later when we create the index)
- Should I fill in the CHTAX tables for carcass conformation and carcass fat and carcass category? Not very good quality and more distracting than helpful, I think.
 - Yes, you should fill in the CHTAX tables in the way of Andrea Hospenthal. The pricing table should also be included.
- Should I transform the Skript File into a Bookdown file? Somehow committing with Git does not work anymore when combined.
 - If something does not work anymore in RStudio the easiest way to fix it is to restart RStudio. Also I have installed the Tex program which is necessary to build a book in bookdown.
- Where can I find the files for the genetic trend figures?
 - https://www.mutterkuh.ch/de/documents/herdebuch_Herdebuchbericht_2017_page_37_or_the_presentation_of_Remo_Ackermann http://www.swiss-limousin.ch/media/pdf/2017_01_31-Limousintag_Remo_Ackermann.pdf .
- How can I include a figure of a reference into my markup file? E.G. Fig. 21.3 Thonney.
 - You can include a figure with the command “knitr::include_graphics()”. You can write the file name into the brackets and the file has to be deposited in the same folder as the markup file.

- How can you create a nice table in R markdown?
 - You can create a R chunk. There you use the function `data.frame` and with `c()` you define you columns top down. With the function “`colnames(name of the data.frame)`” you define the column names from left to right. Then you use the function “`kable()`”. But why do you have always do `library(knitr)`?
- How can you include R results in the text of R markdown?
 - The R chunk needs to be above and can be hid with “`echo = FALSE`”. The you take the defined variables as results into the text with (press two times shift + ^) “. In those quotation marks you fill in “r Variable name”.
- How do I create a R chunk?
 - With “alt” + “cmd” + “i” you can create a r chunk.
- How do I produce the back slash like this ?
 - With the combination “alt” + “shift” + “7”.
- How can I produce curly brackets {}?
 - “alt” + 8 and 9.
- How do I sign variables?
 - You do x_{sign}
- Should I always use the latech \$\$ writing when writing variables? I think it would be clearer.
 - Yes I should do so. It looks better because then it is clear that it is not just a common letter. But abbreviations not.
- Are character and trait synonyms?
 - Yes almost synonyms, trait is more suitable then character, when used in the aspect of breeding.
- How do I write and interpret the summation symbol big sigma?
 - You write it like this: $\sum_{i=1}^n$. The variable below always indicates which value it will perform in the following term. So if $i = 1$ then the following formula $i + 2$ is $1 + 2$. The value on the top of the summation sign is the last value of the row of whole numbers that will be i . For example below $i = 1$, the value on the top is 4 and the following term is $i + 2$ then the whole calculation that has to be performed is $1+2 + 2+2 + 3+2 + 4+2$ and the solution is 18.
- How do I write square roots?
 - You write it like this: $\sqrt{b^2 - 4ac}$
- How do I write division/fraction signs?
 - You write $\frac{x}{y}$
- How do I write matrices?
 - You write it like this:

$$\mathbf{X} = \begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \\ 7 & 8 & 9 \end{bmatrix}$$

- How do I write tables?
 - Like this

```
data.frame(Kalb =c(1,2,3,5,3),
  Geschlecht =c("M","F","F","M","M"),
  Vater =c(1,3,1,4,3),
  Mutter =c(NA,2,2,5,6),
  WWG =c(4.5,2.9,3.9,3.5,5.0))
```

```
##   Kalb Geschlecht Vater Mutter WWG
## 1    1           M     1     NA 4.5
## 2    2           F     3     2 2.9
## 3    3           F     1     2 3.9
## 4    5           M     4     5 3.5
## 5    3           M     3     6 5.0
```

- How should I call Gesamtzuchtwert? Overall breeding value probably.

- No, total genetic merit referring to Peter. Or aggregate genotype.
- Is the covariance (Zusammenhang) between the true and estimated breeding values defined by the heritability of each trait?
 - No, it is defined by the Prediction error variance (PEV_y) and the additive genetic variance-covariance matrix (G) before the selection.
- Should I use a table to collect all known variables, or is a r chunk enough with just the arrows? The advantage of the table is, that it looks tidier.
 -
- How works the shortcut to produce <- at once?
 -
- How do I give figures and tables numbers and labels, so that I can refer to them?
 - By including the name in the top header of the r chunk. Then I can do @table:name of table and reference it in the text.
- How do I achieve to create tables that fit into the frame of a PDF, when knitted?
 -
- How can I merge table rows? E.G. Distinction of T+/- in CHTAX?
 - See
- How do I shortcut in RStudio Zoom Source?
 - “Ctrl” “+” “1”
- Do we have carcass or live weight as data for the breeding valuation for carcass traits?
 - Only carcass weight according to Sophie.
- How can I cite tables or figures in a text of bookdown?
 - Use @ref(tab:conformationclass) for tables, @ref(fig:genetictrendCF).
- Do I have to compute the pedigree for each sex separately? I think I do.
 - Yes
- How do I show solutions of variables in R to the text?
 - You use **r variable**
- How can I cite directly in the text? For example: Focas (1996) observed this special event.
 - Just use Phocas and Colleau (1996).
- How can I shift the diagonal by 3 to the right, so it starts at the third column?
 - By cbind and including a 0-Matrix of the right dimension. Or with a kronecker product.
- How can I multiply a diagonal matrix so it has the same diagonal value repeatedly 23 times and then again the same value 23 times and again until I have 8 times 23 times the same value (184x184 matrix)?
 - You just have to use the command `rep(as.vector(sige),each=mfs+mhs+3)`, then you can repeat the elements of the diagonal vector which results in the required matrix.
- Will I also need to have the relationship matrix 8 times?
 - No, probably not, Kronecker creates in cooperation with G a 184x184 matrix.

- R^{-1} could be confused with the variable R^* which is the response to selection. Would you rename one of them?
 - Yes you should rename the variable for the response to selection. It is now called Q .
 - How can I number formulas, so I can refer to them?
 - You need to frame the formula with the following commands, then you need fill in the brackets of label the name of the required equation. You then refer to the equation in the text with the following commands: Equation 2 or 2.
- (1)
- This only works for PDF, but not for HTML. Should I use the syntax working for both?
 - I think, only PDF has to work properly. PDF is the format I choose to print the thesis.
 - What is the difference between A bullet B and AB ?
 - There is no difference. Both are meaning matrix multiplication.
 - What is n of I_n ?
 - n is the number of traits. I is the identity matrix with off-diagonal elements of 0 and diagonal elements of 1.
 - Is x and z the same?
 - No, x is the x value of a density function (selection border) and z is the y value of the density function (ordinate). It is so called in this paper, but sometimes x is called z in other sources, which was confusing.
 - `Cbind` does not work with C_1 and C_2 . How can I bind them together?
 - The problem is, that after this point we only use the values of the candidate of each sex. Then the binding should work. Or try `rbind()`.
 - How can I transform a matrix back to a numeric value, so that I can use `sqrt()` etc.?
 - You can use `as.numeric()`
 - Why is G^* in combination with a and a^T negative, but G not?
 - Because G was not positive defined and I used squareroots instead of inversion in one formula.
 - Which unit does a have?
 - Sfr. / unit of stdv of the specific trait as in (???)
 - Should I write in “we” or “I” when I write the material and methods part?
 - According to Réka it is important to stick to one of them.
 - How do you compute the additive genetic variance of the traits values in a population? Do you subtract from the phenotypical variance the variance components of the fixed factors (known environmental factors)?
 -
 - How did you compute the heritabilities, covariances and variances of the traits?
 - See Kunz (2018).
 - How could I create a pedigree automatically just by knowing how many full siblings, half siblings and progeny there are?

- Are the phenotypical observations in BLUP all expressed as deviation from the population mean of the base population?
- How should I call “Bankkälber” and “Banktiere”?
 - calves and stirks <http://beef2live.com/story-cattle-terminology-bulls-springers-freemartins-85-103895>
- How should I format abbreviations? At the moment I use abbreviations in equations with latex layout and the non-equation abbreviations without latex layout.
- How should I abbreviate carcass conformation, carcass fat and carcass weight?
 - See Sophie’s presentation. There she uses CC, CF, CW respecteveley.
- Do I need to introduce unit abbreviations like day d?
- I do not like abbreviations, because the block text fluency, how can I avoid them? Especially in tables.
 - According to Sophie I should not avoid them. They allow very compact and clear tables.
- How can I compute the phenotypic correlations from the genetic correlations? I have the genetic covariances and the covariances of the residuals. The sum will be the phenotypic covariances. Phenotypic covariance dividing by phenotypic variances of the two involved traits I get the correlations.
- Should I indicate a transpose with ' or ^T?
- Should I explain all variables in each formula?
- How can I mention a R command in Rmarkdown?
 - You can do it embracing the command with “
- Should I always specify the required dimension of the used matrix?
 - According to Sophie it is not necessary.
- How can I make the bibliography in bookdown work?
 - I had duplicates in my .bib file, because I had some papers in my personal folder and in also in the group folder. Deleting the papers in the personal folder has fixed the problem.
- Should I explain how we computed the intensity of selection?
- May I refer to a presentation that I read and use it as a reference source? For example the presentation from Wageningen.
- How can a single performance have a variance? It should be 0 shouldn’t it? See presentation Wageningen 2017 p. 15.
 - It is not a single performance, but the mean expected performance, which is the mean of the population. The variance is then the variance of the population. You can account for relationships among animal by reducing the covariance by the degree of relationship. Also in presentation Wageningen.
- What do you mean with selection index theory? The method to calculate EBV or the method to calculate aggregate genotypes?
 - I think both, it is a model (simulation) of BLUP to predict the accuracies of future breeding values and a model to combine the breeding values of different traits according to their economical weights to an aggregate genotype.
- How can I refer to a section, chapter?
 - Just label the section header with {#id} then you can refer to it by @ref(id).
- Shouldn’t we compute the prediction error variance with a scenario of more known records? Usually you know the records of parents and grandparents as well, dont you?

- The additional records would not significantly increase the accuracy of the breeding values, but only the model we are computing (according to Urs).
- Should I compute the response to selection for Banktier and Bankkalb separately or together? Should the aggregate breeding value be separate for both groups? Yes I think so.
 - Yes, according to Sophie.
- Can I compute the response to selection with different information sources within a trait? Is it possible to reproduce the results from Peter with Pimentel's approach?
 - According to Urs it is not easily possible. You would need to produce very long vectors.
- Could I also compute the response to selection with provided mean accuracies for breeding values of selection candidates derived from the breeding value estimation?
 - No, it is not that easy. It could be difficult as well and is not necessarily more accurate (Peter).
- What does i.e. mean?
- Should I use the term genetic gain or response to selection?
 - In literature the genetic gain is more often used, but gain is also the live weight increase. This could be confusing.
- How about completely separate “Banktiere” and “Bankkälber”? Use separated variance covariance tables -> residuals only exist within each group.
 - Yes, this makes sense according to Sophie.
- Is the generation interval and intensity of selection for calves and storks different?
- How can I include references in a table caption?
 - <https://tex.stackexchange.com/questions/272475/citations-in-tabular-environment-not-working/290915#290915> As shown here it is very difficult to give a command. Just handwrite it and then use “nosite: | (???)” to make sure the reference is included in the reference list of the document in the end. However this did not work yet.
- Why are the heritabilities slightly different, when computed from the variance components?
 - Because they are false when computed from the variance components.
- How do I need to choose the economical weights for the index?
- How can I describe the selection index theory?
- How exactly works the linear regression of Berry? How can I assess this approach? I need to try it out and compute the response to selection, no?
- How can I find the mistake in my computations of the response to selection?
- How do I choose the appropriate reference type in mendeley?
 - Book, journals are clear, but web pages and laws and presentations not (I could use the type generic for those)
- Is the genetic trend positive if the mean of breeding values is constantly on a high level? Would be a negative genetic trend on a high level just mean that the improvement reduces over time but is still positive? Then many traits would probably show negative genetic trends.
 -
- How should I save figures that should be included in R bookdown? Can I place them in the git_repository?
- Should I use Δ or Q as abbreviation of genetic gain?

- Can I use Thonney (Genetics of Meat Quality) to compare heritabilities of carcass fat with our heritabilities? (Discussion)
 - Not my main task to discuss this.
- Can I include the Sophies' results (variance components) to my results chapter or should I mention them in the discussion part? *No
- Is there any other instrument to assess breeding values beside the genetic gain?
- Should I use the term genetic gain or response to selection?
 -
- How can I structure the M+M part of the thesis?
 - Chunk text chunk, give results of in-between steps.
- How should I structure my Master Thesis?
 - Introduction (short), M+M with subsections of approaches, Results also with subsections, Discussion without subsections, Conclusion that ties to Introduction.
- How can I approximate the generation intervall?
 - I can ask Sophie according to Peter. An approximation will do.
- Should I go from bottom to top (how I computed it) or top to bottom (why I computed it like this) when explaining how to compute response to selection?
 - I should go from top to bottom according to Peter to make clear the aim of the computations from the beginning. This also means that I will be forced to decouple the R chunks from the explanations. I will put the R chunk which are bottom to top into the annex of the paper.
- Should I use tables to show all variable values in M+M? Then I could work with one big code chunk.
 -
- Should I use a single selection path model?
- Should I start with the method to assess the suitability of carcass fat for deriving early maturity and afterwards mention the material? Actually I just need to know the variance components of the breeding value estimation. I shouldn't make it difficult for the reader to know what it all is about.
 -
- How can I make clear that I only use the part of the selection candidate of the PEV?
- Could I also compute the relationship matrix without the other parent and just indicating NA for the second parent? It does not matter I guess.
- How do I assume the proportion of selected animals?
- How about the strategy: Adjusting the correction function of carcass traits of the covariable "age at slaughter"?
- Do I assume mass selection when computing genetic gain like Kause et al. (2014)?
- Should I state like Kause et al. (2014) that carcass fat and carcass conformations are scores? Label (score) in the table.

(2)

$$Q_m^* = \frac{\sum_{y=1}^2 i_y a^T (C_y^*)_m \sqrt{a^T C_y^* a}}{\sum_{y=1}^2 L_y} (\#eq : Qm) \quad (3)$$

Watch @ref(eq:Qm)

$$Q_m^* = \frac{\sum_{y=1}^2 i_y a^T (C_y^*)_m \sqrt{a^T C_y^* a}}{\sum_{y=1}^2 L_y} \quad (4)$$

see Equation 4

```
library(knitr)

## Warning: package 'knitr' was built under R version 3.4.3

library(kableExtra)
x<-data.frame(c("CC", "CF", "CW"), c(0.5, -0.05, 0.52), c(-0.17, 0.73, -0.20), c(0.29, 0.09, 0.63))
colnames(x) <- c("", "CC", "CF", "CW")
kable(x, booktabs=T, caption="calves genetic variance-covariance matrix") %>%
kable_styling(latex_options=c("hold_position")) %>%
  add_header_above(c("", "w"=2, "d"= 1))
```

Table 1: calves genetic variance-covariance matrix

	w		d
	CC	CF	CW
CC	0.50	-0.17	0.29
CF	-0.05	0.73	0.09
CW	0.52	-0.20	0.63

```
x<-data.frame(class = c("C", "H", "T", "A", "X"), profile=c("very convex", "convex", "linear", "concave", "very concave"),
description=c("leg: accentedly wide; back: accentedly wide and full; shoulder: accentedly pronounced", "leg: wide; back: wide and full; shoulder: pronounced", "leg: well developed, quite wide; back: average large; shoulder: accentedly pronounced", "leg: moderateley developed, slim, hollow; back: moderateley developed til slim ; shoulder: flat", "leg: poorly developed, very slim, very hollow; back: slim, thin, pointy wither; shoulder: flat, hollow"))
colnames(x) <- c("class", "profile", "description")
kable(x, booktabs=T, caption="Description and carcass profile of carcass donformation classes") %>%
kable_styling(latex_options=c("hold_position"), full_width =T) %>%
column_spec(3, width="8cm")
```

Table 2: Description and carcass profile of carcass donformation classes

class	profile	description
C	very convex	leg: accentedly wide; back: accentedly wide and full; shoulder: accentedly pronounced
H	convex	leg: wide; back: wide and full; shoulder: pronounced
T	linear	leg: well developed, quite wide; back: average large; shoulder: accentedly pronounced
A	concave	leg: moderateley developed, slim, hollow; back: moderateley developed til slim ; shoulder: flat
X	very concave	leg: poorly developed, very slim, very hollow; back: slim, thin, pointy wither; shoulder: flat, hollow

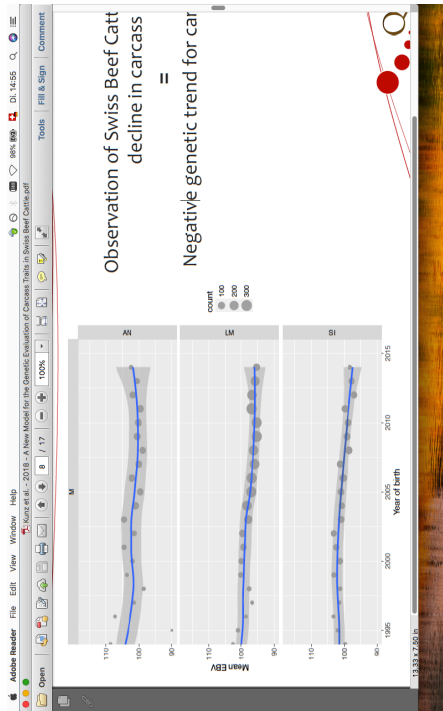


Figure 1: yey

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