10 weeks to deadline (January 30th):

A) 4 weeks of 20 hours (Monday, 21th November-Sunday, 18th December)

2 weeks hollidays (Monday, 19th Decembe-Monday, 2th January)

B) 4 weeks of 50 hours (Tuesday, 3th January-Monday, 30th December)

In A) and B) I will submit one sheet on Mondays with the progress of the previous week. You could give me feedback through email or wait until the biweekly meeting.

A)

Week of N-21: I will prepare a sheet about:

Emphasizes on “why I think it will work”. Find best references about variation in conservation. Discuss the value of conservation to work with low frequency alleles and how to prove it (with priors?). ~~Also, a list of things that I intend to change according to comments from reviewers, and a list of the strongest points of the proposal.~~

Week of N-28: I will update “detailed description”. Emphasizes on:

Interconnection activities. More technical explanations. Better introduction of the link association- function (the use of breeding in biology); importance in general and in the context. Also, a list of things that I intend to change according to comments from reviewers, and a list of the strongest points of the proposal.

30 min meenting?

Week of D-5: I will prepare a sheet about:

Diagrams with dummy data and suggested statistical models in the different stages

Maybe here

Week of D12th: I will update all proposal. Including non-technical parts (summaries…).

1 hour meeting?

Data available?

As a member of the steering committee of FAANG, Prof Groenen has early access to relevant data to be used in the current proposal.

A list of additional, specific researches questions?

B)

Week of J2th: I will add to the proposal comments about the importance. Perhaps, I should focus only on the most convincing fact. Some ideas:

- Potential of breeding as experiment in biology. M: Validation 2: Specific matings between carriers of predicted lethal alleles in chicken. In our case they are favourable, so it makes a lot of sense to experiment in that direction. See if double homocig perform better. Also activity 6

- The use of priors can be particularly helpful for low-input local breeds.

- Conservation is a clever way to select for the most important traits (“conservation is a consequence of breeding”).

- The use of priors enables to accelerate the genetic improvement even in the existence of an infinitesimal model.

- Priors in conservation are somehow more “protected” against the interactions between genes. These interactions may change overtime and add a difficulty to the use of priors in genomic prediction.

- Comparative genomics to get some more insight on the differences between herds (countries) that difficulties the creation of reference populations (out of context? Only for dairy cattle?)

-Comparative genomics to exploit heterosis?

I could also: Work with some real data to improve the “purity” of the writing

Write about “what if it does not work?” (referring to the last activities)

How the research links in department (Genomics and Quantit), and in other Universities

Have an appointment with one contact that works in Conservation

Why I think validation (GP results) will work

Which percetage of SNPs are going to be conserved. Which conservation is expected? Mammals?...

Best references bout priors in GP

Why pigs: This is of particular importance in poultry and pig breeding, where most commercial products are based on 3- or 4-way crosses between different lines.

How much time I will spend in each part

Short, medium and long term

Why this is useful. Porposal Biaty

M: we will disseminate the C-scores both in tabular formats, as well as in the form of custom tracks (i.e. bigwig files) to be used in genome browsers such as Ensembl or UCSC.

Sanne: Biological knowledge was introduced by giving different weights for non-coding and coding variants [36], by giving weights to SNPs that are expected to be on the causal genes, or by giving weights to SNPs that are expected to explain a lot of variation based on RNA sequence information[35]. All these studies have shown that the accuracies barely increase [35, 36]. Overall,

Sanne: Across populations only short distance LD between the QTL and SNP is conserved. The effect of the genetic architecture such as the minor allele frequency, heritability or level of LD could be evaluated by simulations.

Separate: Why the idea is good? Why the project is gonna be succesful?

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4224693/