ABG MSc thesis topics: 2022 - 2023

Version, October 2022

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1. Quantitative genetics

Individualized training populations

Genomic prediction uses methods that allow (very) large number of predictors to be used to estimate the genetic ability of individuals that genotyped only (test population) given that an adequate training population is available. The question is what is adequate. Over time, as data accumulates, training data sets become increasingly heterogeneous. Differences in allele frequency and linkage disequilibrium patterns between the training and test populations can limit prediction accuracy. Prediction should be based on predictors of testing individuals being identical by descent and not identical by state to predictors observed in the training population. Most of the relevant prediction accuracy of an individual testing is generated by the training individuals that have a sizable relationship with the testing individual, but the question is what is sizable. However, these lowly related individuals usually outnumber the number of closely related individuals and although they have a low relationship with the individual to be predicted, together they can have a strong influence on the prediction. It is also known that in ‘pedigree prediction’, i.e. based on the numerator relationship matrix (A) more than 3 generations do not add much. That means relationships smaller than $\frac{1}{2^6} = 0.0156$ do not contribute much. The hypothesis is that prediction accuracy is mainly driven by ‘family’ relationships, i.e. if training and prediction individuals share genes that are IBD. The idea is that it is possible to use predictor variables (SNPs, NIR-wavelengths etc.) to discriminate between individuals that have IBD segments or IBS segments.

Thus, the objective is to study the relationships between/among training and testing individuals to:

- Show that informative individuals truly have part of the genome in common;
- Show that low relationships are due to IBS for example by comparing haplotypes instead of SNPs;
- Show that SSI is not only a statistical ‘trick’ that improves prediction accuracy, but that there is an underlying genetic reason for it.

Duration: 6 months


Supervisor(s): Henri Heuven
Available from: 2022

Modelling erosion of genomic breeding values

Genomic selection has been implemented in most important breeding programs in the last decade. With genomic selection, animals are selected based on genomic breeding values relatively accurately early in life, before performance is recorded on the animals themselves, or close relatives. Genomic breeding values are estimated using estimated SNP effects. Current genomic breeding value estimation models assume that SNP effects are constant across the years spanned by the data used. This assumption is likely violated in practice, which implies that estimated SNP effects and genomic breeding values erode across generations. The aim of this thesis is to develop and validate a model that is able to explicitly model and estimate the extent of this erosion. To enable validation of the model, the work will be based on simulated data.

Supervisor(s): Mario Calus
Available from: 2022

What is the impact of genomic selection on genomic diversity?

Selection in a livestock population aims to improve the future performances of the population. As a result of selection, changes are taking place on the genome, such as changes in allele frequencies and genetic variation. Insights in those changes help to open up the black box of selection and will lead to a better understanding of the effects of selection. One of the outstanding questions is
whether those changes are depending on the used selection strategy (namely phenotypic, pedigree and genomic selection). In this thesis, the aim is to compare the genomic changes in a livestock population under these three different selection strategies, to learn whether the impact on genomic variation is different. This is important to know, because it has implications for how we should preserve valuable genetic diversity in the future. For this thesis, you will use a simulated dataset of a livestock population that was under 50 generations of selection. The student will learn to quantify the genomic changes by performing analyses on runs of homozygosity, selective sweeps and changes in allele frequencies across the genome.

Supervisor(s): Mirte Bosse, Yvonne Wientjes
Available from: 2020

**Improving genomic prediction for crossbred performance without crossbred information**

Crossbred breeding programs aim to improve performance of crossbred animals. Selection takes place in purebred lines, and is usually based on purebred performance measurements. Breeders can decide to collect data on crossbred animals to improve genomic predictions, but this approach is costly and may be difficult in practice. It may therefore be interesting to investigate whether predictions can be improved without collecting crossbred data, for example by improving the model. In this project, you will learn how to simulate a crossbred breeding program that applies genomic selection. The aim is to simulate and evaluate strategies that aim to optimize genomic prediction for crossbred performance, without collecting crossbred information.

Supervisor(s): Pascal Duenk
Available from: 2020

**The long-term effects of genomic selection**

In the beginning of this century, genomic selection has been introduced. Since that time, genomic selection has been rapidly implemented in most of the livestock breeding programs worldwide. However, at the moment, not much is known about the long-term effects of genomic selection and whether enough genetic variation is maintained for future selection. Using an existing simulation program, the student will investigate the impact of the different parameters on the long-term effects of genomic selection. Options are to investigate the impact of the number of loci underlying the trait or the change in breeding goals over time, or to investigate the usefulness of older generations in a reference population for genomic selection. The student will learn to use different selection methods such as pedigree and genomic selection and to investigate the long-term effects of selection.

Supervisor(s): Yvonne Wientjes
Available from: 2020

**Updating genomic predictions without updating the reference population**

With genomic prediction, breeders typically use the same reference population for a number of generations to make selection decisions, because updating the reference population is costly. As a result, the accuracy of genomic prediction reduces every generation, because marker effects may change considerably due to changes in allele frequencies. It may therefore be possible to improve genomic predictions by accounting for these changes in allele frequency. In this project, you will use simulations to investigate the benefit of updating marker effects each generation without updating the reference population. Depending on your interests and skills, you can investigate the benefit for accuracy, response to selection, and profitability of the breeding program. You will learn about simulation of breeding programs, genomic prediction, and you will obtain valuable programming skills.

Supervisor(s): Pascal Duenk
Available from: 2020
Inbreeding and genetic parameters in homing pigeons

Homing pigeons are bred and kept by pigeon enthusiasts for participating in racing contests. In these contests, the pigeons are released from a location far away from their homes (lofts), and points are awarded based on the speed at which they return home. Homing speed seems to have a strong genetic component, because breeders have been able to improve performance over the years by means of selection. However, genetic trends and genetic parameters (such as heritability) for homing speed have never been estimated. One of the problems that pigeon breeders face is the loss of young birds during training. Birds can for example be lost due to predation, accidents, or the inability to find their way back home. In the last 10-20 years, the fraction of young birds that are lost seems to have increased, and a clear explanation for this trend is missing. Inbreeding and unfavorable genetic correlations might play a role here, but this has not been investigated. In this project, you will work on data provided by a pigeon breeder. This data contains a well-documented pedigree, and results from racing contests of the last 13 years. From this data, you could study past and current inbreeding levels, or estimate genetic parameters and breeding values for racing performance or survivability. Which of these research questions you will work on depends on your personal interest.

Supervisor(s): Pascal Duenk
Available from: 2022

Validating the optimal modelling traits when predicting animal breeding values

Optimal modelling has a key role in improving predictability of breeding values of traits of interest. Better predictions increase the genetic gain of the breeding program. When optimizing a prediction model it is important to have a validation strategy that works well for assessing accuracy and bias of model predictions to selection candidates. Different approaches have been attempted to validate accuracy of model predictions such as; theoretical accuracy derived from the prediction error variance, correlation between predicted breeding values and corrected phenotypes, and semi-parametric estimates of population accuracy for prediction of future phenotypes. However, it is little known which approach is most appropriate for traits such as indirectly observed traits, traits with scaling effects for different sexes, traits measured in group records, and traits that are affected by maternal effects. You will investigate validation strategies for these traits in different breeding programs with traditional BLUP selection and GBLUP selection for pig, chicken or fish. In this thesis project you will learn to perform stochastic simulations and learn about the design and optimization of breeding programs and genetic evaluation models.

Supervisor(s): Thinh Tuan Chu, John Bastiaansen

Selecting/restricting training populations for improved prediction accuracy

The essence of genomic prediction is to predict the phenotype of genotyped individuals. This is achieved by using the results of a statistical model that determines the association between phenotype and SNP-genotypes in a so-called training population. The accuracy of this prediction is mainly driven by the genetic relationship between training population and the selection population. Underlying assumption is that the relationship based on the SNPs reflects the relationships based on the QTLs underlying the traits of interest. Genomic prediction works well in a closed breeding population. If, however, the training population consists of a combination of (sub) populations, the relationship (Linkage Disequilibrium) between SNP genotypes and underlying QTL genotypes may not be consistent. For example, SNPs can be segregating in the whole training population, while QTL alleles might be segregating in only part of the training population, which will hamper the prediction accuracy. This has been extensively documented in plants, e.g. corn breeding (Melchinger/Bernardo), and also prediction across breeds in animals results in low accuracies.
A PhD student of De los Campos has recently published an algorithm that could be used to determine which part of the training population is most informative for a given group of genotyped individuals. The idea is that selecting the optimal part of the training population would result in higher prediction accuracy. The goal of this MSc project is to better understand this algorithm and to discover when and how to apply it using real and/or simulated data.


Supervisor(s): Henri Heuven, Pascal Duek
Available from: 2021

**Definition of phantom parent groups in international evaluation of beef cattle**

In national genetic evaluations, recorded animals may miss pedigree information for one or both of their parents. Nevertheless, producers desire to have an animal Estimated Breeding Value (EBV) also for such individuals to make their selection decisions and, therefore, these animals are still included in the genetic evaluations. However, in genetic evaluation models, animals with missing pedigree information are considered as offspring of the same unrelated and unselected animals in the base population, disregarding of their year of birth. This, in turn, may lead to potential bias in the animals’ EBV. In a similar way, when animals are evaluated across countries in an international genetic evaluation, they may miss parental information. To overcome such problem, Phantom Parent Groups (PPG) can be defined. However, in current beef cattle international evaluations PPG are not yet implemented. In this MSc project, after a brief literature review on the topic, you will define PPG for across-country evaluations in Limousine beef cattle European populations. Your goal will be to find the best approach to use for PPG in estimating beef cattle animals’ EBVs. You will have the opportunity to work with real data and to improve programming skills.

Please keep in mind that organizing the data before the start of the thesis might take some time. So please inform us ~3 months in advance about your interest in this topic.

Supervisor(s): Renzo Bonifazi
Available from: 2019

Note: This project has already been carried out, but follow-up research is still available. You can send an email to renzo.bonifazi@wur.nl to discuss the possibilities.

**Data requirements for the estimation of across-genetic correlations in international beef cattle genetic evaluations: a simulation study**

International beef cattle evaluations aim to assess animals’ Estimated Breeding Value (EBV) in different environments, i.e. countries. To accurately estimate animals’ EBV, a crucial aspect to consider is how much the information collected on animals recorded in one country is going to contribute to the genetic merit of its relative in another country. This is achieved by the usage of across-country genetic correlations, which are estimated from animals with recorded relatives in multiple countries, e.g. a popular bull. Such animals ensure the presence of across-country genetic links, called genetic connections. Therefore, to correctly estimate genetic correlations across-country good data structure is required, with many genetic connections in place. However, in beef cattle, compared to dairy cattle, there is a structural lack of genetic connections due to the lower usage of artificial insemination and, in turn, estimating genetic correlations across countries may be difficult and require long time. Moreover, many recorded traits in beef cattle are affected by a maternal genetic effect expressed in the offspring’s phenotype and that requires a particular data structure in place to be accurately estimated. In this project, your goal will be to simulate a beef cattle international dataset with phenotypic and genomic information. You will gain experience with programming, simulation studies and international cattle evaluations. Once the dataset is in
place, you will perform a simulation study with the aim of understanding the required amount and structure of the data to have an accurate estimation of genetic correlations across-country.

Supervisor(s): Renzo Bonifazi
Available from: 2019

Note: This project has already been carried out, but follow-up research is still available. You can send an email to renzo.bonifazi@wur.nl to discuss the possibilities.

Genetics of fish growth in Greek vs. Spanish waters

We have the unique opportunity to do an MSc thesis that includes field work to do measurements on fish that you will subsequently use for quantitative genetic analysis. The question that is asked in this project is whether growing in warmer vs. Colder water puts different (genetic) requirements on fish. To measure this genotype by environment interaction (GxE) we let fish from the same families grow in two different farms, one in Spain and one in Greece. The experiment is part of the EU project MedAID ([http://www.medaid-h2020.eu](http://www.medaid-h2020.eu)). In this project you will analyze phenotypes collected in the project to estimate heritability and genetic correlations of performance in the two different environments.

Supervisor(s): John Bastiaansen, Benan Gulzari
Available from: 2019

Genetic differences in feed digestibility between dairy cows

In recent years, interest for feed efficiency increased, because – among others – of economic reasons, societal issues (feed-food competition) and environmental concerns (e.g., nitrogen pollution). Recently, the Dutch breeding company CRV included feed efficiency in its breeding objective. However, there is still a lack of knowledge on the biological background of differences between cows in feed efficiency. Some studies showed that differences in feed efficiency might be partly explained by feed digestibility. Digestibility is measured as the difference between the feed ingested and the faeces excreted. There are indications that feed digestibility is heritable and that genetic improvement is possible, but as it is a laborious and expensive trait to record, there are few studies on its genetic background. Currently, the breeding company CRV records routinely feed intake on 5 commercial dairy farms. In a combined research project of Animal Breeding and Animal Nutrition, feed digestibility will be measured on approximately 400 genotyped cows on commercial farms. Feed intake data will be provided by CRV and faecal samples will be collected to estimate feed digestibility. The aim is to better understand differences between cows in feed digestibility through the analysis of the genetic background, including estimation of heritability, genetic variance and a genome wide association study. The project also aims to better understand the relationship between feed efficiency and digestibility, so the correlation between digestibility and other traits, including feed related traits, will be examined.

Supervisor(s): Henk Bovenhuis, Eugenie Guennoc
Available from: 2022

Estimation of heritabilities and genetic correlations in production environment of gilthead seabream using genotypic data

Heritabilities and genetic correlations of production traits in fish are commonly calculated with the data collected in the environment where the broodstock is kept, which is generally far away from the commercial production environment. Variance components estimations with the data collected in the commercial production environment are rare. In this project, data of the commercially produced gilthead seabream for human consumption were collected for harvest weight, fillet weight, fillet yield, fat percentage, heart weight and liver weight. Harvest weight, fillet yield and fat percentage of the fish are traits of commercial importance. Heart and liver weights can be used as indicators of overall health. The heritabilities of these traits as well as genetic correlations among them will be estimated using genotypic data by the MSc student. Estimations performed by the MSc student will be an important contribution to fish breeding literature. Interested students will have the opportunity to learn basic programming in R and ASReml.
Improving genomic prediction by using individualized reference populations

Genomic prediction typically uses a single reference population of genotyped and phenotyped individuals, to estimate breeding values for selection candidates that are only genotyped. Over time, as data accumulates, the reference population becomes increasingly heterogeneous. As a result, the differences in allele frequency and linkage disequilibrium patterns between the reference population and selection candidates can limit prediction accuracy. It may therefore be beneficial to use only part of the reference population. But how do we decide which animals to use? One can imagine that the subset of the reference population that maximizes accuracy differs between selection candidates. In theory, for each selection candidate, it would be beneficial to include animals in the subset that are more closely related. Lopez-Cruz and de Los Campos (2021) proposed an approach that identifies, for each selection candidate, an optimal subset from the reference population (i.e., a set of support points) from which predictions are derived. In this project, you will study the relationship between/among reference animals and selection candidates to show that:

- individuals in the subset truly have parts of the genome in common;
- low relationships are due to identity-by-state instead of identity-by-descent;
- SSI is not only a statistical ‘trick’ that improves prediction accuracy, but there is an underlying genetic reason for it.


Supervisor(s): Henri Heuven

2. Genomics

CNV analysis in different pig breeds using 650K SNP genotypes

You will work with a large SNP genotype data set of around 100 pig samples of different breeds. By using PennCNV software you will identify CNVs. You will characterize the CNV regions by looking at overlapping genes. You will look at breed differences and function of the genes involved. Compare results with SNP genotypes from whole genome sequence data and from 60K SNP chip.

Supervisor(s): Martien Groenen, Richard Crooijmans
Available from: 2018

Insights of the Lakenvelder phenotype in farm animals

Coat colouring in farm animals is a complex phenotype. The “Lakenvelder” phenotype is a phenotype occurring in several species. We would like to know how the genetics and genomics behind this trait. Furthermore we would like to have a summary of all genes involved in coat colour over species. We do have SNP genotypes of Lakenvelder chicken and cattle available. A selective sweep analysis in chicken and in cattle Lakenvelder can be performed to find potential new genes associated with this trait.
This project is partly a literature study and SNP data analysis. A comparative study between species will be part of the task.

Supervisor(s): Richard Crooijmans
Available from: 2018

Inheritance of a chromosomal-wide oxford nanopore sequencing in great tit
Large inversions in bird genomes are known to affect different phenotypes. A striking example is the non-canonical reproductive strategy in ruff, which is associated with an inversion that in turn underlies lower testosterone levels. Moreover, inversions have a prominent role in the evolution because they can lead to strong differentiation between the inverted and non-inverted region. Recently, we identified a chromosome-wide inversion on PM1A present in 5-10% of wild great tit (Parus major) populations, which indicates an evolutionary role for the inversion haplotype. This 1A inversion is indeed highly differentiated from the normal version of the chromosome 1A and until this point was demonstrated to occur just in heterozygotic state. From 2017 onwards we will start to breed birds containing the inverted chromosome 1A to allow detailed evaluation of inversion inheritance. The student shall then be able to explore whether the heterozygotic state is mandatory for birds carrying the inversion haplotype. Therefore, the student should illustrate different levels of genomic complexity within inverted and non-inverted 1A chromosomes, discuss associated phenotypes as well as their putative evolutionary roles. This is a collaborative project between Wageningen University & Research (WUR) and Netherlands Institute of Ecology (NIOO-KNAW), supervised by two researchers in each institute and will require knowledge on bioinformatics and genetics.

Supervisor(s): Mirte Bosse (WUR), Veronika Laine (NIOO-KNAW), Marcel E. Visser (NIOO-KNAW)
Available from: 2018

Sugar pig

Milk composition has been under natural selection for thousands of generations. Milk composition affects both the fitness of the mother and the offspring and therefore is optimized to transfer essential ingredients as efficient as possible from mother to offspring. Remarkably, milk contains oligosaccharides which are not digestible by the offspring and therefore seem like a waste of maternal energy. These oligosaccharides, however, provide a selective advantage to specific microbes which are specialized in digesting oligosaccharides and might be beneficial to the host. In humans, FUT2 gene variants have been associated with activity and composition of the gut microbiome. More than a hundred different milk oligosaccharides have been identified and there are large differences between and within species in milk oligosaccharide composition. Part of these differences have been attributed to genetic differences e.g. in expression of certain glycosyltransferases. In humans 4 "milk groups" are distinguished based on milk oligosaccharide composition which can be related to mutations in FUT2 and FUT3. These fucosyltransferase genes are also linked to ABO histo-blood groupings, illustrating that the function of these genes is not limited to fucosylation of milk oligosaccharides. In pigs, polymorphisms in the FUT1 gene have been associated with control of the intestinal expression of enterotoxigenic E. coli (ETEC) F18 receptors; a pathogen causing edema disease and post-weaning diarrhea (e.g. Meijerink et al 1997). The aim of the current study is to use whole genome sequence data to identify variants in genes involved in the production of pig milk oligosaccharides. These genes include among others FUT1 and FUT2.

Supervisor(s): Martijn Derks, Henk Bovenhuis
Available from: 2021

The search for the missing tail

A tail-less might sound odd, but the Drenthe fowl has been around for centuries in the Netherlands. A variant of this breed called ‘Klomphoen’ is the rumpless/ tail-less Drents, as shown in the pictures. The Drenthe Fowl Bolstaart shows striking rounded rump due to the lack of tail, or to be precise, uropygium from which the tail grows. The trait of caudal truncation is kept by farmers for the reason that the rumpless chickens escape better from the attack of foxes, then the predators have no grip because of the absence of the tail. Here we would like to develop a Master thesis study to investigate the genetic nature underlying the tail-less phenotype by using the genetic data of Drenthe Fowl Boolstaart and Drenthe Fowl. It is possible to use the Whole Genome Sequence
data to work on the genetic variants that are associated with the tail-less phenotype. In order to tackle the research question, Genome-wide association study, detection of signal of selection will be possible. We are looking for a student with a basic knowledge of genomics (variations, genome sequencing and functional annotation) and working experience with Linux machine (basic bash coding) and R.

Supervisor(s): Richard Crooijmans
Available from: 2018

**Improvement in imputation accuracy with a line specific reference genome**

The public reference genome of species is based on an single individual of a specific breed. In pig this is a Duroc animal. However, different breeds also have some differences in the genomes, especially with respect to structural variation. In pigs we have generated breed-specific reference genomes using long-read sequences. The line-specific reference genome should be a more accurate reference genome compared to the public reference genome. Our research question is whether this accuracy in the reference genome also leads to more accurate imputation of SNP chips to WGS level. Whole genome sequencing (WGS) is still too costly to do routinely on large number of animals. Imputation from SNP chips up to WGS is therefore a good alternative to create datasets with potential causal variants of sufficient size for e.g., GWAS studies. However, the success of such studies depends largely on the imputation accuracy. We have WGS data available from a pig breed with a line-specific reference genome. You will learn to align this data to this new line-specific reference genome with bioinformatic tools. Afterwards you will impute SNP chips up to WGS using that data aligned to the line-specific reference genome, as well as using the WGS data aligned to the public Duroc reference genome. You will ultimately compare the imputation accuracy across different genomic regions and MAF categories to identify situations were imputation accuracy is improved with a line-specific reference genome.

Supervisor(s): Martijn Derks
Available from: 2022

**Functional genome analysis during development of chicken and pig (apply allele specific analysis to detect genome aneuploidy)**

Summary not yet available.

Supervisor(s): Ole Madsen, Marta Godia Perello
Available from: 2022

**Single cell RNA-seq analysis of organoids**

Summary not yet available.

Supervisor(s): Ole Madsen, Marta Godia Perello

**'Nanopore sequencing’**

Summary not yet available.

Supervisor(s): Ole Madsen, Marta Godia Perello
Available from: 2022

**3. Genetic diversity**

Genetic diversity across local Dutch breeds
In the Netherlands we have a number of unique rare cattle breeds. Efforts have been made to preserve these breeds for the future. Their DNA is stored in the Dutch gene bank, and breeding strategies to maintain genetic diversity in the living population are in place. The breeds look very different, but besides those breed characteristics we know little about the genetic diversity across the different breeds. With whole genome sequence data we can investigate which regions in the genome differ significantly between the breeds and which genes are located in those regions that may explain differences in phenotypes. Are you interested in working with whole genome sequence data on genomic diversity of Dutch local breeds? You will learn to handle whole genome sequence data, to estimate genomic diversity across breeds, and interpret the results.

Inbreeding due to breed characteristics

Is inbreeding higher at loci related to breed appearance? Several local Dutch breeds have very unique breed characteristics. For example the white belt of Dutch belted cattle (Lakenvelder), the white head with coloured blisters around the eyes of the Groninger White Headed (Blaarkop), or the double muscling of Dutch Improved Red cattle (Verbeterd Roodbont). The regions on the genome responsible for these breed characteristic are known. With whole genome sequence data we can characterize these areas and investigate the uniqueness and length of haplotypes in those areas. By comparing those regions to the remainder of the genome we can answer the research question. Are you interested in working with whole genome sequence data on genomic diversity of Dutch local breeds? You will learn to handle whole genome sequence data, to estimate genomic diversity, to identify haplotypes and interpret the results.

Using breeding circles for genetic management of zoo populations

Summary not yet available.

Genetic relationship between free ranging Scottish Highlander herds on the national reserve ‘De Hoge Veluwe’

By using GPS data and SNP genotype (100K) data we want to investigate inbreeding and migration between herds.

Specific selection signatures in dog breeding

Currently there are nearly 400 distinct dog breeds. Dog breeds are highly divergent on appearance, body size, talent, lifespan, and many other phenotypes. These breed-specific traits were selected artificially and fixed by inbreeding. In a long history, dog breeding programs were isolated from Western countries to Oriental countries. This yielded the diversification in many traits between Western and Oriental dog breeds. Since genotype data of more than 6000 dogs from more than 160 dog breeds across the whole world is available which makes it possible to investigate the breed-specific selection signatures. Meanwhile, in this thesis, you will collect the general standard characteristics of dog breeds, like standard height and lifespan, as your phenotypes to be investigated. Optional questions to work on: Based on the genotype data and breeds information you could detect the distinct major selection signature(s) for specific dog breeds, for instance, terrier. The measures you will work on are Fst, inbreeding level, ROH (run of homozygosity), and so on. Furthermore you will interpret how the genes underlying the selection signatures contribute.
to the specific traits or special dog breeds. You could also work on identifying the selection signatures linked to the geographical origin of the breeds. Another one interesting diverse trait is the average lifespans of dog breeds. To investigate the underlying genetic basis of the lifespan in dogs, you will first collect the lifespan parameters of various dog breeds, and then perform GWAS analysis to identify the genes associated with the average lifespan of the dog breeds.

Supervisor(s): Richard Crooijmans, Yun Yu
Available from: 2019

**Inheritance analysis in Tauros cattle: a free ranging cattle population in the Netherlands**

We have 5 different sets of SNP data varying from 20k till 770K with in total more than 500 semi-wild cattle individuals with unknown/ or incomplete pedigree information. By using different methods we want to reconstruct the pedigree.

Supervisor(s): Richard Crooijmans
Available from: 2020

**Evolutionary genomics of common carp (Cyprinus carpio)**

The common carp (Cyprinus carpio) is an iconic fish and important in aquaculture and as model species. Carp is often preferred for experimental work due to its impressive size over its relative, the diminutive zebrafish which is a model for vertebrate development and physiology. To increase its use as an experimental species, but also to facilitate selective breeding, a better understanding of the functioning of the carp genome is required. The carp genome however has an interesting feature: it is tetraploid. The carp and its relative the goldfish originated from a hybrid between two species, around 12 million years ago. That hybridization led to a genome duplication – the genomes of both species were combined into a single nucleus. This situation more or less continues until today. But this leads to many questions concerning the fate of all those duplicated genes – are all genes still active? Only one of the copies is perhaps enough. Or are genes gradually being lost, something you see in other polyploid species. And if both copies of genes are still there, do they perform different functions? We are currently doing a new genome assembly using Nanopore sequencing. This improved genome assembly allows us to these questions. First we try to improve the interpretation of the function of the genome (annotation) by looking at gene expression in the context of the genome assembly. Second, we will compare the two ‘subgenomes’ to see what is lost, what is still there, and what is still there but doing something different. We are also interested in a broader comparative genomic study that includes zebrafish and many other fish species. To this end well generate functional genomic data such as gene expression data, epigenetic modifications, and more, for several species including carp.

Supervisor(s): Annemiek Blasweiler (AFI, ABG), Hendrik-Jan Megens
Available from: 2019

**Inbreeding when matings are out of control**

In many fish species that are grown in aquaculture the reproduction is not completely controlled. Often this means that we can select potential parents but we cannot decide on the individual contributions that parents make to the next generation and/or which parents will mate together. The theory and methods that are generally applied to control inbreeding assume that you can make specific matings and keep offspring of those. In this project you will analyze pedigree data from fish breeding programs that reproduce fish in breeding groups, and use the results to predict the rate of inbreeding in such a program. In addition, you can apply this knowledge to design a breeding program to control the rate of inbreeding at an accepted level. The design work can involve simulation or theoretical derivation of inbreeding rates based on the results from the analysis of the breeding groups.

Supervisor(s): John Bastiaansen
Available from: 2019
From sequence to sushi: genetic diversity in a newly domesticated fish species

The Yellow Tail Kingfish (*Seriola lalandi*) is one of several fish species that has recently made the transition from exclusively wild-caught to being cultured, and is now on its way to becoming a domesticated species. This species has a biology that is similar to tuna (although no direct ‘family relationship’): It lives in the oceans and is very mobile. These fish are found all around the world. The domestication process and related breeding are directed to efficient production and high quality meat. Most of the meat is produced for Sushi, a highly prized product. There is, however, currently hardly any knowledge on the variation in this species in the wild, or in cultured systems. We recently sequenced the genome of the Yellow Tail Kingfish, and conducted physiological experiments and gene expression analyses to gain a better insight in the biology of culturing this species. We have also sequenced 20 Yellow Tail Kingfish that were caught from the wild near South Africa from cultured populations in Chili and Australia. This whole-genome sequence data holds a very large amount of information that can give us knowledge on the evolution of the species and on the variation that is present in the populations that are currently in the process of becoming domesticated. Questions that you can be working on: what is the effective population size? How much variation is there in the genome? What is the pattern of evolution in protein altering-, versus neutral evolution? And is there reason to fear inbreeding depression when a species that may have a very large population size in the wild is transferred to an enclosed and relatively small breeding system?

Supervisor(s): Hendrik-Jan Megens, John Bastiaansen
Available from: 2018

### 4. Sustainability and breeding programs

**Selection traits for alternative housing systems in laying hens**

Cage-free housing systems have been suggested as a welfare-friendly alternative to conventional cage housing of poultry. Such housing systems allow animals to express a wider range of natural behaviours, such as movement in outdoor areas, sand bathing, etc. Modern poultry, however, have been genetically selected for conventional systems and may not be well-suited for cage-free environments. Furthermore, birds housed in cage-free systems experience various behavioural, physical and disease challenges which may negatively affect them. Given the increasingly global trend towards cage-free housing, genetic selection programs must be adapted to select birds appropriate for such housing systems. This involves the development of relevant cost-effective phenotyping strategies, in which a large number of birds are measured and ranked on their performance. Those animals with the best performance will be selected to parent the next generation of birds, ultimately contributing to improved health and welfare of poultry.

In collaboration with a large avian genetics company, animal welfare specialists at the University of Bern in Switzerland and geneticists at the University of Guelph in Canada, this project aims to develop a series of novel traits associated with movement, locomotion and health and welfare traits in poultry for use in breeding programs. Sensor tracking technology applied to commercial laying hens, as well as information on a number of conventional traits, will be collected and analysed within this project. Students will gain knowledge and skills in animal behaviour, genetics, data analysis and statistics. This project aims to develop novel phenotypes that can be used for genetic selection within laying hen breeding programs.

More reading about the observed behavioral patterns and their association with health and disease can be found at:

https://doi.org/10.1016/j.applanim.2019.05.007
https://doi.org/10.1016/j.cbd.2020.100700
https://doi.org/10.3389/fvets.2020.00587

Supervisor(s): Henk Bovenhuis, Prof Christine Baes (University of Bern and Guelph)
Available from: 2022

**Methane traits for dairy cows**
Dairy cattle are a significant contributor to greenhouse gases. There is a possibility that breeders can select cows that produce less methane but are still efficient milk producers. We are exploring methods of recording methane on farm, defining methane phenotypes, and estimating genetic parameters, all of which would contribute to the breeding of low methane producing cows. Two different types of machines have been installed in barns across the Netherlands. Both measure methane of individual cows, but with different methods. The aim of this thesis is to help determine if cows would have the same ranking for methane with the two different methods.

Supervisor(s): Michael Aldridge
Available from: 2019

Genetics of resilience to heat stress in fertility traits

The expectation is that summers will get warmer and the occurrence of heat waves will increase because of global warming. This would increase the need for heat resilient animals Within the EU-project Rumigen we are involved in investigating genetic variation in resilience to heat stress for production and fertility traits. The hypothesis is that fertility is more affected by heat stress than production. In this thesis we would like to investigate to which extent fertility traits like calving interval, interval calving first insemination and interval first last insemination are affected by heat stress. It will be investigated what the critical period is for heat stress affecting these fertility traits. Subsequently, it will investigated if there is genetic variation in the decline in fertility using reaction norm models. If time permits, the student can investigate how trade-offs between fertility and production may be affected by heat stress. The student gets ample opportunity to work with large data sets and different software packages, such as awk, R, ASReml or Gibbs.f90. Ultimately, this thesis gives new traits that could be used to breed heat resilient cattle.

Supervisor(s): Han Mulder, Jeremie Vandenplas
Available from: 2021

Social behaviour in dairy cows

Dairy farming remains one of the most important food production sectors worldwide, providing high quality protein whilst utilizing residual flows from other industries. In modern society, however, dairy production is controversial in terms of sustainability with its high load of greenhouse gas emissions and the delicacy of dairy cow welfare. Breeding for the best animal-in-environment cow is a crucial aspect in optimizing the sectors’ negative impact on society. Dairy cow hierarchy and dominance can affect the animals’ welfare and health, and is potentially heritable. Obtaining insight in this hierarchy, and linked with this, a good phenotype for breeding, has proven difficult. It requires knowledge of the behaviour and interactions between the animals, preferably in a long term and continuous way. In this project, you will look at individual, paired and herd cow behaviour as measured with a on-farm indoor positioning system (ultra-wide band technology) over a time period of 6M to 1Y to gain insight in behaviours that reflect cow dominance. With the current dataset, it is also possible to look at the effect of lactation stage, parity, disease status and weather conditions. Within the project, there is some flexibility to bring in your own ideas or put your own focus if preferred. You will learn about precision livestock farming and (social) cow behaviour and acquire skills in time-series analysis, statistical modelling and programming (preferably python, including data visualisation).

Supervisor(s): Ines Adriaens
Available: 2022

Effects of the altitude on qualitative phenotypic characteristics of local Ethiopian chickens
You will investigate the effect of the environment (variation in altitude) on morphological variability of indigenous chicken populations. The phenotypes will be collected in Ethiopia. So far we have been aiming to utilize the quantitative measurements for landscape genomic studies. You will collect and learn to analyze biogeographic information together with data on qualitative traits from indigenous chicken populations. The traits could include plumage colour, comb type, earlobe colour, shank colour, head shape, shank morphology. Based on the results of analysis you will develop hypotheses for why certain phenotypes might be useful in a particular environment. Field work in Ethiopia to collect data and to work with the researchers at ILRI campus in Addis Ababa could be included. In this case you will collect data on chicken production systems, qualitative morphological data, geographic data (coordinates), and possibly other geospatial and environmental data such as altitude or climate. The correlation of traits with environmental parameters is part of your analyses.

Supervisor(s): Fasil Getachew, John Bastiaansen
Available from: 2019

**Do organic and circular dairy farming require different genetics?**

Are cows that show their best performance under conventional farming conditions the same as the ones that show excellent performance under organic farming conditions? In other words, is there genotype by environment interaction? This has been the topic of an ongoing debate. Nauta (2009) estimated a relatively high genetic correlation between milk yield under conventional and organic production of 0.80. Standard errors of the estimated genetic correlations were high, which did not allow drawing firm conclusions. Since the work of Nauta (2009) the number of organic farms in the Netherlands has increased, allowing for more accurate estimates of genetic parameters. In addition, quantifying genotype by environment interaction will benefit from an accurate definition of “environment” which has been problematic in previous studies as there are considerable differences among organic farms as well as among conventional farms, e.g. in the use of concentrates. The excretion indicator (BEX) is used to calculate specific N and P excretion from dairy cattle on farm level. This data base contains detailed information on several farm characteristics which can be used to better characterise farms (i.e. the environment). How differences in the use of concentrate interact with genetics is a relevant topic in view of the switch to circular agriculture. The aim of the current study is to quantify genotype by environment interaction for dairy farms in the Netherlands. The first project will focus on the difference between organic and conventional farming conditions. The second project will focus on differences in the use of concentrates.


Supervisor(s): Henk Bovenhuis
Available from: 2022

**Difference between morning and evening goat milk composition in relation to heat stress**

In general, we assume that milk composition (fat% and protein%) is similar between morning and evening milk samples. However, we have strong indications that this is not the case for goat milk. Furthermore, we have indications that goat milk composition is (strongly) affected by heat stress. The aim of this study is to quantify differences in goat milk composition between morning and evening milk samples. We hypothesize that this difference is affected by temperature; it is expected that during warm summer days the evening milk sample is stronger affected by heat stress than the morning milk sample.

Supervisor(s): Henk Bovenhuis
Available from: 2022

**How do cultured fish keep their shape?**
Fish for aquaculture are typically selected for growth. Selection for growth can have effects on the shape of fish. In this project we will use image analysis to investigate the genetics of shape and appearance. For this project we collaborate with a fish breeding company in Greece that produces high value fish species: sea bream and sea bass. The company is taking photographs of all the fish in their breeding program at multiple times during their growth. The shape and appearance of the fish, i.e. the exterior traits, are very important because they are sold as whole fish. In horses and cattle it is common to give scores for the exterior of the animals and to breed for this. Fish are also scored in a similar way, but obviously for different traits as horses, cattle or dogs. The important traits in fish are roundness, color, belly shape, etc. In this project you will analyze the digital images of the animals to develop smart and objective measures to describe the exterior of the fish. In a second phase you try to estimate heritabilities for your new measures and investigate how they correlate, genetically, to the current scores given by human judges. The aim is to develop measures that can be included in the breeding program in Greece to improve the appearance of the fish.

Supervisor(s): John Bastiaansen, Hans Komen
Available from: 2018

Growing fish also healthy?

Fish is generally known to be a healthy food for humans. To become a healthy food, farmed fish should be healthy itself. In this study we will investigate the genetic relationship of growth and health of the fish. For this project health is measured as the condition of several organs, like the gills, the heart and the liver that play an important role in supporting the growth of fish. For instance by supplying oxygen, or by metabolizing fatty acids. These organs are expected to be good checkpoints for the overall health of the animal. For this study a large number of fish from a breeding population have been dissected and the health of their organs was scored by a veterinarian. The heritabilities of these scores as well as their correlations with growth will be estimated by you. In addition, you will investigate whether difference in environmental conditions such as the season have an impact on the variation that is observed in organ health. From your results you will make recommendations on what is needed in a breeding program to make sure the fish stay healthy while selecting for improved growth.

Supervisor(s): John Bastiaansen, Hans Komen
Available from: 2018

Fish reproduction

At ABG, we study the reproductive physiology of fish in nature and aquaculture and develop innovative methodology for solving reproduction bottlenecks of captive fish. Research topics include sexual maturation, fertility, and larval development. Closing the production cycle of species difficult to propagate (e.g. European eel) is a focus area. Within this line of research we always have projects running within which up-to-date thesis topics can be formulated.

Supervisor(s): Arjan Palstra, Hans Komen
Available from: 2022

Swimming of fish and use for farming fit fish

At ABG, we study the swimming physiology of fish in nature (e.g. migration) and aquaculture and develop innovative methodology for farming fit fish. Research topics include the use of swimming for phenotyping, for inducing (muscle) growth, for improving health and welfare, and for studying the energy economy with sensor technology. Within this line of research we always have projects
running (e.g. on seabream, yellowtail kingfish, tilapia, zebrafish) within which up-to-date thesis topics can be formulated.

Supervisor(s): Arjan Palstra, Hans Komen
Available from: 2022

Social interactions, breeding for diversity and competition between plants

Global biodiversity is declining rapidly, one of the reasons being the widespread use of pesticides. Increasing biodiversity may be a natural way to make agriculture more resilient to pests, but this will also require other breeding strategies. One way to combat pests by increasing biodiversity is the use of mixed cropping, where a field consists of a mixture of different crop species. This system is also known as "intercropping", and a well-known example is the combination of maize and faba bean. Genetic improvement (breeding) for such systems introduces new challenges, such as heritable competition between the two species. In an ideal system, taking maize and faba bean as example, genetic improvement of the maize should also benefit performance of the faba bean, and vice versa. This topic is very closely related to the quantitative genetic study of social interactions in animal breeding, a field where ABG-WUR has a lot of expertise. In this thesis project we aim to integrate knowledge on social interactions coming from the field of animal breeding with systems for intercropping in plant breeding. An important objective is to design and evaluate experimental setups for the estimation of direct and social breeding values in intercropping systems. This will be done at least by computer simulation, and potentially also in the field. You will develop programming skills (e.g. R or Python) and data analysis skills, and become familiar with the application of quantitative genetics in plant breeding (for which er are currently excellent job opportunities).

Supervisor(s): Piter Bijma (ABG), Peter Bourke (PBR)
Available from: 2021

5. Big data/data science

Data selection for improved association studies

In GWAS studies the goal is to identify QTL affecting complex traits. In many cases the assumption is that the underlying QTL is biallelic (Q/q). However, if the population is heterogeneous this assumption may be wrong and more QTL alleles (Q1/Q2/Q3...) are segregating. Especially because SNPs only have 2 alleles, finding an association between SNP and QTL is easier if data is used where only two QTL alleles are segregating, i.e. in the part of the data that is homogeneous with respect to QTL-effects. The idea is that an algorithm developed by De los Campos for improving prediction accuracy, could be used to select data which is most informative to find QTL in an association study. The goal of this project is to study the algorithm for identifying QTL in heterogeneous data set using real and/or simulated data.


Supervisor(s): Henri Heuven, Pascal Duenk
Available from: 2021
Big data from a school of fish: a computer vision system to extract data from images of fish

In animal breeding, one of the biggest challenges is to measure many phenotypes efficiently and accurately. Measuring animals is time consuming, and measurements taken by humans have a limit on how accurate they are and how many animals can be measured cost-effectively. In fish-breeding, regular imaging of fish is becoming the norm, to facilitate semi-automated phenotyping of the animals. Although improvements can be made by this approach, it does not take full advantage of the image data. Rather, what is needed, is a fully automated image analysis approach, that can take many more measurements. In addition, automated systems result in easily scaling up in numbers of animals measured without increasing labor costs that much, and in higher reproducibility of the measurement. From a scientific perspective the exciting prospect is to capture quantitative aspects of the phenotype that can only be measured subjectively by humans. How do you quantify, for instance ‘shape’, from looking at a picture or when only taking 2 or 3 manual measurements? A computer vision system can measure hundreds of points in a reproducible way. In this project you will develop a prototype of a fully automated fish phenotyping program. The programming part will be done using Python (a general and very popular programming language) and OpenCV (a specialized computer vision library that can be used in Python). However, more importantly, you will investigate and apply new ways to define shape and growth parameters that can be derived from your software. Depending on your interests, this can be approached either from biologically informed phenotype definitions, such as lateral line shape, operculum shape, etc, or from more general ‘big data’ type approaches, collectively called ‘Machine Learning’. Interested students will have the opportunity to learn basic programming in Python.

Supervisor(s): Hendrik-Jan Megens, John Bastiaansen
Available from: 2018

Should we pre-correct big data for the estimation of heritabilities and breeding values?

Analysis of big data becomes increasingly important in animal breeding. The size of data sets for estimation of heritabilities and breeding values is growing all the time, also because of the increasing availability of genomic data. To be able to analyze such large data sets efficiently, two-step procedures are becoming common. In the first step, the data are pre-corrected for systematic effects, for example due to the herd or sex of the individual, or the litter the individual is born in, etc. In the second step, heritabilities or (genomic) breeding values are estimated, or a genome-wide association study is performed to identify SNPs affecting the trait of interest. This two-step procedure simplifies the analysis of big data. However, our recent research suggests that pre-correction may create errors (bias) in the estimation of heritabilities and breeding values. Even though pre-correction is widely used in animal breeding, this topic has received little attention until now.

In this thesis project you will investigate the consequences of pre-correction of big data for the estimation of heritabilities and (genomic) breeding values. This includes a combination of data simulation and subsequent analysis, and the use of an actual data set from a Dutch breeding company. The aim is to better understand the effects of data pre-correction, and ideally to find a solution for bias due to pre-correction.

During this thesis project, you will learn to program in R (or Julia or Python if you prefer), to estimate heritabilities and breeding values with ASREML, and to perform genomic prediction. You will also learn how to conduct data simulation. Hence, in this thesis project, you will considerably strengthen your data analysis and programming skills. The analysis of a data set of a Dutch breeding company will also extend your professional network in the field of animal breeding. If you perform very well, you will have the opportunity to write a scientific publication about your research (rather than a thesis report), to be submitted to a peer-reviewed journal.

Supervisor(s): Piter Bijma, Pascal Duenk
Available from: 2022
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