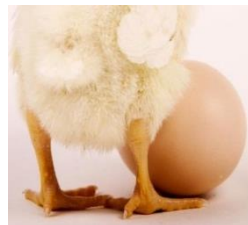


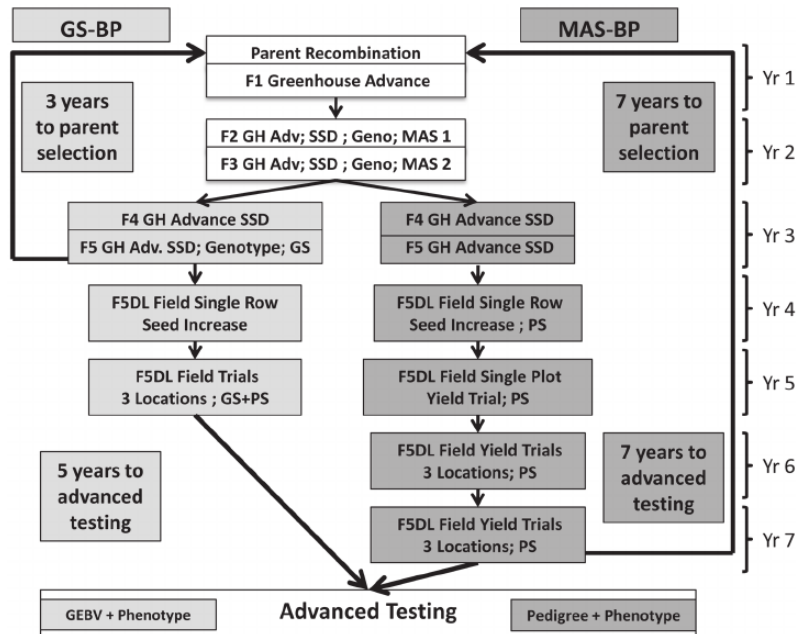
# Modular Breeding Program Simulator

Torsten Pook & Henner Simianer

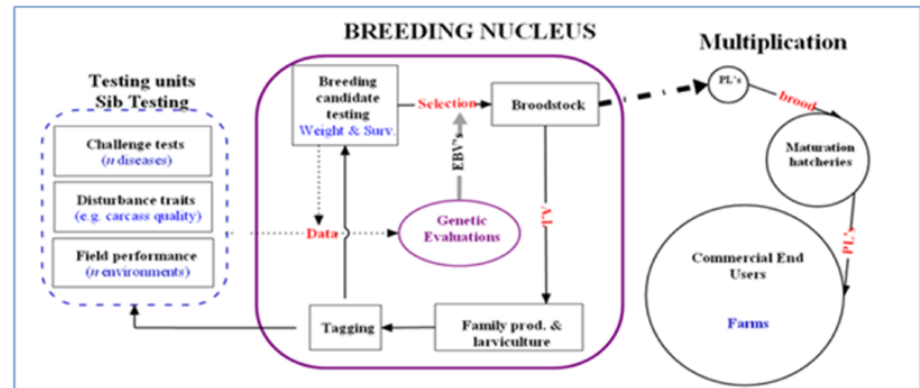




# Modern breeding programs are complex by nature



(Wheat breeding: Heffner et al., 2010)



(Fish breeding: Rye 2012)



# What are we interested in?

- What is our breeding objective?
    - Maintenance of genetic diversity
    - Genetic progress
    - Economic efficiency
    - Risk (variability of the outcome)
  - How to control it?
    - How many animals to use
    - Generate genotype / phenotype data of all animals
    - Mating scheme
    - Selection technique
    - And much more...
- Complex optimization problem!



# Possible ways to answer this?

- Experience of the breeder
- Simulation study
- Cohort-based deterministic (ZPLAN+)
  - Reliant on underlying theory
  - E.g. Breeders equation:

$$R = i \cdot h \cdot \sigma_a$$

R: response to selection

i: selection intensity

h: heritability

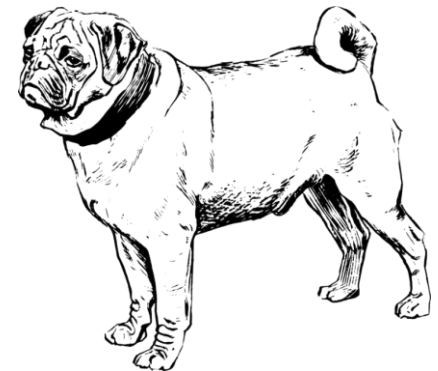
$\sigma_a^2$ : additive genetic variance

- Good approximation but formulas are limited to specific application and are constructed to handle „easy“ scenarios
  - Stochastic individual-based simulation



# What is MoBPS?

- **Modular Breeding Program Simulator**
- R-package (<https://github.com/tpook92/MoBPS>)
  - Highly efficient (Computational relevant parts written in C/C++)
  - Highly flexible (Cohort-based design)
  - Pre-implemented functions
  - Variety of different trait architectures
- Web-based application ([www.mobps.de](http://www.mobps.de))





# About the R-package

- Distributed via github: basically weekly updates
- Design philosophy:
  - Generate a tool that is able to simulate all breeding programs
  - When something is not yet possible and we see a general value in it, we are going to add it

## **Version 1.4.15 (29.10.19)**

Solve issues with running MoBPS without miraculix

Added BayesA,B,C, BL, BRR to BGLR options for BVE

New function: get.genotyped() to export which individuals are genotyped

Renamed ogc\_cAc to ogc.cAc for general uniformity

Updated documentation (especially for web-based application)

Minor update for miraculix (v0.9.7) - not MoBPS related

Added frozen version of the current that (Submission-version)

## **Version 1.4.10 (22.10.19)**

Mostly improvements to reduce memory requirement

New function: add.diag(). R-matrix is not required anymore

Clean-up of memory in ssGBLUP

Better handling of duplicated individuals (generated via copy.individuals)

## **Version 1.4.3 (16.10.19)**

MoBPSmaps 0.1.6 (Including maps for Wheat and Sorghum)

Removed typos in summary.population()

Updates to creating.diploid for trait generation via n.additive/dominant etc.

## **Version 1.4.2 (14.10.19)**

Variety of additions to json.simulation and user-interface

Added direct-mixed-model BVE for individuals without phenotype (vanRaden 2008)

Added use of Parent/Grandparent mean as breeding values

Further updates for miraculix/RandomFieldsUtils for compiler independent computing



# About the R-package

- Internally everything based on single individuals including the simulation of meiosis and recombination
- A variety of implemented functions:
  - Breeding values estimation
  - Single-step GBLUP
  - Optimum Genetic Contribution
  - Genome editing
- Trait architectures:
  - QTL-based: additive, dominance, qualitative/quantitative epistasis
  - Genomic values of parents + inbreeding coefficients
  - Correlated traits



# About the R-package

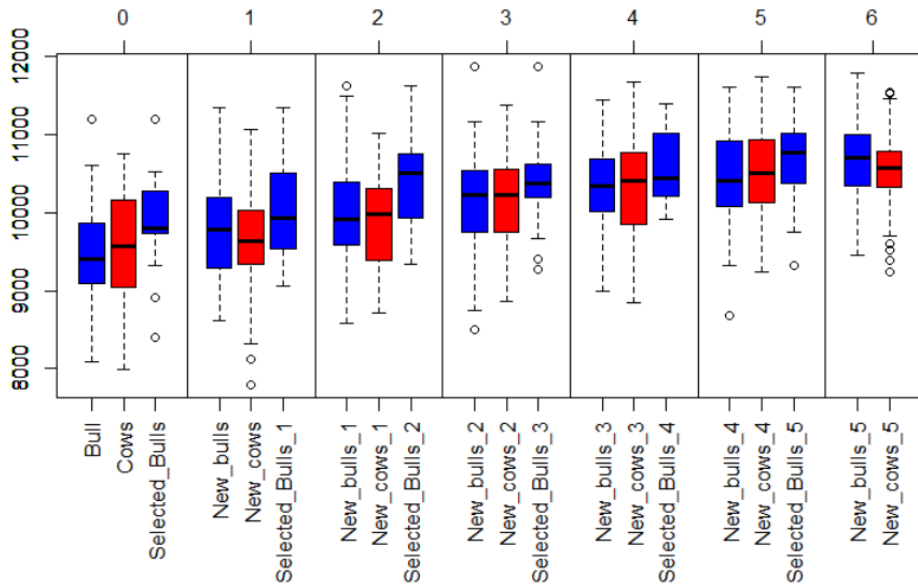
- Flexible storage structure
  - General information
  - Individual specific information
- Bitwise-storing of founder haplotypes
  - On-the-fly computation of genotypes & haplotypes
- R-package miraculix developed by Martin Schlather
  - Bit-wise computation and storage
  - 10 times faster than regular matrix multiplication in R
  - 15 times less memory



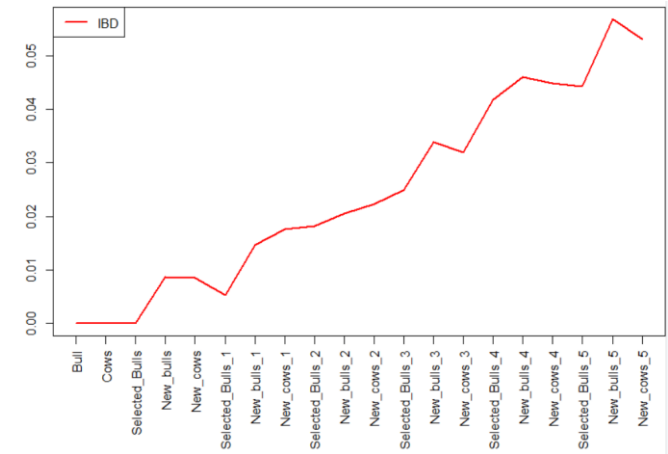


# About the R-package

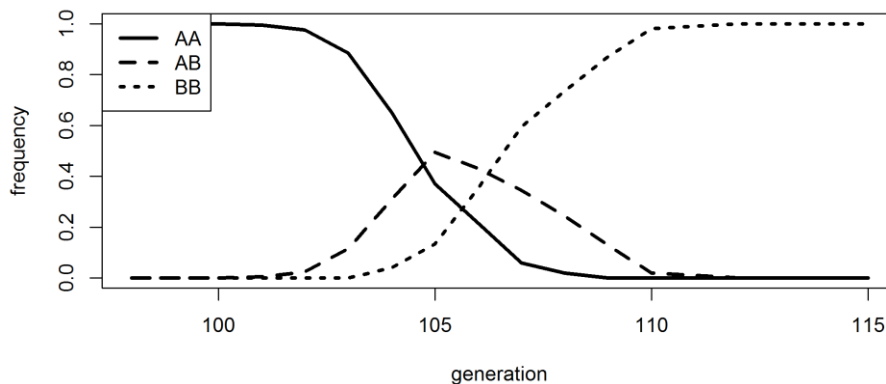
Genetic gain:



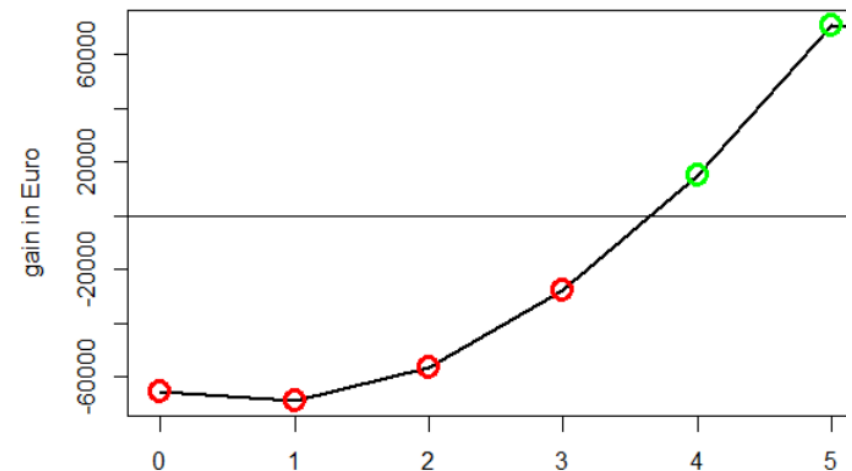
Inbreeding:



Genetic variation:



Economic gain:





# About the R-package

```
breeding.diploid <- function(population, mutation.rate = 10^-5, remutation.rate = 10^-5, recombination.rate = 1,
  selection.m = "random", selection.f = NULL, new.selection.calculation = TRUE, selection.function.matrix = NULL,
  selection.size = 0, ignore.best = 0, breeding.size = 0, breeding.sex = NULL, breeding.sex.random = FALSE,
  used.generations.m = 1, used.generations.f = NULL, relative.selection = FALSE, class.m = 0, class.f = 0,
  add.gen = 0, recom.f.indicator = NULL, recom.f.polynom = NULL, duplication.rate = 0,
  duplication.length = 0.01, duplication.recombination = 1, new.class = 0L, bve = FALSE, sigma.e = NULL, sigma.g = 100,
  new.bv.child = "mean", computation.A = "vanRaden", delete.haplotypes = NULL, delete.individuals = NULL,
  fixed.breeding = NULL, fixed.breeding.best = NULL, max.offspring = Inf, store.breeding.totals = FALSE, forecast.sigma.g = TRUE,
  multiple.bve = "add", multiple.bve.weights = 1, store.bve.data = FALSE, fixed.assignment = FALSE,
  reduce.group = NULL, reduce.group.selection = "random", selection.criteria = c(TRUE, TRUE), selection.criteria.type = c("bve", "bve"),
  same.sex.activ = FALSE, same.sex.sex = 0.5, same.sex.selfing = TRUE, selfing.mating = FALSE, selfing.sex = 0.5,
  praeimplantation = NULL, heritability = NULL, multiple.bve.scale = FALSE, use.last.sigma.e = FALSE,
  save.recombination.history = FALSE, martini.selection = FALSE, BGLR.bve = FALSE, BGLR.burnin = 500,
  BGLR.iteration = 5000, copy.individual = FALSE, dh.mating = FALSE, dh.sex = 0.5, n.observation = 1,
  bve.0isNA = TRUE, phenotype.bv = FALSE, standardize.bv = FALSE, standardize.bv.level = 100,
```

Only two functions are needed to perform all simulations.

You just have to memorize 260 input parameters and read our 58 page user manual and you are good to go!

```
add.architecture = NULL, ncore = 1, ncore.generation = 1, z.integer = FALSE, store.elect.ireq = FALSE,
backend = "doParallel", randomSeed = NULL, randomSeed.generation = NULL, Rprof = FALSE, miraculix = FALSE,
miraculix.mult = NULL, fast.compiler = 0, miraculix.cores = 1, store.bve.parameter = FALSE, miraculix.chol = TRUE,
best.selection.ratio.m = 1, best.selection.ratio.f = NULL, best.selection.criteria.m = "bx", best.selection.criteria.f = NULL,
best.selection.manual.ratio.m = NULL, best.selection.manual.ratio.f = NULL, bve.class = NULL, parallel.generation = FALSE,
name.cohort = NULL, display.progress = TRUE, max.ticks = Inf, combine = FALSE, repeat.mating = 1, time.point = 0,
creating.type = 0, multiple.observation = FALSE, new.bv.observation.gen = NULL,
new.bv.observation.cohorts = NULL, new.bv.observation.database = NULL, bve.gen = NULL, bve.cohorts = NULL,
bve.database = NULL, sigma.e.gen = NULL, sigma.e.cohorts = NULL, sigma.e.database = NULL, sigma.g.gen = NULL,
sigma.g.cohorts = NULL, sigma.g.database = NULL, gwas.gen = NULL, gwas.cohorts = NULL, gwas.database = NULL,
bve.insert.gen = NULL, bve.insert.cohorts = NULL, bve.insert.database = NULL, reduced.selection.panel.m = NULL,
reduced.selection.panel.f = NULL, breeding.all.combination = FALSE, depth.pedigree = Inf, copy.individual.keep.bve = TRUE,
bve.avoid.duplicates = TRUE, report.accuracy = TRUE, share.genotyped = 1, singlestep.active = FALSE,
remove.non.genotyped = TRUE, added.genotyped = 0, fast.what = FALSE, offspring.bve.parents.gen = NULL,
offspring.bve.parents.database = NULL, offspring.bve.parents.cohort = NULL, offspring.bve.offspring.gen = NULL,
offspring.bve.offspring.database = NULL, offspring.bve.offspring.cohort = NULL){
```



# A uniform language for breeding programs

- Every breeding program can be represented as a combination of boxes (nodes) and arrows (edges), (Simianer et al., in prep.)
- Nodes: cohorts of animals with certain properties
- Edges: breeding actions (e.g. selection, aging, reproduction)

## Edit Node

### *Node Young Cows*

Name *i*

Number of individuals *i*

Founder *i* ☒

Genotype generation type *i*

Upload genotypes (plink/vcf) *i*  dataset.vcf

Path genotypes

Phasing required *i* ☒

Sex *i*

Phenotyping Class *i*

Housing Cost Class *i*

Proportion of genotyped individuals *i*

## Edit Edge

### *Edge Young Cows\_Selected Cows*

Breeding Type *i*

Time needed *i*  Month

Selection Type *i*

Calculate reliability *i* ☐

Selection Index *i*

Selection Proportion *i*

Use offspring for BVE *i* ☐

Relationship Matrix *i*

Depth of Pedigree (# generation back) *i*

BVE Method *i*

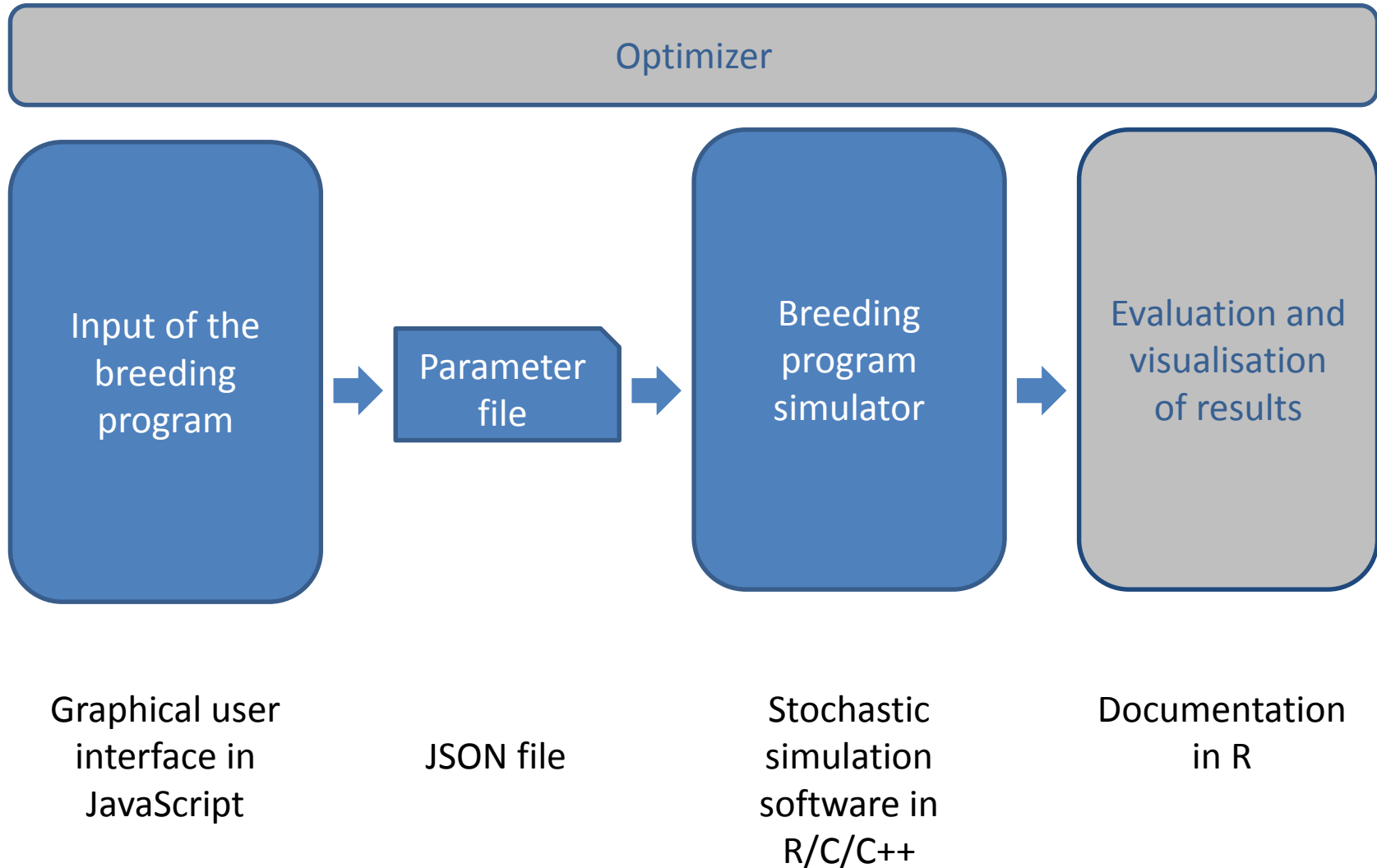
Cohorts used in BVE *i*

Young Cows

Selected Cows



# Web-based application





# Web-based application

- Available at [www.mobps.de](http://www.mobps.de)

## MoBPS Login

<input type="text"/>
<input type="password"/>
<input type="button" value="Login"/>

[Email Me:](#) For Questions and new account generation

Test-account during EAAP:

User: EAAPguest

pw: eaap2019

[GitHub:](#) For the R-package and source code

MoBPS was developed in the context of the EU project [IMAGE](#)  
Copyright © 2017 -- 2019 Torsten Pook



GEORG-AUGUST-UNIVERSITÄT  
GÖTTINGEN

**CiBreed**  
Center for Integrated Breeding Research





# General

- All projects are linked to your personal account and can only be accessed by you

<<>> New Project Save Project Copy Project Import Project Export Project Delete Project Show/Hide Info Show/Hide Warnings

Navigation Close

## MoBPS

Load a new/existent project from your own database:

Project:  Version: (most recent)

Exemplary Templates:

You are assigned to User Class Admin. This enables you to use 20 Cores and maximum run time of 120 hours

### General Information

Project Name

Advanced settings ☐

Species

Time Unit

Genetic Data ☐ Use Ensembl Map ☐ Upload Own Map (vcf/plink) ☐ Create customized Map

Ensembl Dataset

Max. Number of SNPs

Please choose a species first.

### Phenotype Information

Add new phenotype

General information

Phenotype information

Optional information

Breeding Scheme

R Simulation/ Results

Export/ Import

User: Torsten

Logout

Change Password



# General

- In case a project is not running check if there are warnings
  - still in development but potentially helpful!

The screenshot displays the MoBPS web application interface. At the top, a navigation bar contains several buttons: '<<>>', 'New Project', 'Save Project', 'Copy Project', 'Import Project', 'Export Project', 'Delete Project', 'Show/Hide Info', and 'Show/Hide Warnings'. The 'Show/Hide Warnings' button is circled in red. On the left, a sidebar menu lists various sections: 'General information', 'Phenotype information', 'Optional information', 'Breeding Scheme', 'R Simulation/ Results', 'Export/ Import', 'User: Torsten', 'Logout', and 'Change Password'. The main content area is titled 'MoBPS' and includes a section for loading a project from a database with dropdown menus for 'Project', 'Version', and 'Exemplary Templates'. Below this, a message states: 'You are assigned to User Class Admin. This enables you to use 20 Cores'. The 'General Information' section contains input fields for 'Project Name', 'Species', 'Time Unit', 'Genetic Data', 'Ensembl Dataset', and 'Max. Number of SNPs', along with radio buttons for 'Use Ensembl Map', 'Upload Own Map (vcf/plink)', and 'Create customized Map'. A 'Warnings' panel on the right lists three warnings: 'Warning 0 : Please specify a Project Name.', 'Warning 1 : Please specify a Species.', and 'Warning 2 : Please specify an Ensembl Dataset.' A red text box at the top of this panel reads: 'Attention, there are 3 warnings! R Simulation most likely cannot be run unless they are fixed.'



# General

- Jump to particular parts of the web-interface via the navigation bar

The screenshot displays the MoBPS web interface. At the top, a light blue navigation bar contains several buttons: '<<>>', 'New Project', 'Save Project', 'Copy Project', 'Import Project', 'Export Project', 'Delete Project', 'Show/Hide Info', and 'Show/Hide Warnings'. Below this, a vertical navigation bar on the left lists various sections: 'General information', 'Phenotype information', 'Optional information', 'Breeding Scheme', 'R Simulation/ Results', 'Export/ Import', 'User: Torsten', 'Logout', and 'Change Password'. A red oval highlights the first five sections. The main content area is titled 'MoBPS' and includes a section for loading a new or existing project from a database, with dropdown menus for 'Project', 'Version' (set to 'most recent'), and 'Exemplary Templates'. A message states: 'You are assigned to User Class Admin. This enables you to use 20 Cores and maximum run time of 120 hours'. Below this is the 'General Information' form, which includes fields for 'Project Name', 'Advanced settings' (checkbox), 'Species', 'Time Unit' (set to 'Weeks'), 'Genetic Data' (radio buttons for 'Use Ensembl Map', 'Upload Own Map (vcf/plink)', and 'Create customized Map'), 'Ensembl Dataset', and 'Max. Number of SNPs'. The 'Phenotype Information' section at the bottom has an 'Add new phenotype' button.

<<>> New Project Save Project Copy Project Import Project Export Project Delete Project Show/Hide Info Show/Hide Warnings

Navigation Close

General information

Phenotype information

Optional information

Breeding Scheme

R Simulation/ Results

Export/ Import

User: Torsten

Logout

Change Password

## MoBPS

Load a new/existent project from your own database:

Project:  Version:

Exemplary Templates:

You are assigned to User Class Admin. This enables you to use 20 Cores and maximum run time of 120 hours

### General Information

Project Name

Advanced settings ☐

Species

Time Unit

Genetic Data ☐ Use Ensembl Map ☐ Upload Own Map (vcf/plink) ☐ Create customized Map

Ensembl Dataset

Max. Number of SNPs

Please choose a species first.

### Phenotype Information

Add new phenotype





# General

- To activate more complex features of the tool activate advanced settings

<<>>

New Project

Save Project

Copy Project

Import Project

Export Project

Delete Project

Show/Hide Info

Show/Hide Warnings

Navigation Close

General information

Phenotype information

Optional information

Breeding Scheme

R Simulation/ Results

Export/ Import

User: Torsten

Logout

Change Password

## MoBPS

Load a new/existent project from your own database:

Project:  Version:

Exemplary Templates:

You are assigned to User Class Admin. This enables you to use 20 Cores and maximum run time of 120 hours

### General Information

Project Name ⓘ  
Advanced settings ⓘ  
Species ⓘ  
Time Unit ⓘ  
Genetic Data ⓘ  
Ensembl Dataset ⓘ  
Max. Number of SNPs ⓘ

☐  
  
  
☒ Use Ensembl Map  
☐ Upload Own Map (vcf/plink)  
☐ Create customized Map  
Please choose a species first.

### Phenotype Information ⓘ

Add new phenotype

Advanced settings ⓘ

Test-Mode ⓘ

Parallel Computing + Multiple Simulation ⓘ

Complex Trait architecture ⓘ

Culling Module ⓘ

Subpopulation Module ⓘ

Economic Module ⓘ

Advanced Edge/Node options ⓘ

☒  
☒  
☐  
☒  
☒  
☒  
☒  
☒



# Design your genome

## General Information

Project Name ⓘ

Cattle\_Traits\_Empty

Advanced settings ⓘ  
Species ⓘ  
Time Unit ⓘ  
Genetic Data ⓘ  
Ensembl Dataset ⓘ  
Max. Number of SNPs ⓘ

Enter the name of your project.  
You can load  
save/download/delete your  
project via the action bar and  
load different version to return  
to.

☐

Cattle ▼

Month ▼

☒ Use Ensembl Map

☐ Upload Own Map (vcf/plink)

☐ Create customized Map

Illumina BovineLD BeadChip ▼

10000



# Design your traits

## Phenotype Information ⓘ

Add new phenotype

Show/Hide 3 phenotypes

Show/Hide QTLs

Show/Hide residual correlation

Show/Hide genetic correlation

Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# polygenic loci ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor	
Milk	liters	9300	900	0.35	1000	0	0,30	<input checked="" type="checkbox"/>	X
Fat	%	3.9	0.4	0.4	1000	0	100	<input checked="" type="checkbox"/>	X
Protein	%	3.4	0.3	0.38	100	0	100	<input checked="" type="checkbox"/>	X

## Residual Correlation ⓘ

	Milk	Fat	Protein
Milk	1	0.1	0.3
Fat	0.1	1	-0.2
Protein	0.3	-0.2	1

## Genetic Correlation ⓘ

	Milk	Fat	Protein
Milk	1	0.3	0.4
Fat	0.3	1	0.1
Protein	0.4	0.1	1



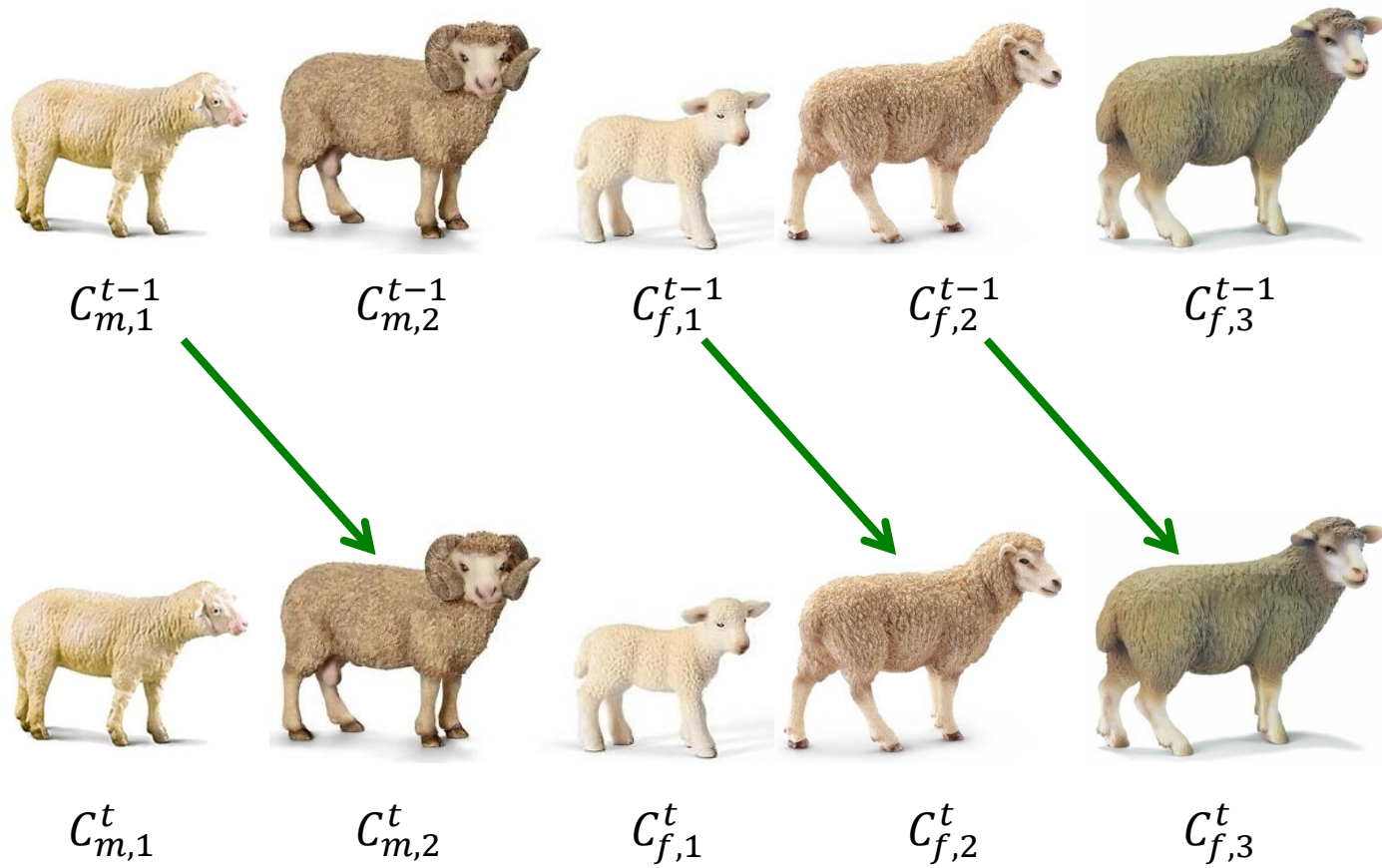
# Available modules

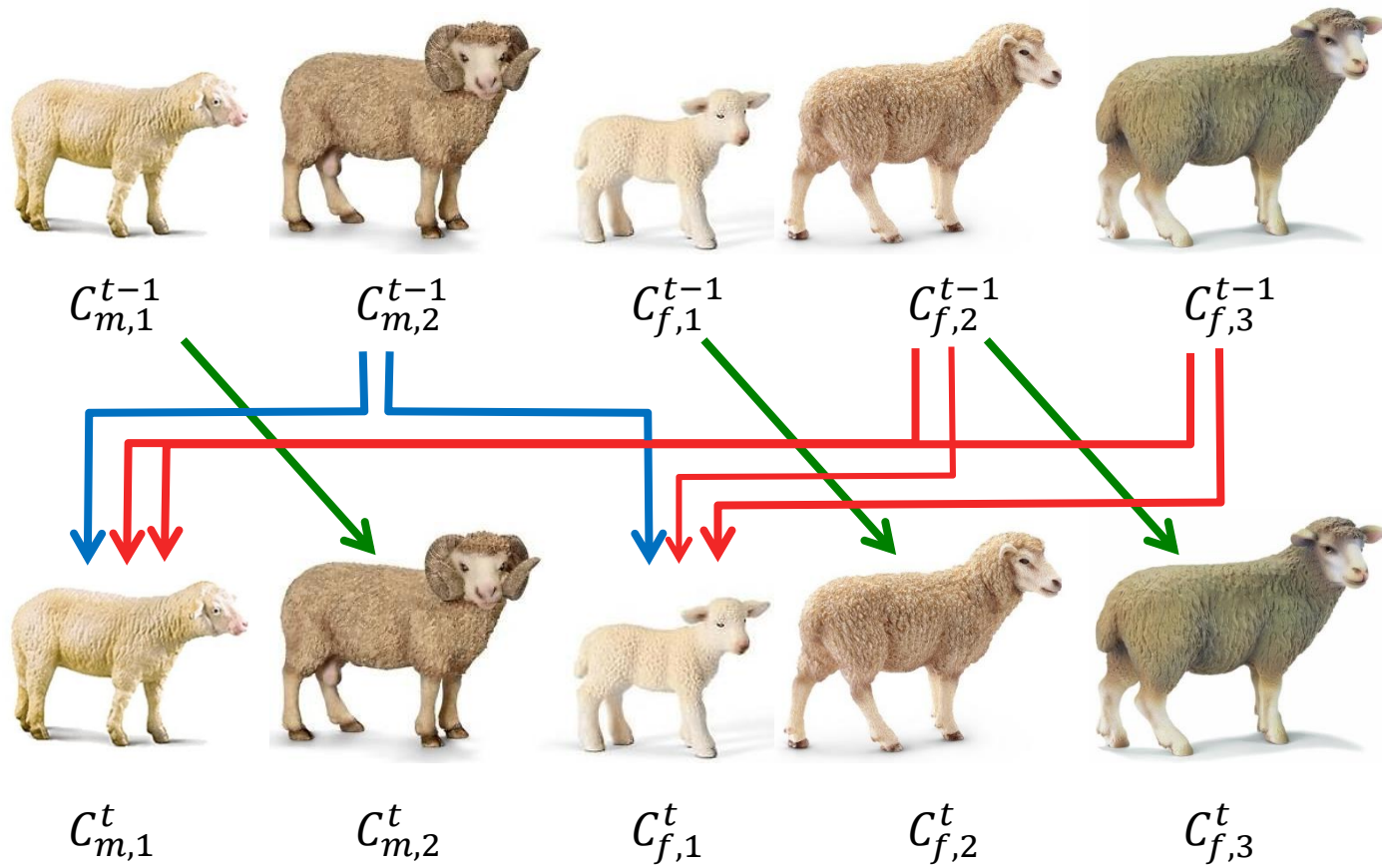
- Design your Genome
- Design your Traits
- Multiple Subpopulations
- Design your Selection Index
- Reasons for Culling
- Economy Parameters
- Draw your Breeding Scheme
- Analyze your Population



# List of tasks

- Task 1: Simulation of a goat breeding program
  - Focus on the use of MoBPS output functions
- Task 2: Introgression scheme
  - Use of the flash interface to draw breeding programs
- Task 3: Cock rotation
  - Advanced breeding program for conservation breeding
- Task 4: Simulation of a cattle breeding program
  - Use of the R-package itself (this workshop is no R-tutorial!)
- Task 5: Crossbreeding in a pigs
  - Import of a genomic map and genotype data
- Case studies:
  - Controlling inbreeding via introgression between sheep flocks
  - Simulation of the female side of a cattle breeding program of a local german farm
  - Comparision of genomic gains obtained by different selection indexes







# And this is how it looks in MoBPS

## Breeding Scheme ①

*Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!*

### Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

➤ Selection

➤ Reproduction

➤ Aging

➤ Combine

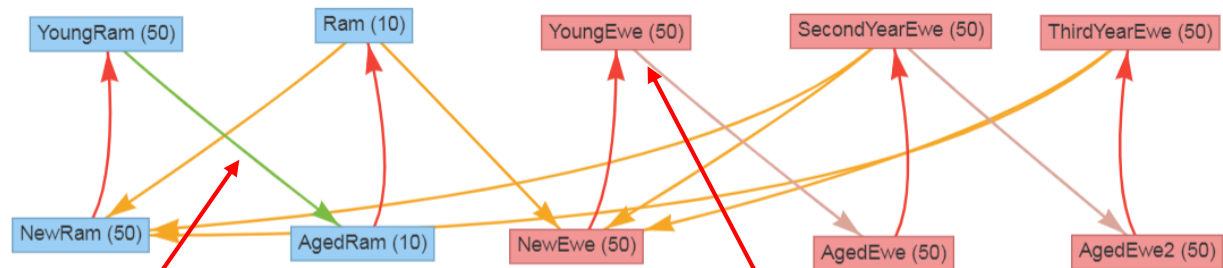
➤ Repeat

➤ Split

➤ Cloning

➤ Selfing

➤ DH-Production



### Edit Edge

#### Edge YoungRam\_AgedRam

Breeding Type ①

Selection ▼

Time needed ①

0 Weeks

Selection Type ①

BVE ▼

BVE Method ①

Direct Mixed-Model ▼

Selection Proportion ①

0.2 (calculated based on # Individuals)

Relationship Matrix ①

VanRaden ▼

Cohorts used in BVE ①

Manual select ▼

YoungRam:Same Repeat x

Ram:Same Repeat x

YoungEwe:Same Repeat x

SecondYearEwe:Same Repeat x

Select cohorts for manual select: ①

### Edit Node

#### Node YoungEwe

Name ①

YoungEwe

Number of individuals ①

50

Founder ①

☒

Genotype generation type ①

Random-sampling ▼

Sex ①

Female ▼

Phenotyping Class ①

Fully phenotyped ▼

save cancel



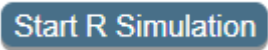


# Task I

Everyone of you has his own account:

Username: yourlastname (No capital letters)!

Password: save

- MoBPS interface: [www.mobps.de](http://www.mobps.de)
  - 1.1) Change your password (via navigation bar)
  - 1.2) Open the template „Sheep\_breeding“
  - 1.3) Simulate the project 
  - 1.4) How did the genomic values of the new rams change over time?
  - 1.5) Look at inbreeding rates for the new rams.



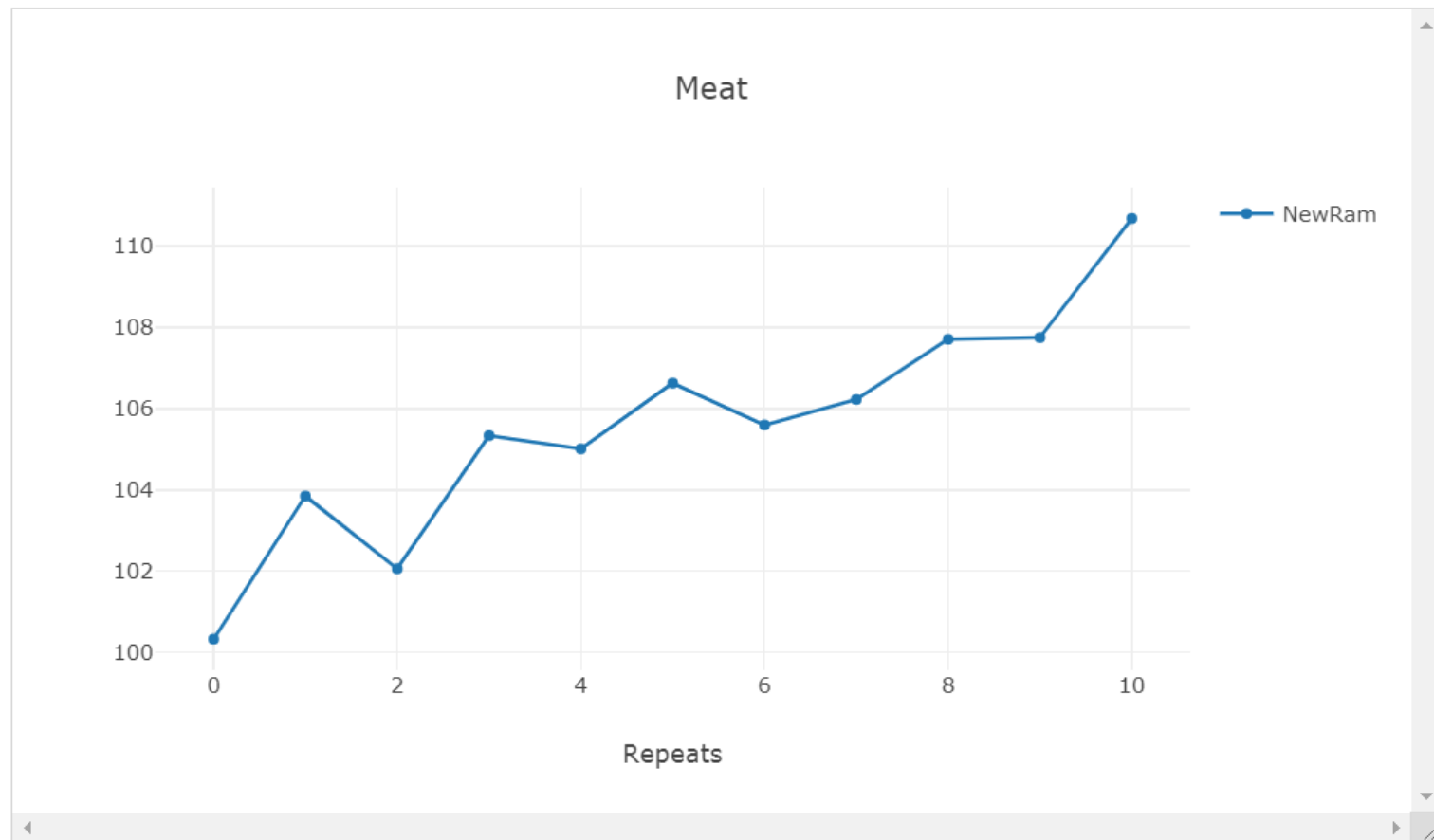
# Solutions – Task I

## *Results: True Breeding Values*

Select plotting type: By Repeats ▼

Select cohorts (multiple selection possible): Plot Results

NewRam (10 Repeats) ✕





# Solutions – Task I

## Results: True Breeding Values

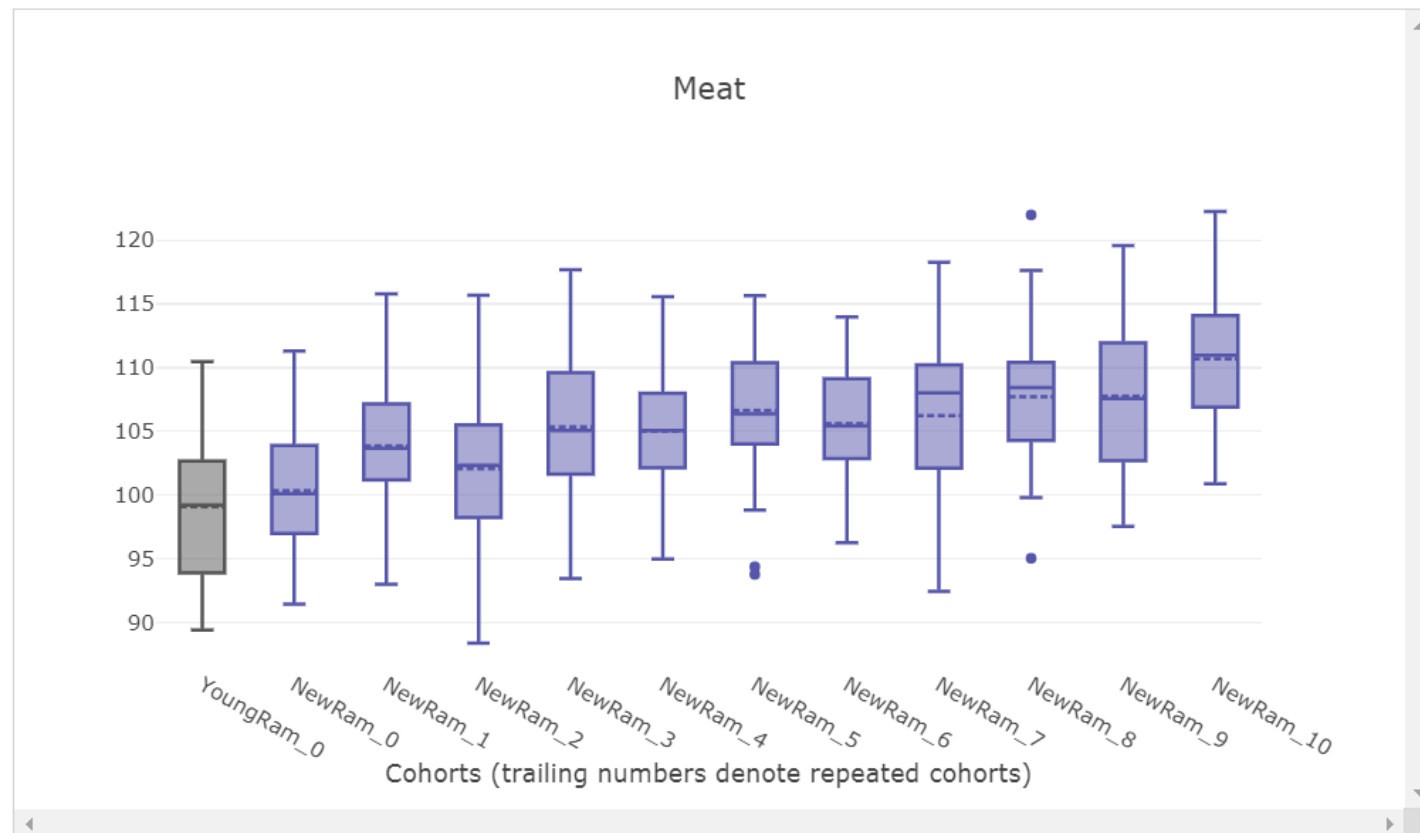
Select plotting type: By Cohorts ▾

Select cohorts (multiple selection possible): Plot Results

YoungRam (0 Repeats) ×

NewRam (10 Repeats) ×

× ▾





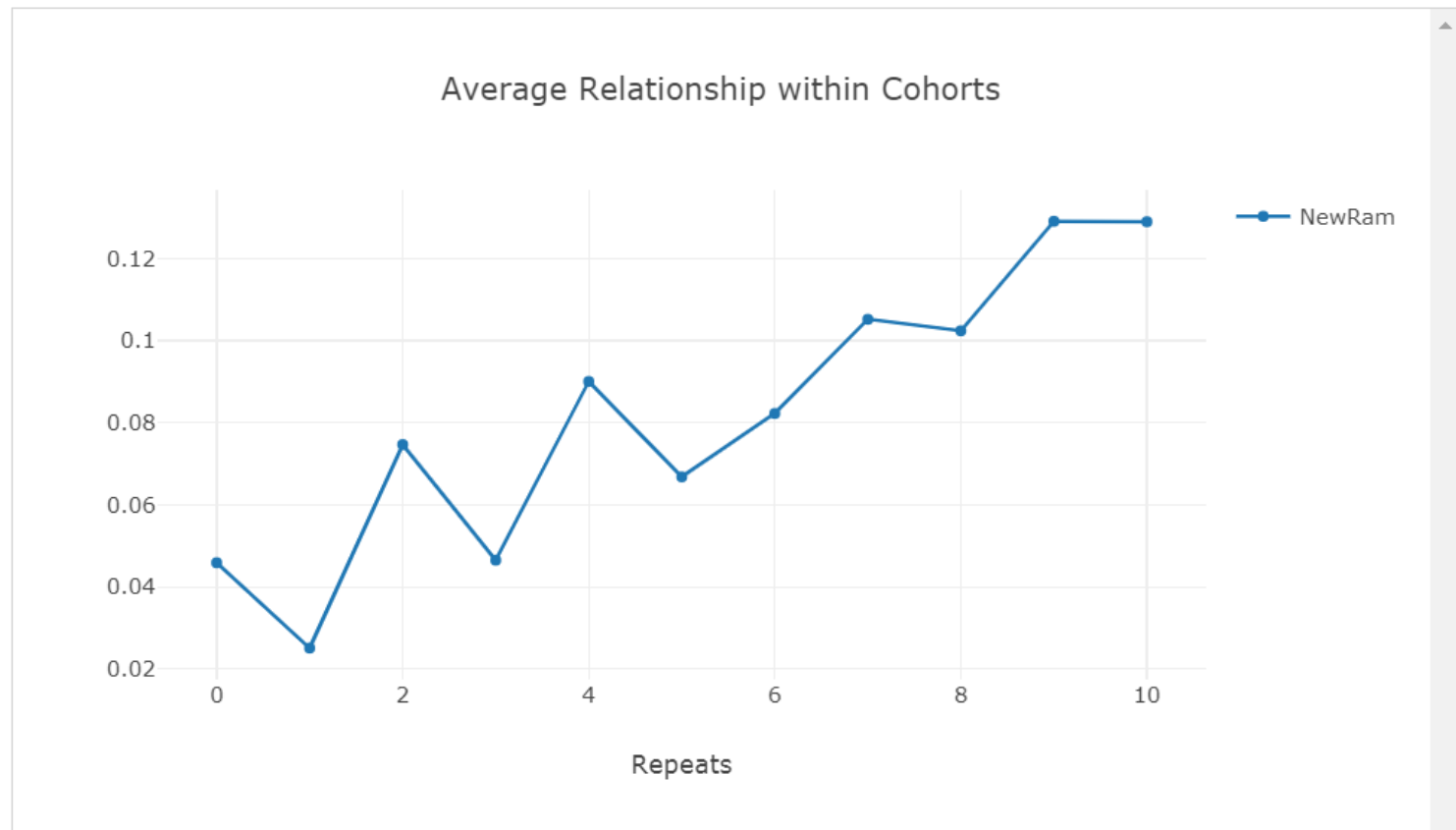
# Solutions – Task I

## *Results: Relationship and Inbreeding within Cohorts*

Select plotting type: By Repeats ▼

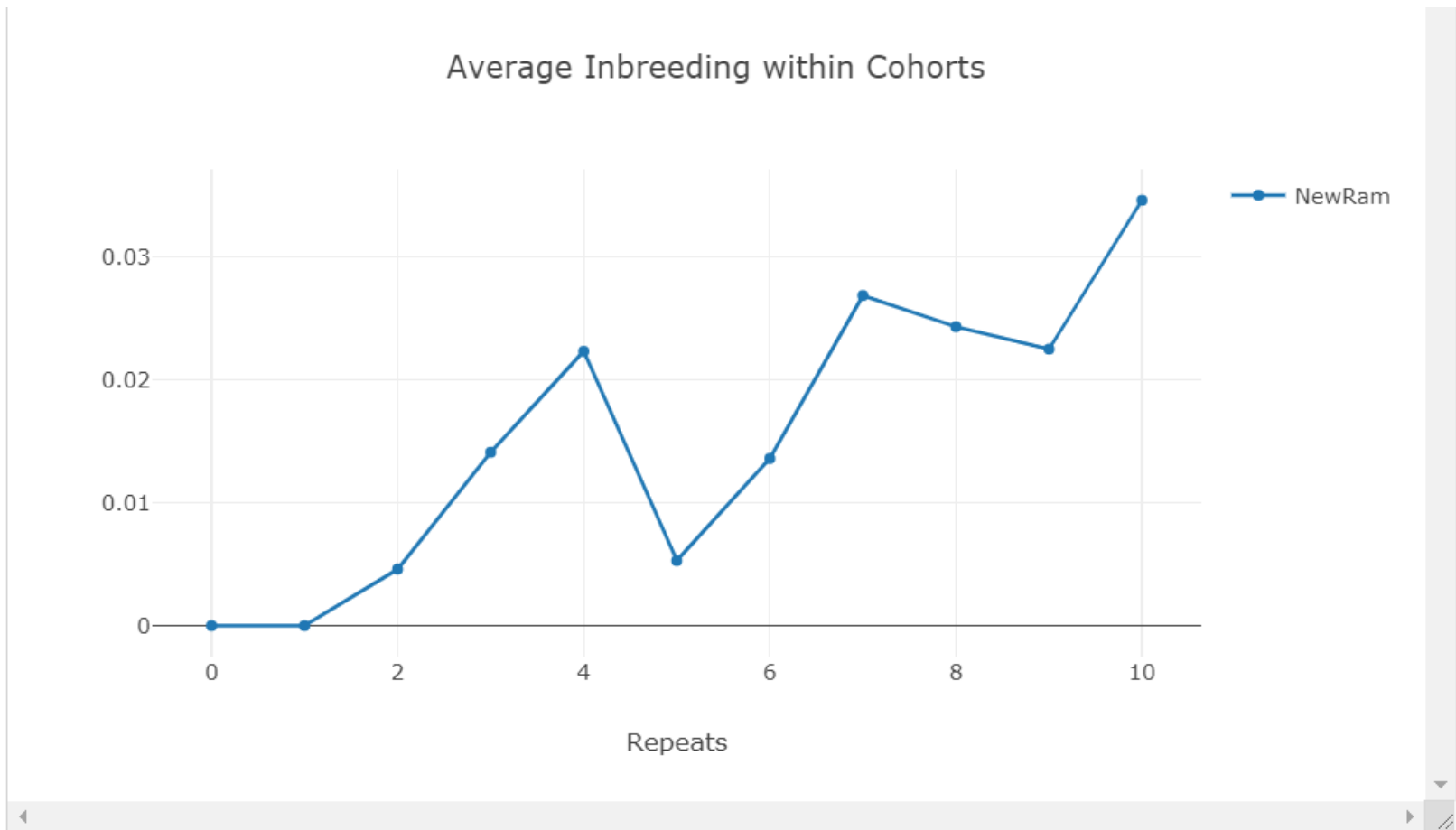
Select cohorts (multiple selection possible): Plot Results

NewRam (10 Repeats) x





# Solutions – Task I





# Introducing genetic material

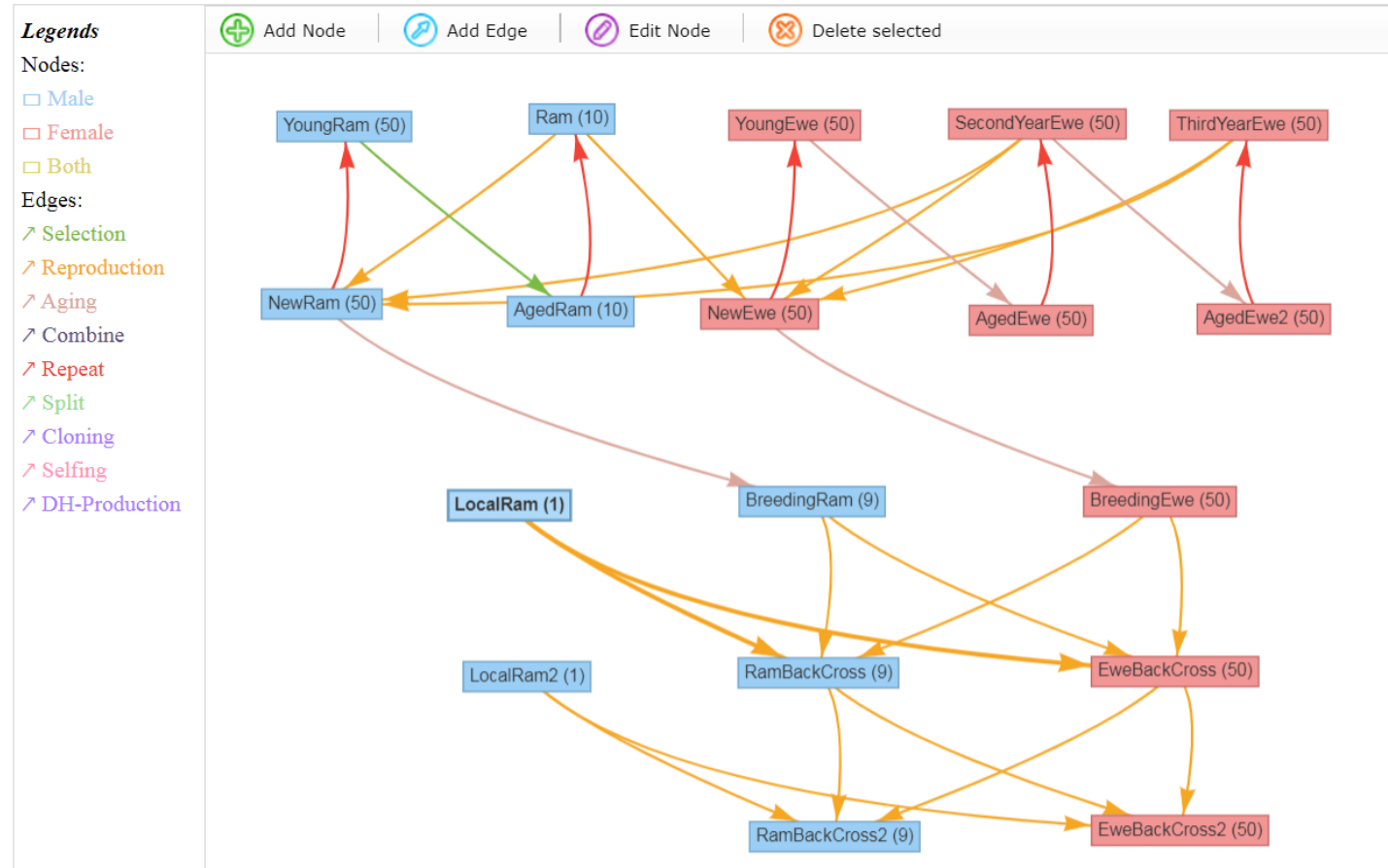
- Open the template „Sheep\_diversity“
- Task:
  - 2.1) Perform two generations of back-crosses. Use 9 rams from the breeding population and 1 local ram as paternal parent.
  - 2.2) Look at the allele frequency of the major QTL in the new cohorts. What allele frequency would you expect?
  - 2.3) Use 10 local rams and 50 rams from the breeding population. Apply selection on the male side perform introgression while at least maintaining the performance level in terms of the meat-trait.
  - 2.4) How does the allele frequency in the major QTL for the fitness trait change over time?



# Solutions – Task II

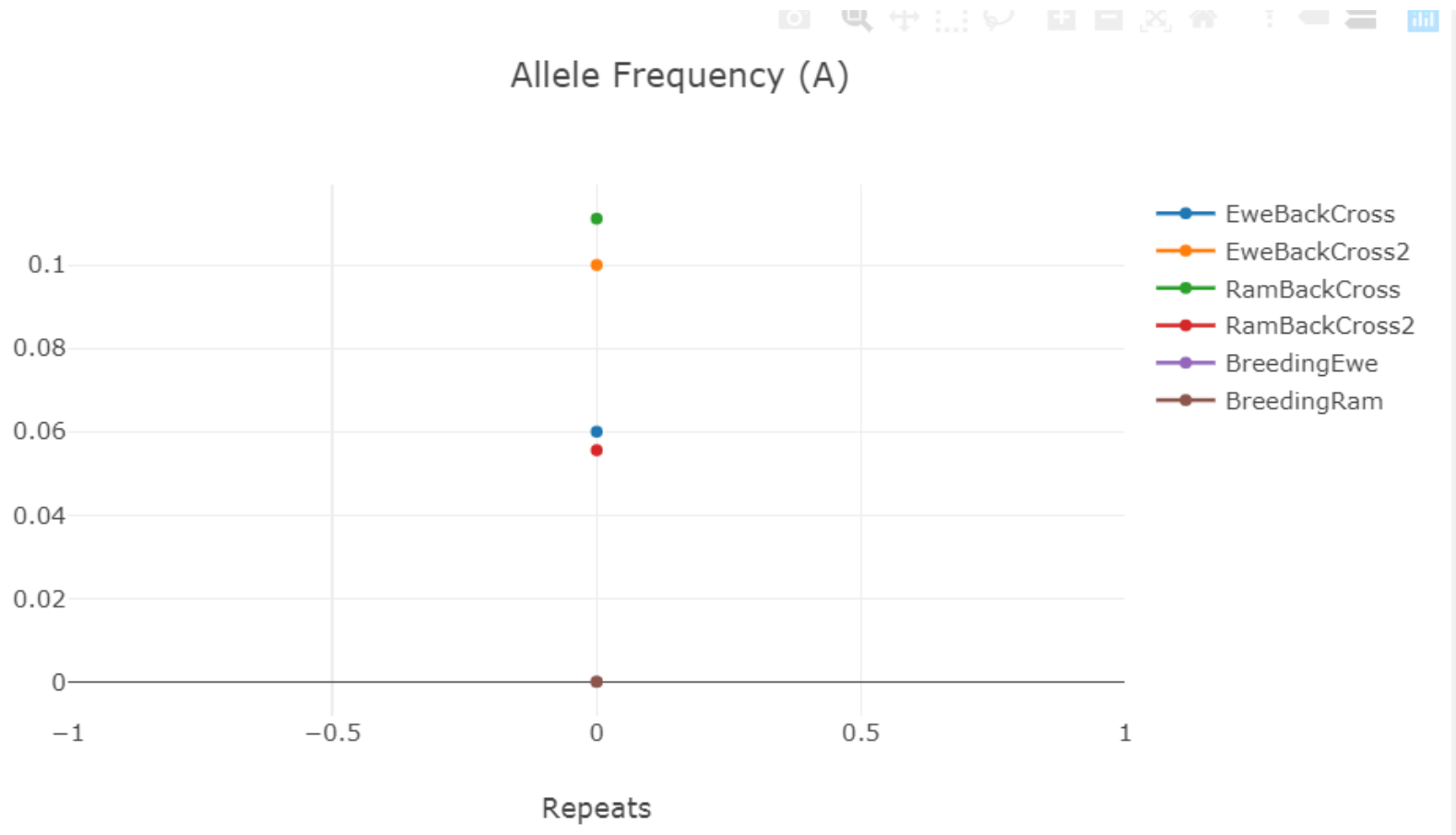
## Breeding Scheme ①

**Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!**





# Solutions – Task II



- Only 10% of the males carry the allele. Therefore we would expect  $p = 0.05$  in the first back cross.





**Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!**





# Solutions – Task II

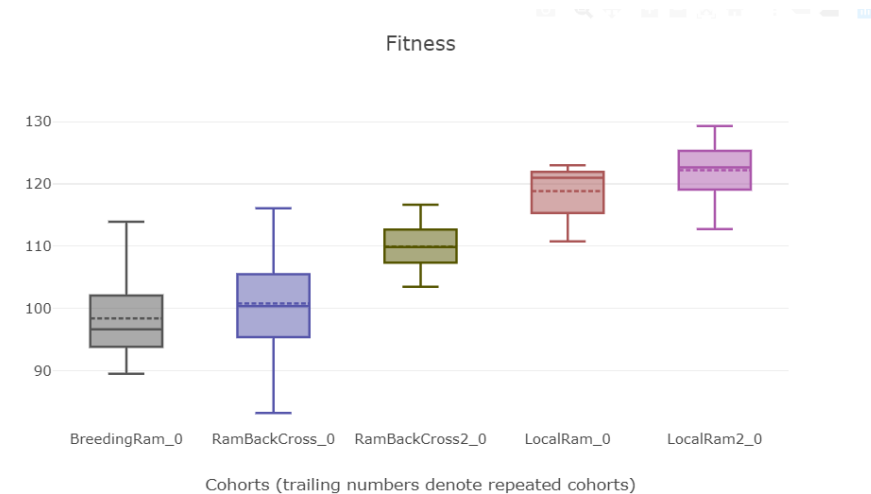
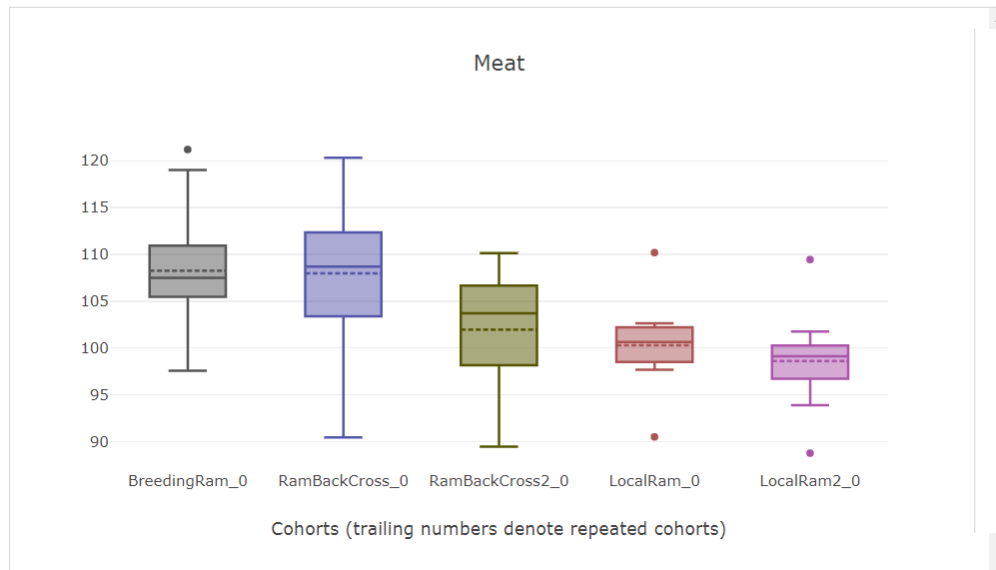
- Selection with equal weight on both traits

**Results: True Breeding Values**

Select plotting type: By Cohorts ▾

Select cohorts (multiple selection possible): Plot Results

BreedingRam (0 Repeats) ✕ RamBackCross (0 Repeats) ✕ RamBackCross2 (0 Repeats) ✕ LocalRam (0 Repeats) ✕  
LocalRam2 (0 Repeats) ✕





# Solutions – Task II

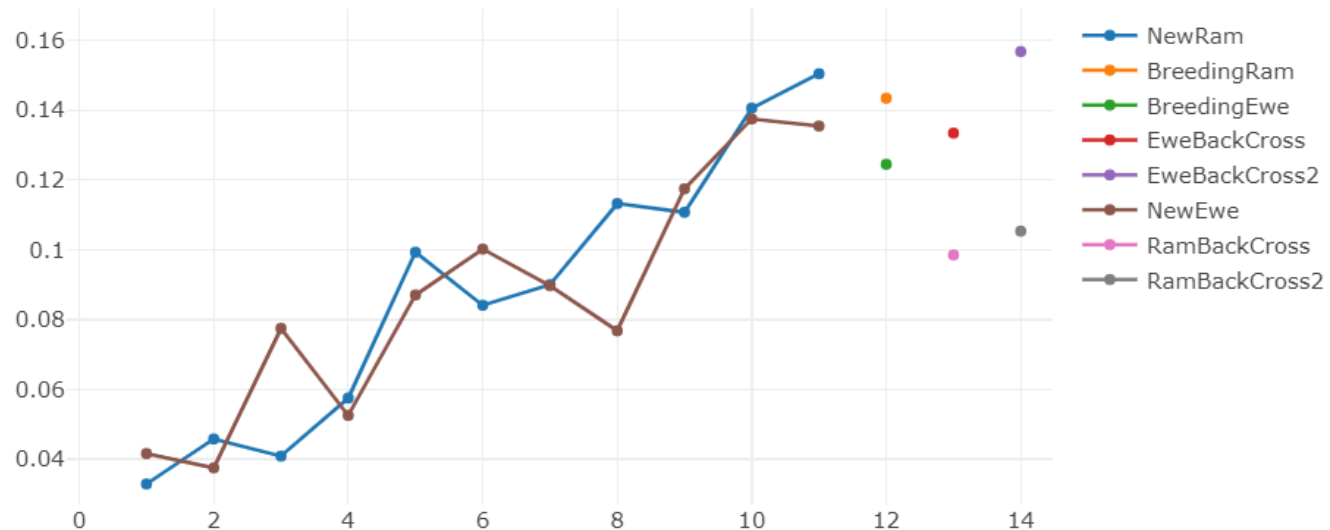
## Results: Relationship and Inbreeding within Cohorts

Select plotting type:

Select cohorts (multiple selection possible):

NewRam (10 Repeats) × BreedingRam (0 Repeats) × BreedingEwe (0 Repeats) × EweBackCross (0 Repeats) ×  
EweBackCross2 (0 Repeats) × NewEwe (10 Repeats) × RamBackCross (0 Repeats) × RamBackCross2 (0 Repeats) ×

Average Relationship within Cohorts





# Solutions – Task II

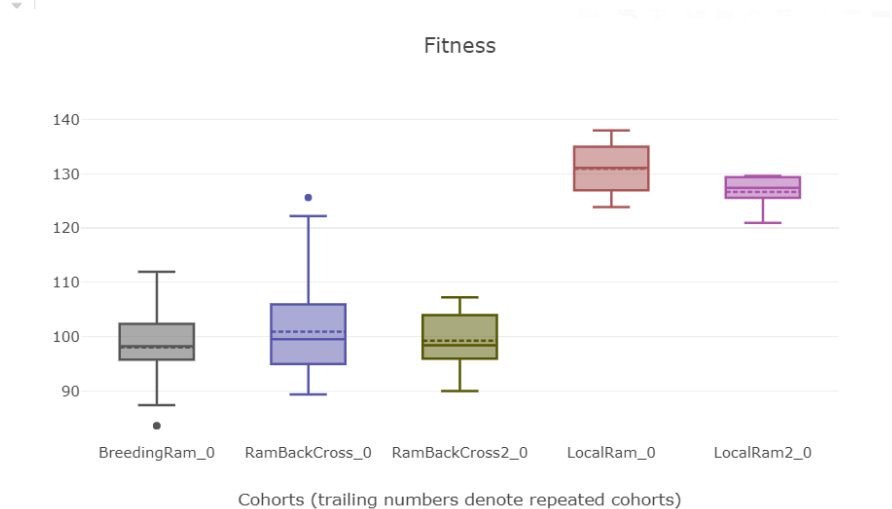
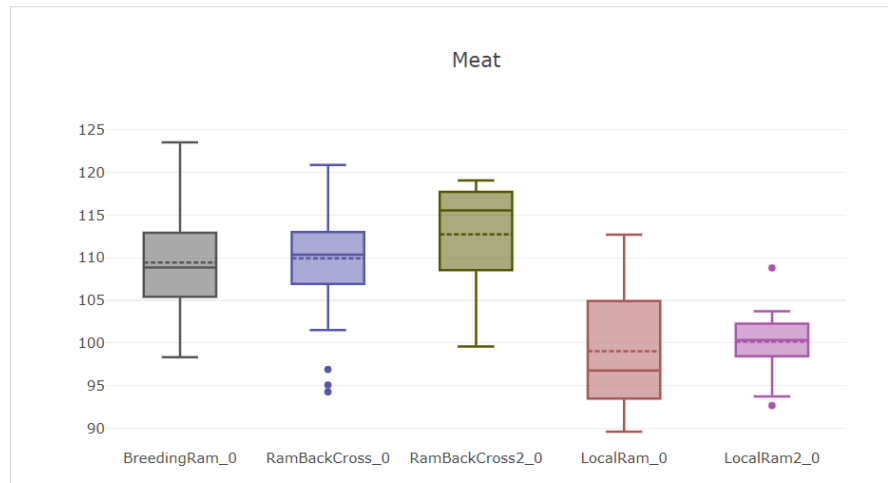
- 3 Index Points on Meat and 1 Index Point on Fitness

## Results: True Breeding Values

Select plotting type:

Select cohorts (multiple selection possible):

BreedingRam (0 Repeats) × RamBackCross (0 Repeats) × RamBackCross2 (0 Repeats) × LocalRam (0 Repeats) ×  
LocalRam2 (0 Repeats) ×





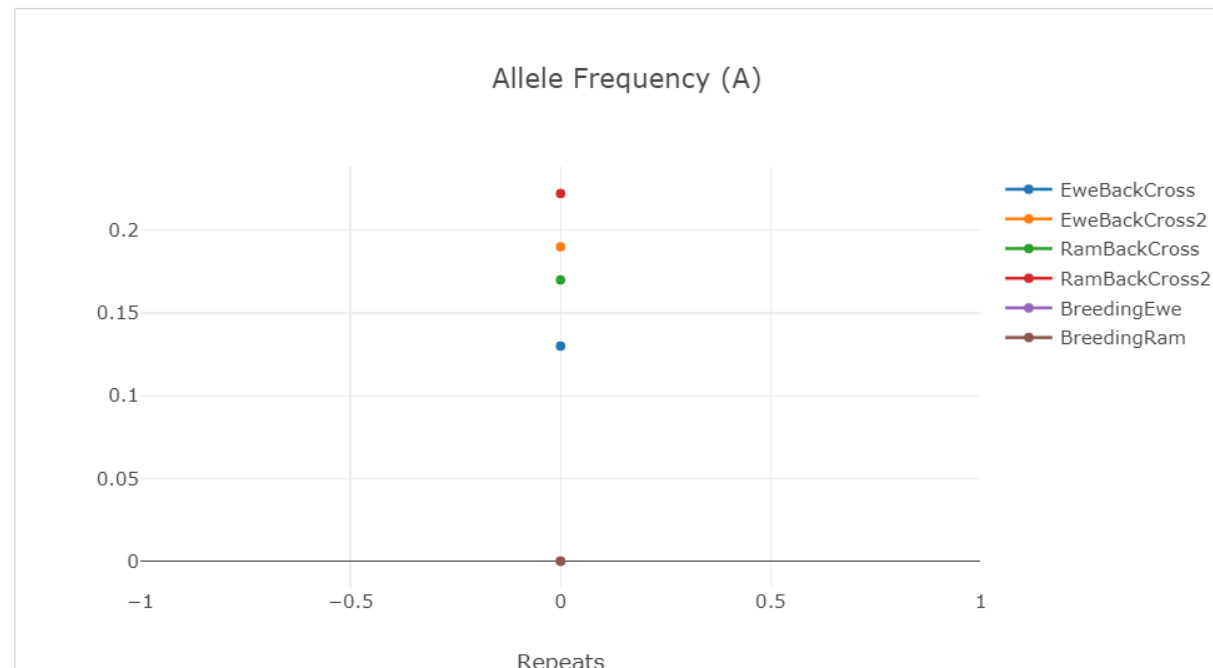
# Solutions – Task II

Results: Major QTLs (Allele Frequency, exp./obs. Heterozygosity)

Select Trait :  Select QTL :

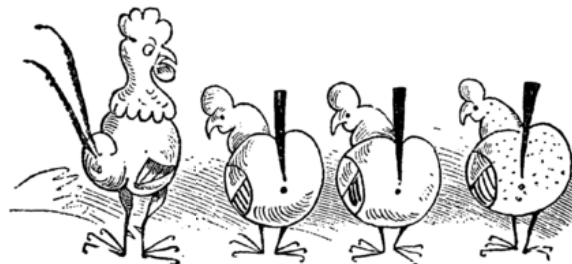
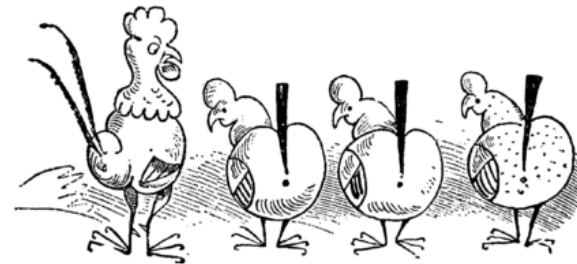
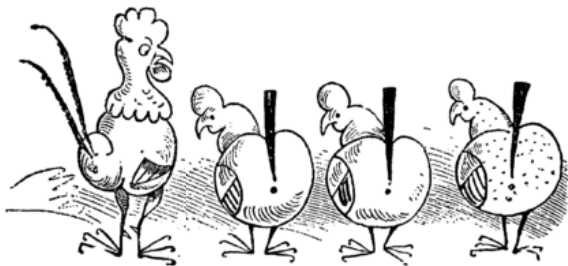
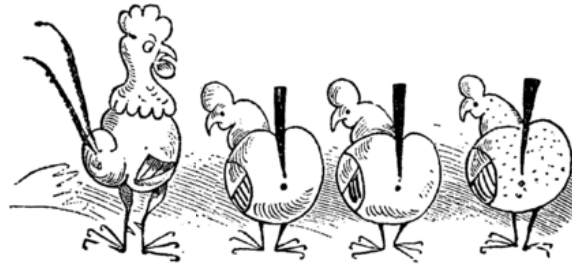
Select Cohorts (multiple selection possible):

EweBackCross (0 Repeats) × EweBackCross2 (0 Repeats) × RamBackCross (0 Repeats) ×  
RamBackCross2 (0 Repeats) × BreedingEwe (0 Repeats) × BreedingRam (0 Repeats) ×



- More weight on fitness leads to higher allele frequency in the major QTL

# Conservation breeding





# Task III

3.1) Simulate 20 generations of a breeding program

– Assume: 5 Boxes with 5 hen and 1 cock each

3.2) How do inbreeding rates compare to a random mating environment?

3.3) Can you think of further modifications of the breeding program to reduce inbreeding



# Solutions – Task III

## Breeding Scheme ①

*Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!*

### Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

↗ Reproduction

↗ Aging

↗ Combine

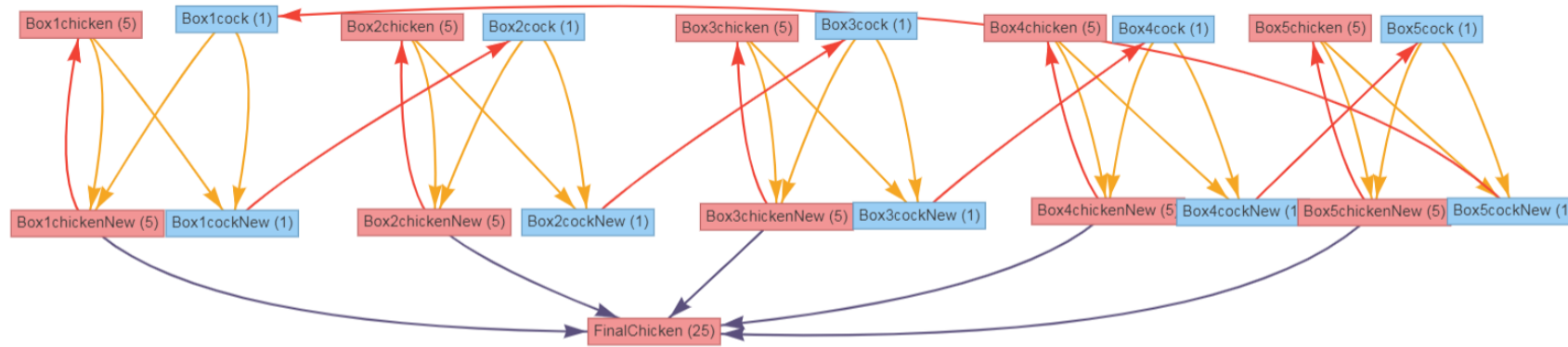
↗ Repeat

↗ Split

↗ Cloning

↗ Selfing

↗ DH-Production







# Solutions – Task III

## *Results: Relationship and Inbreeding within Cohorts*

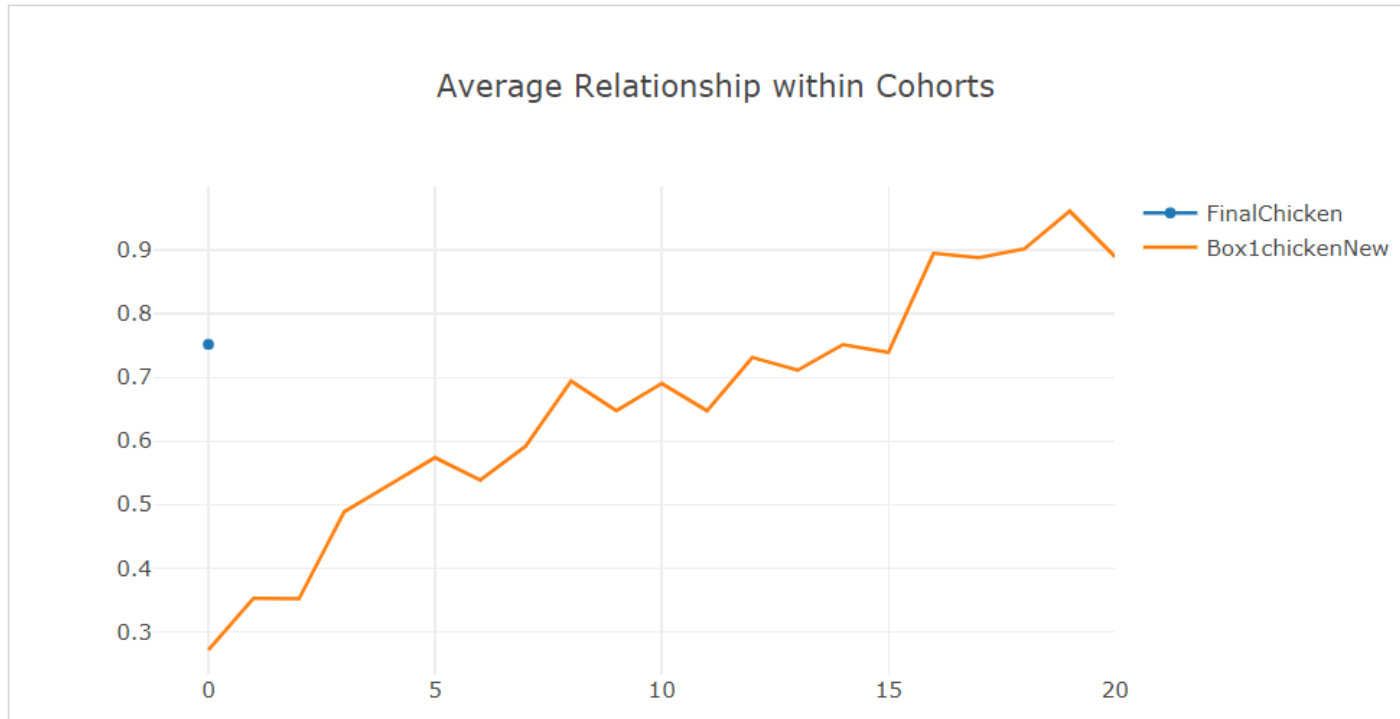
Select plotting type: By Repeats ▾

Select cohorts (multiple selection possible): Plot Results

FinalChicken (0 Repeats) ×

Box1chickenNew (20 Repeats) ×

×



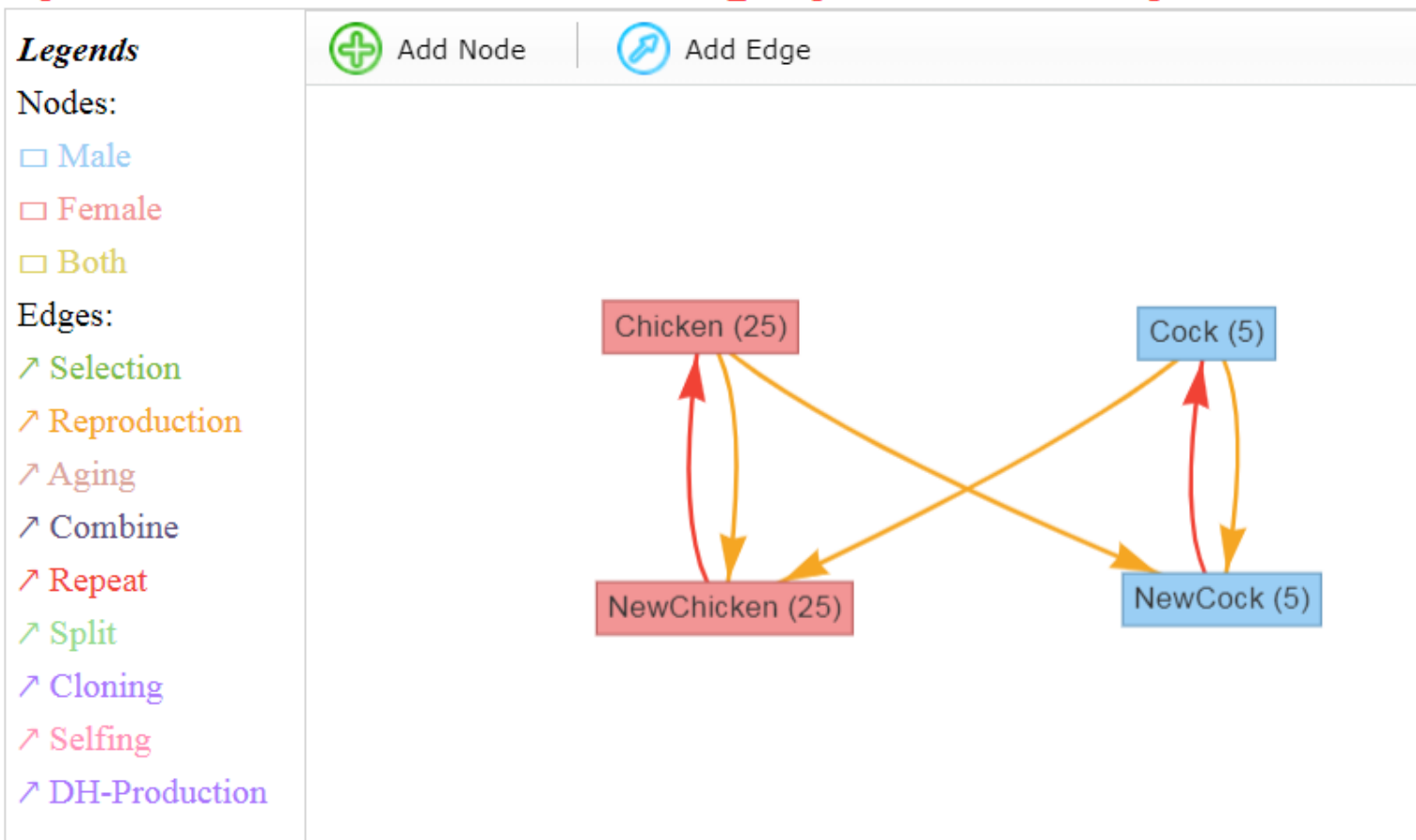
Note that inbreeding between the boxes is lower than for a single cohort!



# Solutions – Task III

## Breeding Scheme ⓘ

*Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like AB1*





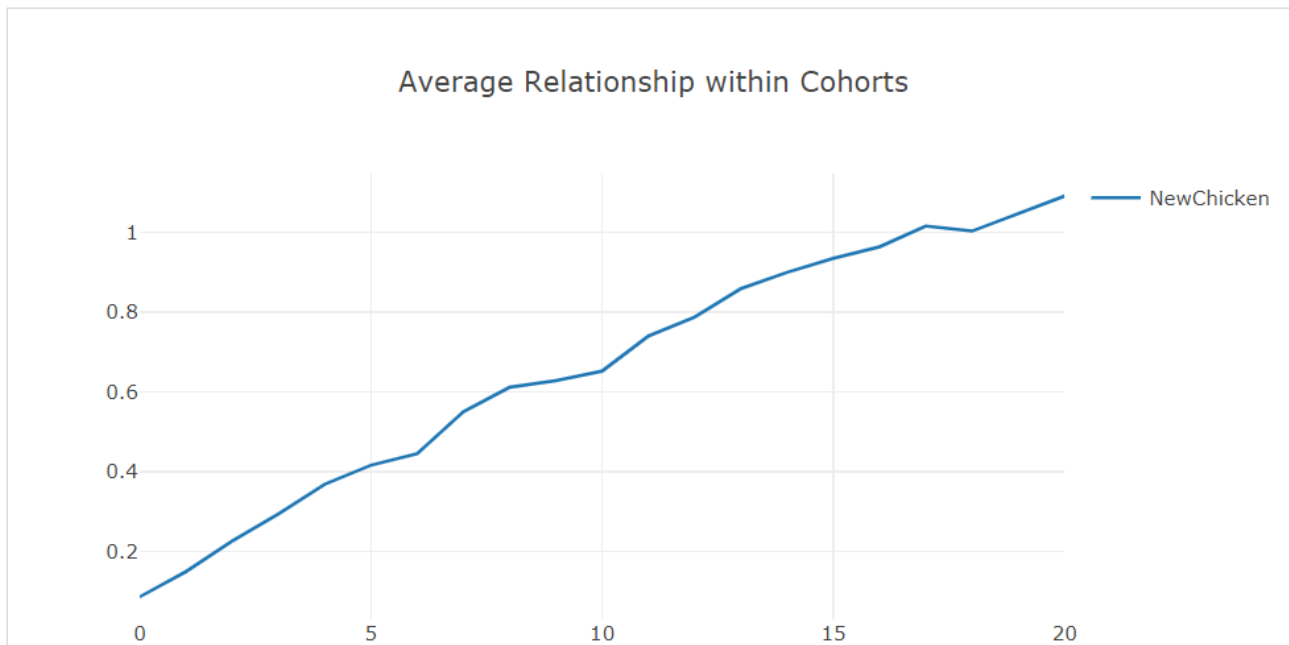
# Solutions – Task III

## *Results: Relationship and Inbreeding within Cohorts*

Select plotting type:

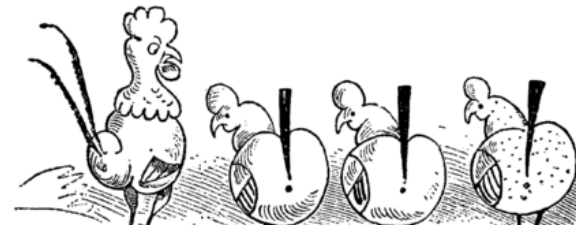
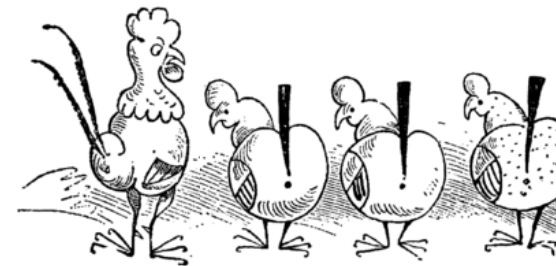
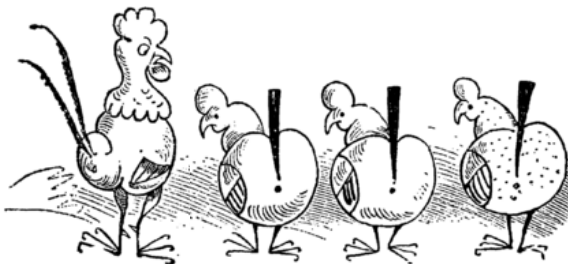
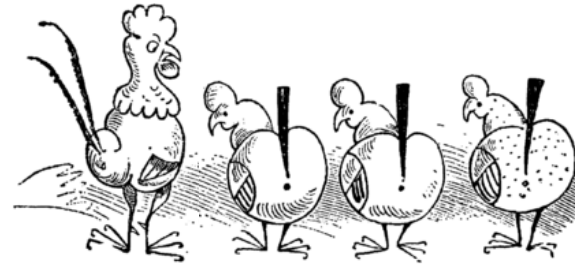
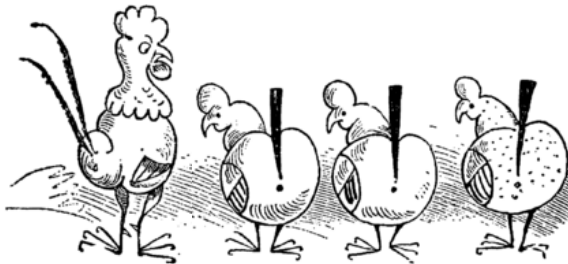
Select cohorts (multiple selection possible):

NewChicken (20 Repeats)



# Solutions – Task III

- Task 3.3)
  - Use each hen exactly once for reproduction of new hens
  - Do not always rotate to the same cohort





# Working outside of the Web-interface

- Our server provides:
  - 64 GB Memory
  - 20 cores

→ Not enough for large scale simulation studies!
- Option 1: Use the R-package directly
- Option 2: Export json-file from the interface



# Task IV

- Export the json-file of the template „Simple\_Cattle“
- Install R (<https://cran.r-project.org/>)
- R-package MoBPS (<https://github.com/tpook92/MoBPS>)
  - Make sure to install version 1.4.22!
  - You also need the R-package jsonlite
- Simulate the breeding program (`(json.simulation() )`)
- Generate a summary of your population (`( summary() )`)
- Generate a histogram of the phenotypes of the cohort: „CowsSecondYear“ (`( get.pheno() )`)
- Compare LD between the cohorts „Bull“, „NewBulls\_5“ and „SelectedBulls“ (`(ld.decay() )`):
- Export the genotypes of the cohort „NewBulls\_5“ and „NewCows\_5“ to PLINK files  
(`ped/map`) (`(write.pedmap() )`)



# Task IV - Solutions



Navigation Open

## MoBPS

Load a new/existent project from your own database:

Project:  Version:   
Exemplary Templates:

You are assigned to User Class Admin. This enables you to use 20 Cores and maximum run time of 120 hours

### General Information

Project Name ⓘ	<input type="text" value="Simple_Cattle"/>
Advanced settings	<input type="checkbox"/>
Species ⓘ	<input type="text" value="Cattle"/>
Time Unit ⓘ	<input type="text" value="Years"/>
	<input type="radio"/> Use Ensembl Map

- Load in the Project „Simple\_Cattle“
- Press the „Export Project“ – button in the navigation
- R-related: task1.R



# Task IV - Solutions

Install Packages

Install from:  
Package Archive File (.zip; .tar.gz) ▼

Package archive:  
C:/Users/pook/Desktop/R-Stuff/MoBPS\_1.4.22.tar.gz Browse...

Install to Library:  
C:/Users/pook/Documents/R/R-3.6.0/library [Default] ▼

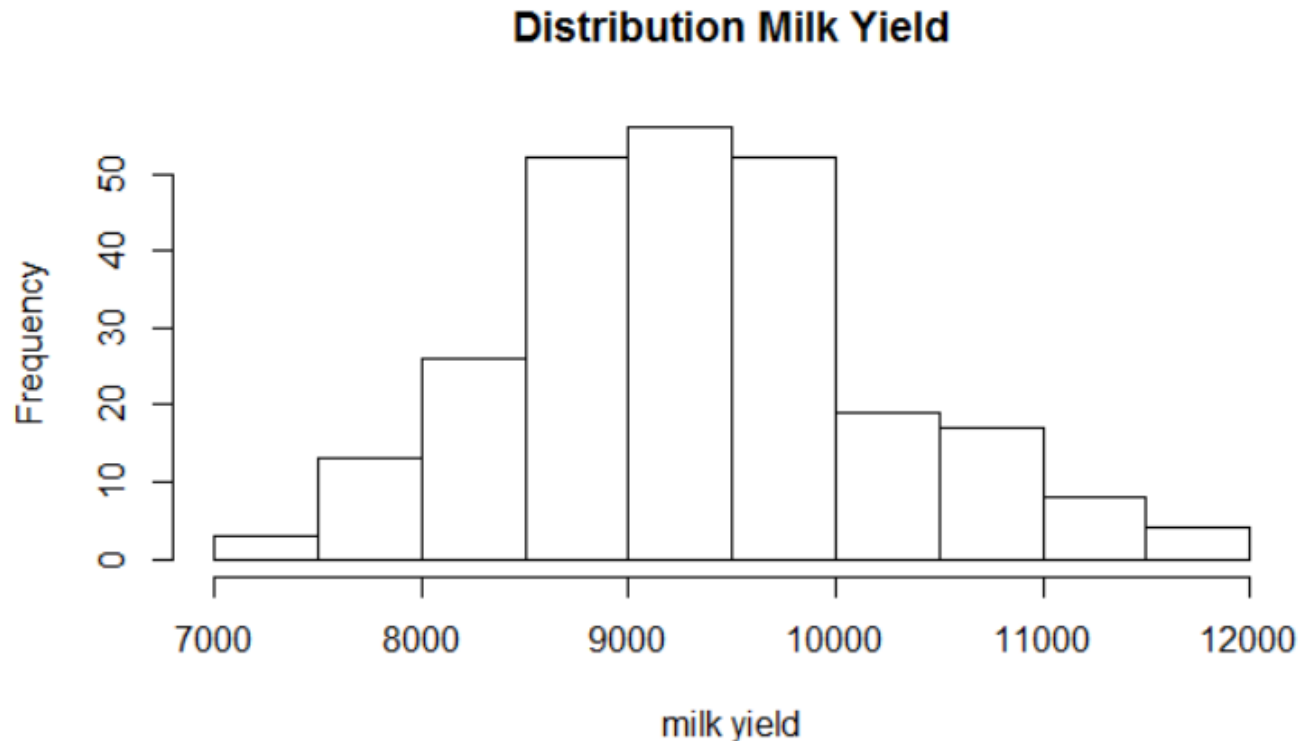
Install Cancel





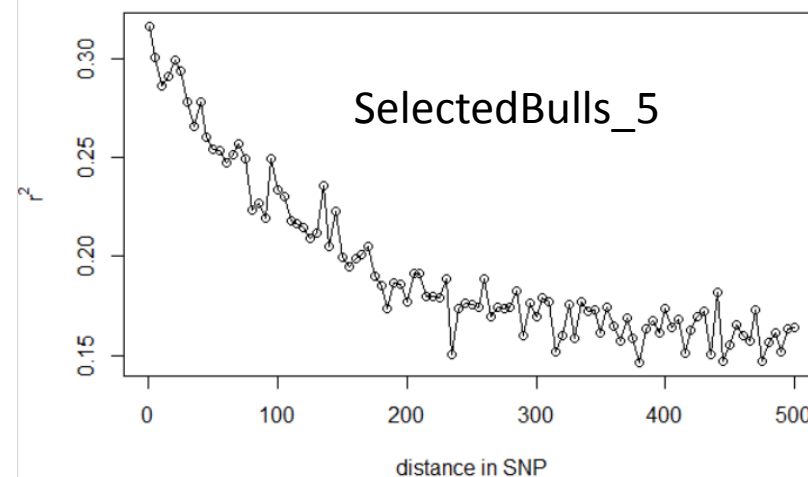
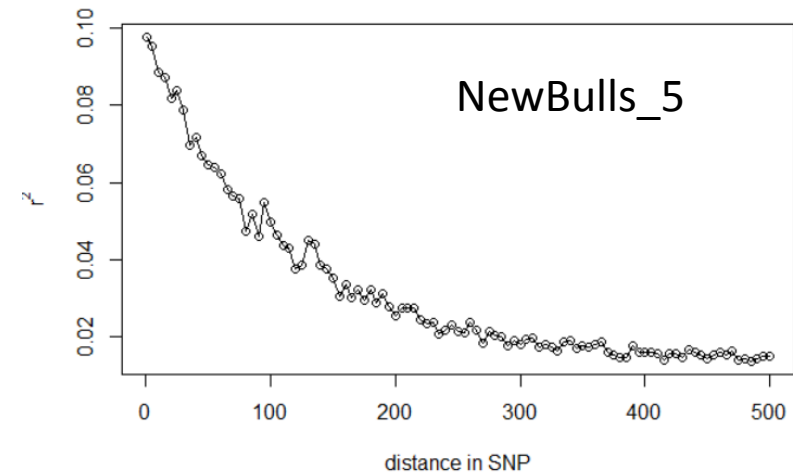
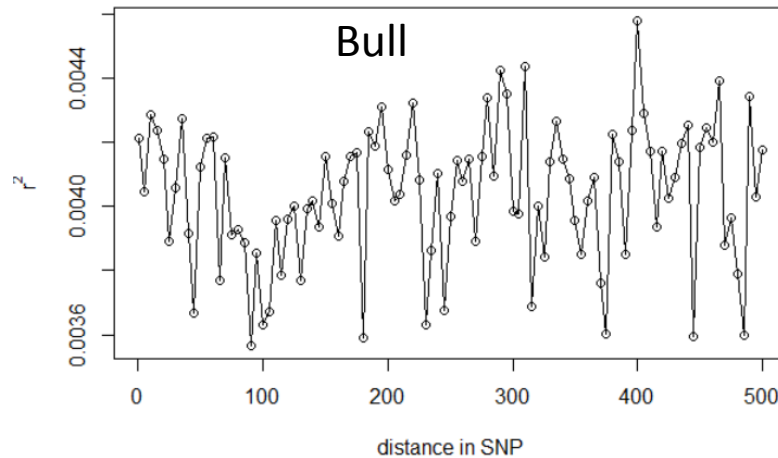
# Task IV - Solutions

- Simulations contain random factors therefore results can deviate slightly!





# Task IV - Solutions



- By far highest LD for the group of selected individuals



# Task V

5.1) Download the genotype and phenotype data from [https://github.com/tpook92/MoBPS/tree/master/IMAGE\\_workshop](https://github.com/tpook92/MoBPS/tree/master/IMAGE_workshop)

- Pig1.peg and pig2.ped are genotypes of 250 boars each
- Pig3.ped and pig4.ped are genotypes of 250 sows each
- Pig.map contains a map file

5.2) Active the Module „Complex trait architecture“

5.3) Generate a trait with 500 qualitative epistatic QTL

5.4) Simulate a pig breeding program that is using Cross breeding



# Task V - Solutions

## General Information

Project Name ⓘ	<input type="text" value="PigCross"/>
Advanced settings	<input checked="" type="checkbox"/>
Test-Mode ⓘ	<input type="checkbox"/>
Parallel Computing + Multiple Simulation ⓘ	<input type="checkbox"/>
Complex Trait architecture ⓘ	<input checked="" type="checkbox"/>
Culling Module ⓘ	<input type="checkbox"/>
Subpopulation Module ⓘ	<input type="checkbox"/>
Economic Module ⓘ	<input type="checkbox"/>
Advanced Edge/Node options ⓘ	<input type="checkbox"/>
Species ⓘ	<input type="text" value="Pig"/>
Time Unit ⓘ	<input type="text" value="Weeks"/>
Genetic Data ⓘ	<input type="radio"/> Use Ensembl Map <input checked="" type="radio"/> Upload Own Map (vcf/plink) <input type="radio"/> Create customized Map
Upload Map File ⓘ	<input type="text" value="Datei auswählen"/> pig1.map <input type="button" value="Upload Map"/>
Own Map Path	UserMaps/Torsten_pig1.map

## Phenotype Information ⓘ

Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# additive QTL ⓘ	# dominant QTL ⓘ	# qualitative epistatic QTL ⓘ	# quantitative epistatic QTL ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor
Pheno 1		100	10	0.3	0	0	500	0	0	0	<input checked="" type="checkbox"/>



# Task V - Solutions

## Breeding Scheme ①

*Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!*

### Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

↗ Reproduction

↗ Aging

↗ Combine

↗ Repeat

↗ Split

↗ Cloning

↗ Selfing

↗ DH-Production



Add Node



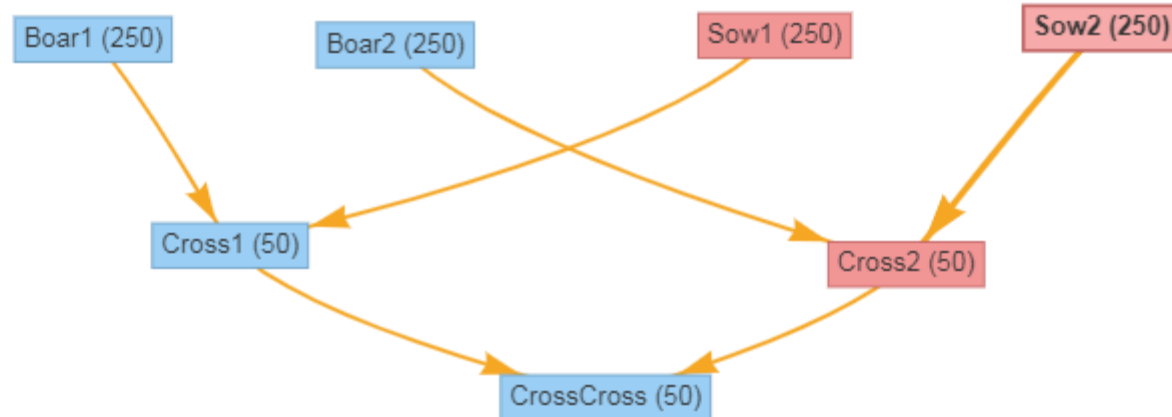
Add Edge



Edit Node



Delete selected





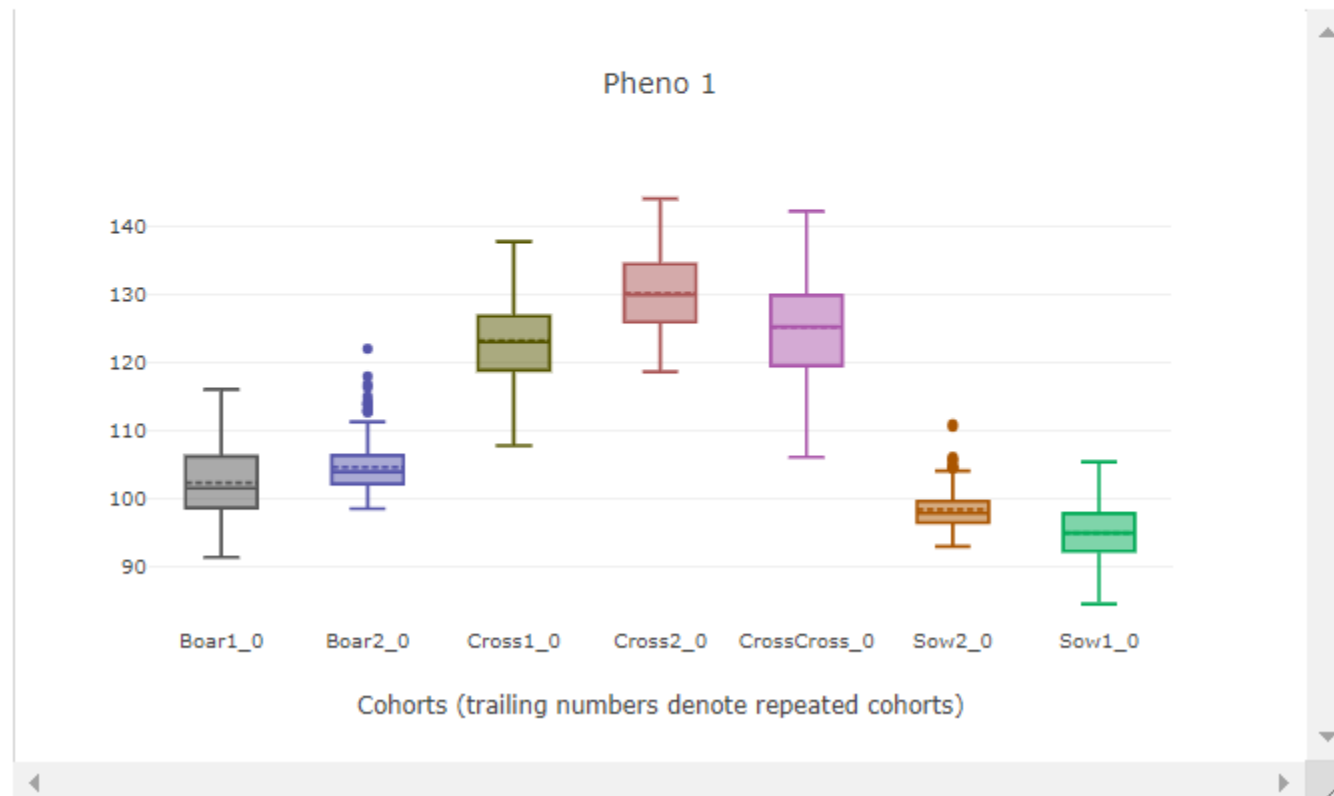
# Task V - Solutions

## Results: True Breeding Values

Select plotting type: By Cohorts ▾

Select cohorts (multiple selection possible): Plot Results

Boar1 (0 Repeats) × Boar2 (0 Repeats) × Cross1 (0 Repeats) × Cross2 (0 Repeats) × CrossCross (0 Repeats) ×  
Sow2 (0 Repeats) × Sow1 (0 Repeats) ×





# Task V - Solutions

- About importing genotype / phenotype data
- MoBPS will be linked to the IMAGE database and therefore provide some exemplary genotype data to be used
- Uploaded genotype data is stored on our server!
- Solutions for confidential data:
  1. Sign a confidential agreement with us
  2. Use the R-package directly
  3. How the MoBPS webinterface on your own server.  
We are happy to assist you in setting this up.



# Case Study

- Think before simulating anything more complex!
  - How does the breeding program look like?
    - Breeding scheme
    - Traits
    - Just because the simulation is not crashing does not mean that what you entered is reasonable // what you wanted to enter!
  - What are in parameters we are interested in?
  - Is there the is of confounding effects?
  - What results would we expect?
    - Simulations are executed to get a better hand on the problems
    - They should never be used as the only basis for the decision





Additional information regarding all case studies is available on request!

This should be seems as some potential examples to inspire your own breeding scheme



# Case Study I

- Simulation of two sheep populations
- Population 1 is much larger and was selected for Milk
- Population 2 is basically not selected
- Objective: Introduce genetic material from the other population to increase genetic diversity



# Case study I

## General Information

Project Name ⓘ	<input type="text" value="Sheep"/>
Advanced settings ⓘ	<input type="checkbox"/>
Species ⓘ	<input type="text" value="Sheep"/>
Time Unit ⓘ	<input type="text" value="Weeks"/>
Genetic Data ⓘ	<input checked="" type="radio"/> Use Ensembl Map <input type="radio"/> Upload Own Map (vcf/plink) <input type="radio"/> Create customized Map
Ensembl Dataset ⓘ	<input type="text" value="IlluminaOvineSNP50"/>
Max. Number of SNPs ⓘ	<input type="text" value="5000"/>

### Residual Correlation ⓘ

	Meat	Milk
Meat	1	-0.4
Milk	<input type="text" value="-0.4"/>	1

Enter Phenotypic correlation

### Genetic Correlation ⓘ

	Meat	Milk
Meat	1	-0.4
Milk	<input type="text" value="-0.4"/>	1

## Phenotype Information ⓘ

<input type="button" value="Add new phenotype"/>	<input type="button" value="Show/Hide 2 phenotypes"/>	<input type="button" value="Show/Hide QTLs"/>	<input type="button" value="Show/Hide residual correlation"/>	<input type="button" value="Show/Hide genetic correlation"/>				
Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# polygenic loci ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor
Meat		<input type="text" value="100"/>	<input type="text" value="10"/>	<input type="text" value="0.3"/>	<input type="text" value="1000"/>	<input type="text" value="1"/>	<input type="text" value="0"/>	<input checked="" type="checkbox"/>
Milk		<input type="text" value="100"/>	<input type="text" value="10"/>	<input type="text" value="0.3"/>	<input type="text" value="1000"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input checked="" type="checkbox"/>

SNP for Meat	SNP ID ⓘ	bp	chromo	Effect AA	Effect AB	Effect BB	Allele Freq. (B) ⓘ	Optional Info
1			1	<input type="text" value="0"/>	<input type="text" value="5"/>	<input type="text" value="10"/>	<input type="text" value="0.5"/>	

Upload File for Genotype



# Case study I

## General Information

Project Name ⓘ	<input type="text" value="Sheep"/>
Advanced settings ⓘ	<input type="checkbox"/>
Species ⓘ	<input type="text" value="Sheep"/>
Time Unit ⓘ	<input type="text" value="Weeks"/>
Genetic Data ⓘ	<input checked="" type="radio"/> Use Ensembl Map <input type="radio"/> Upload Own Map (vcf/plink) <input type="radio"/> Create customized Map
Ensembl Dataset ⓘ	<input type="text" value="IlluminaOvineSNP50"/>
Max. Number of SNPs ⓘ	<input type="text" value="5000"/>

## Phenotype Information ⓘ

<input type="button" value="Add new phenotype"/>									<input type="button" value="Show/Hide 2 phenotypes"/>	<input type="button" value="Show/Hide QTLs"/>	<input type="button" value="Show/Hide residual correlation"/>	<input type="button" value="Show/Hide genetic correlation"/>
Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# polygenic loci ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor				
Meat		<input type="text" value="100"/>	<input type="text" value="10"/>	<input type="text" value="0.3"/>	<input type="text" value="1000"/>	<input type="text" value="1"/>	<input type="text" value="0"/>	<input checked="" type="checkbox"/>				
Milk		<input type="text" value="100"/>	<input type="text" value="10"/>	<input type="text" value="0.3"/>	<input type="text" value="1000"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input checked="" type="checkbox"/>				

SNP for Meat	SNP ID ⓘ	bp	chromo	Effect AA	Effect AB	Effect BB	Allele Freq. (B) ⓘ	Optional Info
1			1	<input type="text" value="0"/>	<input type="text" value="5"/>	<input type="text" value="10"/>	<input type="text" value="0.5"/>	

Upload File for Genotype



# Case study I

## Residual Correlation ⓘ

	Meat	Milk
Meat	1	-0.4
Milk	<input type="text" value="-0.4"/>	1

Enter Phenotypic correlation

## Genetic Correlation ⓘ

	Meat	Milk
Meat	1	-0.4
Milk	<input type="text" value="-0.4"/>	1

## Creating own Selection Indexes (Optional) ⓘ

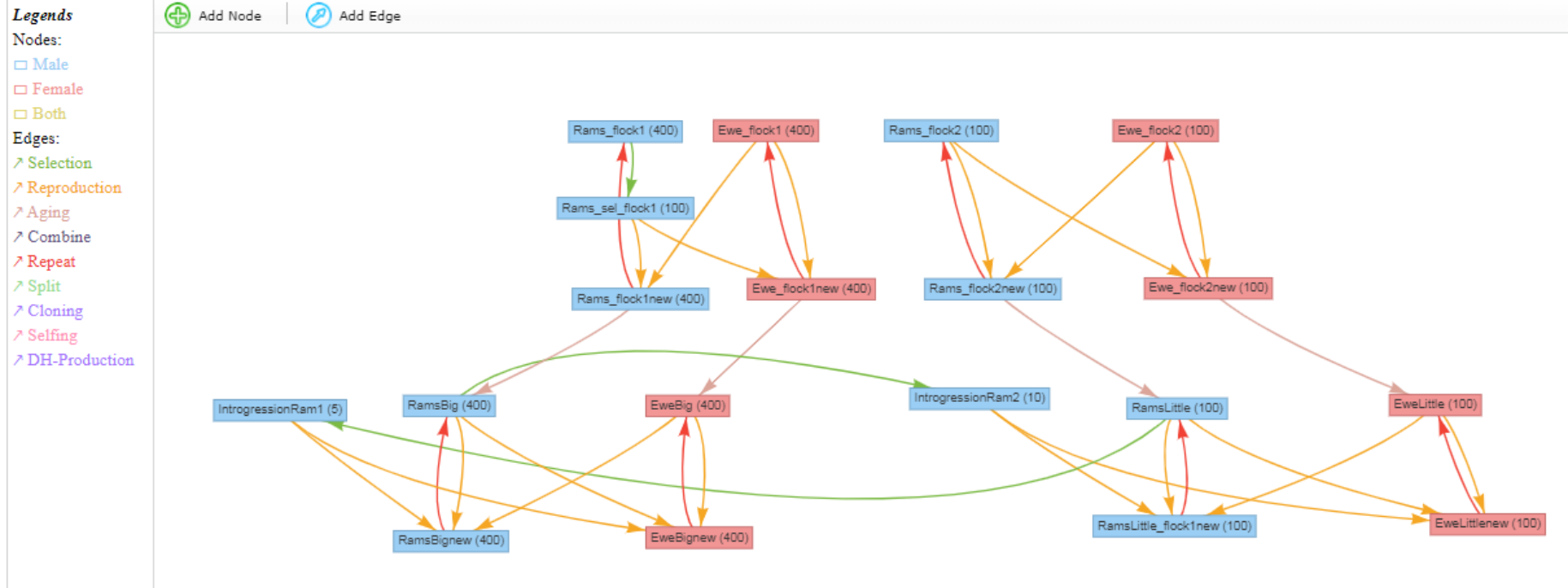
SI ⓘ	Meat	Milk	
Default Index	<input type="text" value="1"/>	<input type="text" value="1"/>	
Non	<input type="text" value="0"/>	<input type="text" value="0"/>	
Milk_focus	<input type="text" value="0"/>	<input type="text" value="1"/>	<input type="button" value="x"/>
Meat_focus	<input type="text" value="1"/>	<input type="text" value="0"/>	<input type="button" value="x"/>



# Case study I

## Breeding Scheme ①

*Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!*



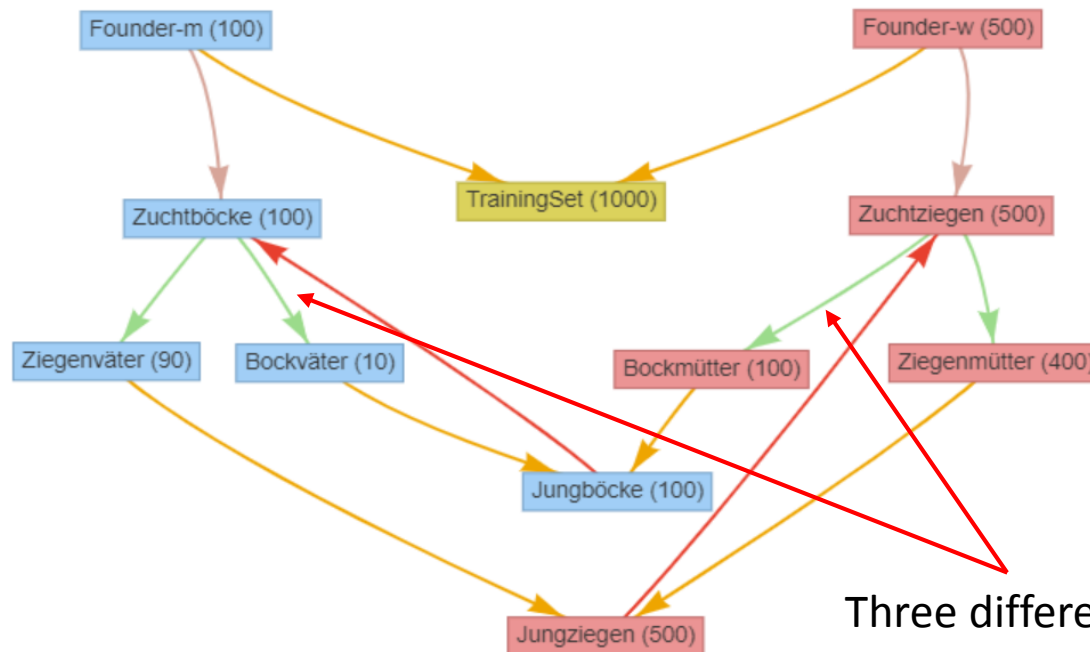
# Case study II

- Is it beneficial to use BLUP and/or GBLUP instead of phenotypic selection in goats?
- Trait structure (excuse the German!)

Merkmal	MW	SD	GEW	Gen. Parameter			Zuchttiere	
				MKG	TZN	EXT	m	w
Milchmenge	700	70	40	0.25	-0.20	0.30		X
Tägl. Zunahme	200	20	40	-0.06	0.40	0.50	X	X
Exterieurnote	7	0.5	20	0.09	0.17	0.30	X	



# Case study II



Only the best goats are used to breeding of the new bucks.  
Less selection for does

Three different types of selection

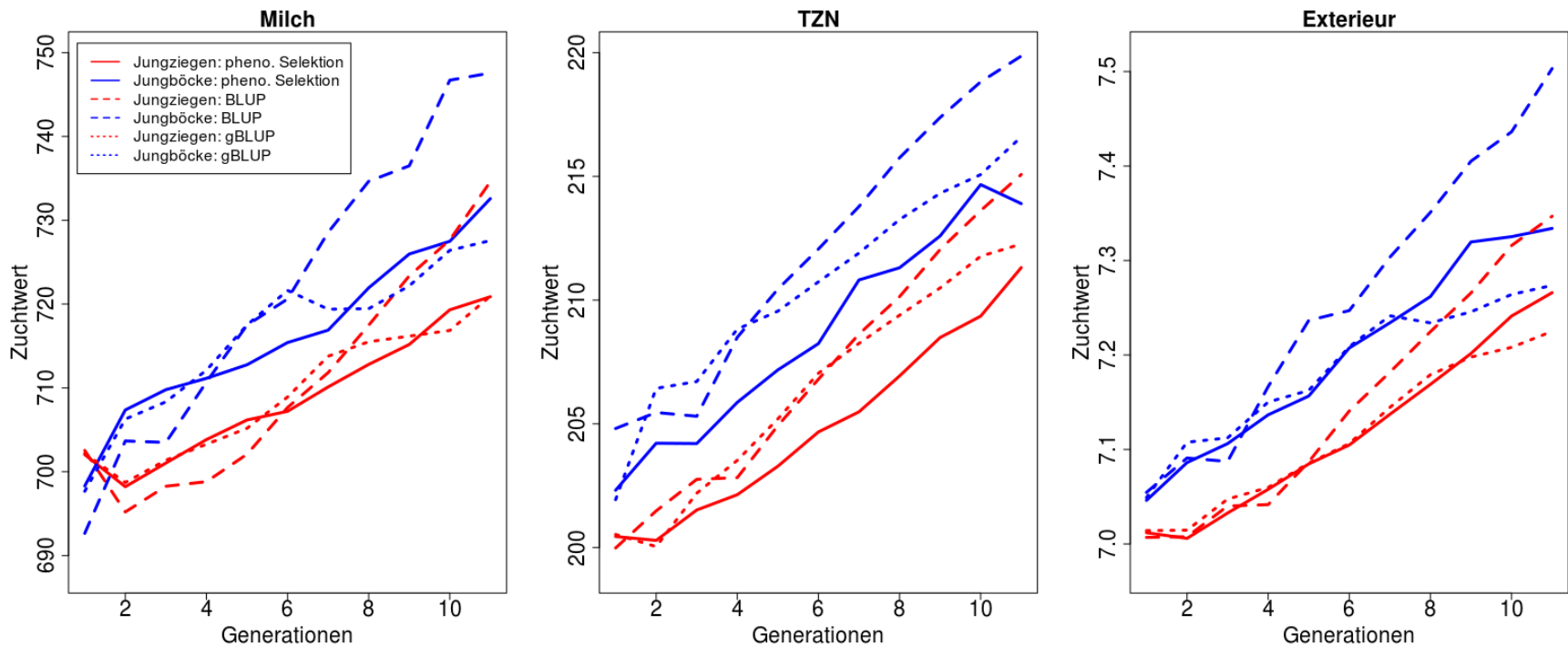
1. phenotypic
2. Pedigree BLUP
3. Genomic BLUP





# Case study II

- Pedigree BLUP performs on the same level as GBLUP
  - Note there are no repeats to generate new training data
  - Training and current population become for distant





# Case study III

- Analyze the impact of different selection indexes on genetic gains
- In particular:
  - How much do we lose by putting a strong focus on breeding for hornless cows

# Case Study III

- Traits we want to look at

## Phenotype Information ⓘ

<a href="#">Add new phenotype</a> <a href="#">Show/Hide 7 phenotypes</a> <a href="#">Show/Hide QTLs</a> <a href="#">Show/Hide residual correlation</a> <a href="#">Show/Hide genetic correlation</a>								
Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# polygenic loci ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor
RZM	Punkte	100	21.91	0.3	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZN	Punkte	100	30.98	0.09	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZE	Punkte	100	30.98	0.15	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZS	Punkte	100	40	0.15	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZR	Punkte	100	84.85	0.02	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZK	Punkte	100	56.57	0.045	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
Hornlosigkeit		100	0	1	0	1	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>

SNP for Hornlosigkeit	SNP ID ⓘ	bp	chromo	Effect AA	Effect AB	Effect BB	Allele Freq. (B) ⓘ	Optional Info
1			1	1	1	0	0.98	<input type="button" value="x"/>

SI ⓘ	RZM	RZN	RZE	RZS	RZR	RZK	Hornlosigkeit	
Default Index	1	1	1	1	1	1	1	
Non	0	0	0	0	0	0	0	
RZGMiesenberger	45	20	15	7	10	3	0	<input type="button" value="x"/>
Studenten	26	24	14	13	12	11	0	<input type="button" value="x"/>
Uni Goettingen	30	22	13	13	12	10	0	<input type="button" value="x"/>
Uni Kassel	21	28	15	14	11	11	0	<input type="button" value="x"/>
Hornlosigkeit	45	20	15	7	10	3	50	<input type="button" value="x"/>



# Case Study III

- Selection indexes we want to compare

SI ⓘ	RZM	RZN	RZE	RZS	RZR	RZK	Hornlosigkeit	
Default Index	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	
Non	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	
RZGMiesenberger	<input type="text" value="45"/>	<input type="text" value="20"/>	<input type="text" value="15"/>	<input type="text" value="7"/>	<input type="text" value="10"/>	<input type="text" value="3"/>	<input type="text" value="0"/>	<input type="button" value="x"/>
Studenten	<input type="text" value="26"/>	<input type="text" value="24"/>	<input type="text" value="14"/>	<input type="text" value="13"/>	<input type="text" value="12"/>	<input type="text" value="11"/>	<input type="text" value="0"/>	<input type="button" value="x"/>
Uni Goettingen	<input type="text" value="30"/>	<input type="text" value="22"/>	<input type="text" value="13"/>	<input type="text" value="13"/>	<input type="text" value="12"/>	<input type="text" value="10"/>	<input type="text" value="0"/>	<input type="button" value="x"/>
Uni Kassel	<input type="text" value="21"/>	<input type="text" value="28"/>	<input type="text" value="15"/>	<input type="text" value="14"/>	<input type="text" value="11"/>	<input type="text" value="11"/>	<input type="text" value="0"/>	<input type="button" value="x"/>
Hornlosigkeit	<input type="text" value="45"/>	<input type="text" value="20"/>	<input type="text" value="15"/>	<input type="text" value="7"/>	<input type="text" value="10"/>	<input type="text" value="3"/>	<input type="text" value="50"/>	<input type="button" value="x"/>



# Case study III

- The second subpopulation performs worse to the milk trait (-20)
- Target QTL for being hornless is fixated

## Multiple Subpopulations ⓘ

Subpopulation	Sampled allele frequency (p) ⓘ	Sampled allele frequency (q) ⓘ	Share of fixated markers in A ⓘ	Share of fixated markers in B ⓘ	Nr. of Markers with manual chosen allele frequency	Deviation from Mean for Trait RZM	Deviation from Mean for Trait RZN	Deviation from Mean for Trait RZE	Deviation from Mean for Trait RZS	Deviation from Mean for Trait RZR	Deviation from Mean for Trait RZK	Deviation from Mean for Trait Hornlosigkeit
Population 1	1	1	0.1	0.1	0							
Hornlos	1	1	0.1	0.1	1	-20						

Type a Subpopulation name ⓘ Creating new Subpopulation

SNP for Hornlos	SNP ID ⓘ	bp	Chromosome	Allele Freq. (B) ⓘ	Optional Info
1			1	0	

# Case Study III

- Traits we want to look at

## Phenotype Information ⓘ

<a href="#">Add new phenotype</a> <a href="#">Show/Hide 7 phenotypes</a> <a href="#">Show/Hide QTLs</a> <a href="#">Show/Hide residual correlation</a> <a href="#">Show/Hide genetic correlation</a>								
Phenotype ⓘ	Unit ⓘ	Pheno. Mean ⓘ	Pheno. SD ⓘ	Heritability ⓘ	# polygenic loci ⓘ	Major QTL ⓘ	Value per unit (€) ⓘ	Show Cor
RZM	Punkte	100	21.91	0.3	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZN	Punkte	100	30.98	0.09	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZE	Punkte	100	30.98	0.15	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZS	Punkte	100	40	0.15	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZR	Punkte	100	84.85	0.02	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
RZK	Punkte	100	56.57	0.045	1000	0	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>
Hornlosigkeit		100	0	1	0	1	0	<input checked="" type="checkbox"/> <input type="button" value="x"/>

SNP for Hornlosigkeit	SNP ID ⓘ	bp	chromo	Effect AA	Effect AB	Effect BB	Allele Freq. (B) ⓘ	Optional Info
1			1	1	1	0	0.98	<input type="button" value="x"/>

SI ⓘ	RZM	RZN	RZE	RZS	RZR	RZK	Hornlosigkeit	
Default Index	1	1	1	1	1	1	1	
Non	0	0	0	0	0	0	0	
RZGMiesenberger	45	20	15	7	10	3	0	<input type="button" value="x"/>
Studenten	26	24	14	13	12	11	0	<input type="button" value="x"/>
Uni Goettingen	30	22	13	13	12	10	0	<input type="button" value="x"/>
Uni Kassel	21	28	15	14	11	11	0	<input type="button" value="x"/>
Hornlosigkeit	45	20	15	7	10	3	50	<input type="button" value="x"/>

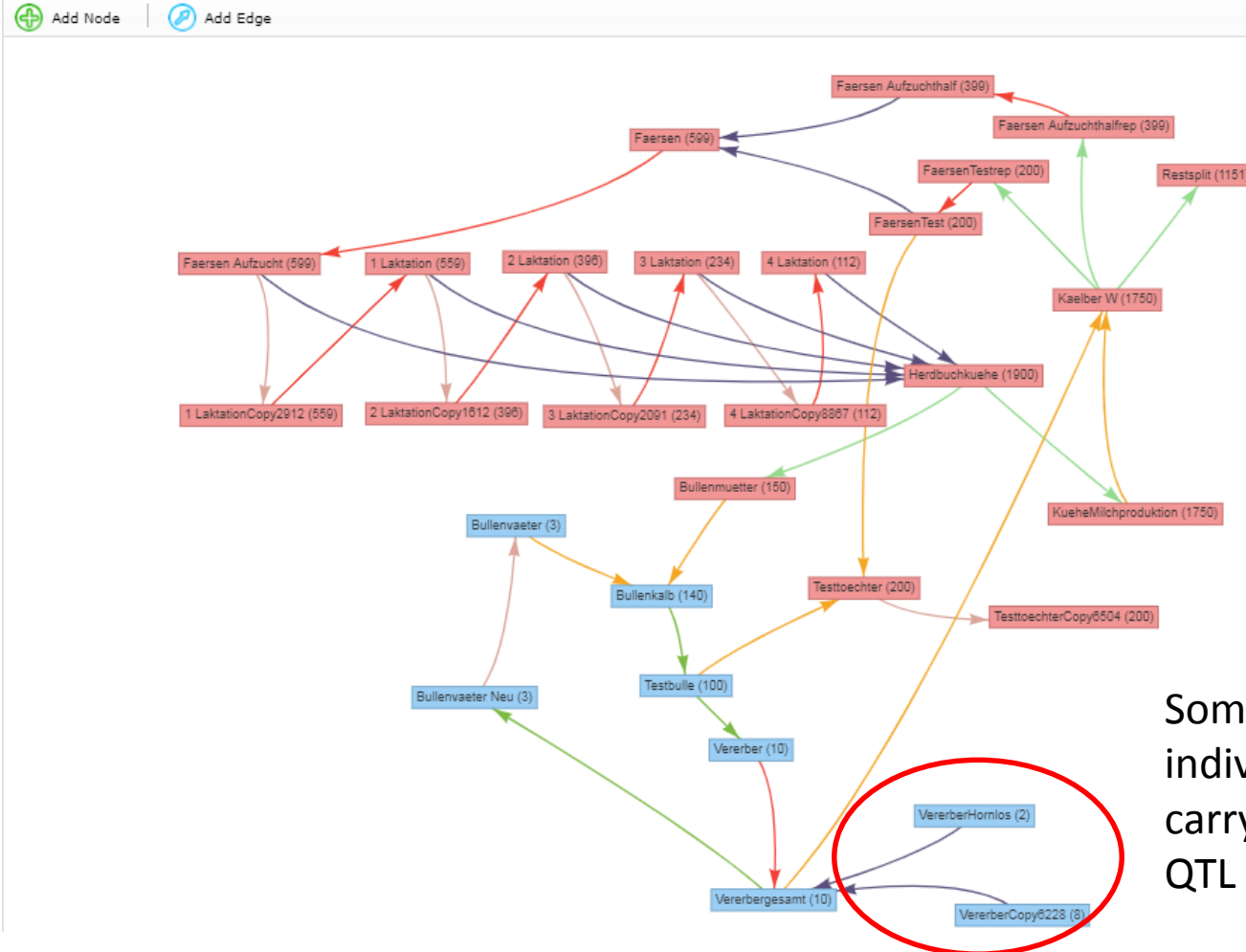


# Case Study III

## Breeding Scheme

Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!

- Legends**
- Nodes:**
- Male
  - Female
  - Both
- Edges:**
- Selection
  - Reproduction
  - Aging
  - Combine
  - Repeat
  - Split
  - Cloning
  - Selfing
  - DH-Production



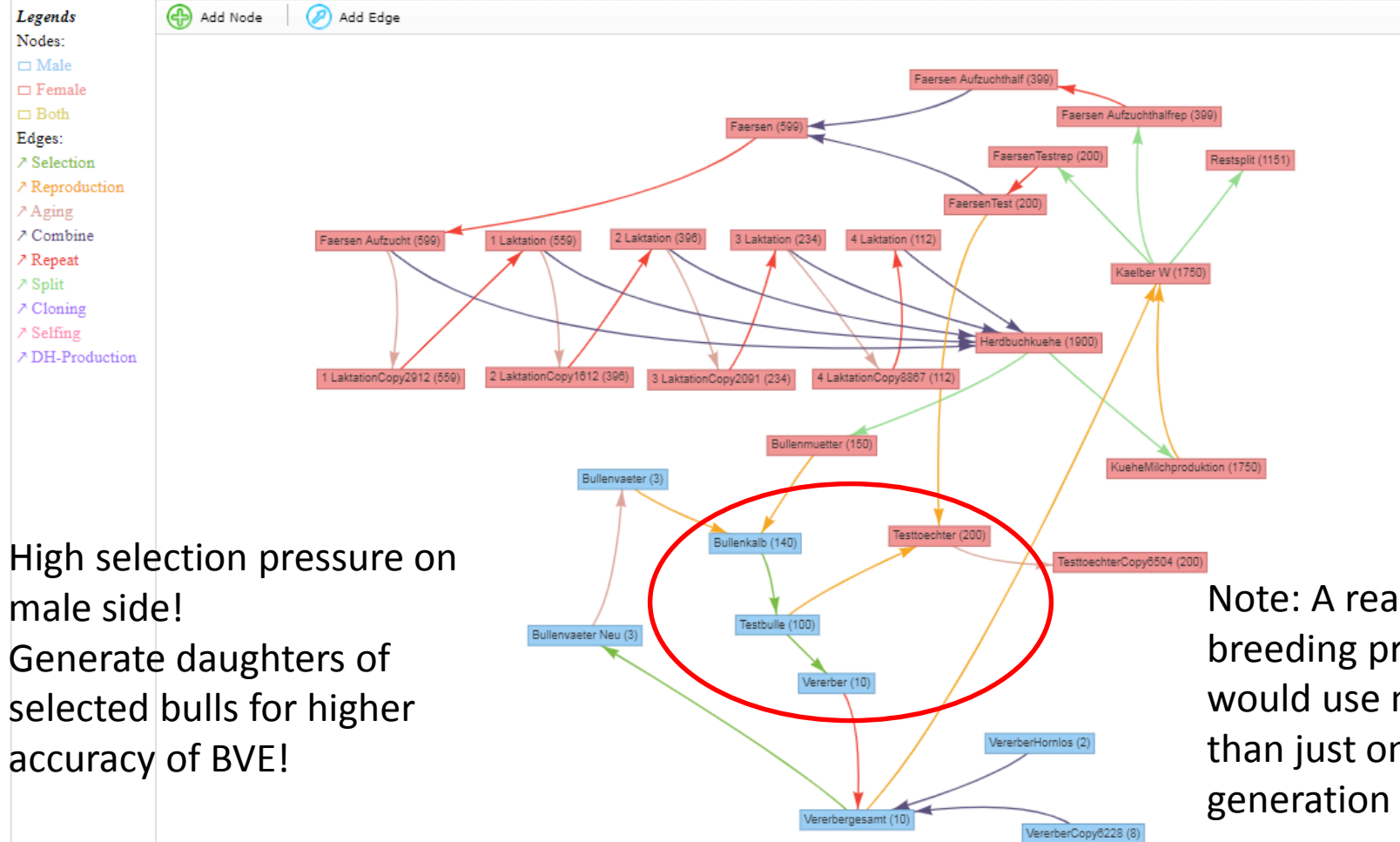
Some founder individuals that carry the hornless QTL



# Case Study III

## Breeding Scheme ①

Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!

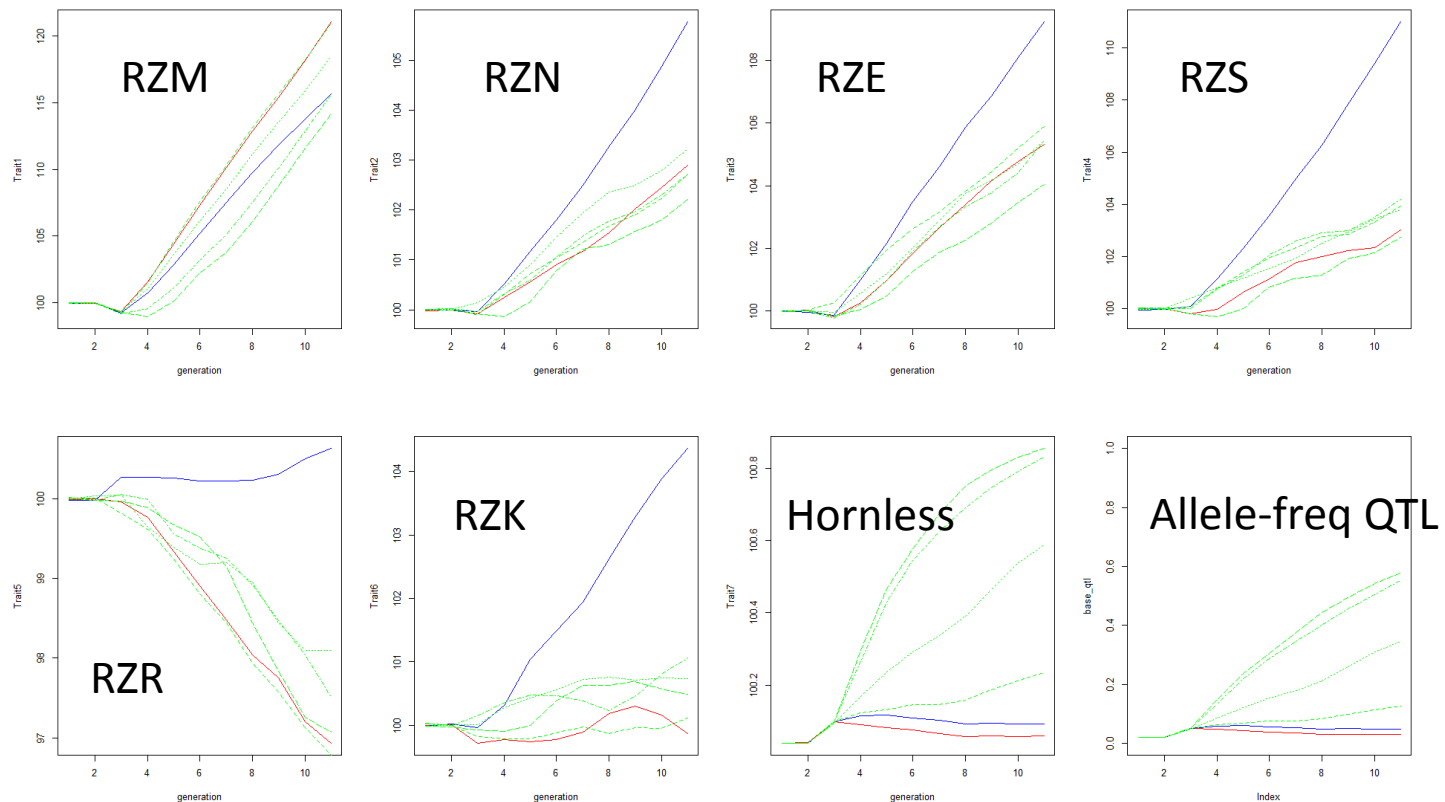






# Case Study III

- Red: currently applied index
- Blue: Index proposed by students
- Green: Variants with different weights on being hornless





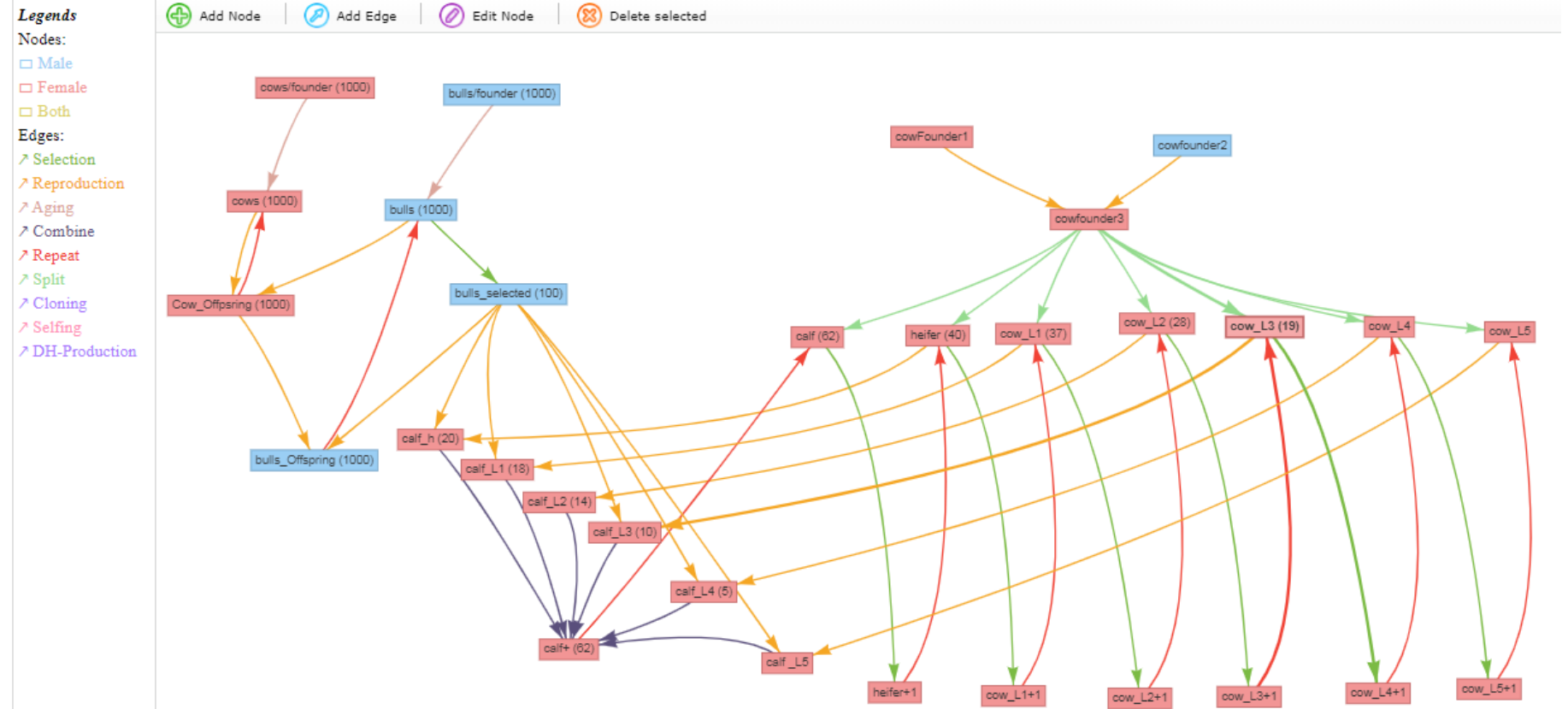
## Case study IV

- Analyze potential gains of the use of genomic prediction for the female side of a cattle breeding program
- Simulation of the cattle population of a local German farm
- Focus on the female side of the breeding program



## Breeding Scheme ①

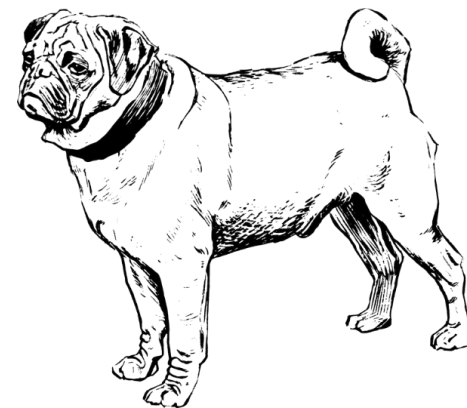
**Important: Please AVOID node names with : and \_ . In particular avoid trailing numbers like ABC\_1. Repeated nodes will use this syntax!**





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- European Union's Horizon 2020 Research and Innovation Program
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University of Goettingen



\*Fun fact: The german word for pug is Mob

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