

Optimization of introgression breeding programs with MoBPS

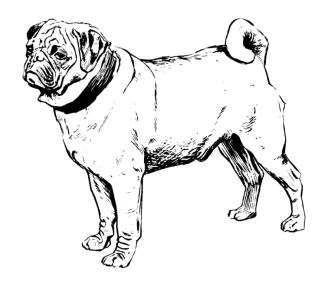
- T. Pook^{1,2}, A. Ganesan^{1,2}, N.T. Ha^{1,2}, M. Schlather^{2,3}, H. Simianer^{1,2}
- ¹ University of Goettingen, Animal Breeding and Genetics Group, Goettingen, Germany
- ² University of Goettingen, Center for Integrated Breeding Research, Goettingen, Germany
- ³ University of Mannheim, School of Business Informatics and Mathematics, Mannheim,

Germany

What is MoBPS?



- Modular Breeding Program Simulator
- Answer common questions when designing breeding programs:
 - How many animals to use?
 - Generate genotype/phenotype data of all animals?
 - Mating scheme?
 - Selection technique?
 - And much more ...



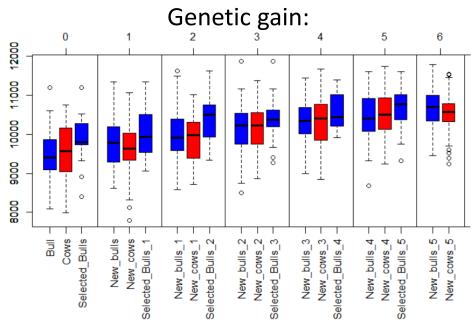
What is MoBPS?



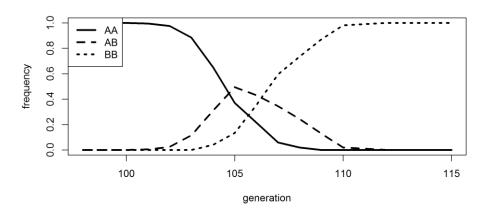
- Modular Breeding Program Simulator
- R-package (https://github.com/tpook92/MoBPS)
 - Highly efficient (Computational relevant parts written in C/C++)
 - Highly flexible (Cohort-based design)
 - Pre-implemented functions
 - Variety of different trait architectures

Functions to analyze your breeding program

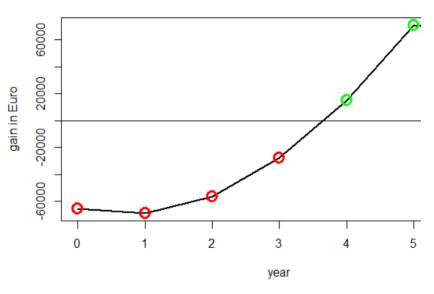




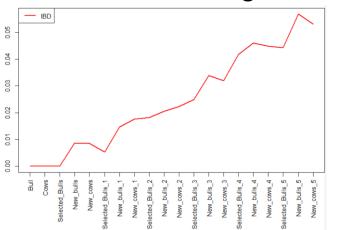
Genetic variation:



Economical:



Inbreeding:



```
breeding.diploid <- function (population, mutation.rate=10^-5, remutation.rate=10^-5, CRIF
....recombination.rate=1, selection.m=c("random"), selection.w=NULL, CRIDE
.....new.selection.calculation= TRUE, selection.function.matrix= NULL, CRIE
.... selection.size=c(0,0), breeding.size=0, breeding.gender=0.5, CRIF
.....breeding.gender.random=FALSE, used.generations.m=1, CRIF
     used.generations.w=NULL, relative.selection=FALSE, migration.level.m = 0, CRIF
.... migration.level.w = 0, add.gen=0, recom.f.indicator=NULL, recom.f.polynom=NULL, CRLE
          · duplication.rate=0, duplication.length=0.01, duplication.recombination=1, CRIF
.... new.migration.level=0L, bve=FALSE, bve.database= NULL, sigma.e = 100, CRIF
.....sigma.s.=.100, new.bv.observation.=.NULL, new.bv.child="mean", CRIF
        computation.A="vanRaden", delete.haplotypes=NVLL, delete.individuals=NVLL, CRIE
.... fixed.breeding=NULL, fixed.breeding.best=NULL, max.offspring=c(Inf,Inf), CRIF
     store.breeding.totals=FALSE, forecast.sigma.s=TRVE, multiple.bve="add", CRIF
        multiple.bve.weights=c(1), store.bve.data=FALSE, fixed.assignment=FALSE, CRIF
···········reduce.group=NVLL, reduce.group.selection="random", selection.critera=c(TRVE,TRVE), CRIF
   .... same.sex.activ=FALSE, same.sex.gender=0.5, same.sex.selfing=TRUE, CRIDE
.... selfing.mating=FALSE, selfing.gender=0.5, praeimplantation=NULL, CRIDE
sigma.e.database=NULL, heritability=NULL, multiple.bve.scale=FALSE, CRIF
```

Only two functions are needed to perform all simulations.

You just have to memorize 250 input parameters and read our 58 page user manual and you are good to go!

```
best1.from.group=NVLL, best2.from.group=NVLL, store.comp.times=TRUE, CRIEF
    store.comp.times.bve=TRUE, store.comp.times.generation=TRUE, CRIEF
.....special.comb=FALSE, max.auswahl=Inf, predict.effects=FALSE, SNP.density=10, CRIE
.... use.effect.markers=FALSE, use.effect.combination=FALSE, import.position.calculation=NULL, CRIF
          special.comb.add=FALSE, BGLR.save="RKHS", BGLR.save.random=FALSE, oqc=FALSE, CRIF
.....emmreml.bve=FALSE, nr.edits=0, gene.editing.offspring=FALSE, gene.editing.best=FALSE, CRIF
     gene.editing.offspring.gender=c(TRUE, TRUE), gene.editing.best.gender=c(TRUE, TRUE), CRIE
         qwas.u=FALSE, approx.residuals=TRUE, sequenceZ=FALSE, maxZ=5000, maxZtotal=0, CRIF
.... gwas.database=NVLL, delete.gender=1:2, gwas.group.standard=FALSE, CRIDE
 .....new.bv.observation.gender=c(1,2),.v.gwas.used="pheno",.gen.architecture.m=0,CRIF
          qen.architecture.w=NULL, add.architecture=NULL, ncore=1, ncore.generation=1, CRID
         · Z.integer=FALSE, store.effect.freg=FALSE, backend="doParallel", randomSeed=NULL, CRIF
    randomSeed.generation=NULL, Rprof=FALSE, miraculix=FALSE, miraculix.mult=NULL, CRIF
.... fast.compiler=0, miraculix.cores=1, store.bve.parameter=FALSE, CRIF
        print.error.sources=FALSE, miraculix.chol=FALSE, bve.database.insert=1, CRIF
.... best.selection.ratio.m=1, best.selection.ratio.w=NVLL, best.selection.criteria.m="by", CRIE
best.selection.criteria.w=NULL, best.selection.manual.ratio.m=NULL, CRIF
```



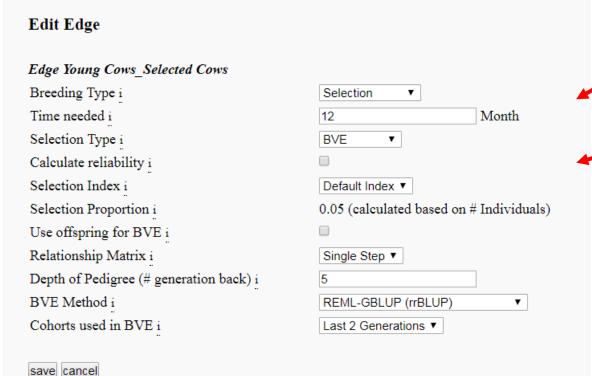
Modular representation of a breeding program

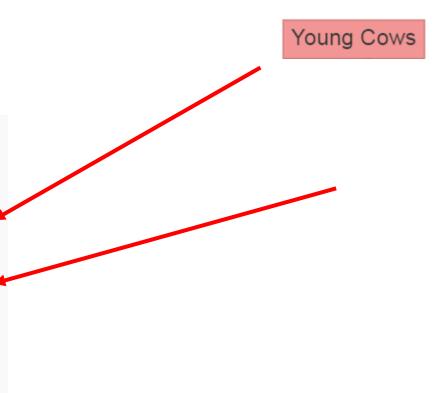


Graph-based representation

Nodes: Groups of animals

Edges: Breeding Actions





Web-based application



www.mobps.de

MoBPS Login

Username			
Password			
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			

Test-account during EAAP: User: EAAPguest pw: eaap2019

MoBPS was developed in the context of the EU project <u>IMAGE</u> Copyright © 2017 -- 2019 Torsten Pook







Design your Genome



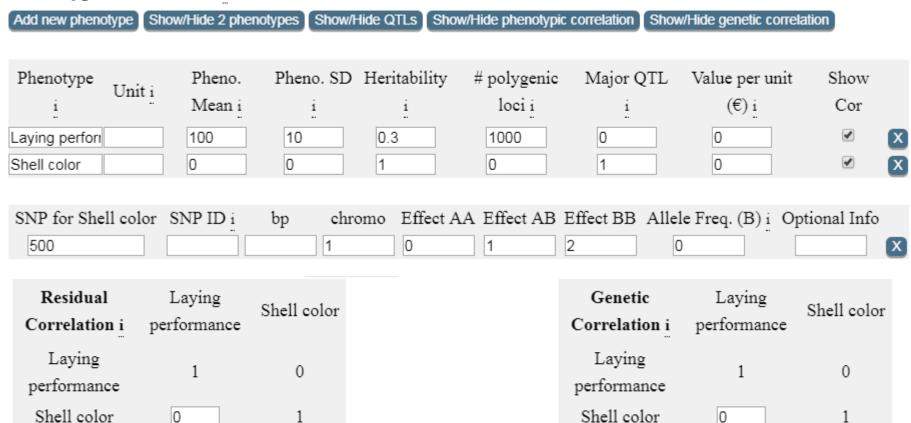
General Information

Project Name i		<u>EAAP</u> chicken
Advanced settin load save/download/delete your project		
Species i	via the action bar and load different	
Time Unit i	version to return to.	s ▼
		Use Ensembl Map
Genetic Data i		Upload Own Map (vcf/plink)
		Create customized Map
Ensembl Dataset i		Affymetrix Chicken600K Array ▼
Max. Number of SNPs i		50000

Design your Traits



Phenotype Information i



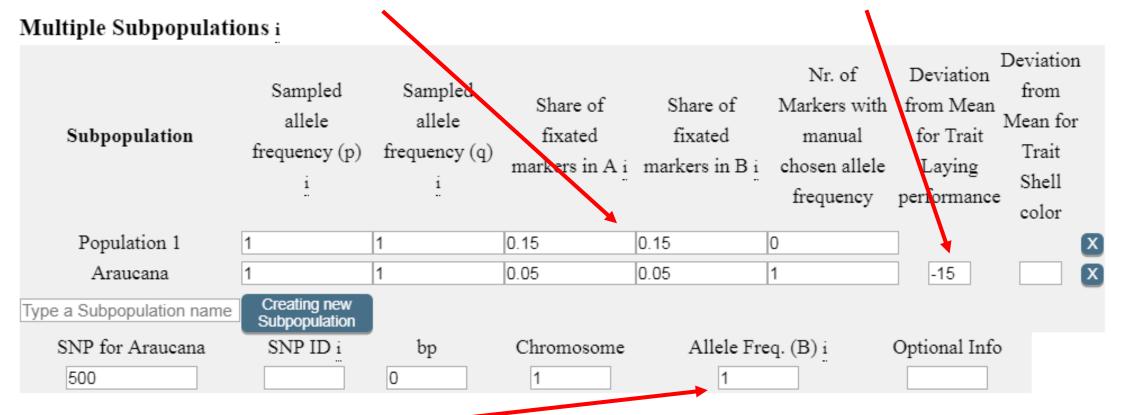
Enter Phenotypic correlation instead of residual correlation

Design your Subpopulations





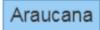
Worse laying performance



Web-based application

- http://www.mobps.de/
- 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



White-Layer





Araucana ♂ x WL ♀



Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

∠ Reproduction

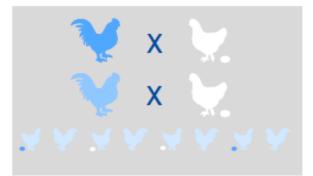
∠ Aging

∠ Combine

∠ Repeat

↗ Split





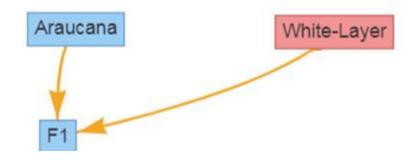
WL-content without selection: 75 %/87.5 %



BC2 ♂ x BC2 ♀

F1 ♂ **x** WL ♀

BC1 ♂ **x WL** ♀





Legends

Nodes:



□ Female

□ Both

Edges:

→ Selection

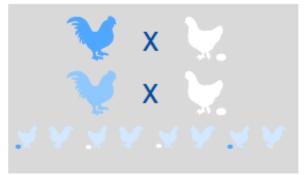
∧ Reproduction

∠ Aging

∠ Combine

∠ Repeat

↗ Split



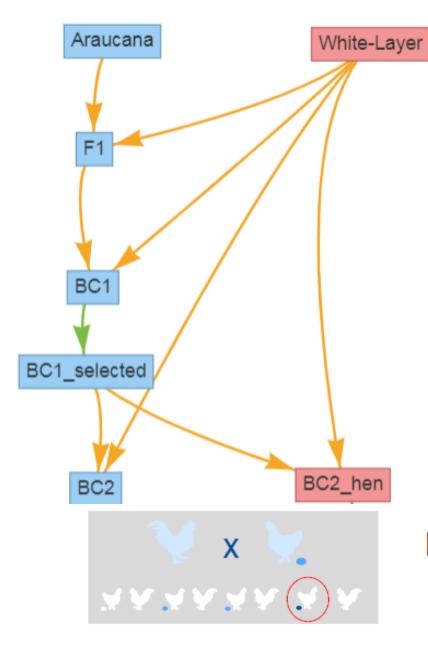
WL-content without selection: 75 %/87.5 %



BC2 ♂ x BC2 ♀

F1 ♂ **x WL** ♀

BC1 ♂ **x WL** ♀





Legends

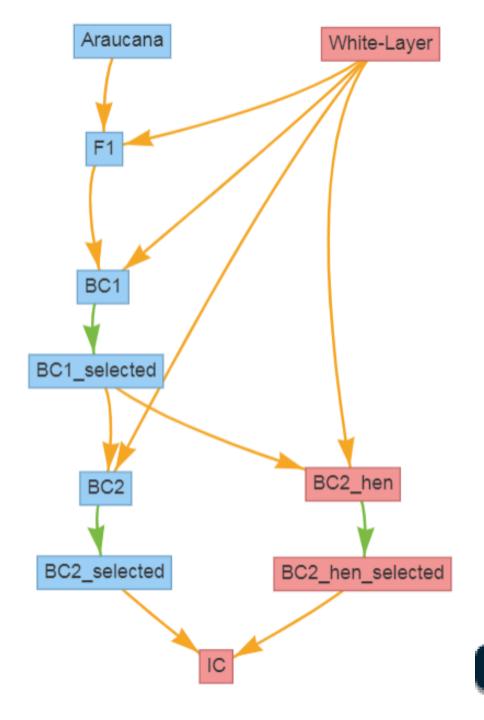
Nodes:

- □ Male
- □ Female
- □ Both

Edges:

- → Selection
- → Reproduction
- → Aging
- ∠ Combine
- ∠ Repeat
- ∠ Split

BC2 ♂ x BC2 ♀





Legends

Nodes:

- □ Male
- □ Female
- □ Both

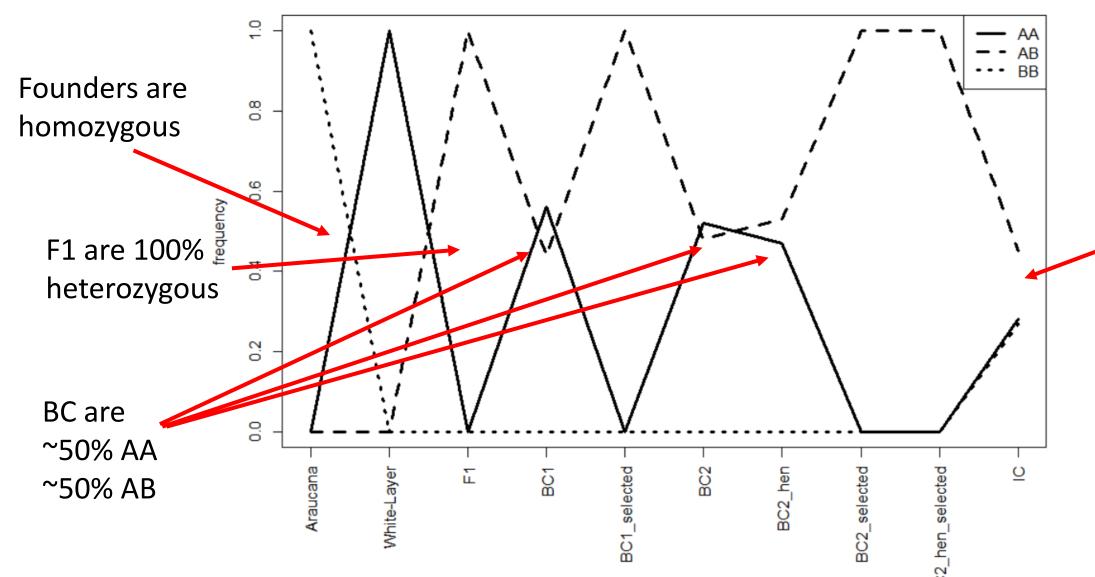
Edges:

- → Selection
- → Reproduction
- → Aging
- ∠ Combine
- ∠ Repeat
- ∠ Split

Start R Simulation

Results are as you would expect



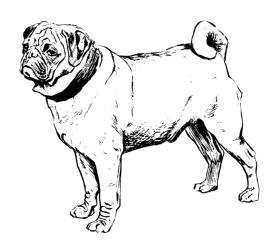


IC are
~25% AA
~50% AB
~25% BB

Summary



- R-package: MoBPS
 - Simulation of breeding programs
 - Highly efficient
 - Flexible in design
- Web-based application at http://www.mobps.de/
- During EAAP:
 - Test User: EAAPguest
 - Password: eaap2019
- We are interested in collaborations with both academia and companies!



Acknowledgments



- European Union's Horizon 2020 Research and Innovation Program
 - Grant agreement n° 677353 IMAGE
- Animal Breeding and Genetics Group University of Goettingen





