

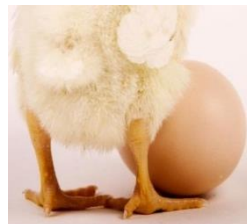
Optimization of introgression breeding programs with MoBPS

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

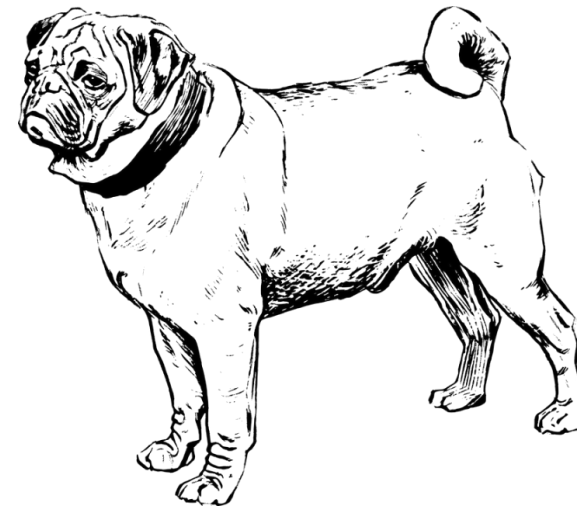
³ University of Mannheim, School of Business Informatics and Mathematics, Mannheim,
Germany





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 ...





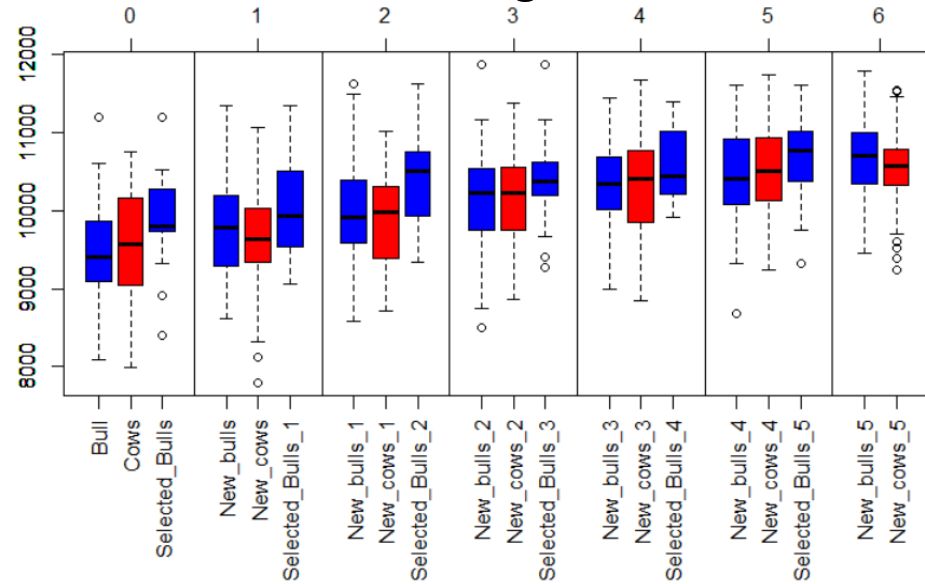
What is MoBPS?

- **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

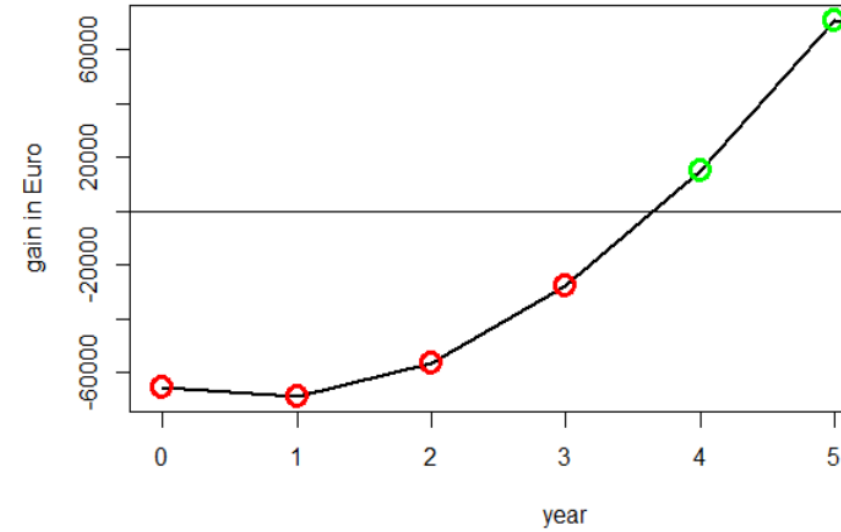
Functions to analyze your breeding program



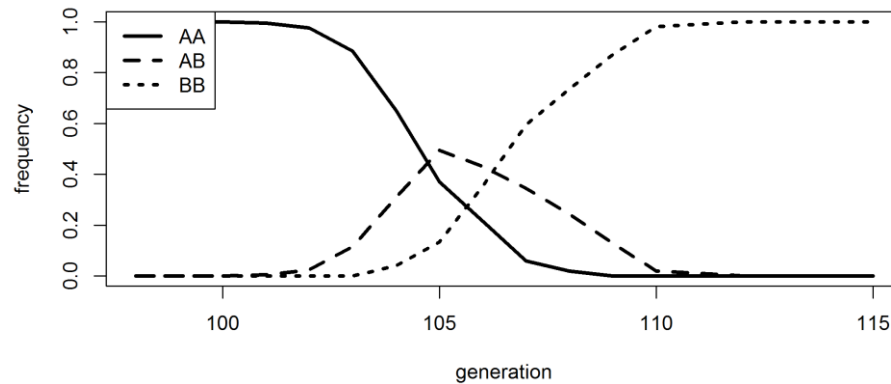
Genetic gain:



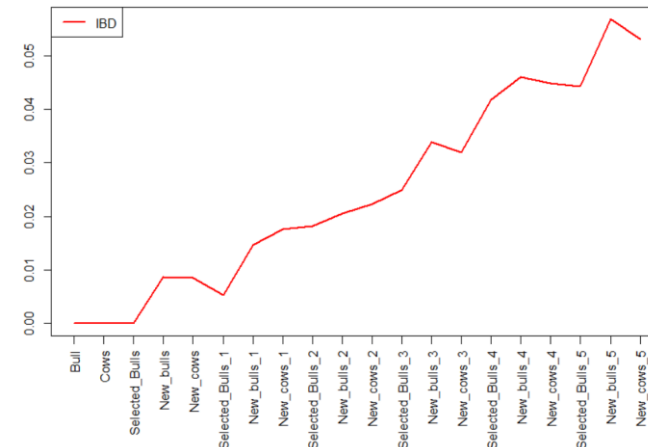
Economical:



Genetic variation:



Inbreeding:





Modular representation of a breeding program

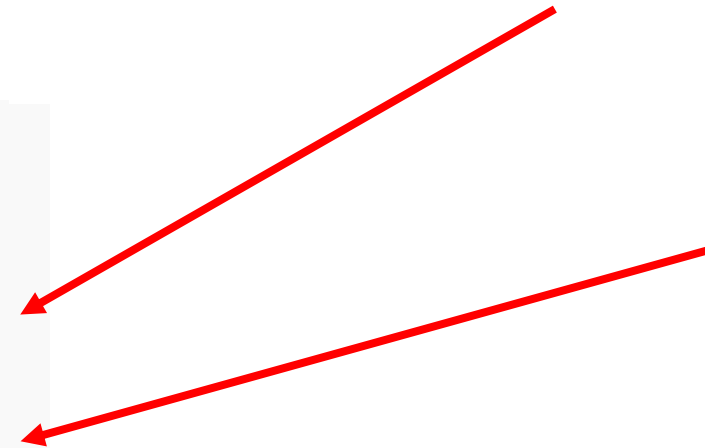
- Graph-based representation
 - Nodes: Groups of animals
 - Edges: Breeding Actions

Young Cows

Edit Edge

Edge Young Cows_Selected Cows

Breeding Type <small>i</small>	Selection ▾
Time needed <small>i</small>	12 Month
Selection Type <small>i</small>	BVE ▾
Calculate reliability <small>i</small>	<input type="checkbox"/>
Selection Index <small>i</small>	Default Index ▾
Selection Proportion <small>i</small>	0.05 (calculated based on # Individuals)
Use offspring for BVE <small>i</small>	<input type="checkbox"/>
Relationship Matrix <small>i</small>	Single Step ▾
Depth of Pedigree (# generation back) <small>i</small>	5
BVE Method <small>i</small>	REML-GBLUP (rrBLUP) ▾
Cohorts used in BVE <small>i</small>	Last 2 Generations ▾



Web-based application



- www.mobps.de

MoBPS 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 [IMAGE](#)
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GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN

CiBreed 
Center for Integrated Breeding Research



Design your Genome



General Information

Project Name <small>i</small>	<input type="text" value="EAAPchicken"/>
Advanced settings <small>i</small>	
Species <small>i</small>	<input type="text" value="Chicken"/>
Time Unit <small>i</small>	<input type="text" value="Days"/>
Genetic Data <small>i</small>	<input checked="" type="radio"/> Use Ensembl Map <input type="radio"/> Upload Own Map (vcf/plink) <input type="radio"/> Create customized Map
Ensembl Dataset <small>i</small>	<input type="text" value="Affymetrix Chicken600K Array"/>
Max. Number of SNPs <small>i</small>	<input type="text" value="50000"/>

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.

Design your Traits



Phenotype Information ⋮

Phenotype i	Unit i	Pheno. Mean i	Pheno. SD i	Heritability i	# polygenic loci i	Major QTL i	Value per unit (€) i	Show Cor i	✕
Laying perform	<input type="text"/>	<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"/>	✕
Shell color	<input type="text"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="1"/>	<input type="text" value="0"/>	<input type="text" value="1"/>	<input type="text" value="0"/>	<input checked="" type="checkbox"/>	✕

SNP for Shell color	SNP ID i	bp	chromo	Effect AA	Effect AB	Effect BB	Allele Freq. (B) i	Optional Info	✕
<input type="text" value="500"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="1"/>	<input type="text" value="0"/>	<input type="text" value="1"/>	<input type="text" value="2"/>	<input type="text" value="0"/>	<input type="text"/>	✕

Residual Correlation i	Laying performance	Shell color
Laying performance	<input type="text" value="1"/>	<input type="text" value="0"/>
Shell color	<input type="text" value="0"/>	<input type="text" value="1"/>

Genetic Correlation i	Laying performance	Shell color
Laying performance	<input type="text" value="1"/>	<input type="text" value="0"/>
Shell color	<input type="text" value="0"/>	<input type="text" value="1"/>

Enter Phenotypic correlation instead of residual correlation

Design your Subpopulations



Less fixates markers in the wildrace

Worse laying performance

Multiple Subpopulations i

Subpopulation	Sampled allele frequency (p) i	Sampled allele frequency (q) i	Share of fixated markers in A i	Share of fixated markers in B i	Nr. of Markers with manual chosen allele frequency	Deviation from Mean for Trait Laying performance	Deviation from Mean for Trait Shell color
Population 1	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="0.15"/>	<input type="text" value="0.15"/>	<input type="text" value="0"/>		
Araucana	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text" value="0.05"/>	<input type="text" value="0.05"/>	<input type="text" value="1"/>	<input type="text" value="-15"/>	<input type="text"/>

Type a Subpopulation name Creating new Subpopulation

SNP for Araucana	SNP ID i	bp	Chromosome	Allele Freq. (B) i	Optional Info
<input type="text" value="500"/>	<input type="text"/>	<input type="text" value="0"/>	<input type="text" value="1"/>	<input type="text" value="1"/>	<input type="text"/>

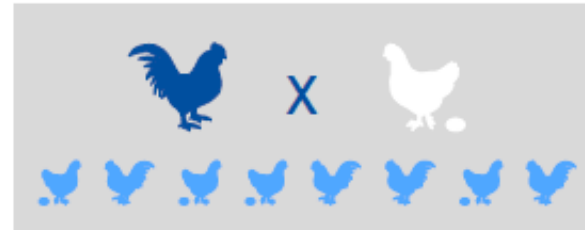
Beneficial QTL

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

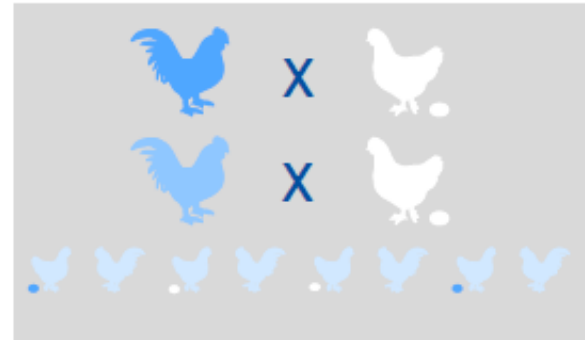
Araucana

White-Layer



WL-content: 50 %

Araucana ♂ x WL ♀



WL-content without selection: 75 %/87.5 %

F1 ♂ x WL ♀

BC1 ♂ x WL ♀



BC2 ♂ x BC2 ♀

Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

↗ Reproduction

↗ Aging

↗ Combine

↗ Repeat

↗ Split



Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

↗ Reproduction

↗ Aging

↗ Combine

↗ Repeat

↗ Split



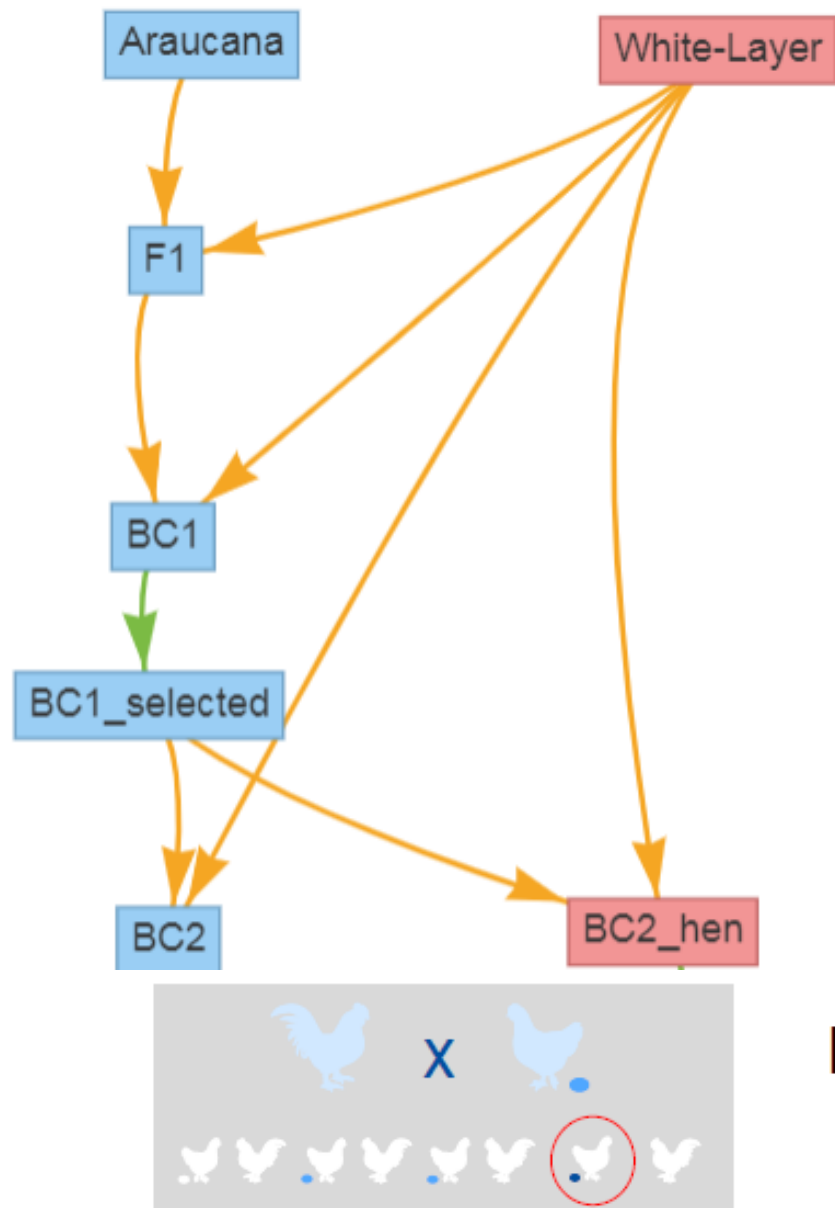
WL-content without selection: 75%/87.5%

F1 ♂ x WL ♀

BC1 ♂ x WL ♀



BC2 ♂ x BC2 ♀



Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

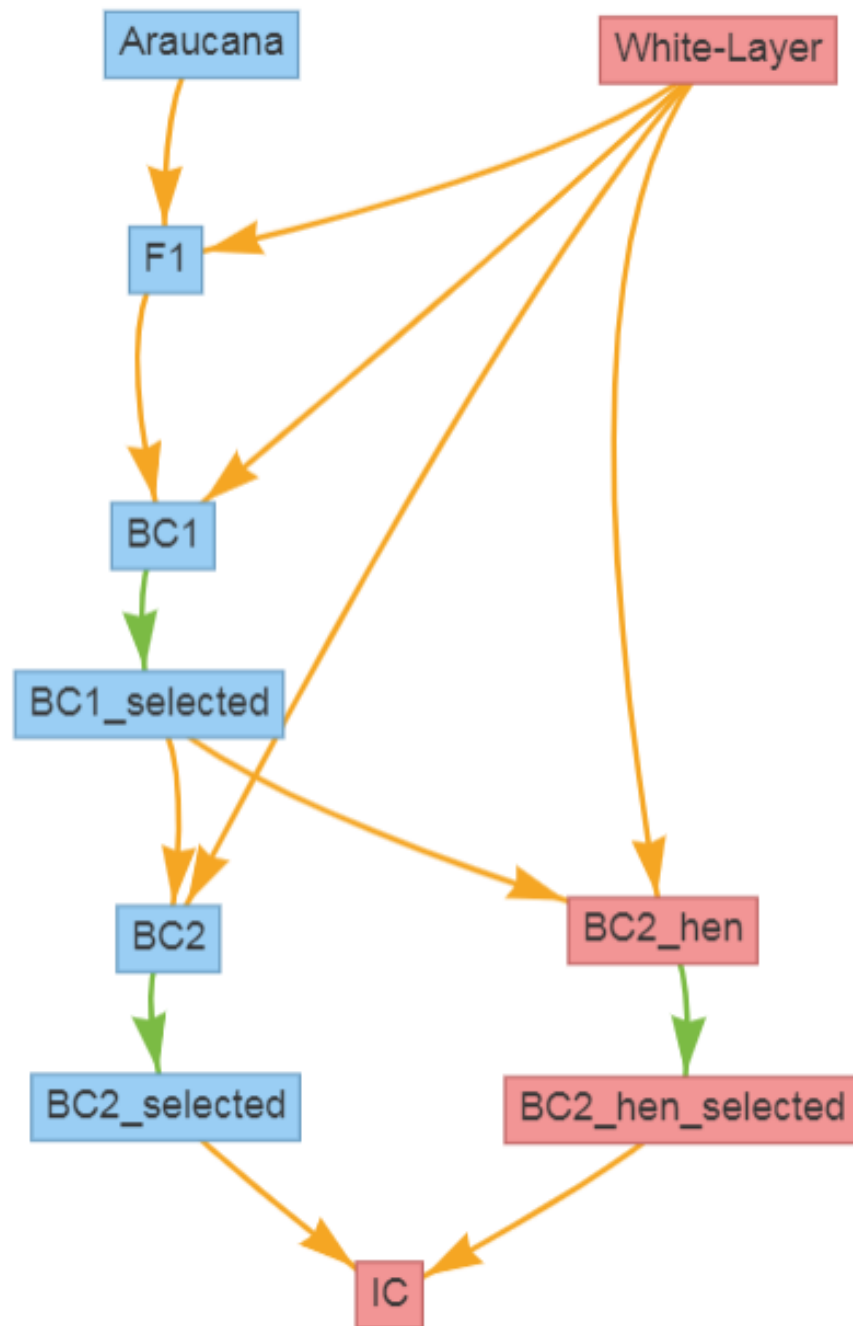
↗ Reproduction

↗ Aging

↗ Combine

↗ Repeat

↗ Split



Legends

Nodes:

□ Male

□ Female

□ Both

Edges:

↗ Selection

↗ Reproduction

↗ Aging

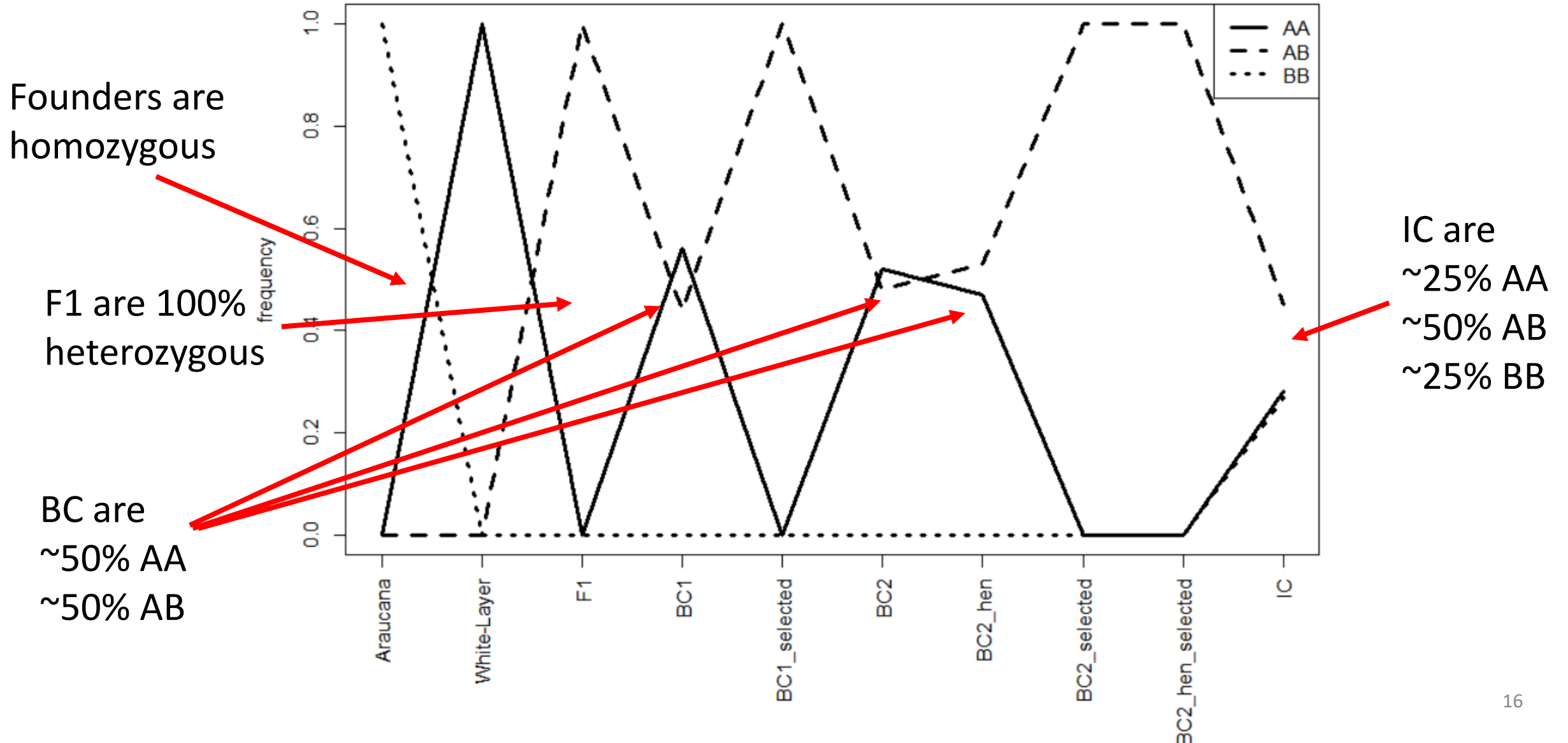
↗ Combine

↗ Repeat

↗ Split

Start R Simulation

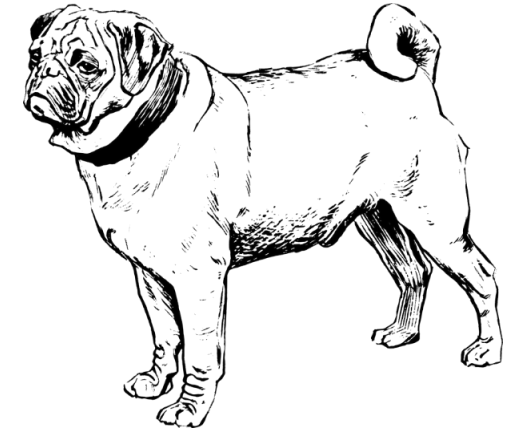
Results are as you would expect



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!



Thank you for your attention!

Acknowledgments



- European Union's Horizon 2020 Research and Innovation Program
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- Animal Breeding and Genetics Group
University of Goettingen

