



Session 2

Strategic Research Center

GenSAP

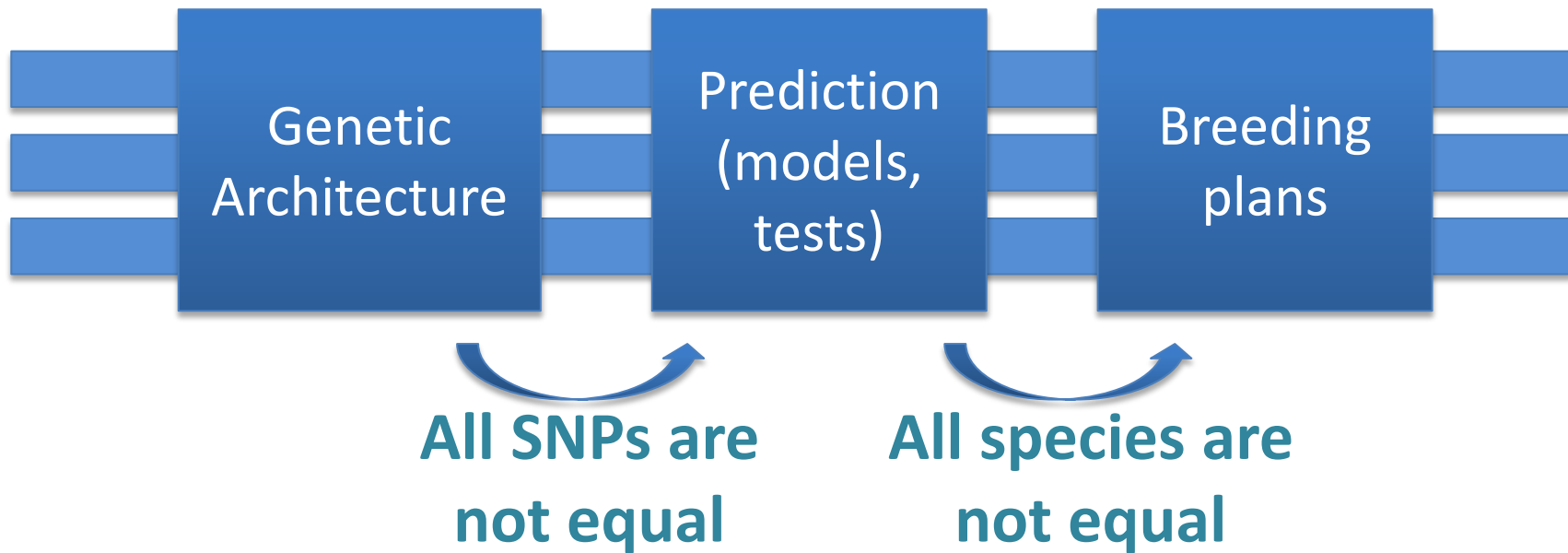
Genomic Selection in Animals and Plants



**Genomic Prediction: towards use of full
sequence and large populations**
Luc Janss, QGG, Aarhus University

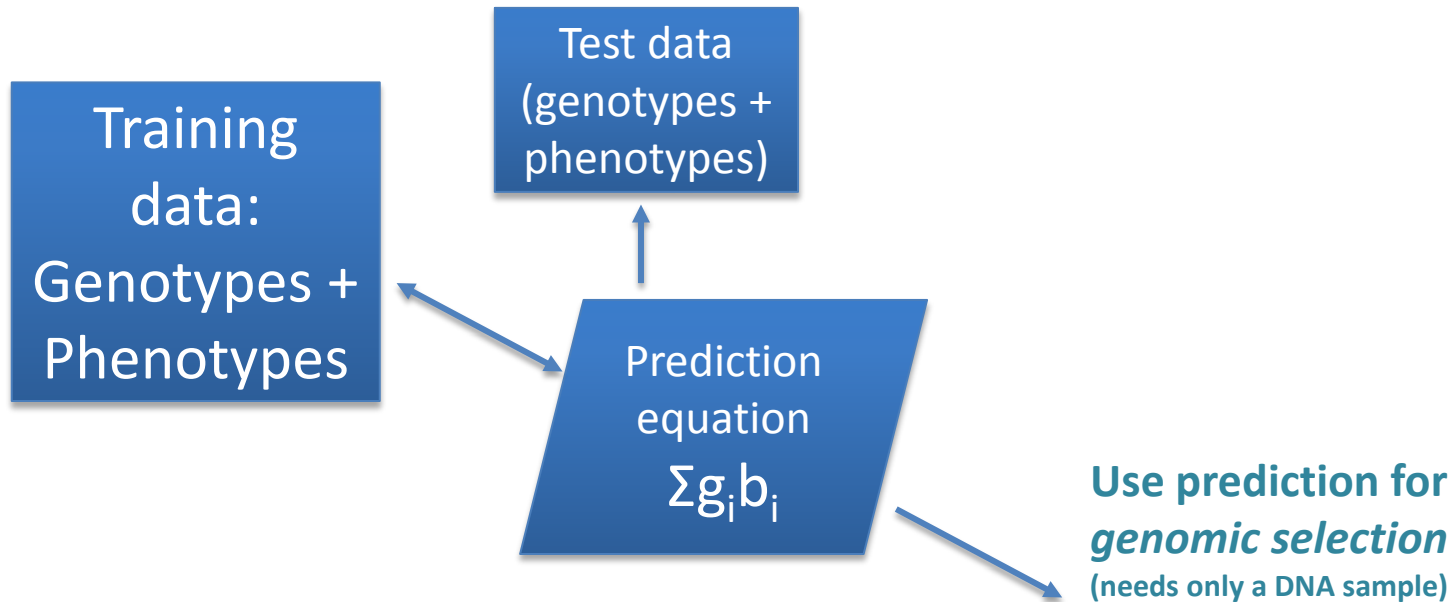


GenSAP lay-out





Principles of Genomic Prediction and Genomic Selection



Prediction works using whole-genome models (and fails when using mapping approaches)





Current Status Genomic Prediction

- Used in cattle, pigs, pilots in wheat, maize, attempts in human
- Current method: “GBLUP”
 - Equal weighting of SNPs
 - ‘Relationship’ approach
- Performs well
 - Within populations of small effective size
 - With strong structure and relationships between training / testing populations
- Limitations regarding # individuals, phenotypes, combining different SNP densities, ...

Current genome-based prediction systems work well, but only in particular (limited) cases



Main challenges

- All SNPs are *not* equal
- ‘Relationship’ approach limits application
- Computational procedures not up to speed with genomics technology
- Merging in whole population data



Animals and SNP densities in cattle

| | SNPs | # Animals |
|--------------------------|-----------------------------|--------------------------|
| Ungenotyped | - | 10.000.000 + |
| Elite cows | 7K | 100.000 + |
| Breeding bulls | 54K | 40.000 |
| Sample of breeding bulls | 777K | 4.000 |
| Elite bulls | Full sequence (20M SNPs) | 1.000 (approx 250 DK) |

Imputing all to full sequence is not an option



GenSAP Solutions

- Better LD with causal variants
 - Use full sequence
 - Use bioinformatics knowledge
- Better models allowing unequal weighting of SNPs
 - Variable selection models
- Build extensions
 - Plant specific genetics (selfing, polyploidy)
 - Interactions (GxE, dominance)
- Integration in population predictions (BLUP)
 - Modified BLUP for unequal weighting of SNPs
 - Improved ‘single step’ methods (larger, multi-trait, ...)



Program

Session 2:

- 13:45 Genomic prediction models: towards use of full sequence and large populations
Senior Researcher Luc Janss, QGG, AU
- 14:00 The 1000 bull genomes project - reconstructing the past genetic history of cattle, and accelerating future gains
Research Leader Ben Hayes, Dept. of Primary Industries, Victoria, Australia
- 14:45 Coffee break
- 15:15 Genomic selection using QTL information
Senior Scientist Didier Boichard, INRA, France
- 15:35 Visions and perspectives for genomic prediction in animals, plants and humans
Professor Daniel Gianola, University of Wisconsin-Madison, USA
- 15:55 The benefits of haplotypes as predictors of genetic merit
PhD Student Beatriz Castro Dias Cuyabano, QGG, AU
- 16:15 Poster session & reception