

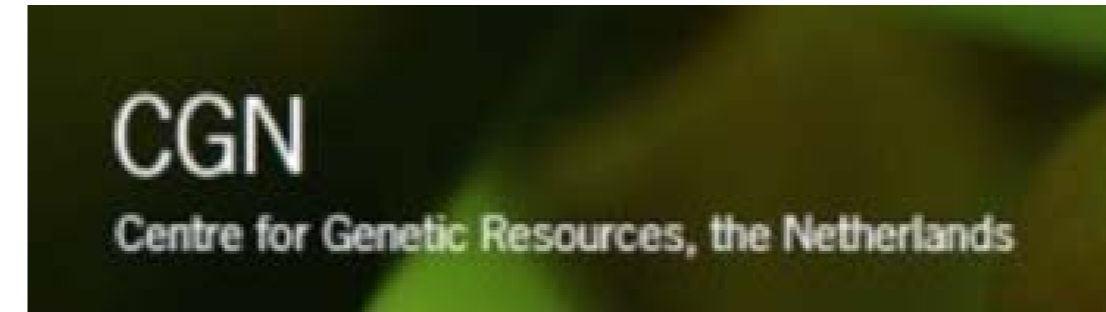
The use of whole genome sequence data for prioritisation decision in genetic diversity conservation

Sonia E Eynard^{1, 2, 3, 4}, Jack J Windig^{1, 4}, Mario PL Calus¹

¹ Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands, ² AgroParisTech, UMR 1313 Génétique Animale et Biologie Intégrative, 16 rue Claude Bernard, 75231 Paris 05, France, ³ INRA, UMR 1313 Génétique Animale et Biologie Intégrative, 78350 Jouy-en-Josas, France, ⁴ Centre for Genetic Resources the Netherlands, Wageningen UR, P.O. Box 16, 6700 AA Wageningen, the Netherlands



Animal Breeding & Genomics Centre



Objectives

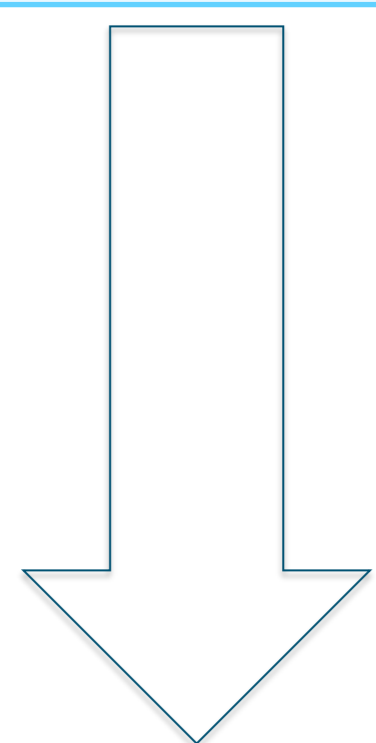
Which individuals are selected for genetic diversity conservation when using

- 1) Pedigree
- 2) SNP
- 3) Whole Genome Sequence information?

Introduction

Scheme selection decision

Information on individuals
Phenotypes, Genotypes, Relationships



Select individuals

Conclusions

The use of rare variants, in whole genome sequence, is expected to affect selection decision for genetic diversity conservation

Estimated relationships

Pedigree	SNP chip	Whole Genome Sequence (WGS)
• Genealogic record	• Subset of markers	• All markers • 3X more Rare variants than in SNP

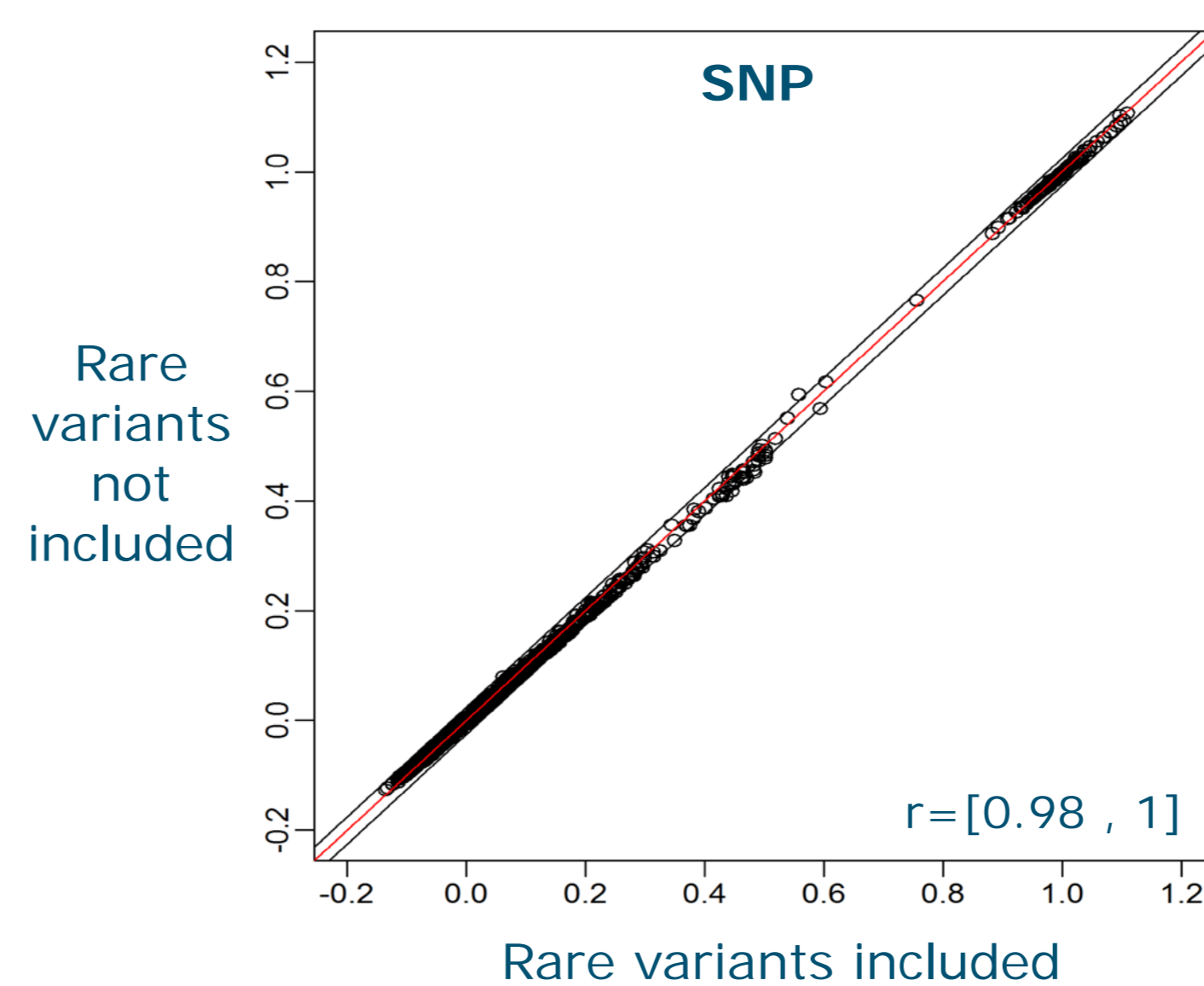


Figure 1. Linear regression of estimated relationships from SNP data including or non including rare variants

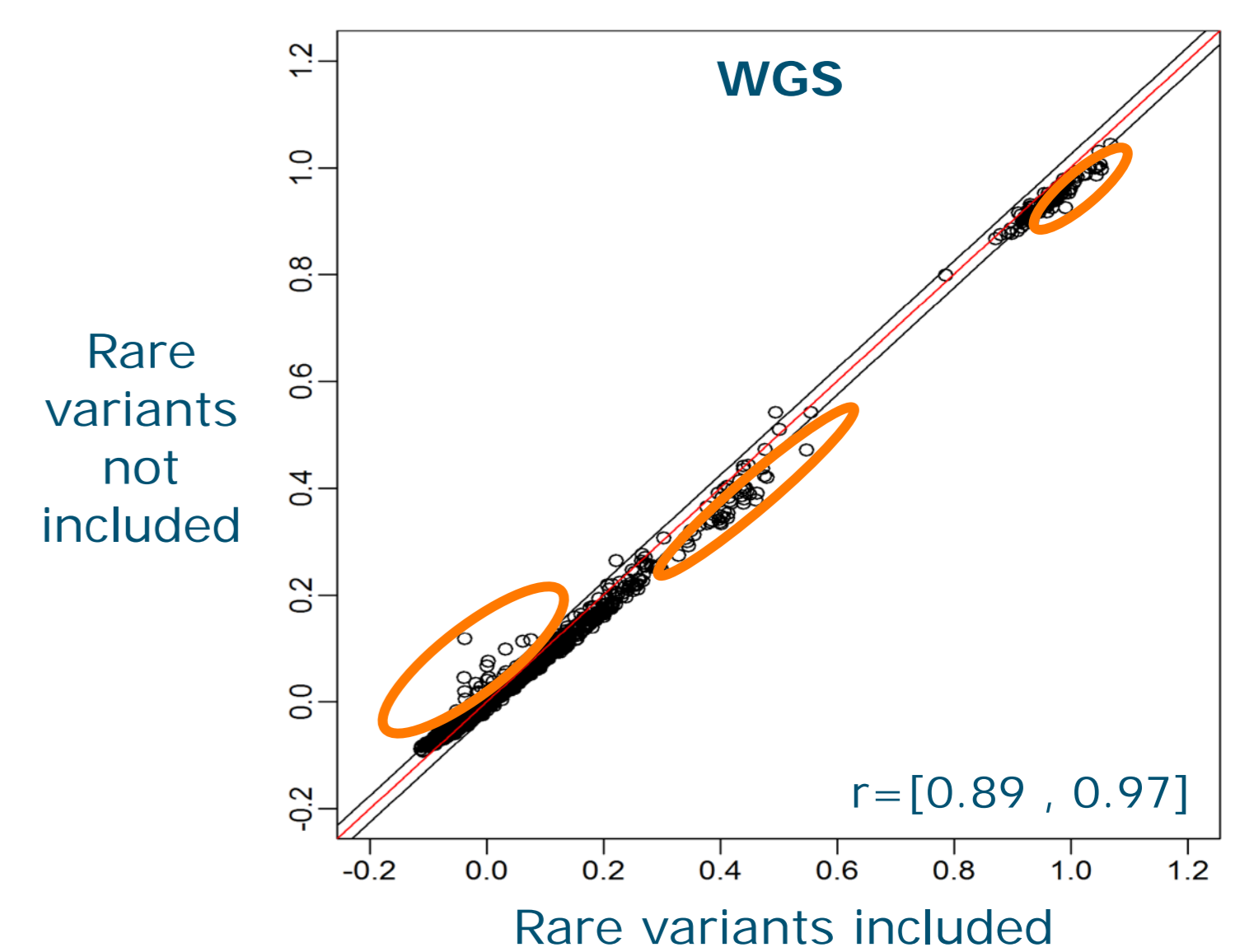


Figure 2. Linear regression of estimated relationships from whole genome sequence data including or non including rare variants

- WGS: change in estimated relationships when rare variants included
- Potential for selection for genetic diversity conservation

Optimal Contribution Selection (OCS)

- Maximise genetic level selected individuals AND
- Minimise relatedness parent population
- Used for prioritisation of individuals to maintain genetic diversity

Approach

Group 1: Selection candidates



Group 2: Selected individuals



Pedigree information

Both All and Common markers SNP

Common markers WGS

All markers (including rare variants) WGS

Acknowledgements

Funding: Erasmus Mundus EGS ABG / Dutch Ministry of economic Affairs KB-12-005-03-001 CGN

Data: 1000 bull genomes consortium



Sonia E Eynard
EGS ABG PhD Candidate
Animal Breeding and Genomics Centre
Wageningen UR Livestock Research
sonia.eynard@wur.nl
sonia.eynard@gmail.com

Postal address: PO box 338
6700 AH Wageningen, the Netherlands
Visitors address: Radix Building (107) E0.214
Droevendaalsesteeg 1
6708 PB Wageningen, the Netherlands

Tel: +31(0)3174-83936

Literature:
Stock KF & Reents R. **Genomic selection: status in different species and challenges for breeding.** *Reprod Domest Anim* 2013
Henryon M, Berg P & Sørensen AC. **Invited review: Animal-breeding schemes using genomic information need breeding plans designed to maximise long-term genetic gains.** *Livest Sci* 2014
Engelsma KA, Veerkamp RF, Calus MPL & Windig JJ. **Consequences for diversity when prioritizing animals for conservation with pedigree or genomic information.** *J Animal Breeding and Genetics* 2011
Meuwissen THE. **Maximizing the response of selection with a predefined rate of inbreeding.** *JAnimal Sci* 1997