

Genome wide diversity: heterozygosity vs. IBD

Krista A Engelsma, MPL Calus, SJ Hiemstra, P Bijma and JJ Windig

Animal Breeding & Genomics Centre
Centre for Genetic Resources, The Netherlands

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Krista.Engelsma@wur.nl



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Introduction

- Genetic diversity in livestock
- Loss of diversity
- Average diversity (pedigree) – diversity on specific regions on the genome (non-neutral trait, i.e. growth and fertility)
- Dense marker maps (SNPs)
- Predict diversity on untyped regions (i.e. unknown QTL)



Genetic diversity evaluation



- Molecular / population genetics
 - Heterozygosity
 - % individuals that have 2 different alleles

- Quantitative genetics
 - Average relatedness
 - % DNA that is identical by descent (IBD)



Aim

Estimation of genetic diversity on untyped regions over the genome

- **Compare two methods: IBD and heterozygosity**
- **Which method best predicts genetic diversity between markers?**

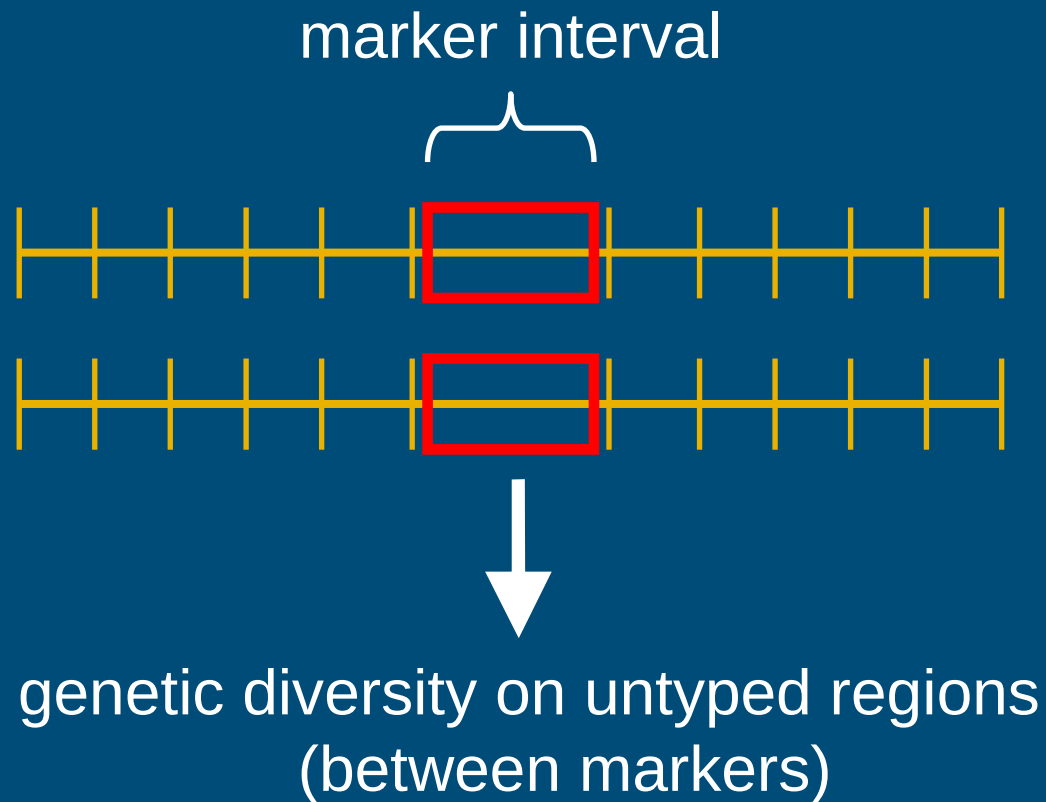


Simulation

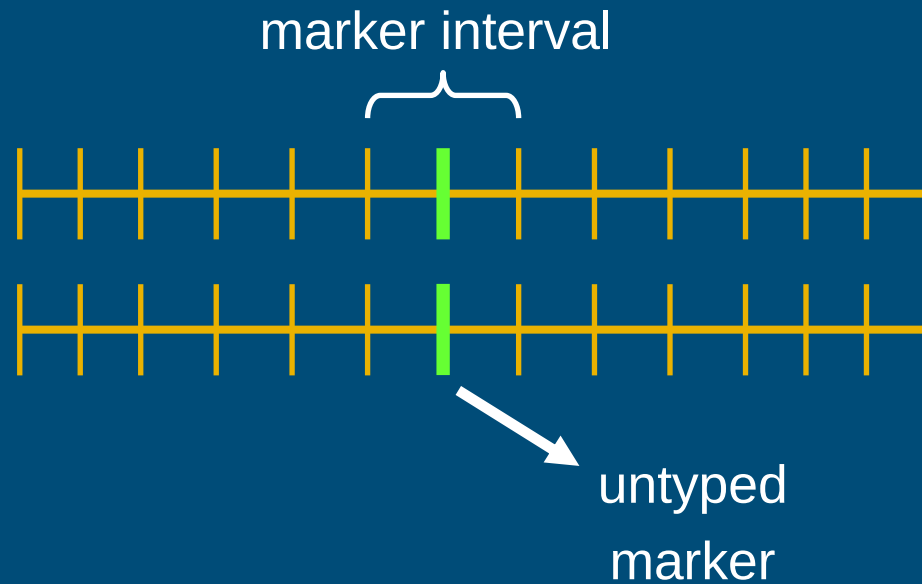
- 1 chromosome of 1 Morgan
- 1,800 SNP markers
- Effective population size = 100
- 100 + 3 generations
- 3 generations: 2,100 genotyped animals



Genetic diversity over the genome



True genetic diversity

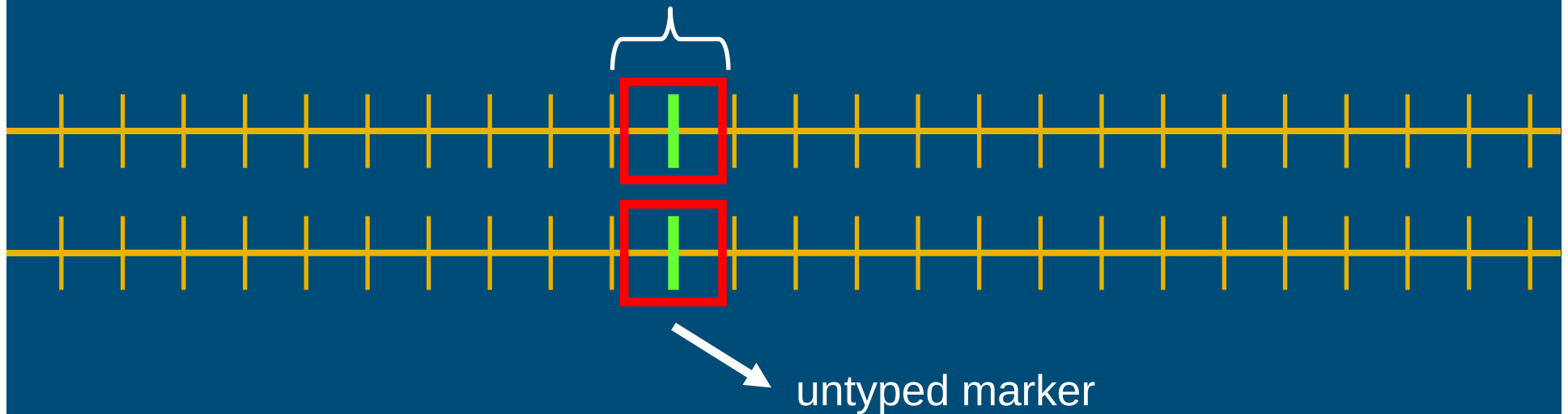


- Heterozygosity of the untyped marker



Genetic diversity estimation

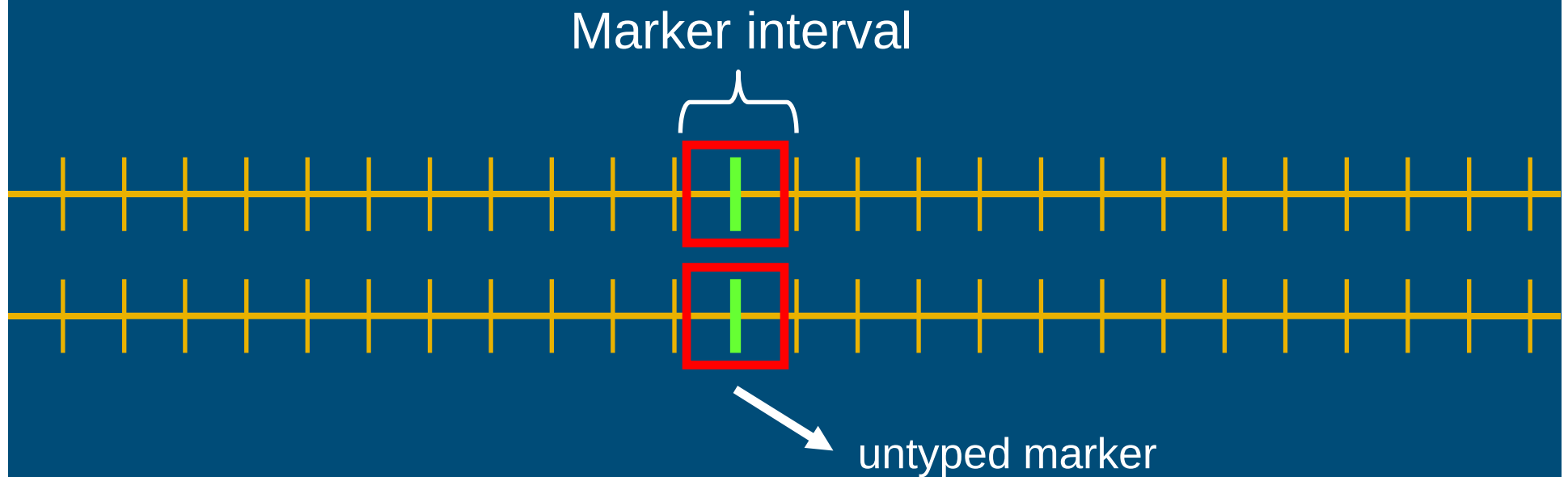
Marker interval



- Predict genetic diversity on untyped region using adjacent markers



Genetic diversity estimation

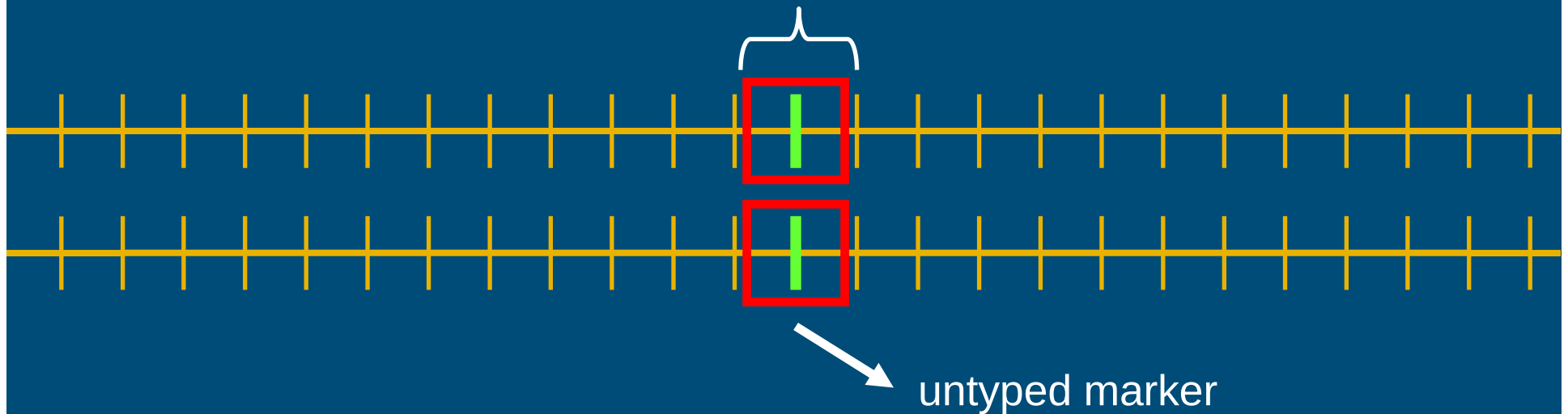


- Predict genetic diversity on untyped region using adjacent markers



Genetic diversity estimation

Marker interval

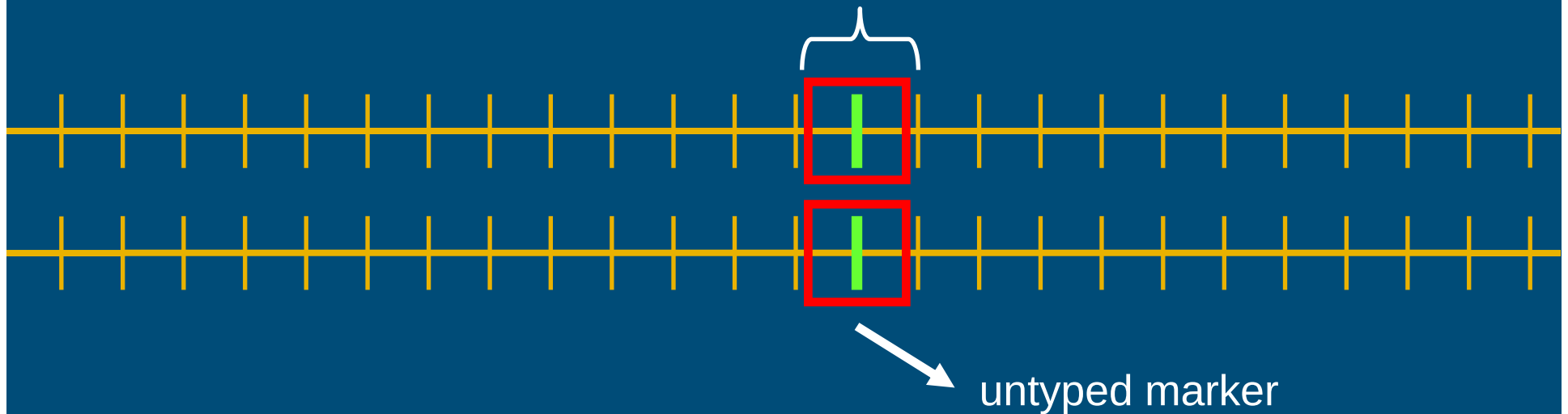


- Predict genetic diversity on untyped region using adjacent markers



Genetic diversity estimation

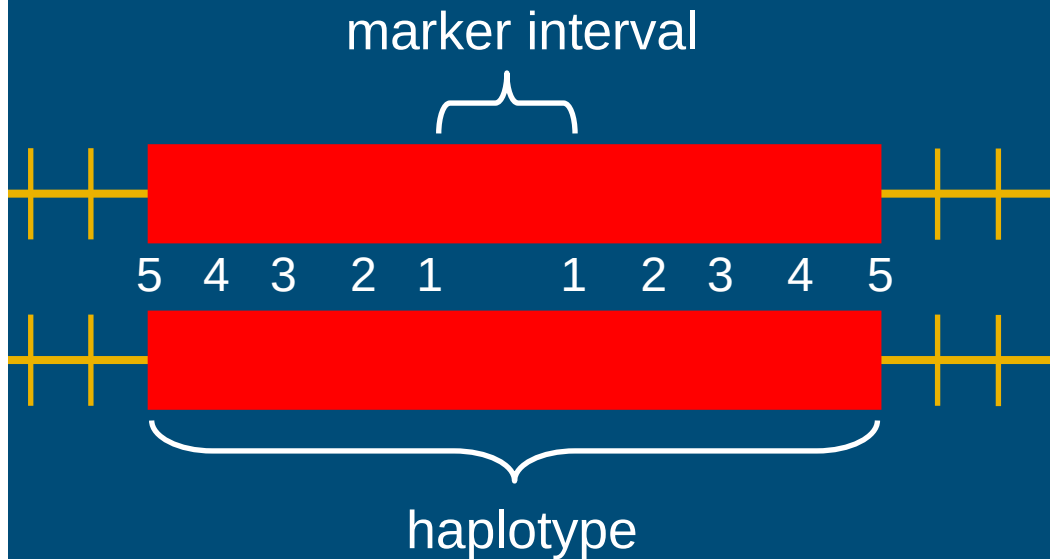
Marker interval



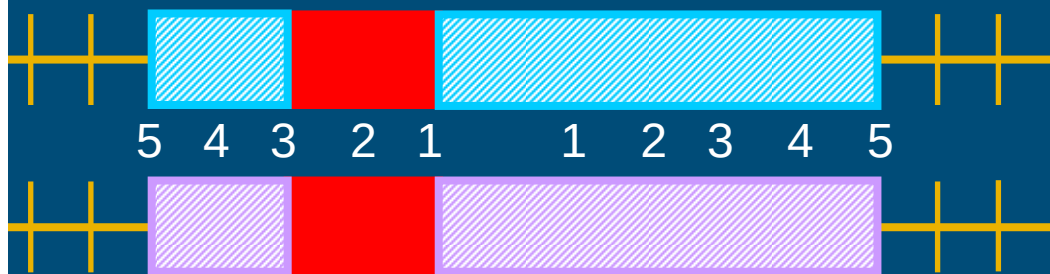
- Predict genetic diversity on untyped region using adjacent markers



IBD-based genetic diversity



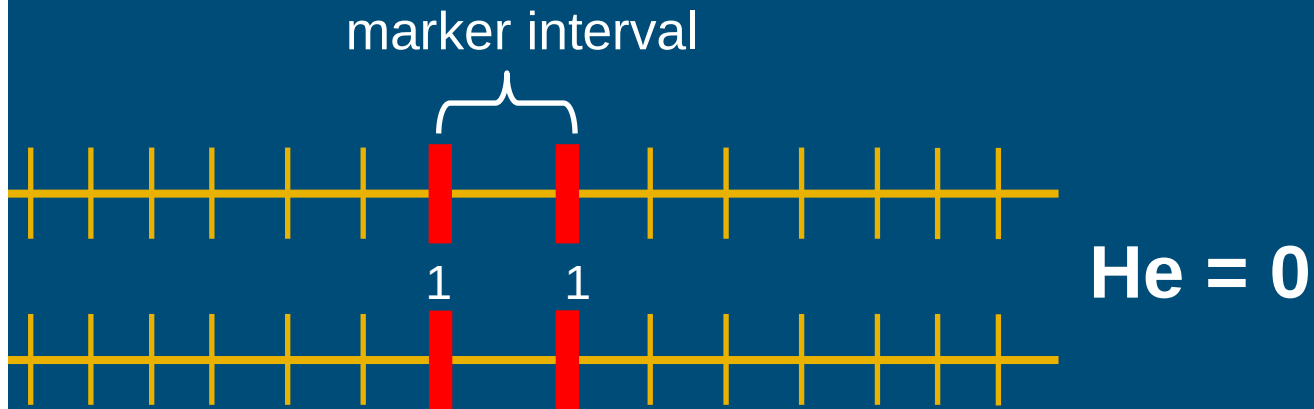
Long stretch AIS:
- recent common ancestor
- high $P(\text{IBD})$



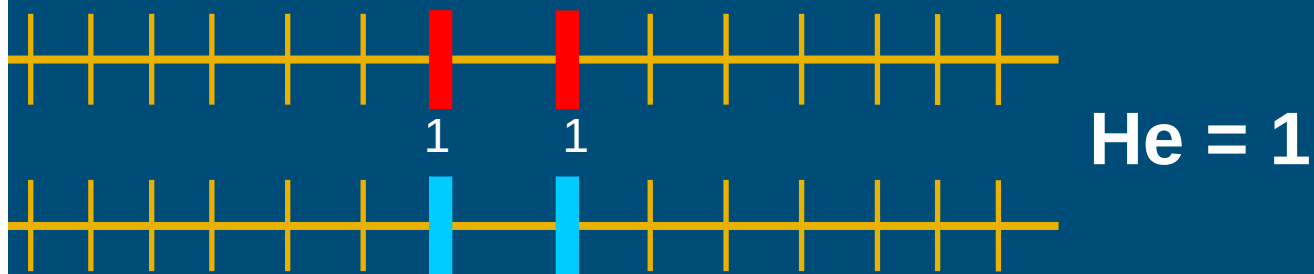
Small stretch AIS:
- lower $P(\text{IBD})$



Heterozygosity



Average $He = (He \text{ left marker} + He \text{ right marker})/2$



Population level



■ IBD

- Diversity-IBD = $1 - \text{average } P(\text{IBD})$
(Details in Meuwissen (1997))

■ Heterozygosity

- $H_e = \# \text{ heterozygotes} / \# \text{ animals}$



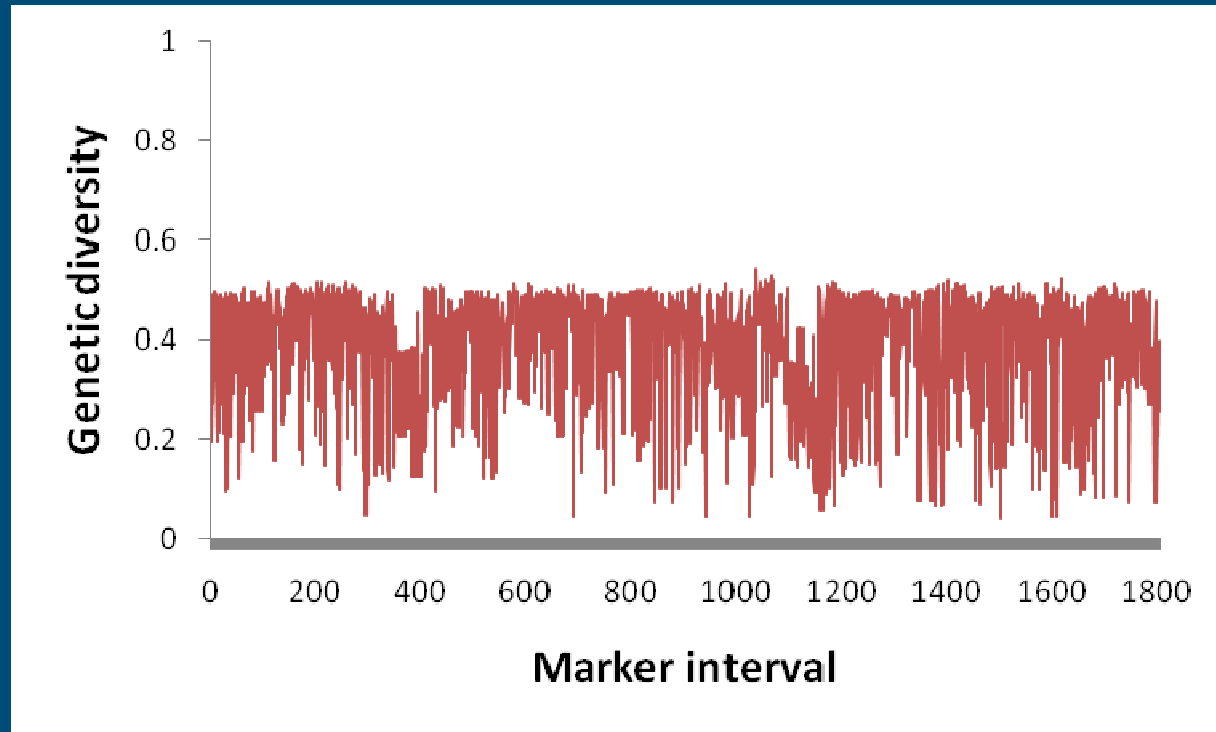
Results



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Genetic diversity over marker intervals



True diversity

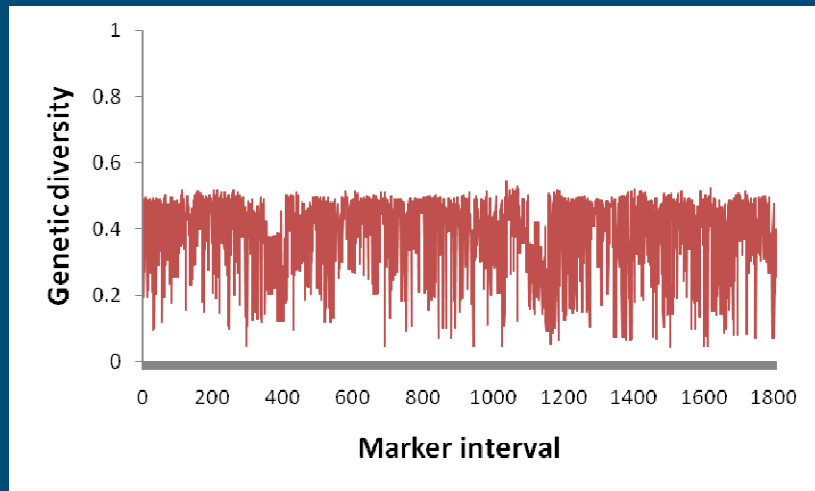
→ Large variation between markers



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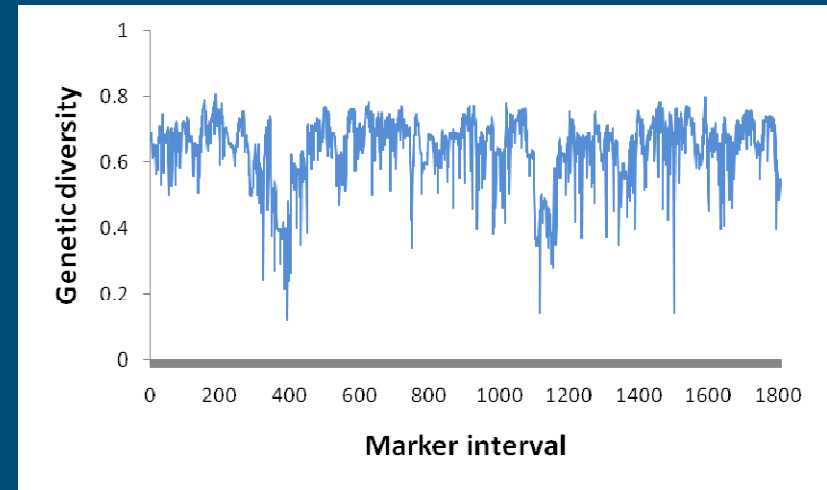
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Genetic diversity over marker intervals

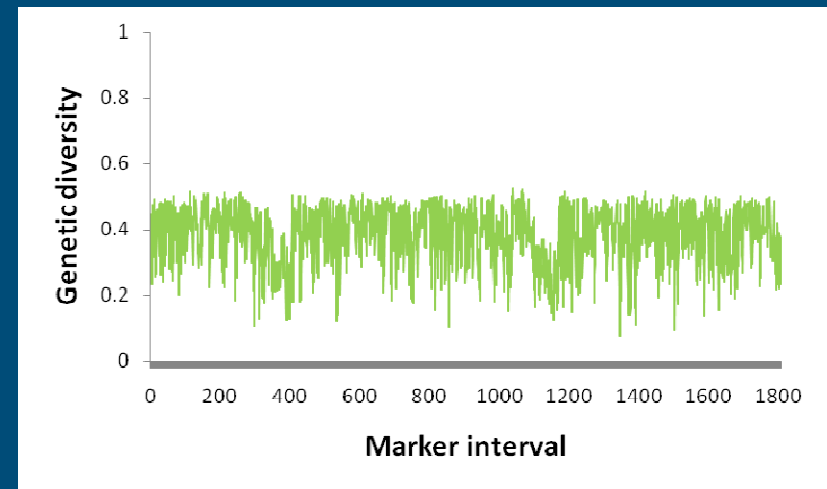


True diversity

IBD



He



→ Difference in level



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Correlations: IBD vs. heterozygosity

Marker intervals

	True	4	10	20	40
IBD	0.27	0.42	0.57	0.72	0.82
He	0.16	0.23	0.38	0.57	0.70



Conclusions

- IBD-method better predictor for genetic diversity on untyped regions of the genome
- More insight into genetic diversity on specific regions of the genome
- Can be taken into account when selecting animals for conservation



Questions?

- IBD-method better predictor for genetic diversity on untyped regions of the genome
- More insight into genetic diversity on specific regions of the genome
- Can be taken into account when selecting animals for conservation

