Pedigree vs. Genomic Inbreeding

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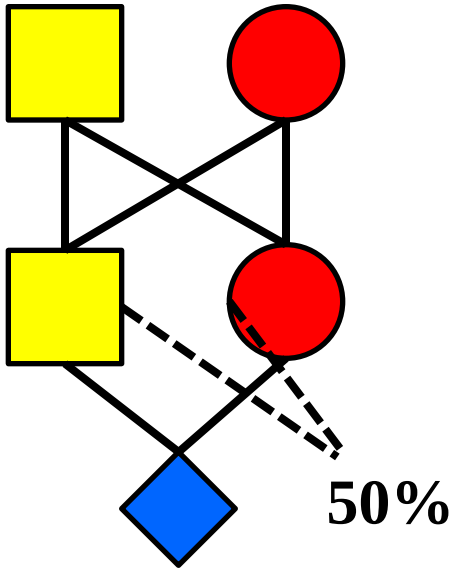
ICBF industry meeting 02/02/2016

Inbreeding

- Inbreeding arise due to mating of closely related animals
- Offspring have a greater likelihood of having two copies of the same variant (homozygous) ***AA or BB***
- Homozygous variant arise due to
  - Identical by state
  - Identical by decent

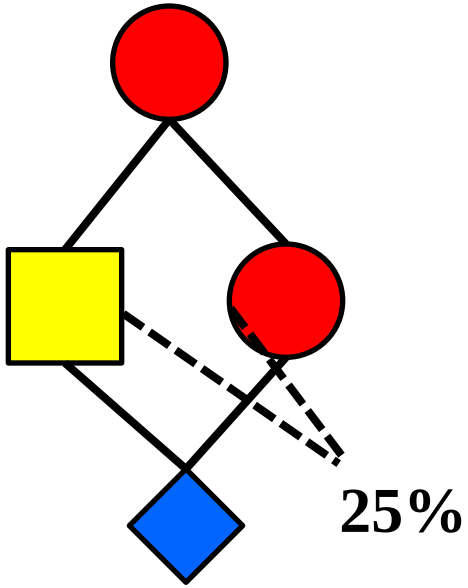
Pedigree inbreeding

Full-sibs



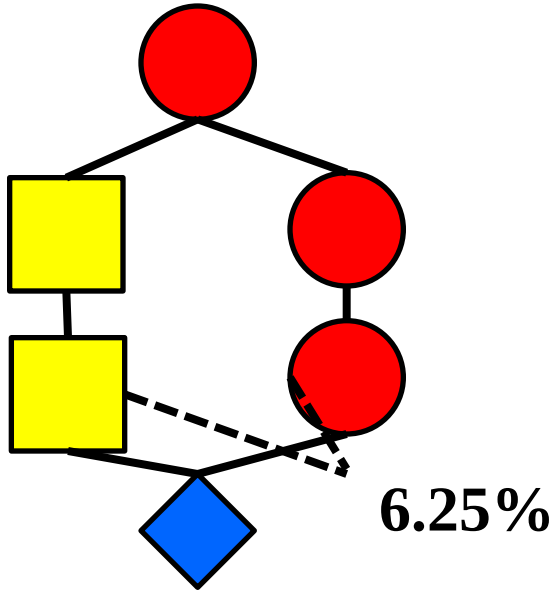
25%

Half-sibs



12.5%

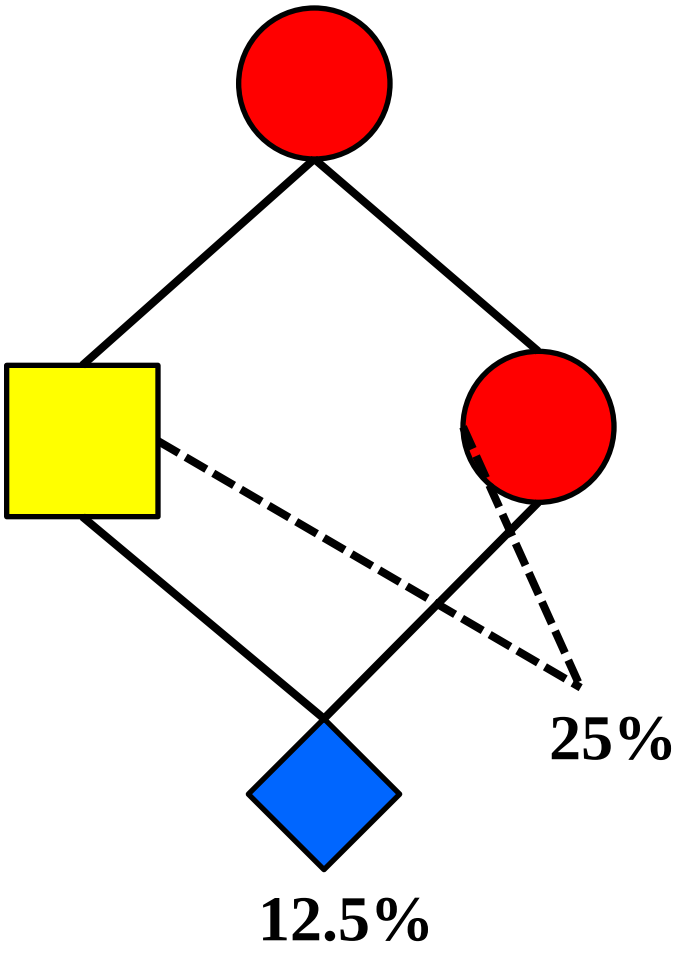
Half 1st cousins

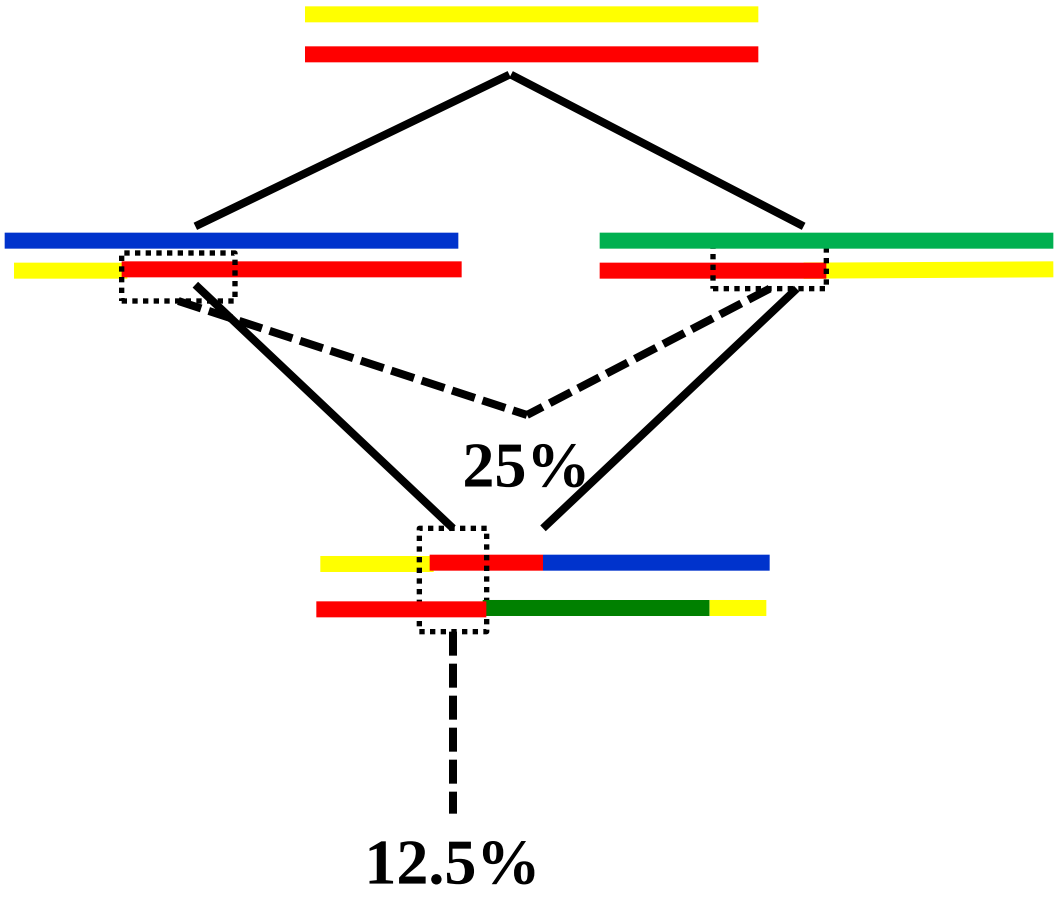


3.125%

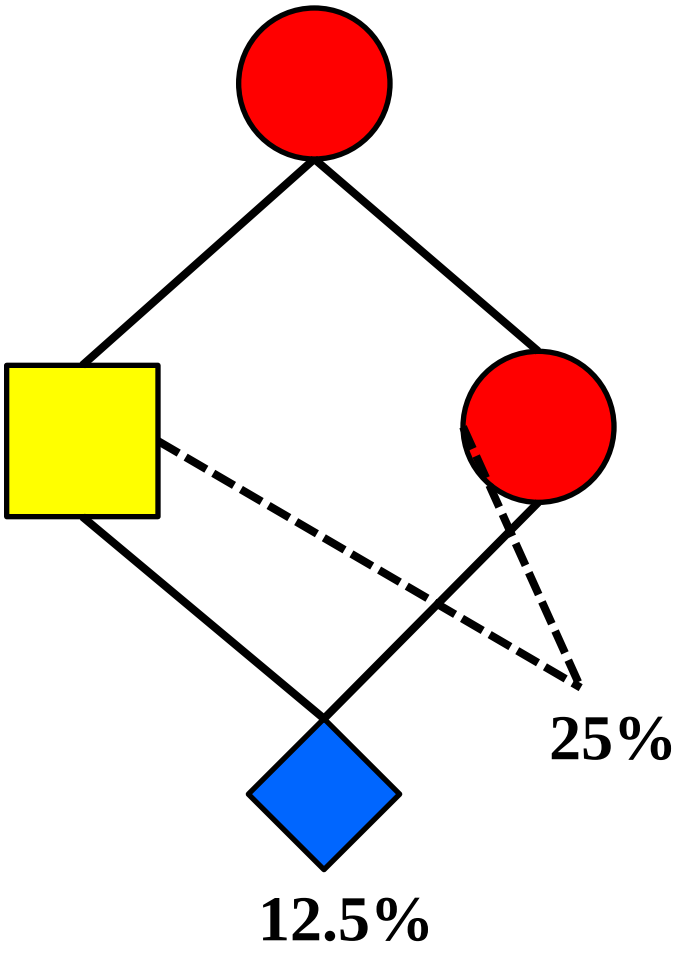
The inbreeding coefficient is $\frac{1}{2}$ the relationship of the parents

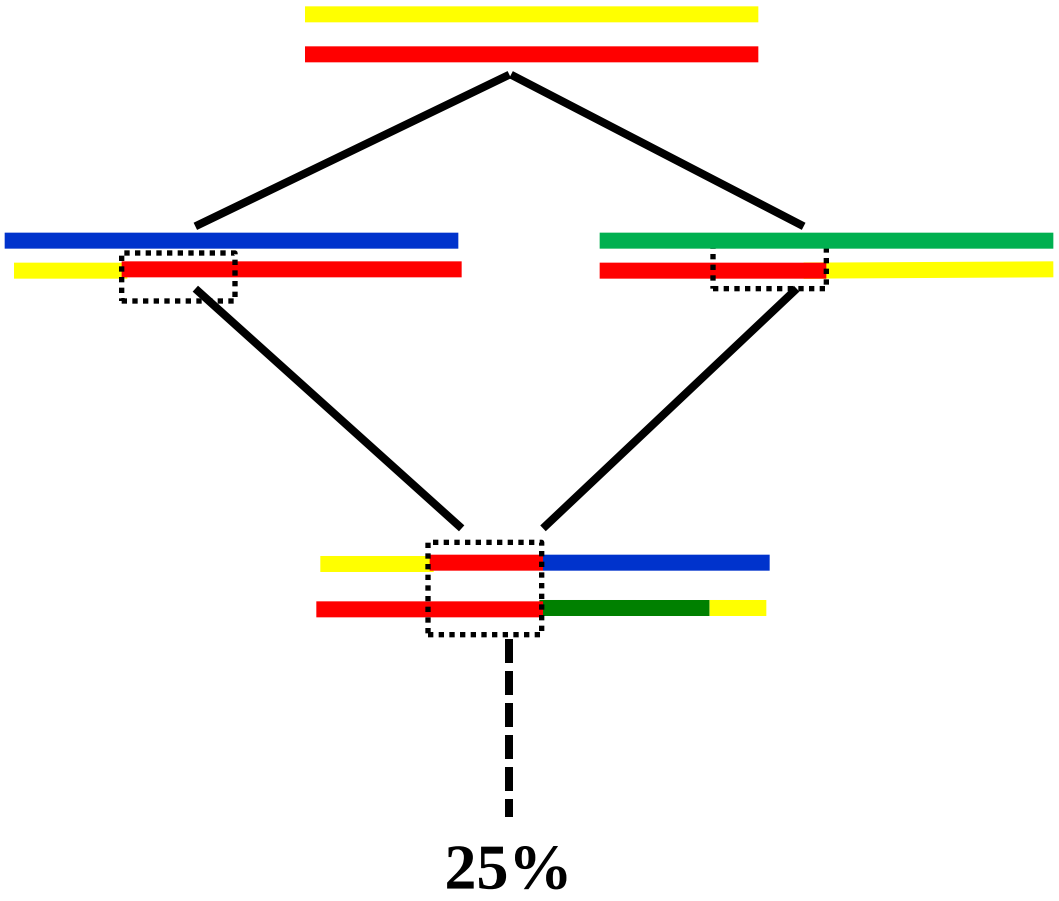
Genomic inbreeding



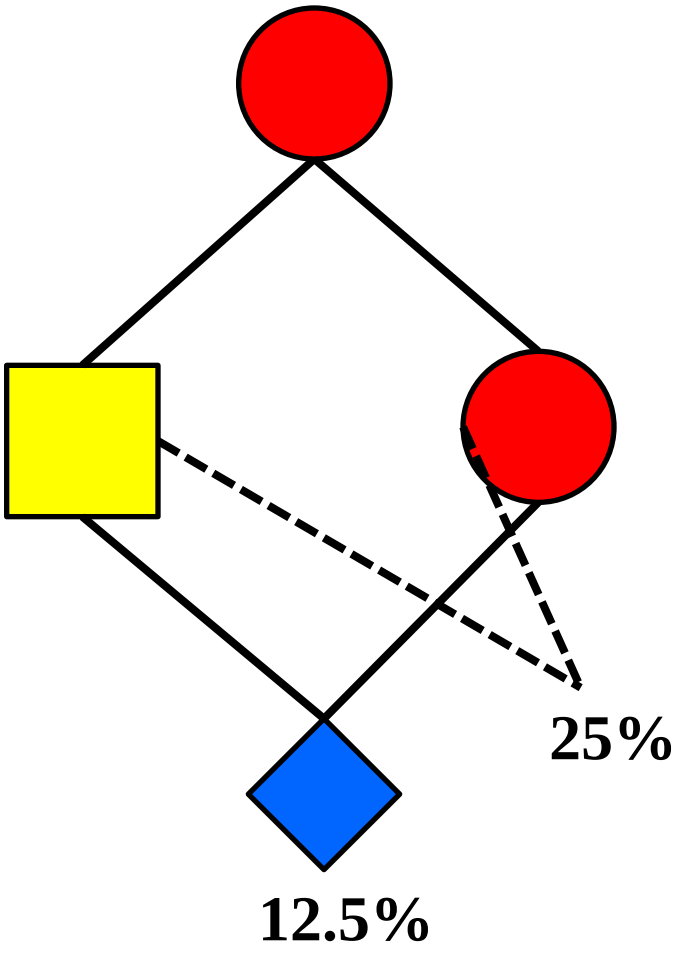


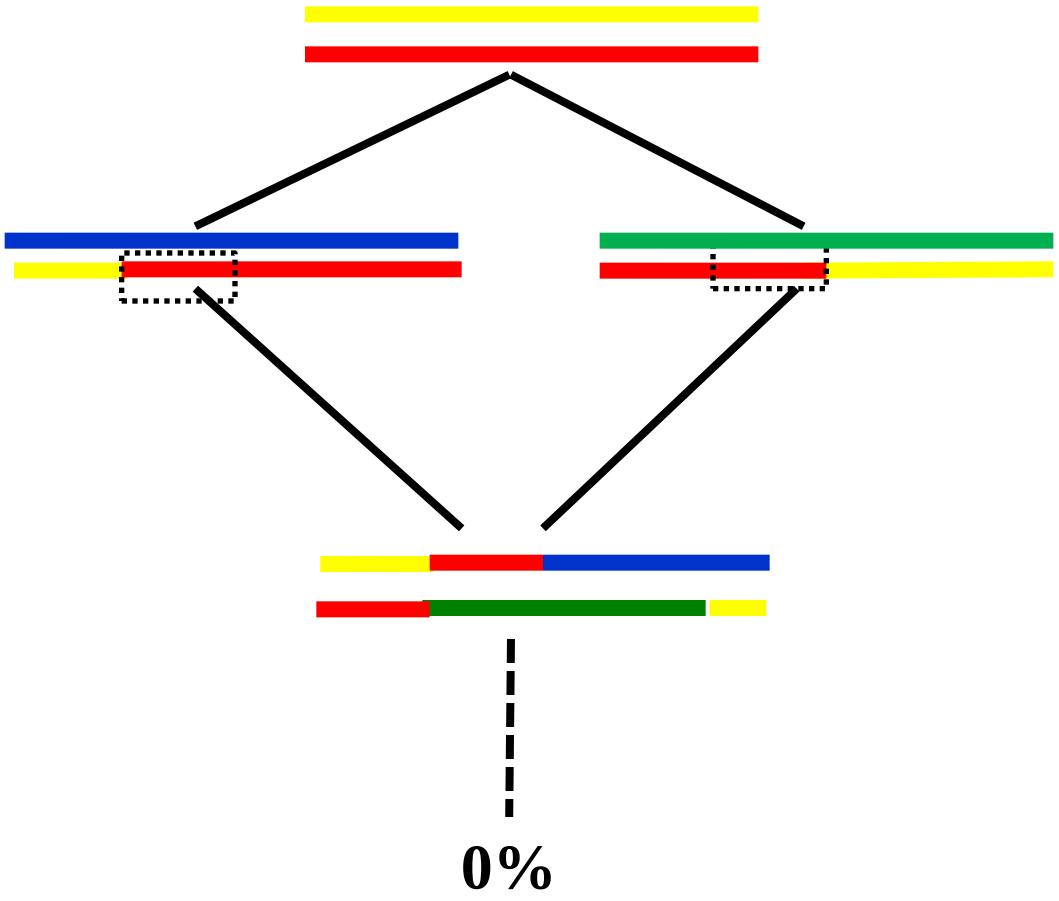
Genomic inbreeding



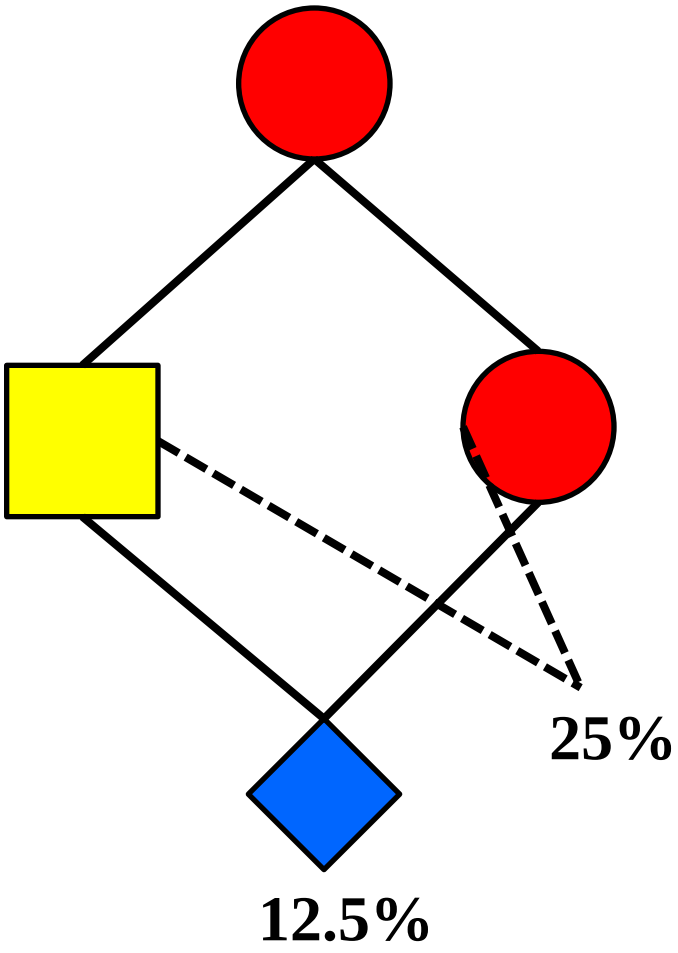


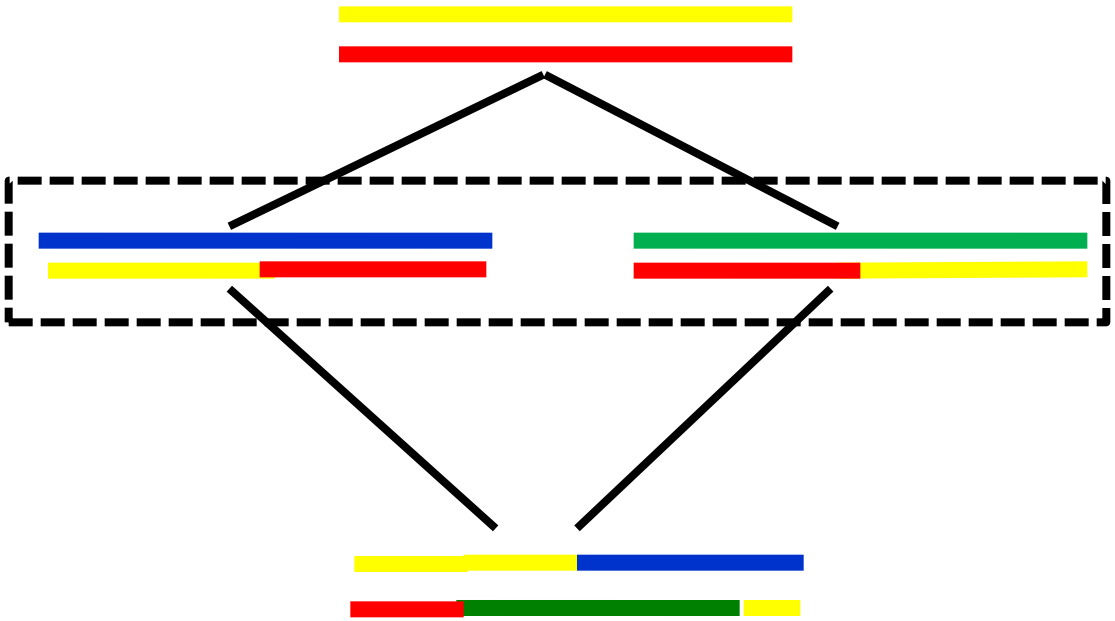
Genomic inbreeding





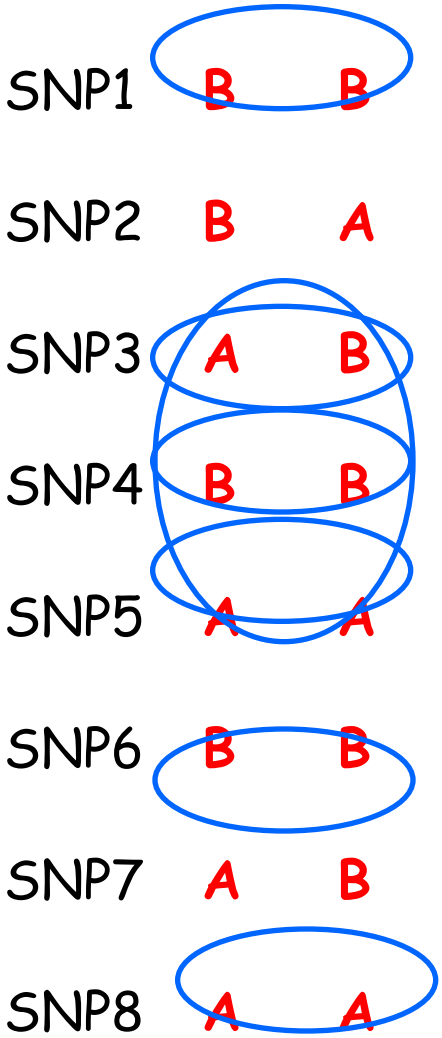
Genomic Relationship





The genomic relationship of these two animal is 0

Measure of genomic inbreeding

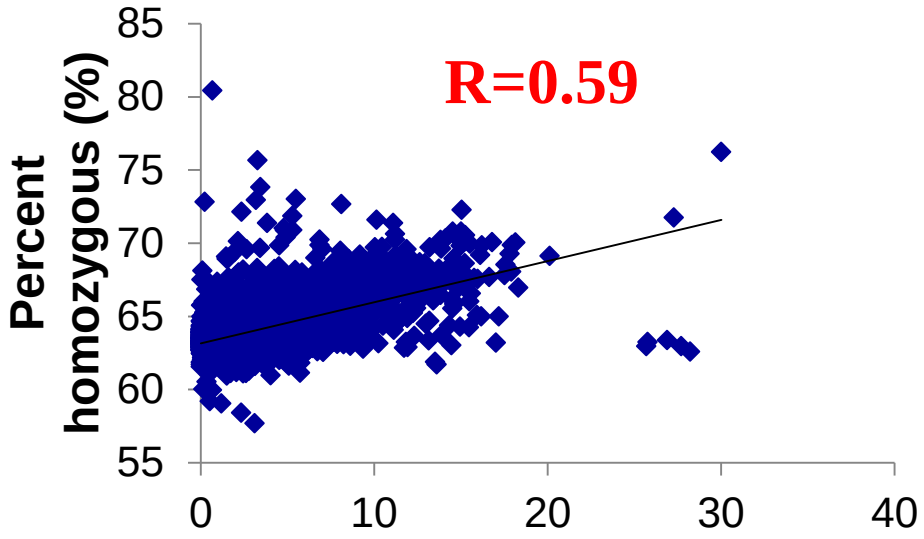


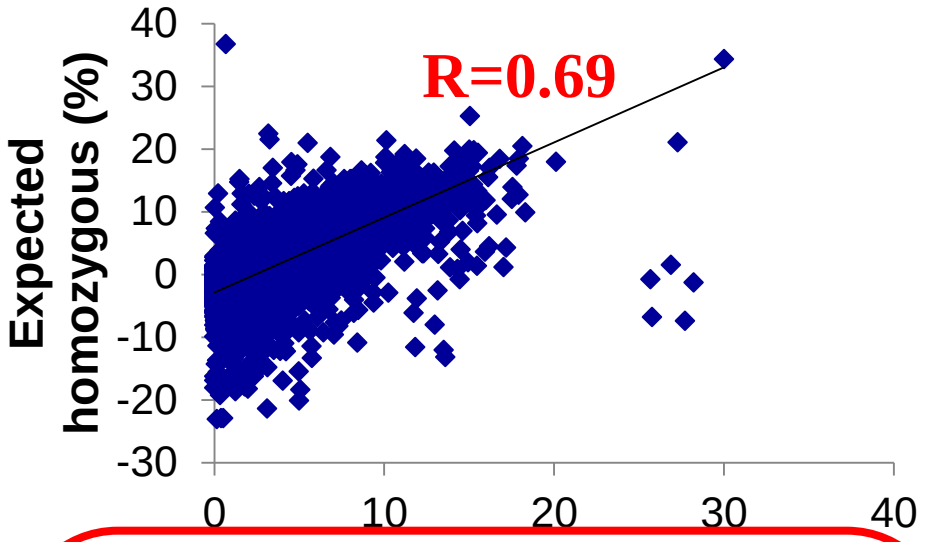
- Percentage homozygous
  - The proportion of the genome that have the same variant
    - 60% homozygous
  - Adjusting for base level of homozygosity in population
    - 10% homozygosity
- Runs of homozygosity
  - The proportion of the genome that have consecutive variant that are the same
    - 30% in ROH

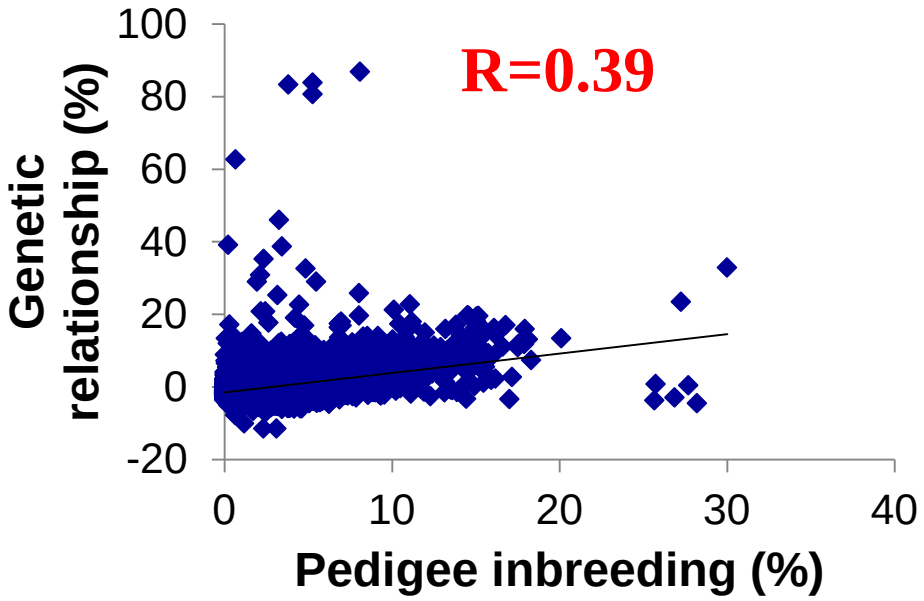
Genetic relationships

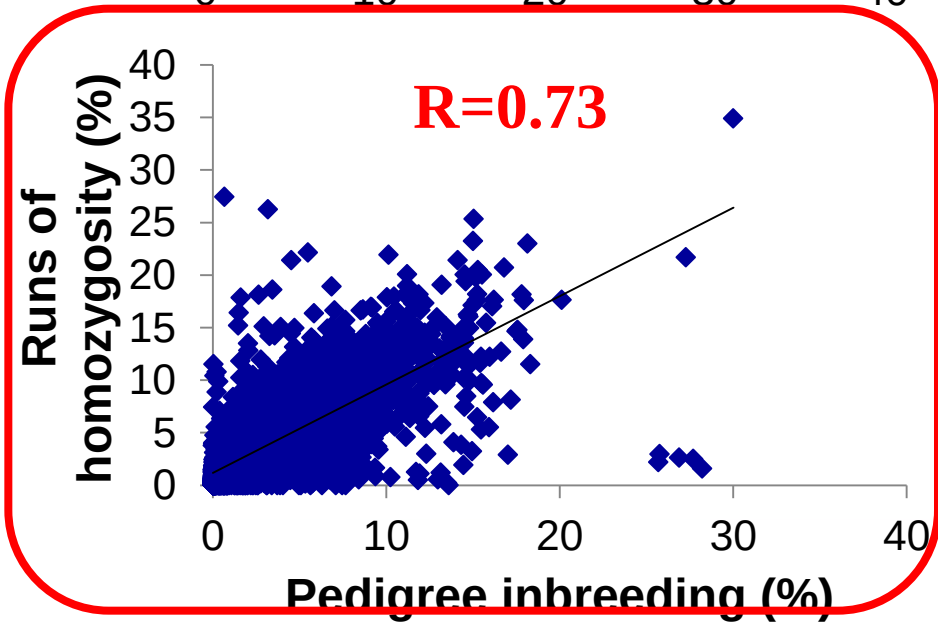
- Using genotypes rather than pedigree information to measure relationship of an animal to itself
  - Homozyosity rather than traditional inbreeding is measured
  - "Inbreeding" can be less than zero
- Adjustments to genomic inbreeding to reflect actually inbreeding

Correlations



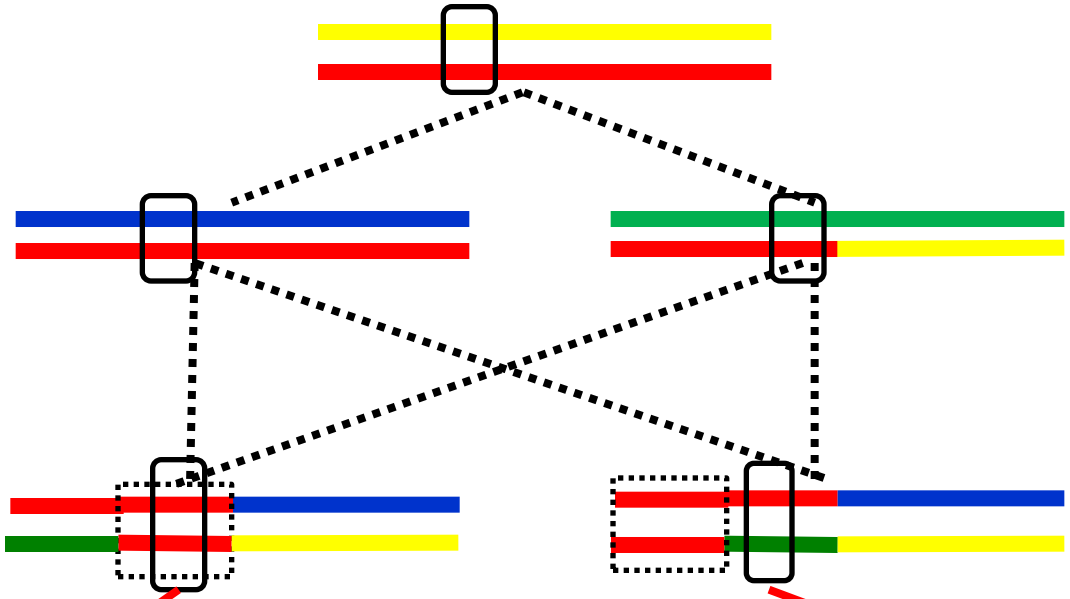






Inbreeding depression

The effect of inbreeding is dependent on what part of the DNA is inherited from the common ancestor



Both animals are 25% inbreed

Affected by inbreeding

Not affected by inbreeding

Inbreeding depression

- Lethal recessive diseases

AB

AB AB

25%	50%	25%
BB	AB	AA
Affected	Carrier	Normal

The lethal recessive variant is in 50% of his offspring

Lethal recessive disease	% in population
CVM	2.5%
DUMPS	0.5%
Brachyspina	1.7%
BLAD	0.7%

Sire advice

- Currently sire advice is based on pedigree information
- Where both sire and dam are genotyped genomic relationships can be used more accurately than pedigree relationships
- With genomics
  - Avoid mating carriers lethal disease
  - Mate animals with complementary genotypes for best production

Conclusion

- Genomic information can be used to
  - More accurate define the relationship between animal
  - Provide a more accurate measure of the inbreeding of an animal

- Not all inbreeding has a negative effect on performance

- Sire advice will be updated to include genomic information