# *Variation in genome sharing among non-inbred pigs*

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# *Introduction*

❑ Prediction of BVs with a genomic relationship matrix depends on how precise the genome sharing of relatives with the same pedigree relationship is measured.

❑ The realized values of genome sharing deviate due to Mendelian sampling and linkage.

❑ Two approaches: IBD and eIBS methods
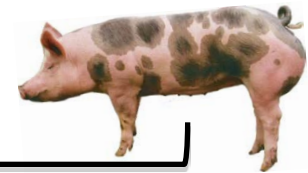
# *Objectives*

1. To estimate the empirical variation in genome sharing of relatives from a pig population, using either identity-by-descent (IBD) or identity-by-state (IBS) based estimators.

2. To compare the *estimated* values of the variances against their *theoretical* values (Hill and Weir, 2011) for different pedigree relationships.

# *Data*

- 411 pigs
- outbred 3-generation Duroc × Pietrain resource population (Edwards et al. 2008. J Anim. Sci., 86: 241-253)

- Genotypes: Porcine SNP60 Beadchip.

- **84254 pairwise relationships**

4 $F_0$ Duroc ♂          15 $F_0$ Pietrain ♀



56 $F_1$ (50♂ x 6♀)

336 $F_2$

60K chip

http://www.nldb.gov.lk/animals/pig%20-%20Duroc.jpg,
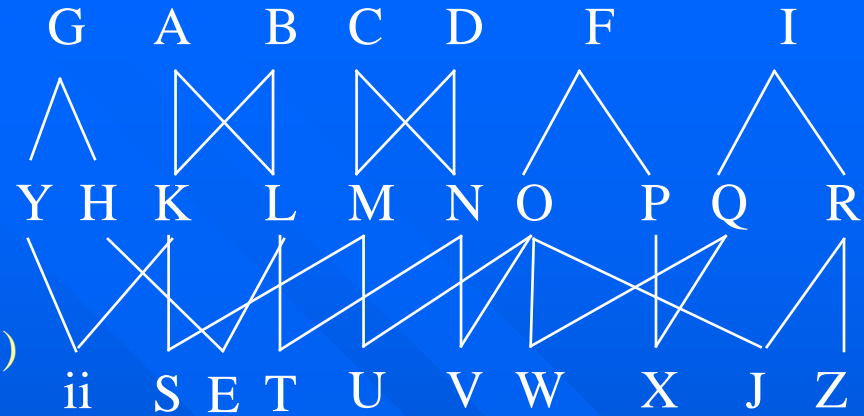http://www.hesbayebrabanconne.be/IMG/jpg/cochon.jpg,
http://www.illumina.com/products/porcinesnp60_dna_analysis_kit.ilmn

# Unilineal relatives

*Lineal descendants:*

**PO**: Parent-offspring  (AK)

**GG**: Grandparent-grandoffspring  (AS)

G   A   B   C   D   F   I

Y   H   K   L   M   N   O   P   Q   R

ii   S   E   T   U   V   W   X   J   Z

*Half sibs and their descendants:*

**HS**: Half sibs  (OP)

**HUN**: Half uncle-nephew (QZ)

**HFC**: Half cousins  (XZ)

*Descendants of full sibs:*

**UN**: Uncle-nephew (KT)

**FC**: First Cousins  (SV)

# Bilineal relatives

**FS**: Full sibs (KL)

DHFC: Double half first cousins (XJ)

3FC: Three-way cousins  (iiE)

DFC: Double first cousins (ST)

(WX) EHS: Half sibs, mothers(fathers)HS

(UV) TQS: Half sibs, mothers(fathers) FS

# *Genomic relationship estimates*

**IBD-based**

$$\hat{G}_{xy\,(\text{IBD})} = \frac{1}{L} \sum_{k=1}^{K} l_k \left[ \tfrac{1}{2} P\left(\text{IBD}_k = 1 \,\middle|\, \mathcal{M}\right) + P\left(\text{IBD}_k = 2 \,\middle|\, \mathcal{M}\right) \right]$$

length of each segment
delimited by 2 SNP

posterior probabilities of IBD sharing
software PEDIBD (Li et al., 2010)

- HMM approach
- accounts for pedigree
  and LD between SNP

**IBS-based**

$$\hat{G}_{xy\,(\text{IBS})} = \left( \frac{Z\,Z'}{\sum\limits_{k=1}^{K} 2p_k q_k} \right)_{xy}$$

- Theoretical variance:  formulae from Hill & Weir (2011) for non inbred individuals based on genetic maps.

- Porcine genetic maps (Tortereau et al. 2012. BMC Genomics 13:586).
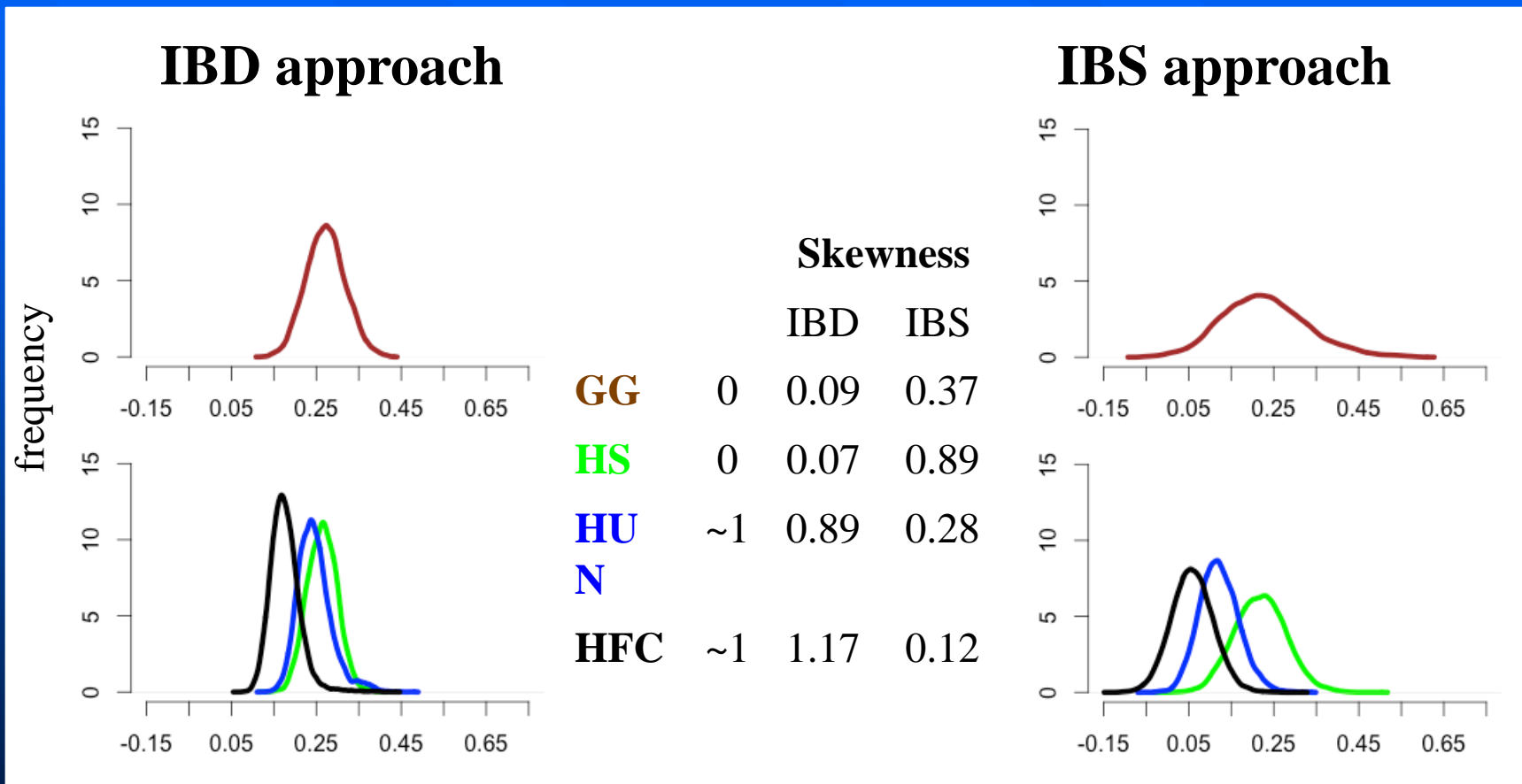
# *Results*

# Correlations among methods

## *Probability > | r | under $H_0$ : $\rho = 0$*

|  | gIBD | gIBS |
|---|---|---|
| **Expected relationship** $(a_{ij})$ | **0.875** <br> $P < 0.0001$ | **0.797** <br> $P < 0.0001$ |
| **gIBD** | **—** | **0.721** <br> $P < 0.0001$ |

# Standard Deviations of actual relationships

| | Relationship | $R$ | $N$ | Theoretical | IBD | IBS |
|---|---|---|---|---|---|---|
| Lineal | PO | 0.500 | 784 | 0.0000 | 0.0000 | 0.0573 |
| | GG | 0.250 | 1344 | 0.0437 | 0.0456 | 0.0993 |
| | HS | 0.250 | 7061 | 0.0352 | 0.0353 | 0.0609 |
| | HFC | 0.062 | 22944 | 0.0235 | 0.0351 | 0.0495 |
| Bilineal | FS | 0.500 | 639 | 0.0498 | 0.0577 | 0.0826 |
| | TQS | 0.375 | 816 | 0.0449 | 0.0480 | 0.0711 |
| | DFC | 0.250 | 544 | 0.0395 | 0.0478 | 0.0581 |
| | DHFC | 0.125 | 5408 | 0.0332 | 0.0450 | 0.0504 |

# *Empirical distribution for estimated actual relationships*



**IBD approach**

**IBS approach**

| Skewness | | |
|---|---|---|
| | IBD | IBS |
| **GG** | 0 | 0.09 | 0.37 |
| **HS** | 0 | 0.07 | 0.89 |
| **HUN** | ~1 | 0.89 | 0.28 |
| **HFC** | ~1 | 1.17 | 0.12 |

As expected from theory, for IBD-based estimates the distributions are ✛ skewed as **R** becomes smaller.

# *Empirical distribution for estimated actual relationships*
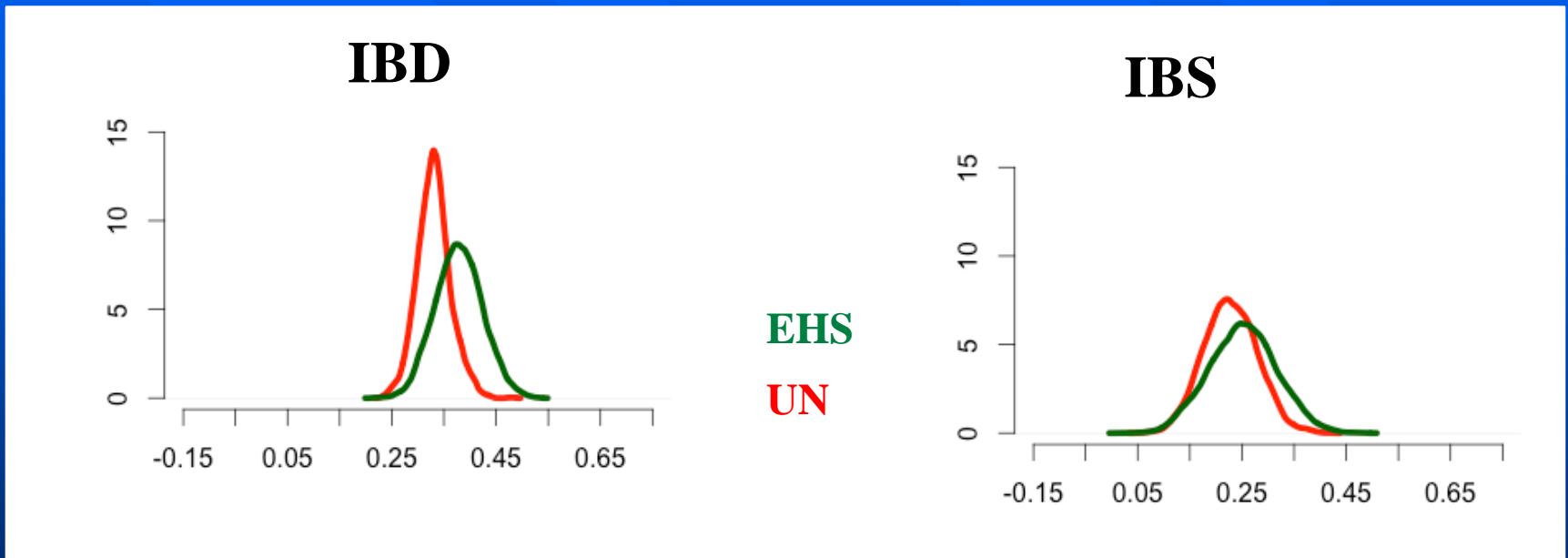


**The overlap in the amount of sharing of quite different pedigree relationship classes was <u>higher for IBS</u> estimates.**

# *Correlations with true relationships Simulation results*

| | gIBD | gIBS | gIBS "Tunning" |
|---|---|---|---|
| **True relationship** | **0.79** 0.0036 | **0.65** 0.0049 | **0.67** 0.0046 |

# *Final comments*

❑ The SD(gIBD) was always smaller than the SD(gIBS), being on average, 18.5% and 70.7% higher respectively, when compared to the theoretical SD.

❑Results suggest that the IBD-based method can detect **more accurately the degree of genome sharing between relatives** and could be used to compute realized relationships for predicting BVs with genomic information.

❑ **gIBD** was more strongly correlated to *true relationship* than **gIBS** with simulated data.
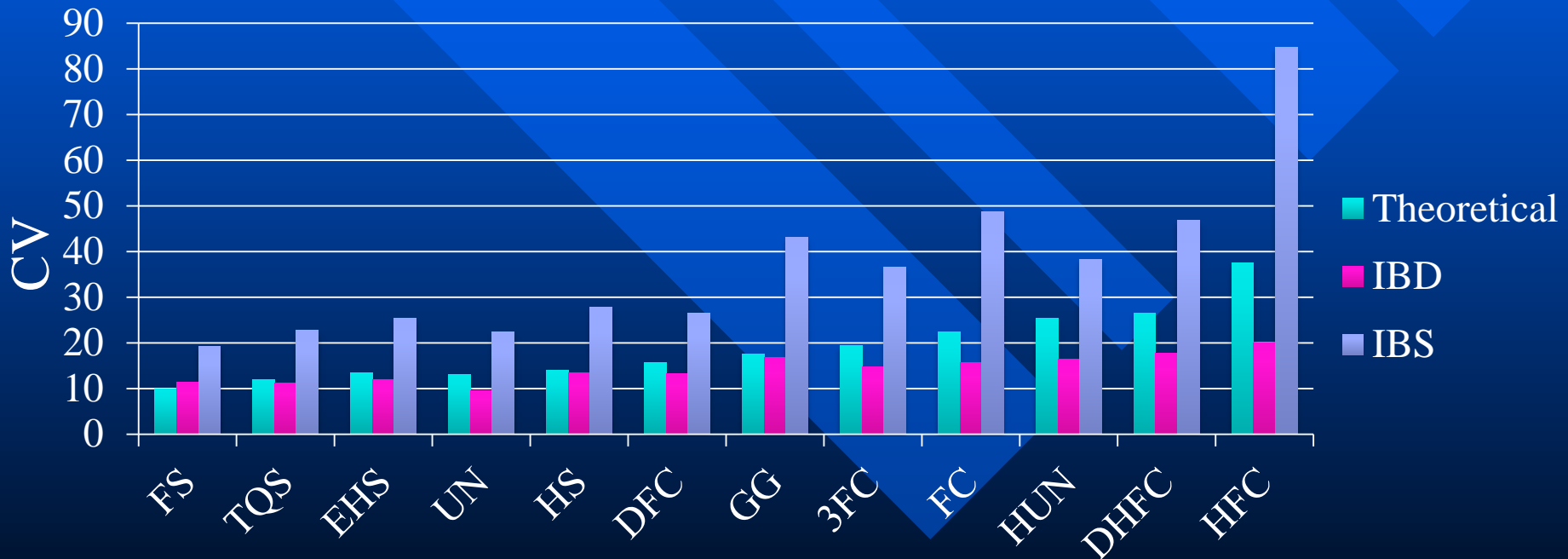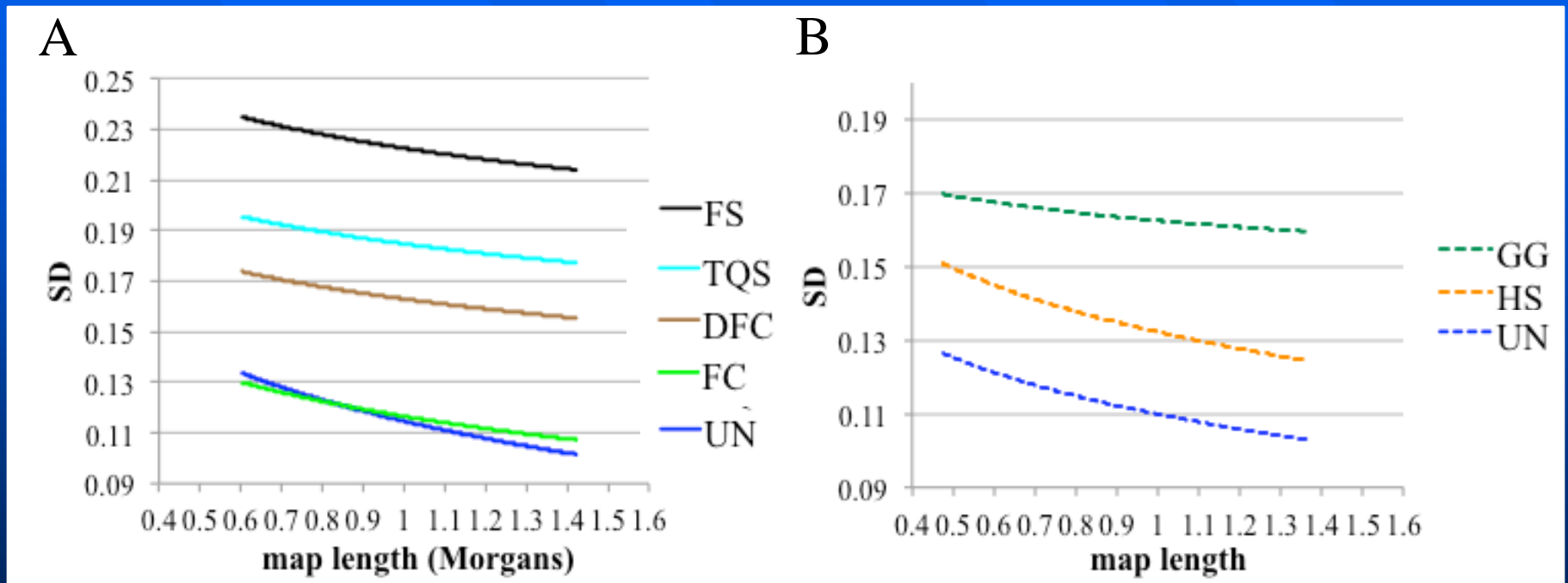
*Thank you!*

# *Coefficient of variation*

As expected from theory, as animals become less related, the SD becomes smaller whereas the CV becomes larger.

**CV(IBD) is always closer to the theoretical value than CV(IBS).**

# *IBD-based estimated SD and map length*

IBD-based estimated SD behaves as its theoretical value: it decreases with increased chromosome map length (Figure A).



For relationships with the same mean, the estimated SD declines less rapidly with map length for lineal descendants than for those involving half sibs, showing the fastest decline for descendants of full sibs (B)