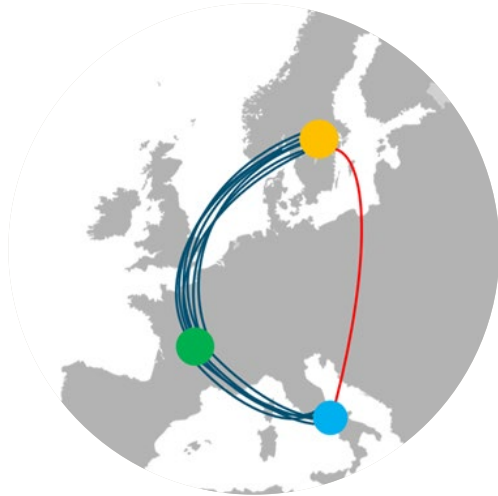


Using genomic data to estimate genetic correlations between countries with different levels of connectedness

Bonifazi R, GM Neufeld, T Pook, J Vandenplas, MPL Calus

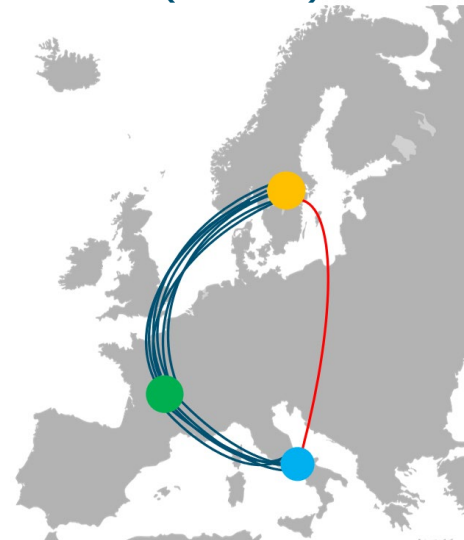


International evaluations

- Compare animals' genetic values **across countries**
- **Differences:** trait definition, scale and genetic bases, GxE
- Multi-trait models: **countries as different correlated traits**
- r_G between countries < 1
- Impact on international (G)EBVs → **Crucial** for international evaluations

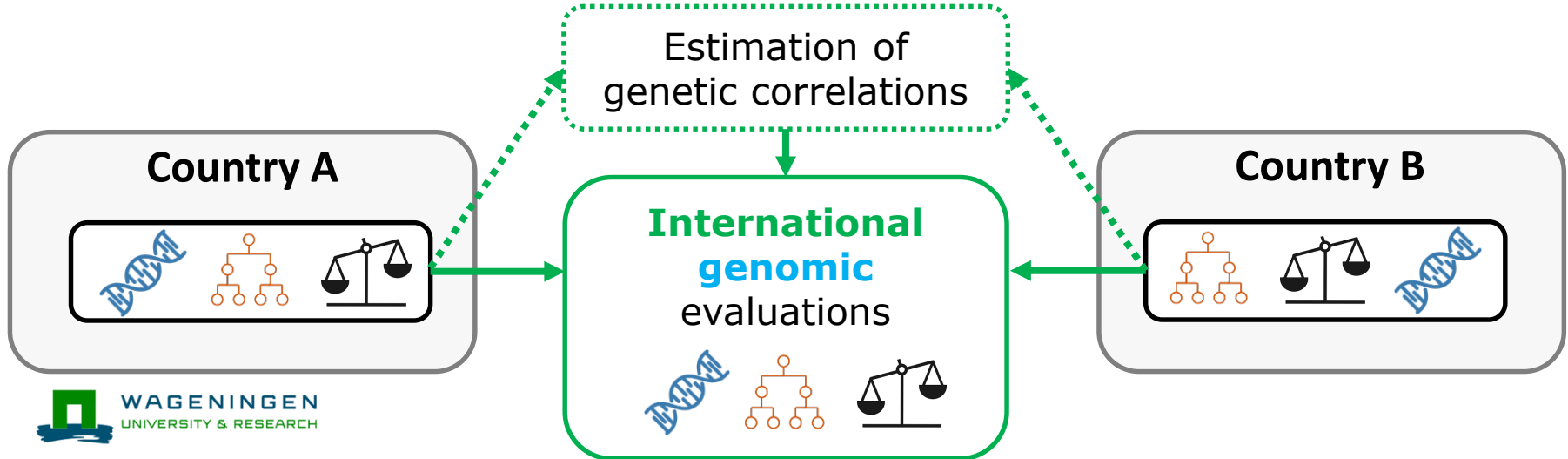
Estimation of r_G between countries

- Requires **genetic connections** between countries
- “Common Bulls” (CB)
- Beef cattle, small (dairy) populations → low use AI/low #CB → low connections
- **Maternally influenced traits** → “Common Maternal Grand-Sires” (CMGS)
- Estimation methods: **pedigree-based**
- **Low connectedness** → **issues**:
 - Long computational times, large SE
 - Impossible to estimate r_G



Genomic data in international evaluations

- Interbeef **single-step** evaluations (Bonifazi et al. 2022, GSE)
- **Genomic data** to estimate r_G between countries
- Disconnected populations (according to **pedigree**) → **Connected via genomic information** (e.g. Wientjes et al. 2015, 2018, GSE)



Aim of the study

Investigate if **genomic data** help
to **estimate r_G between countries**
more accurately than **pedigree**
at **different level of connectedness**

Simulated data and (genetic) parameters

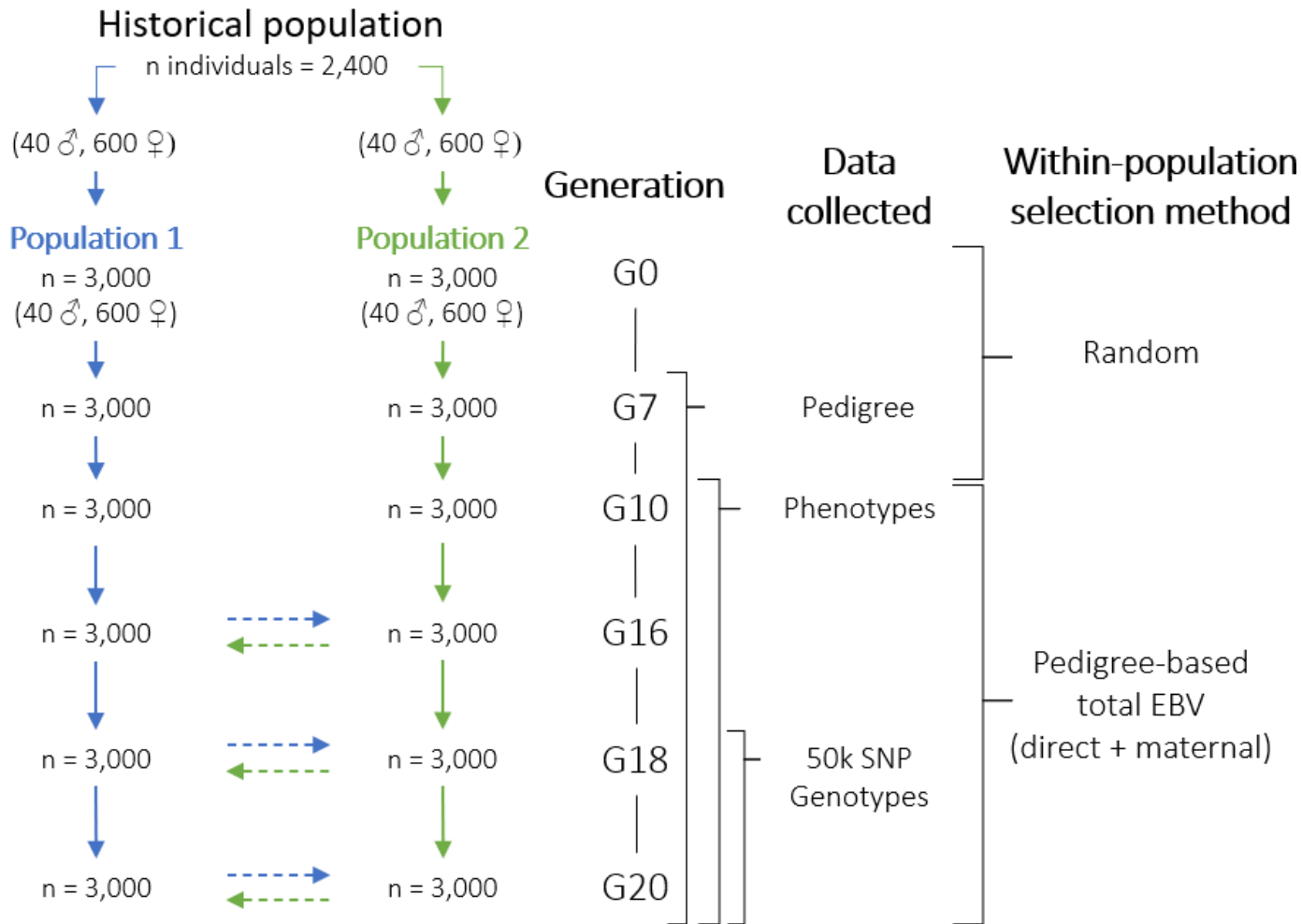
- Two **beef cattle** populations of **same breed**
- Maternally affected trait:** weaning weight
- Genetic parameters** (Bonifazi et al. 2020, GSE)



	h^2 & r_G	POP ₁		POP ₂	
		Dir	Mat	Dir	Mat
POP ₁	Dir	0.30			
	Mat	-0.2	0.15		
POP ₂	Dir	0.80	0	0.30	
	Mat	0	0.70	-0.2	0.15

Layout

- Mimic current beef situation
(Bonifazi *et al.* 2023, GSE)
- Different sires exchange levels

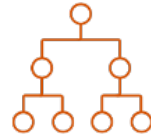


Scenarios: connectedness between POPs

Scenario	n. CB	n. off. from CB	GS	Mean n. CMGS	Mean n. grand-off. from CMGS	Mean GS _{CMGS}
Disconnected	0	0	0	0	0	0
Low	10	1,500	0.02	8	2,322	0.04
Medium	20	3,000	0.05	16	4,544	0.07
High	80	12,000	0.18	63	15,364	0.23

- Names based on GS thresholds of Bonifazi et al. 2020, GSE
- 10 replicas

Estimation of r_G : sources of information



A-matrix	10 gen.	11 gen.	-
H-matrix	10 gen.	11 gen.	3 gen.
G-matrix ¹	3 gen.	4 gen.	3 gen.

- Pedigree 14 generations → 11 generations (space limitations)
- H as Legarra et. al. 2009, JDS (scaling G inbreeding to A_{22})
- G as VanRaden 2008, JDS, method 1
- ¹ Maternal effects → need prev. gen. relationships (effectively computed as H-mat)

Software



<https://github.com/tpook92/MoBPS>

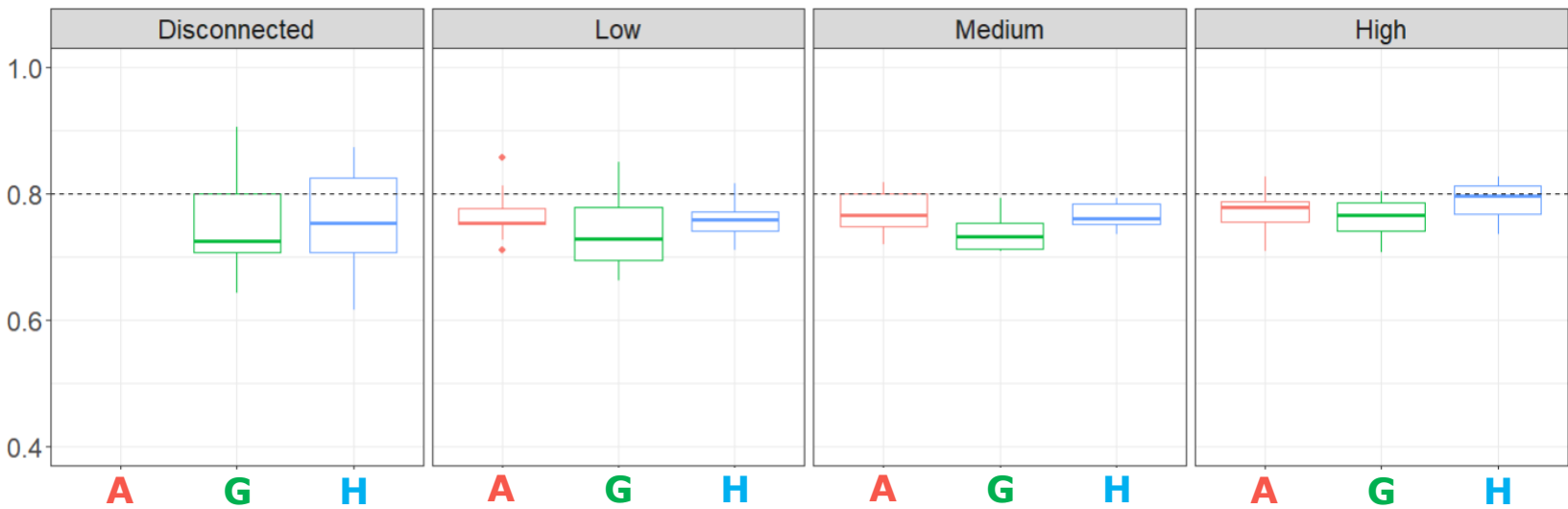
- Simulation: *MoBPS* (*miraculix* & *RandomFieldUtils*)
- GRM: *calc_grm* (Calus and Vandenplas, 2013, WUR)
- r_G estimation: *mtg2* (CORE GREML: maternal effects) ¹
- **Mimic current Interbeef**
- **Bivariate model**: countries as correlated traits (no residual corr.)
- **Raw data**
- Starting values: within-country (co)variances, 0 across-country

Results

- Genetic correlations
- Standard errors
- Computational resources

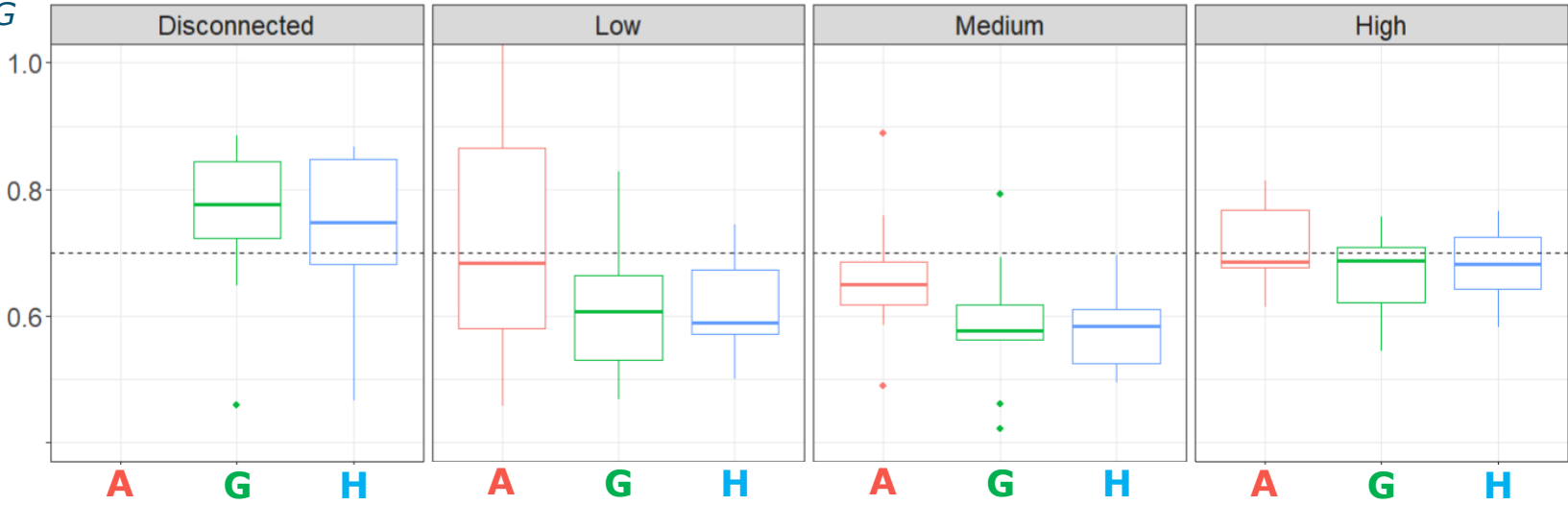
Direct r_G

Simulated = 0.8

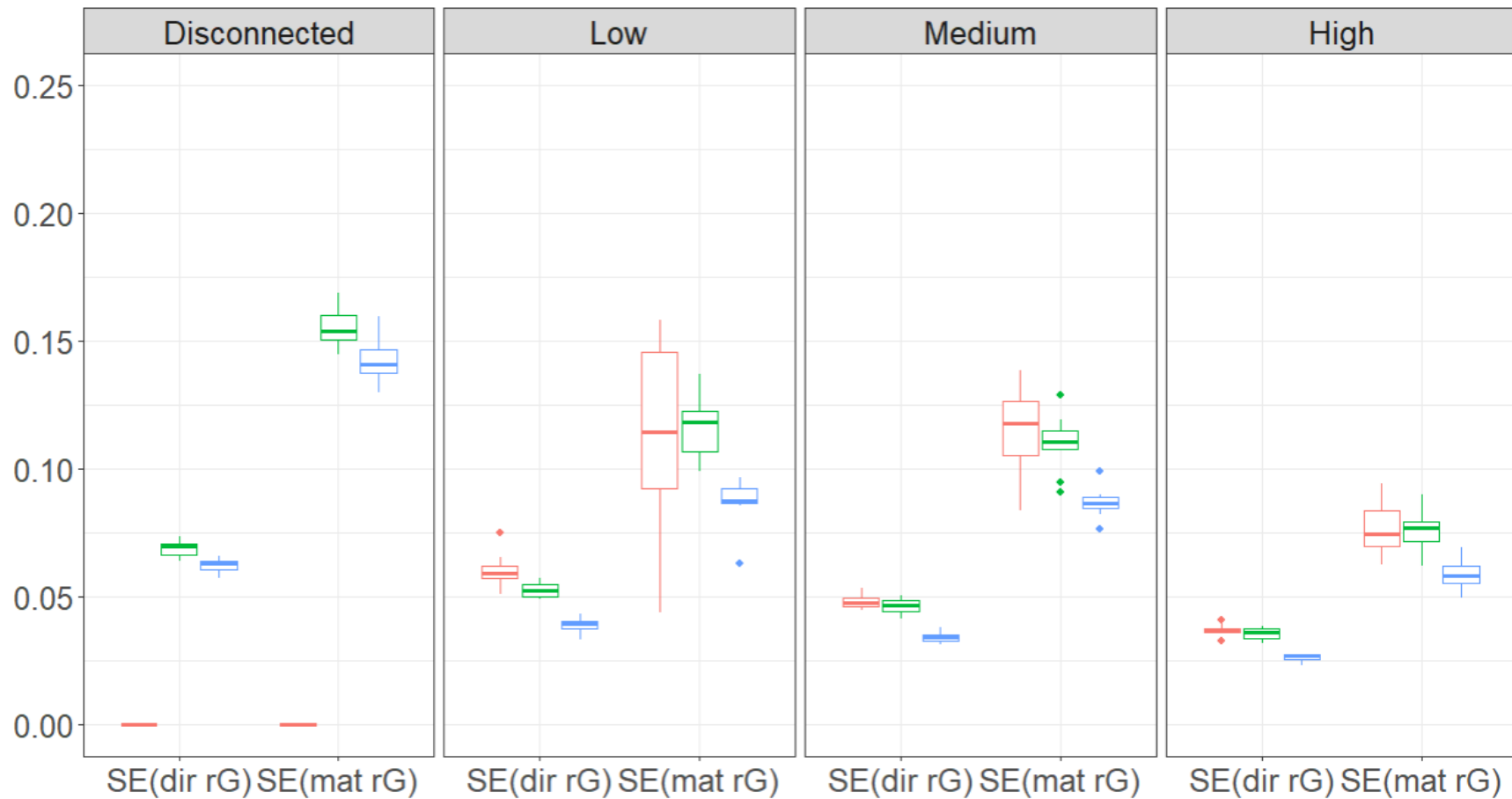


Maternal r_G

Simulated = 0.7



Standard Errors ▢ A ▢ G ▢ H



Computational requirements

	A	G	H
Animals in matrix	66,000	24,000	66,000
Elapsed time (hours)	3.1	7.3	2.9
RAM peak usage (Gbytes)	106	13	102

Averages across scenarios and replicas

Conclusions

- **Genomic data more accurate estimates of r_G between countries** and **smaller SE** for:
 - **disconnected** and **low connected**: beef cattle, small (dairy) populations (e.g. AYR, GUE, JER)
 - **maternal r_G**
- Medium/high connected: no benefits (e.g. HOL)
- **G** with 3 gen. (pheno & geno) similar to **H**, but less comput. resources
- Real data: unbalanced, <5 off/dam, large datasets (connected sub-set → include genomic info in connectedness measures)

Acknowledgements

Martin Schlather, Universität Mannheim



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Interbeef, Interbull, ICAR, national organisations



Take-home messages

- **Genomic data more accurate estimates** of r_G **between countries** and **smaller SE** for:
 - **disconnected** and **low connected**: beef cattle, small (dairy) populations (e.g. AYR, GUE, JER)
 - **maternal r_G**
- Useful for beef cattle, small (dairy) populations

Thanks for your attention