



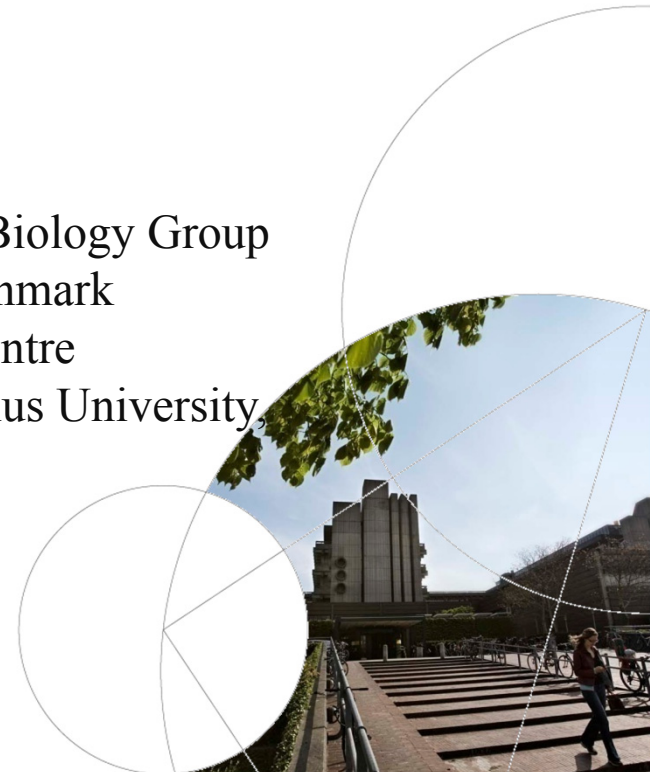
Prediction of genomic breeding values for feed efficiency and related traits in pigs

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Overview

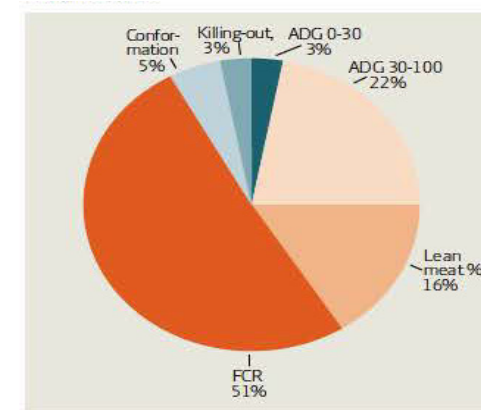
- Introduction
 - Feed efficiency and Residual feed intake
 - Objectives of this study

- Methods
 - Genomic prediction using GBLUP and Bayesian approaches
 - Partitioning of genomic variance based on genomic annotation

- Results, Conclusion and Future perspectives

Feed efficiency and Residual feed intake (RFI)

- Feed efficiency is a complex trait with large economic impact
- Measured by food conversion ratio, **RFI** or residual and gain
- $\text{RFI} = \text{observed feed intake (DFI)} - \text{expected DFI}$
- The expected DFI predicted from production (Daily gain) and maintenance requirements (Backfat/middle metabolic weight)
- $\text{RFI} = \text{net feed efficiency}$



Benefit of selection for **low RFI pigs**



reduce feed
consumption
or feed cost



no change in Daily Gain &
Back fat



less impact on
environment



improve meat quality

Residual feed intake (RFI) in Danish Duroc pigs

- Moderately heritable ($h^2 = 0.38$)
- Favorable genetic correlations with (DFI) (0.88) and FCR (0.87)
- 3 QTLs for RFI explain very little genomic variance → No Marker assisted selection

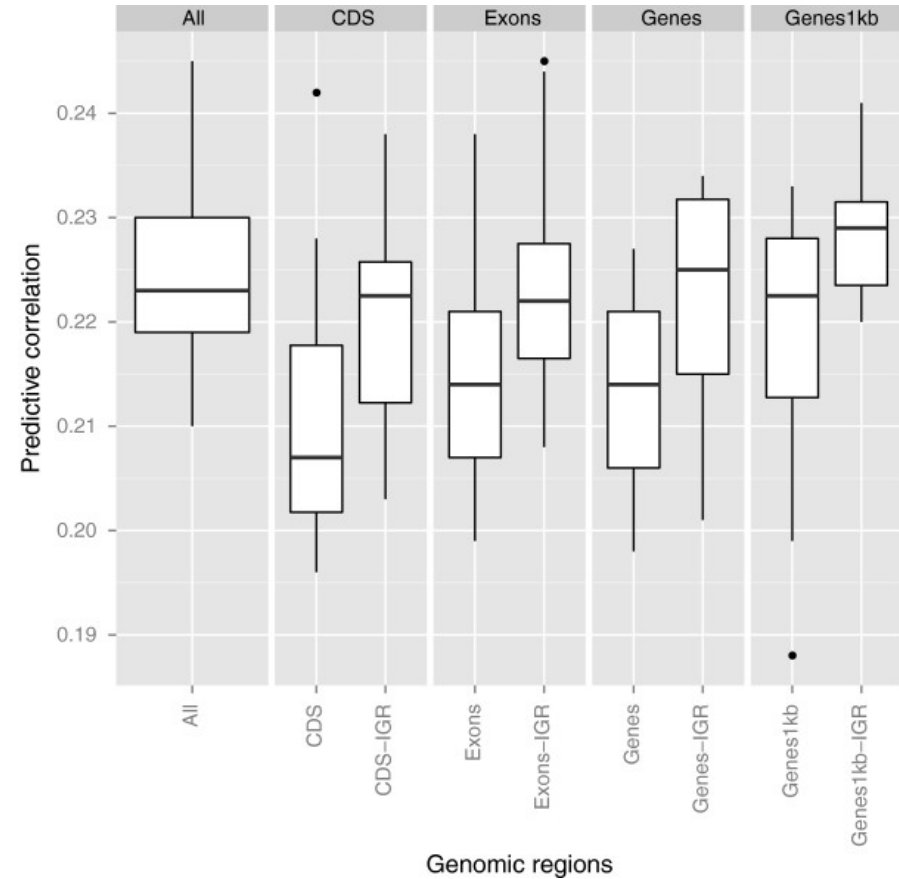


RFI2

Objective 1: To compare prediction performance (accuracy, bias) of different genomic prediction methods (GBLUP and Bayes)

Genomic annotation

- Genomic annotation /genomic regions influenced predictive ability for production traits (Morota et al,2014, BMC genomics)



Objective 2: To investigate the influence of genomic annotation on genomic contribution and prediction accuracy

Population

1,272 Duroc pigs (2008-2012)



Jan, 1st, 2012



Training pop = 968 pigs

Estimated SNP effects used Bayesian

Lasso and Bayesian Alphabet methods

$$y = 1\mu + Xb + M\beta + e$$

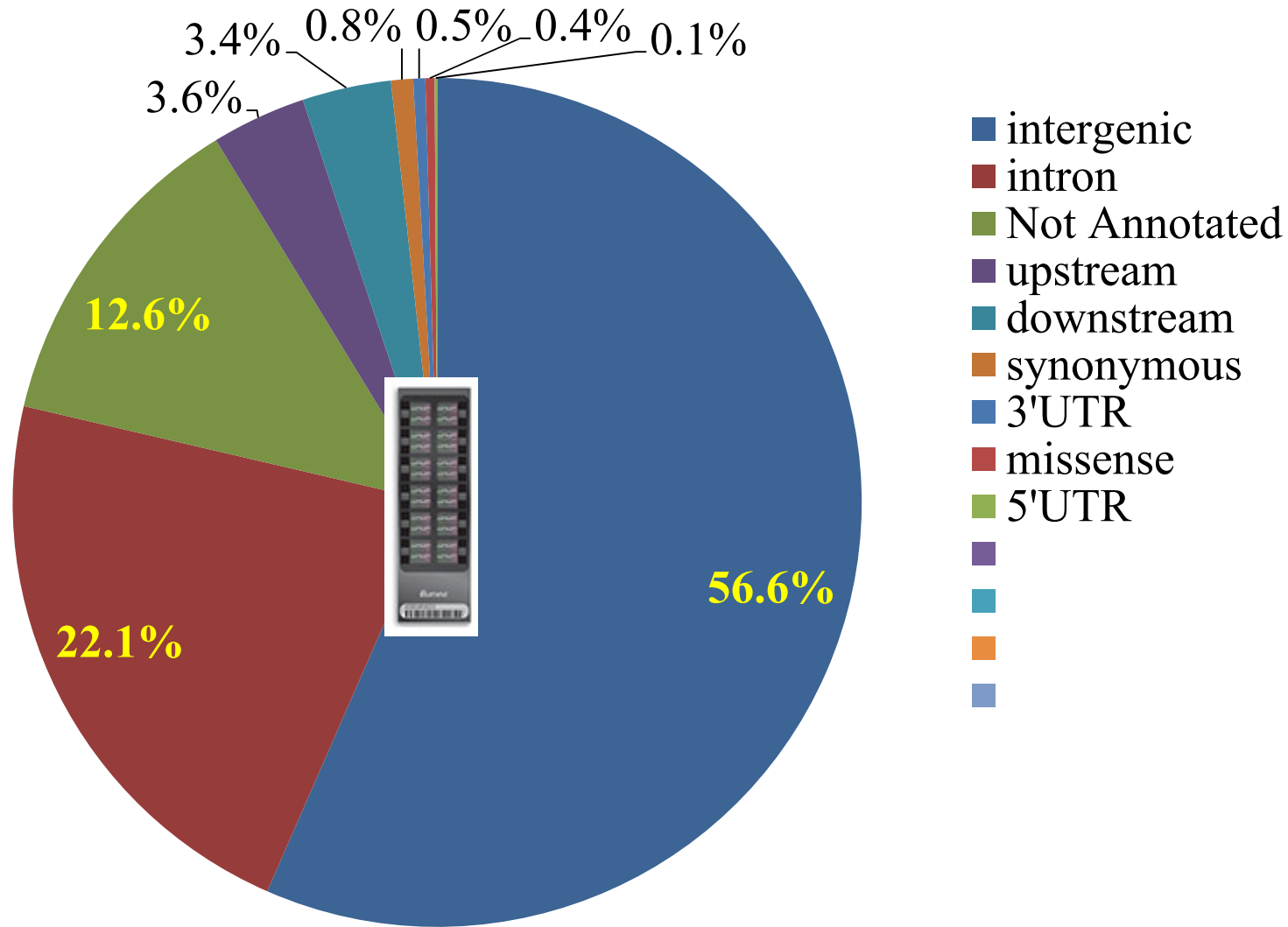
Testing pop = 304 pigs

$$\text{Accuracy} = \frac{\text{cor}(y_c; \text{GEBV})}{\sqrt{h^2}}$$

$$(y_c = \hat{g}_{ebv} + \hat{e} \text{ from animal model})$$

Bias = coefficient of $\text{lm}(y_c \sim \text{GEBV})$

Genomic annotation (60K) using Variant Effect Prediction



Accuracy of genomic prediction

<u>Method</u>	<u>DFI</u>	<u>RFI</u>
GBLUP	0.517	0.517
BL	0.515	0.509
Bayes A	0.528	0.535
Bayes B	0.508	0.519
Bayes C π	0.531	0.532

- Accuracy of genomic prediction ~ 0.51- 0.53 for both traits
- Accuracy was not significantly differed compared to GBLUP ($p < 0.05$)
- Prediction was biased (1.1 - 1.4)

Genomic variance partitioning

Genomic region	SNP	DFI		RFI	
		Var.exp (%)	Var.exp per SNP	Var.exp (%)	Var.exp per SNP
Downstream	1110	3.82	3.45E-05	3.68	3.31E-05
Upstream	1,211	4.09	3.38E-05	3.89	3.21E-05
Genic	8,084	27.28	3.37E-05	28.31	3.50E-05
Intergenic	18,974	61.99	3.27E-05	61.4	3.24E-05

- Variance contribution (%) was linearly associated with number of SNPs
- Variance explained per SNP was as similar as a **expected** value ($1/30234 = 3.31\text{E-}05$)

Prediction accuracy of genomic regions

Genomic region	DFI		RFI	
	Acc	Mean.Acc Random ¹	Acc	Mean.Acc Random ¹
Downstream	0.231	0.378	0.290	0.384
Upstream	0.455	0.385	0.425	0.391
Genic	0.511	0.458	0.493	0.483
Intergenic	0.471	0.500	0.477	0.498

- Genic region and upstream regions improved prediction accuracy,
but not significant ($p < 0.05$)

Discussion

Similar accuracy among the prediction methods

- ✓ Highly Polygenic trait – no major genes or QTLs (Do et al, 2014, BMC Genetics)
- ✓ Pig 60K SNP chip does not contain SNPs of many important genes in feed efficiency/intake: *MC4R*, *LEPTIN*, *CCK8*...

Little impact of genome annotation on prediction accuracy

- ✓ High LD in DuroCS (Wang et al, 2013, BMC Genetics)
- ✓ Poor annotation (12% SNP not annotated)
- ✓ SNP chip design ignores rare variants

Conclusion and future perspective

- ✓ Choice of prediction method
- ✓ Genomic regions
- ✓ Accuracy prediction $\sim 0.5 \rightarrow$ could GEVVs replace for feed intake measurement?

"Little" impact on predictive ability of RFI and DFI

- Ongoing: Examine sources of prediction bias
Include QTLs, candidate genes and biological pathways in prediction model

Improve prediction performance by  of biology



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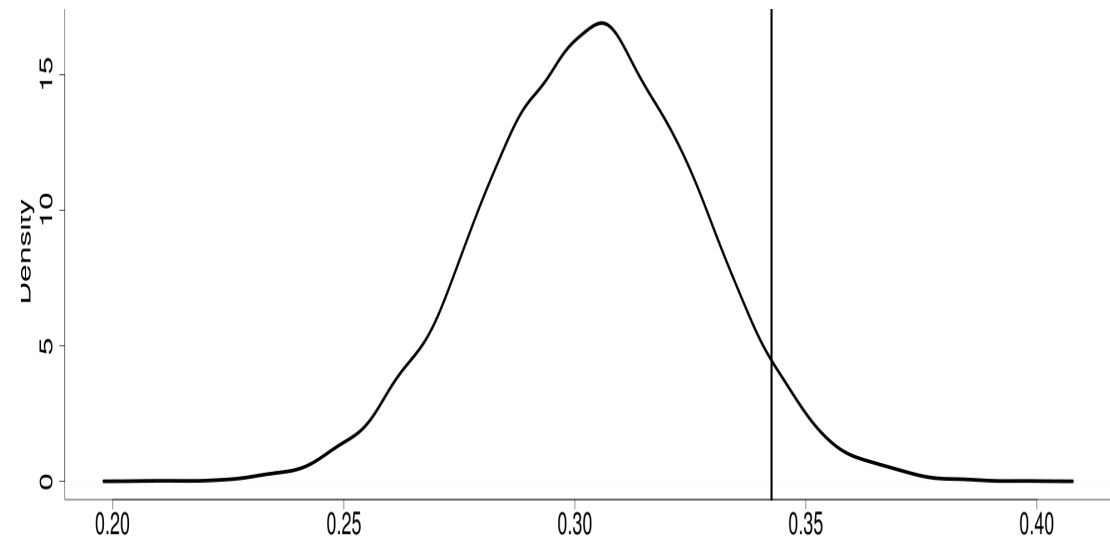


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Define significant threshold for group annotation

- Random sample 1000 time number of SNPs same to each annotated class
- Computed the EBVs of animals using each of 1000 groups
- Compute accuracy for each group on test pop
- Compute 95% quantile
- Draw conclusion based on compare accuracy of class to 95% quantile from random group



95%
quantile
accuracy

Class	60K	QC
3_prime_UTR	282	154
5_prime_UTR	58	36
downstream_gene	2095	1110
intergenic	34979	18974
intron	13662	7347
intron,nc_transcript	144	51
intron,NMD_transcript	53	28
missense	219	109
missense,splice_region	6	2
non_coding_exon,nc_transcript	32	10
splice_donor	2	1
splice_region,intron	54	32
splice_region,synonymous	17	12
stop_gained	4	2
stop_lost	1	1
synonymous	518	305
upstream_gene	2226	1211
Not Annotated	7807	847