

Future Beef cross

“to calculate accurate breeding values for feed efficiency, methane emission and eating quality”

2019-2023

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- Phd student at QGG Aarhus University
- Contribution to FutureBeefCross
 - Generation and editing of phenotypes
 - Estimating genetic parameters for
 - Growth
 - Feed intake
 - Methane
 - Meat quality (reference animals)



SEGES

Huiming Liu

- Genomics
 - Imputation
 - SSGBLUP
 - Validation
 - Implementation



Mahmoud Shirali

- Modelling
 - Random regression
 - Body weight
 - Feed intake
 - RFI
 - Methane
 - Meat quality
 - IMF
 - Marbelling score



Experimental setup

Project started January 2020

Beef on Dairy crosses on Holstein dams

- Belgian Blue
- Charolaise
- Angus

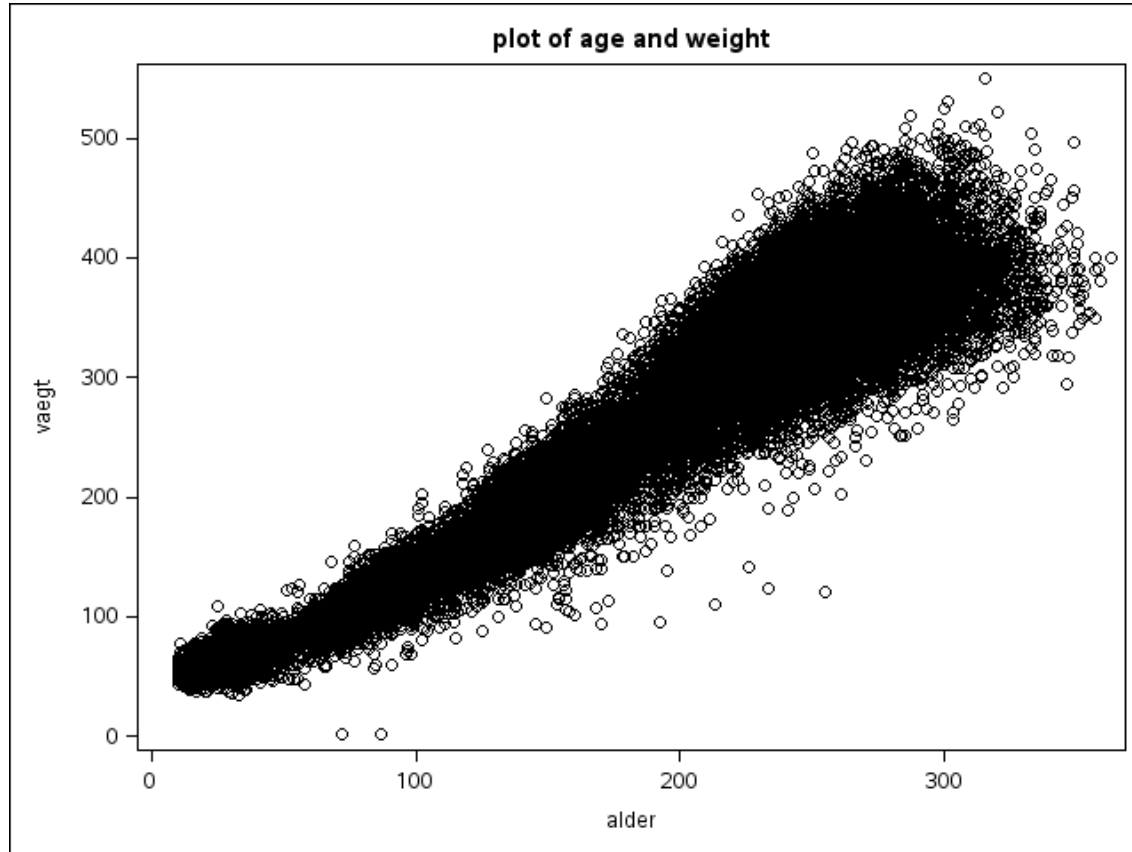
5 commercial slaughter calf herds

- 8 sniffers connected to 6 feed boxes each
- Calves enter for 21 days on average

Feedboxes from Allflex danmark



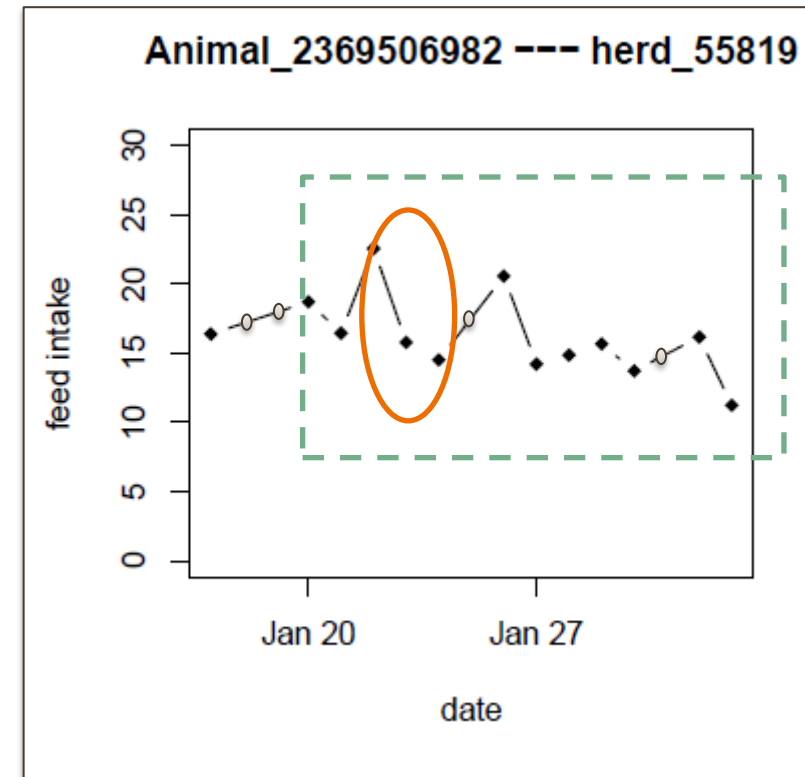
Raw daily feed and body weight data



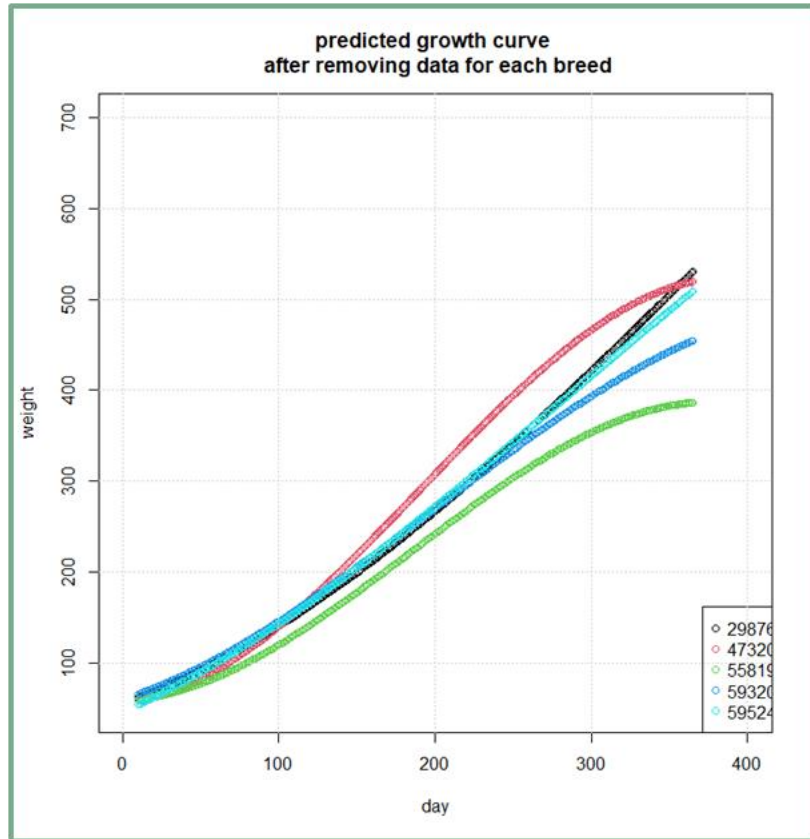


Daily feed intake cleaning procedures

- 3 days prior to missing period, substitute the value with the running mean.
- Allow data to be missing for 3 days.
- Keep only periods with above 5 consecutive days.



Pre phenotypic prediction



Animal_4350213885 --- herd_47320

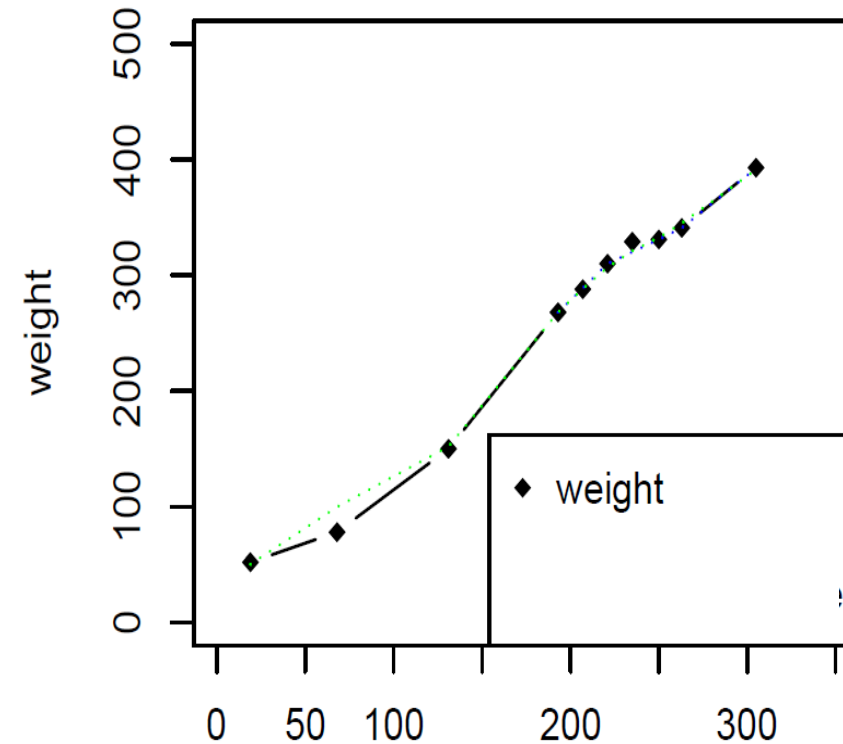




Table 1: Descriptive statistics for growth and feed intake traits¹ across breed² groups of Belgian Blue, Charolaise and Angus sired crossbred slaughter calves on Holstein dams. Data is represented as mean with standard deviation in parenthesis.

Trait	BBL		CHA		AAN	
	Bulls	Heifers	Bulls	Heifers	Bulls	Heifers
n	1874	1567	419	300	459	211
Age (d)	220 (29.8)	230 (34.6)	191 (36.8)	210 (48.0)	199 (35.6)	224 (44.7)
mid_BW (kg)	322 (56.3)	302 (48.8)	283 (65.5)	278 (74.1)	291 (66.5)	300 (62.0)
ADG (kg/d)	1.485 (0.382)	1.348 (0.302)	1.598 (0.419)	1.408 (0.318)	1.597 (0.437)	1.208 (0.351)
DMI (kg/d)	6.48 (1.30)	6.81 (1.34)	5.96 (1.28)	6.41 (1.54)	6.20 (1.51)	6.98 (1.43)
FCR (kg DM/kg*d ⁻¹)	4.56 (1.36)	5.26 (1.44)	3.93 (1.31)	4.67 (1.40)	4.02 (1.36)	5.09 (1.46)

¹ Traits: mid test body weight (mid_BW), average daily gain (ADG), dry matter intake (DMI), feed conversion ratio (FCR=DMI/ADG)

² Breeds of sire BBL: Belgian Blue, CHA: Charolaise, AAN: Angus

Genetic results



Table 2: Results from the genetic parameter analysis of traits¹ in Belgian Blue, Charolaise and Angus sired crossbred slaughter calves on Holstein dams. Heritability is presented on the diagonal, phenotypic correlations above the diagonal and genetic correlation below the diagonal. Standard error of the estimate is presented in the parenthesis.

Traits	mid_BW	ADG	DMI	FCR
mid_BW	0.30 (0.06)	0.21	0.46	0.08
ADG	0.73 (0.17)	0.06 (0.03)	0.37	-0.67
DMI	0.39 (0.13)	0.52 (0.20)	0.19 (0.04)	0.24
FCR	0.03 (0.20)	0.03 (0.31)	0.64 (0.17)	0.08 (0.03)

¹ Traits: mid test body weight (mid_BW), average daily gain (ADG), dry matter intake (DMI), feed conversion ratio (FCR=DMI/ADG)

Based on animal model

$$Y = Xb + Za + e$$

Fixed effects:

- HYM (1,...,159)
- Sex (1,2)
- Sire Breed (BBL, CHA, ANG)
- Age (sex)

Random effect:

- a: $\text{Var}(a) = A\sigma_a^2$
- e: $\text{Var}(e) = I\sigma_e^2$



Genotype data

- Pedigree for XXX was traced back for 3 generations
 - 2469 HOL -> 843 HOL females
 - 76 BBL females
-
- 19991 extra HOL: used for DairyCross – born after 2021 – MD chip
 - 276 extra BBL: Their sires have XXX offspring

Map



- Map1: EuroG_MDv2_XT_DEN_20006795X370693_A1.txt (67817 SNPs).
- Map2: EuroG_MDv3_mapUCD12.txt (75314 SNPs).
- Merge Map1 and Map2 by name and position.
- The positions need to exist in HOL, BBL and XXX.
- We end up with 62102 SNPs

Imputation Scenarios

Scenarios		HOL	BBL	Cross	SNPs	Results
Test1	Purebred HOL were imputed	2469 Imputed females	316	1762	only keep the manifest positions -> 6887	1529 errors by FImpute3
Test2	Purebred HOL were imputed	351 Imputed mothers of XXX	352	1762		1530 errors
Test3	Purebred HOL were imputed	864 Imputed female ancestors	352	1762		1533 errors

Heritability – ADG and DMI/FCR – bivariate model



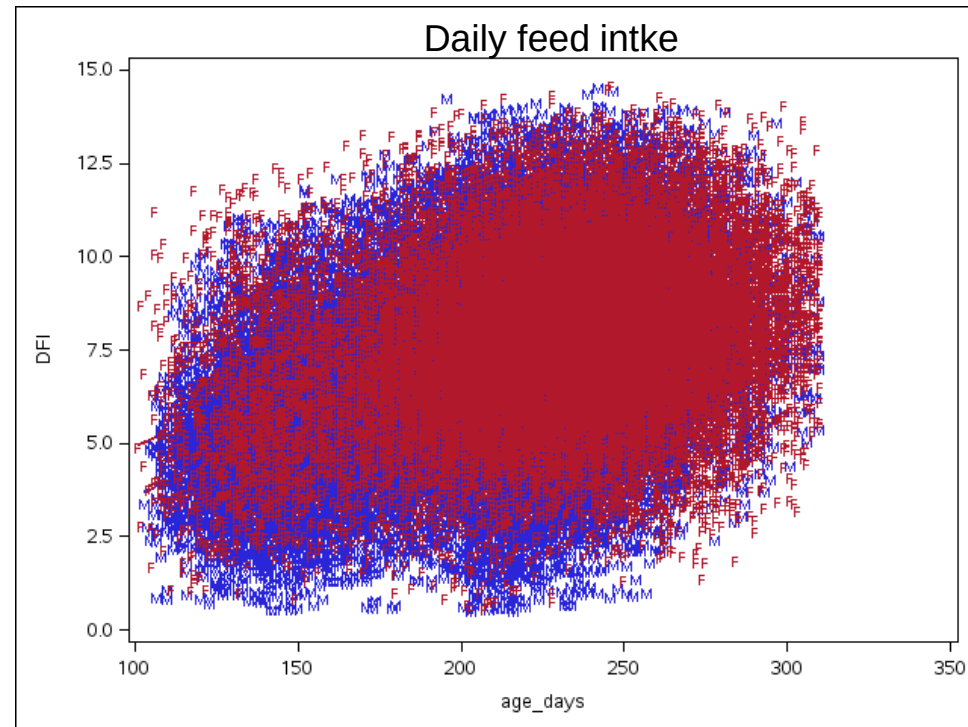
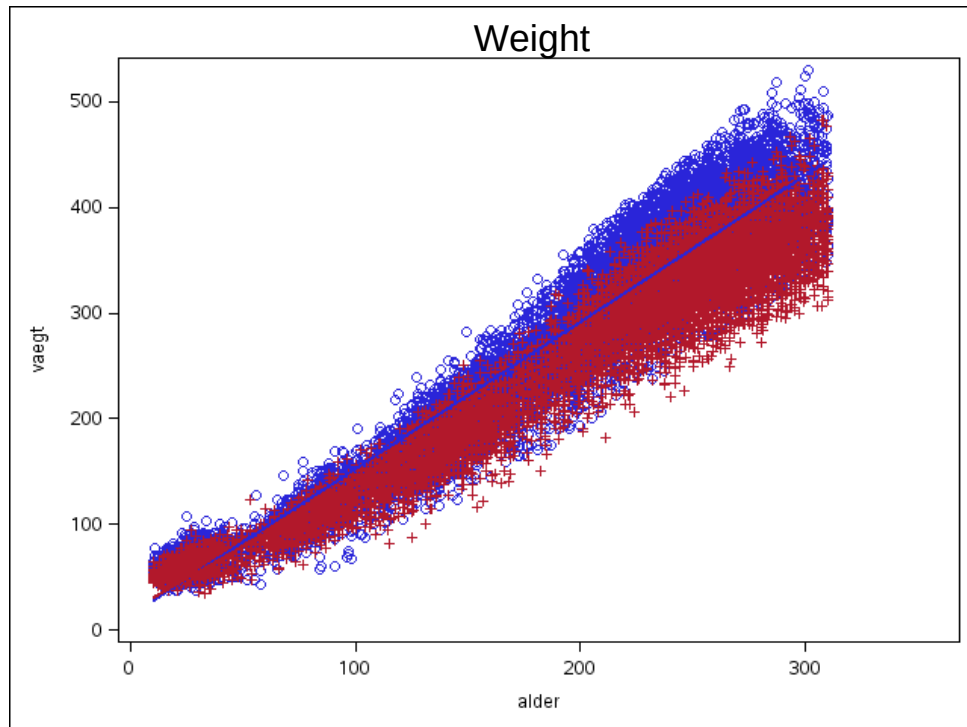
Trait	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$		σ_p^2
	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	
ADG	0.008(0.004)	0.011(0.004)	0.093(0.004)	0.092(0.004)	0.083(0.037)	0.100(0.037)	0.116
DMI	0.156(0.049)	0.164(0.045)	1.001(0.047)	0.994(0.043)	0.135(0.041)	0.141(0.037)	1.74
FCR	0.205(0.074)	0.171(0.057)	1.202(0.067)	1.235(0.056)	0.145(0.051)	0.121(0.039)	1.76



Cor between corrected phenotype and (G)EBV

Trait	Cor	
	PBLUP	SS-GBLUP
ADG	0.096	0.107
DMI	0.211	0.210
FCR	0.113	0.128

BW and DFI data

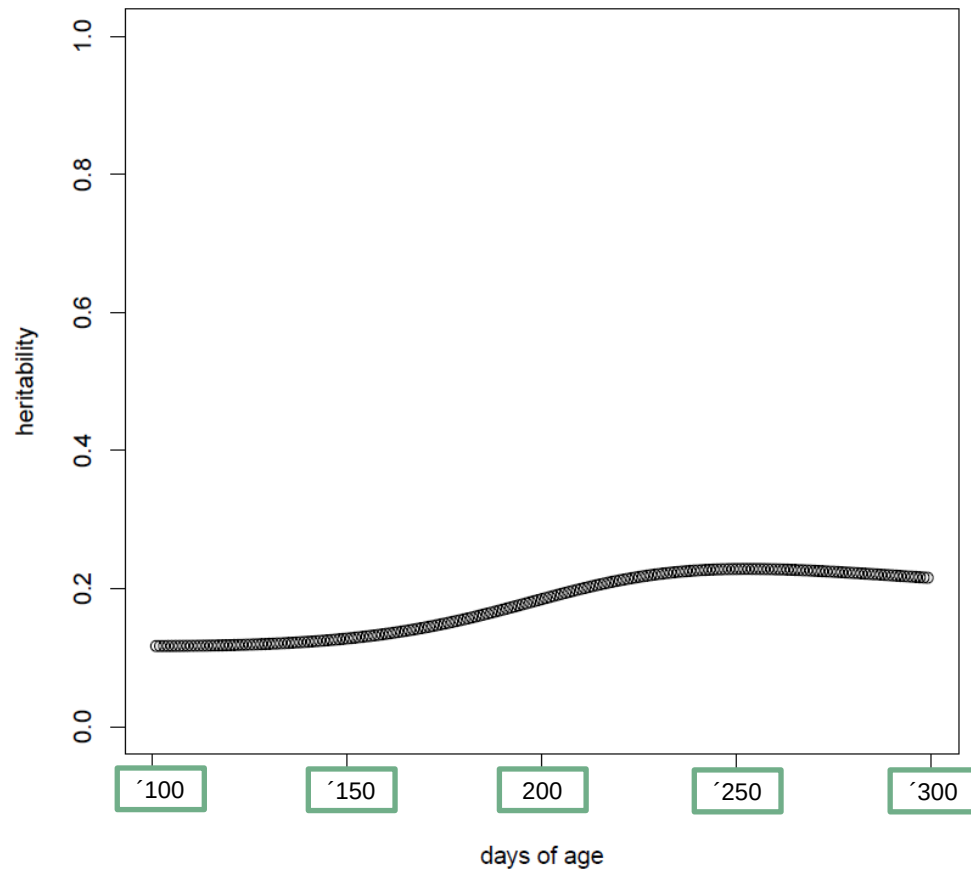


Random regression analysis with legendre polynomials

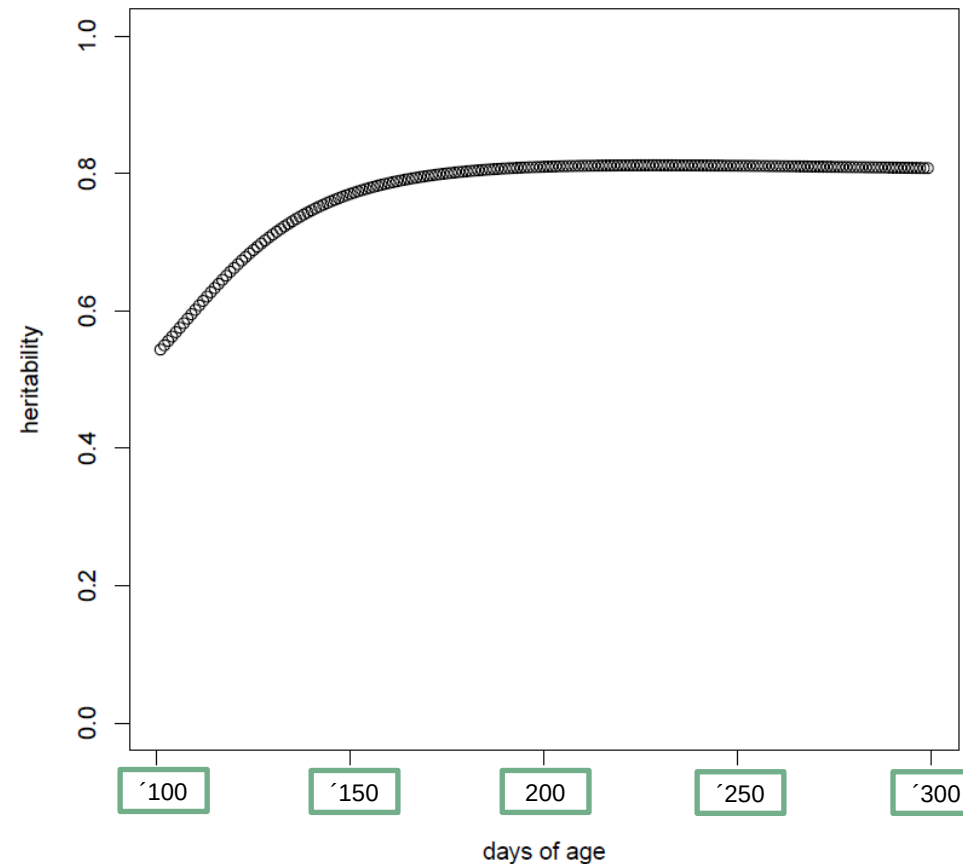


$$y = \text{Sirebreed} + \text{gender} + \text{herdYearMonth} + b(\text{start age}) + l_{q1}(t)' \text{sirebreed} + l_{q2}(t)' a_k + l_{q2}(t)' p_k + e$$

heritability of DFI



heritability of BW



Meat quality

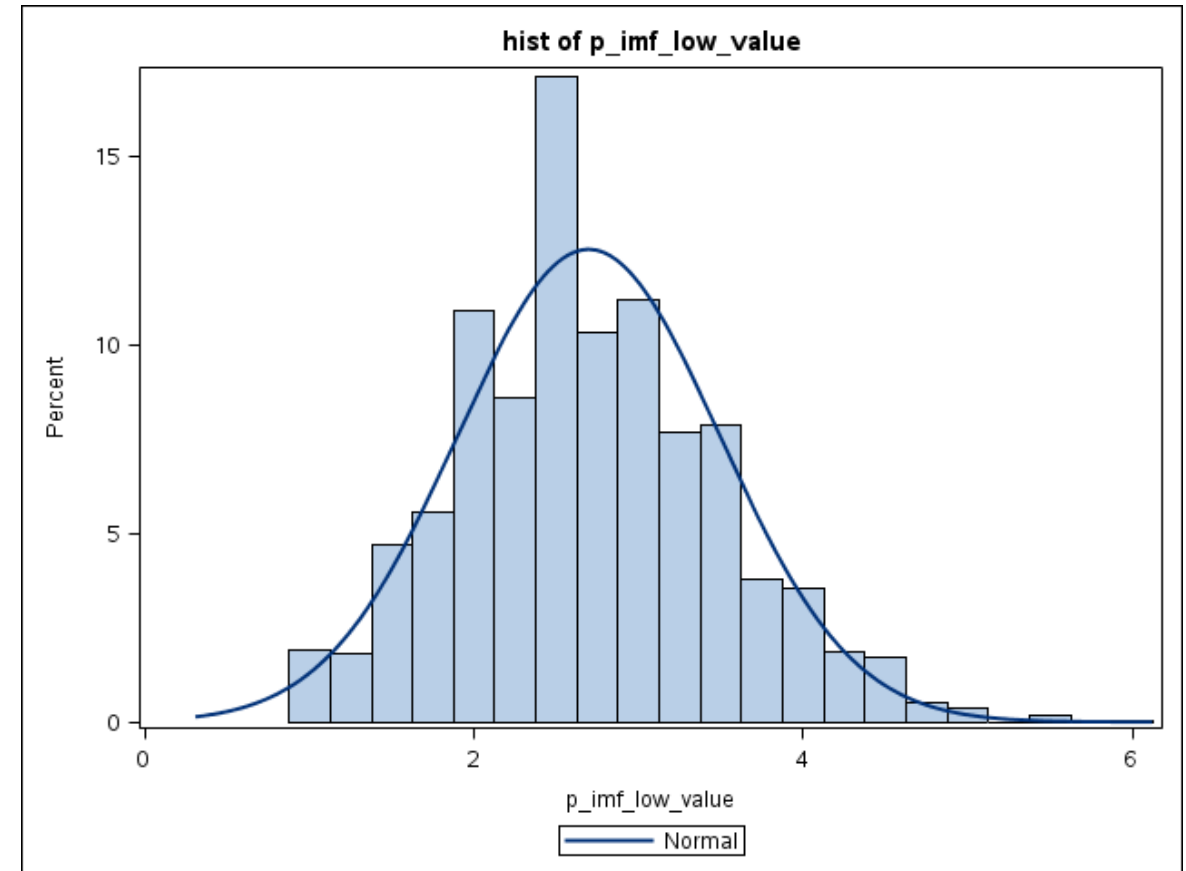
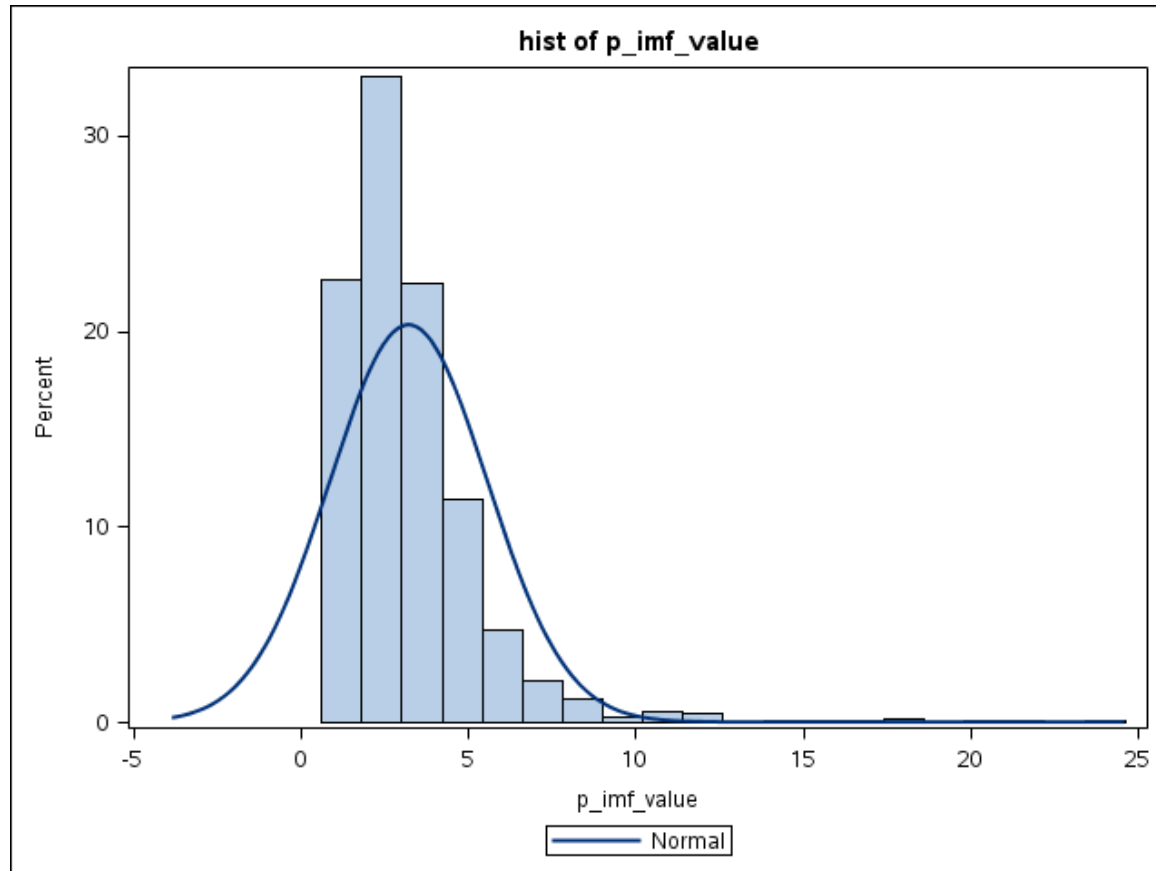


Chemical and mechanic tests performed by AU Food (Fie Drachmann)
Basis for the algorithm used on all animals

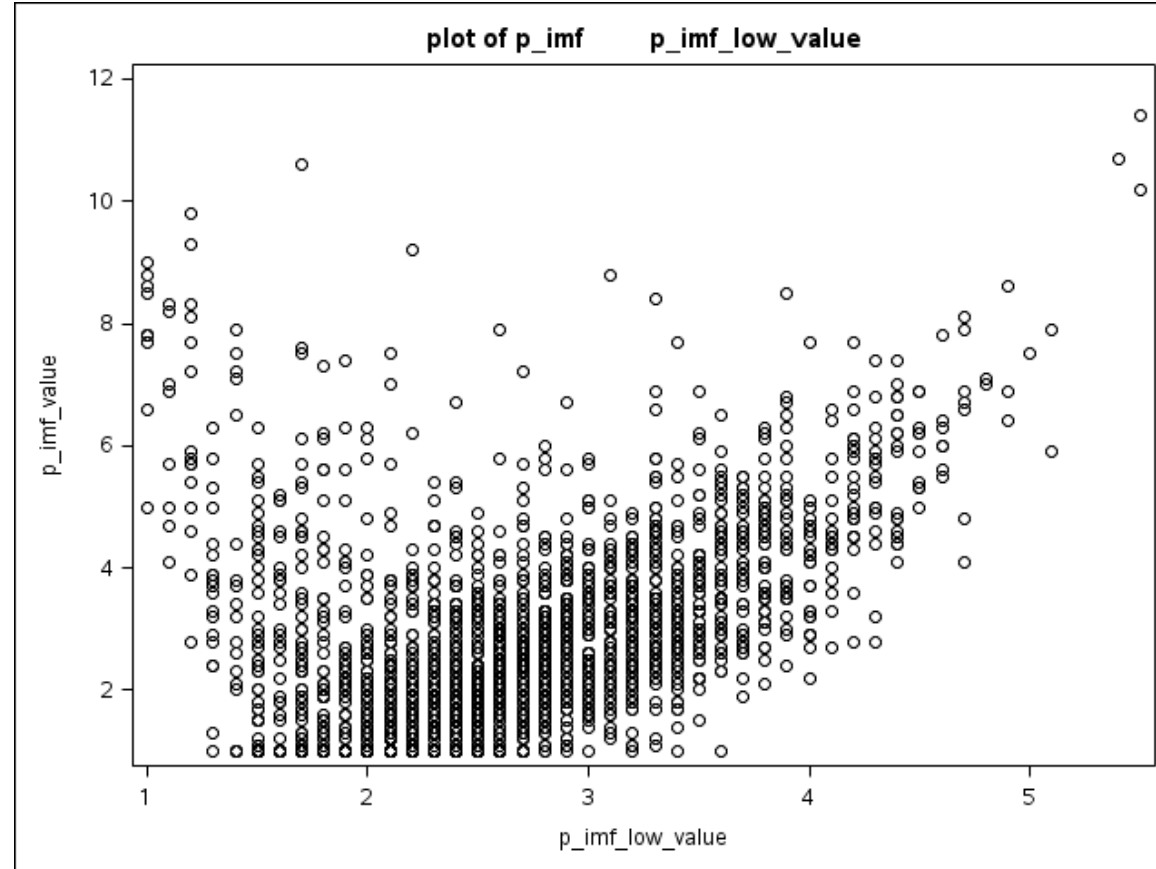
Sire breed	Number of animals	Year	Number of animals
AAN	302	2021	403
BBL	1155	2022	1238
CHA	254	2023	70

Name	Mean	SD	Q1	Q3
Carcass weight	221	21	205	235
eye_muscle_area	33	6	29	37
p_imf_value	3.2	2.3	1.9	3.9

Suddenly we have 2 IMF values



Association between IMF and IMF_low



IMF will be replaced by **Marbelling Score** from July 2023

- Marbelling Score will be based on a model trained on image data and visual scoring

Marbelling Score will be used by Danish Crown and most likely it will have an economic value from late 2024

Genetic parameters for IMF



$$Y = Xb + Za + e$$

fixed effects of slaughter year and month with herd interaction, sex of male and female, sire breeds of Belgium Blue, Angus, and Charolaise, and fixed regression of carcass weight.

Traits	Genetic	Residual	Phenotypic	Heritability
IMF	0.5 (0.18)	2.1 (0.17)	2.6	0.19
IMF BBL	0.14 (0.09)	1.88 (0.11)	2.02	0.07
EMA	6.44 (2.02)	18.97 (1.74)	25.42	0.25
EMA BBL	9.76 (3.1)	16.88 (2.48)	26.64	0.37

Methane data

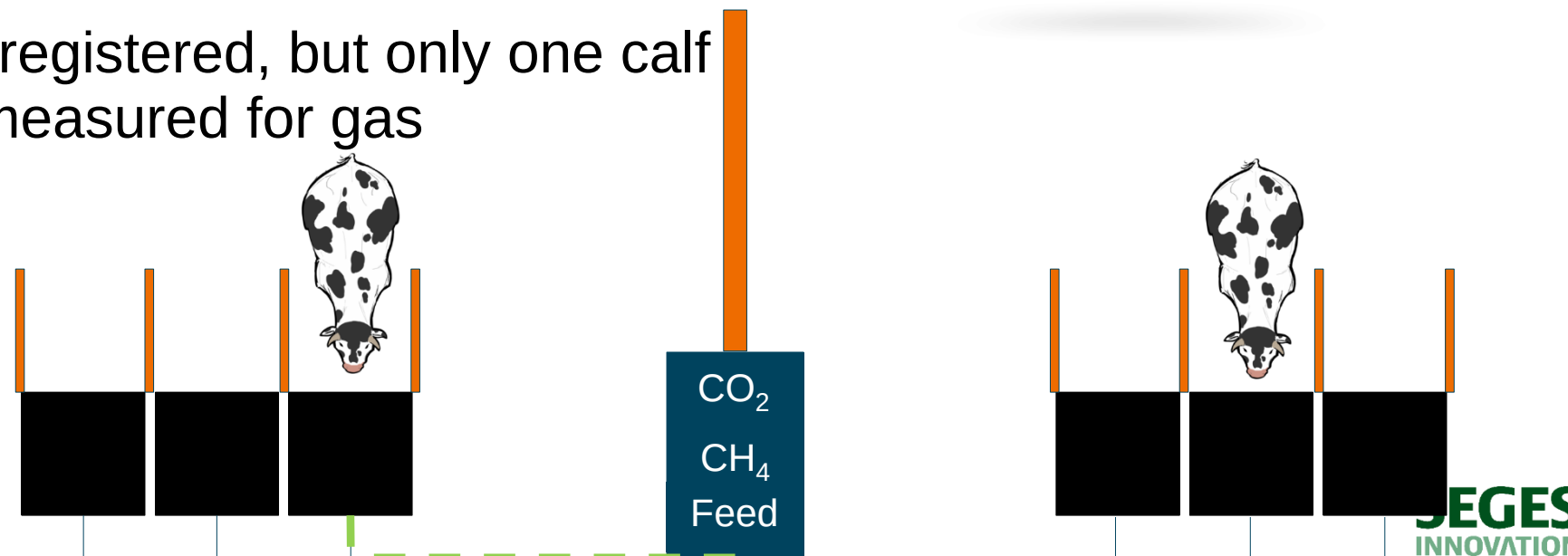


Based on sniffers

- Guardian[®] NG, Edinburgh Instruments Ltd.

Measures CH₄ and CO₂ concentrations continuously

All feed visits are registered, but only one calf at a time can be measured for gas concentrations



Methane data

Generation of phenotypes is well underway

Sniffer data is registered on

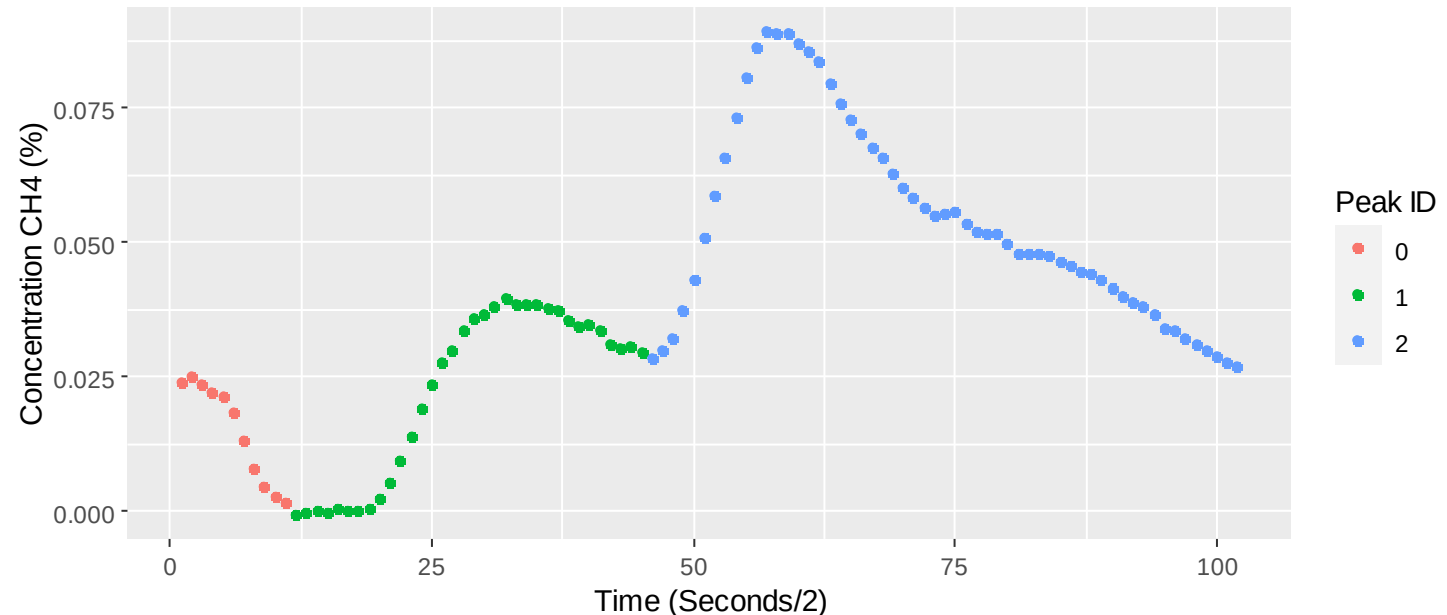
- 3463 BBLxHOL
- 916 CHAxHOL
- 902 AANxHOL

CH₄ concentration is repeatable

- ICC = 0.33



Example of a methane visit



Methane phenotypes



Multiple phenotypes to be tested (May 2023)

- Peak length and frequency
- Peak characteristics (Slope increase and decrease)
- Mean CH_4 concentration
- Daily CH_4 emission (Madsen equation)
- CH_4 relative to production
 - DMI
 - ADG



Thanks you for attending this
meeting



Scope:

“to calculate accurate breeding values for feed efficiency, methane emission and eating quality”

- Develop genomic breeding value for eating quality, feed efficiency and methane
- The right beef bulls can be selected for the production of crossbred calves

WP1: Recording eating quality

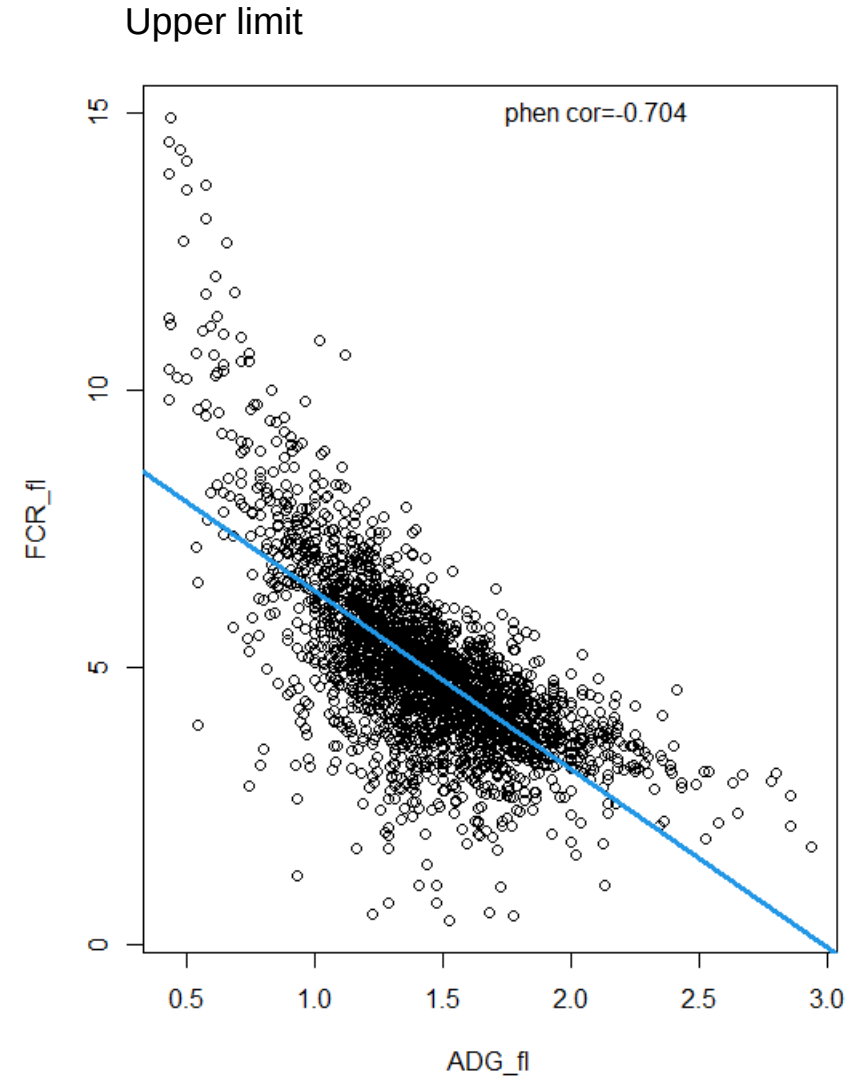
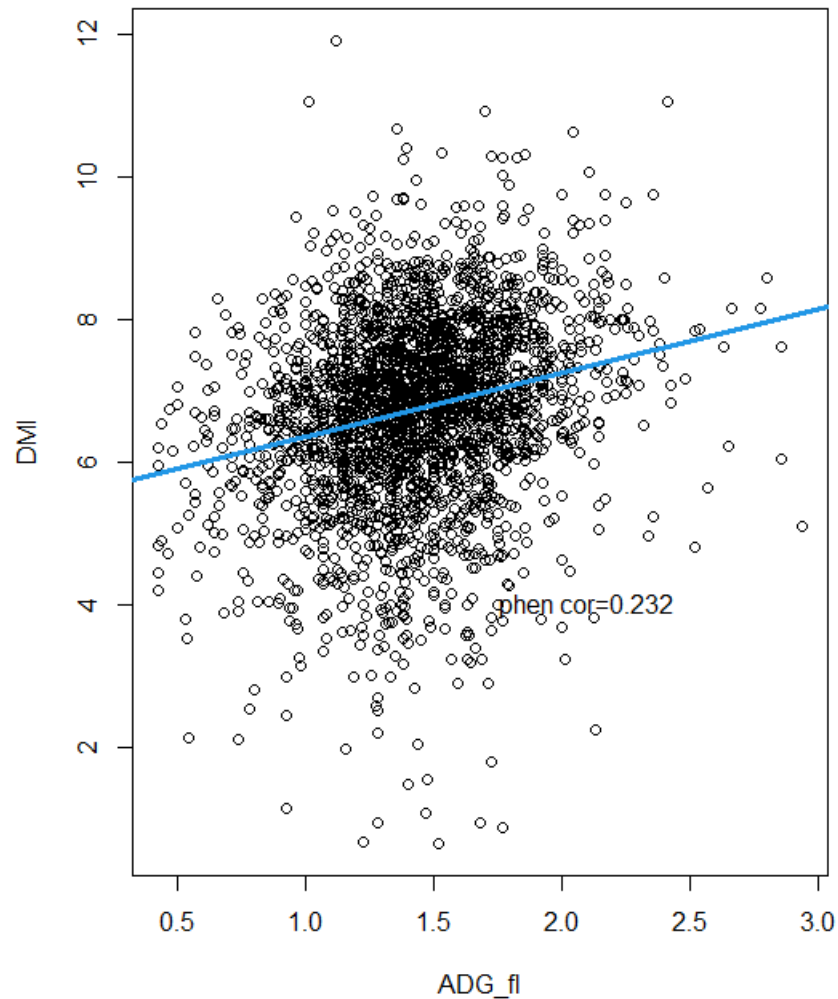
WP2: Recording feed and methane data

WP3: Genetic parameter estimation

WP4: Genomic breeding value estimation

WP5: Dissemination of results

Using dry matter intake instead of DFI across herds



Distribution of offspring (BBL sire)

There are 72 BBL sires

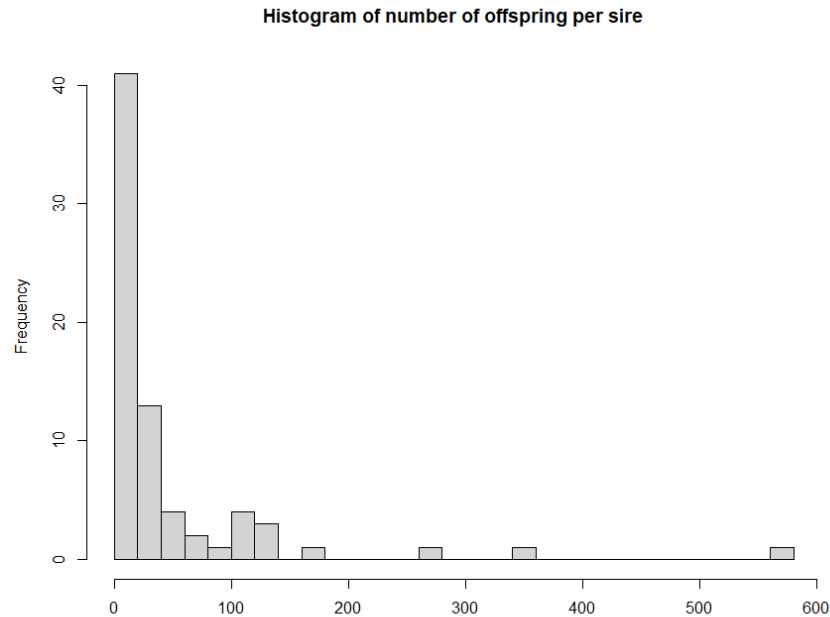
The id_nor of the sires with more than 150 offspring with phenotypic records are:

BBLGBRM000000020140889 – 166 XXX offspring

BBLDNKM000003882201721 – 353 XXX offspring

BBLDNKM000006725800035 – 572 XXX offspring

BBLDNKM000007155901731 – 265 XXX offspring



BW in different herds

	29876	47320	49238	55819	59316	59320	59524
AAN	105	237	1	44	133	171	59
BBL	340	1918	51	597	205	267	118
CHA	174	98	12	92	197	243	25
HOL	19	682	27	31	11	14	58

Heritability – ADG and DFI – bivariate model

Trait	Period	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$	
		PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP
	First-last date (FBC)	0.008(0.004)	0.011(0.005)	0.103(0.004)	0.100(0.004)	0.070(0.036)	0.100(0.040)
ADG	180-310 days chunk	0.014(0.005)	0.017(0.004)	0.081(0.004)	0.079(0.004)	0.149(0.050)	0.172(0.039)
	All	0.004(0.001)	0.004(0.001)	0.015(0.001)	0.015(0.001)	0.204(0.051)	0.211(0.043)

Trait	Multi with ADG	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$	
		PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP
	FBC	0.304(0.105)	0.334(0.099)	2.282(0.101)	2.261(0.093)	0.117(0.040)	0.129(0.037)
DFI	180-310	0.339(0.106)	0.338(0.100)	2.280(0.004)	2.259(0.094)	0.118(0.040)	0.130(0.037)
	All	0.335(0.110)	0.036(0.101)	2.295(0.001)	2.282(0.095)	0.127(0.041)	0.135(0.037)

Heritability – ADG and FCR – bivariate model

Trait	Period	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$	
		PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP
	First-last date (FBC)	0.008(0.004)	0.011(0.005)	0.103(0.004)	0.100(0.004)	0.070(0.036)	0.100(0.040)
ADG	180-310 days chunk	0.014(0.005)	0.017(0.004)	0.081(0.004)	0.079(0.004)	0.149(0.050)	0.172(0.039)
	All	0.004(0.001)	0.004(0.000)	0.015(0.001)	0.014(0.000)	0.204(0.051)	0.210(0.04)

Trait	Period	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$	
		PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP
	First-last date (FBC)	0.198(0.120)	0.294(0.136)	3.895(0.143)	3.819(0.147)	0.048(0.029)	0.071(0.032)
FCR	180-310 days chunk	0.469(0.168)	0.612(0.170)	3.379(0.160)	3.270(0.153)	0.122(0.042)	0.157(0.042)
	All	0.184(0.063)	0.176(0.054)	1.400(0.061)	1.411(0.055)	0.116(0.039)	0.111(0.033)

Genetic correlation between ADG and DFI/FCR

		ADG_FBC	ADG_180	ADG_all
DFI	BLUP	0.33(0.27)	0.23(0.23)	0.30(0.19)
	SSGBLUP	0.40(0.21)	0.30(0.18)	0.32(0.16)
FCR	BLUP	-0.67(0.21)	-0.84(0.09)	-0.21(0.21)
	SSGBLUP	-0.74(0.14)	-0.86(0.06)	-0.17(0.18)

LR to assess potential bias due to design of cross-validation analysis

- Estimators of bias ($\hat{\Delta}$), dispersion ($\hat{b}$), accuracy ($\widehat{acc}$) and ratio of accuracies ($\hat{\rho}$) in LR method were used to evaluate the impact of different methods on crossbred performance.
- Reference and testing populations

You have complete (*whole*) records, pedigree and (perhaps) markers. Consider a cut-off date. Records before these date make the *partial* data set: y_p whereas all records make the *whole* data set: y_w . Then you run two genetic evaluation with either the *partial* data or the *whole* data, and you keep the entire pedigree and markers in both. In these manner, you have EBVs for all animals in both cases, $\hat{u}_p$ and $\hat{u}_w$ respectively.

- EBVs of focal individuals were denoted as $\hat{u}_p$ and $\hat{u}_w$ based on the partial and the whole dataset, respectively. Focal individuals of partial dataset were defined as the set of crossbreed animals which were born after November 1, 2021.

Bias and slope



- 1 **Bias** This is measured using $\hat{\Delta}_p = \bar{\hat{u}}_p - \bar{\hat{u}}_w$. The expectation is 0 (no bias). A positive value means that animals with *partial* information are overevaluated.
- 2 **Slope** Also calledr over/underdispersion. This is measured using $\hat{b}_p = \frac{cov(\hat{u}_p, \hat{u}_w)}{var(\hat{u}_p)}$ or, equivalently, computing the slope b_1 of the linear regression “whole on partial” $\hat{u}_w \sim b_0 + b_1 \hat{u}_p + \epsilon$. The expectation is 1 (no over- neither under-dispersion), values lower than 1 mean that selected candidates are overestimated. This is the kind of bias commonly reported in dairy cattle studies.
- 3 **Accuracy** The first estimator of *absolute* reliability is an estimator of “selected” reliability: $\widehat{acc}_p^2 = \frac{cov(\hat{u}_p, \hat{u}_w)}{\sigma_{u^*}^2}$. The denominator $\sigma_{u^*}^2$ is the variance of animals in the focal group (and not the variance of the base generation σ_u^2).

Ability to rank within the animals, but not for predicting genetic progress (cantt compare with less selected e.g. females)
- 4 **Ratio of accuracy** The first statistic is the correlation between *partial* and *whole* EBVs: $\hat{\rho}_{wp} = \frac{cov(\mathbf{u}_p, \mathbf{u}_w)}{\sqrt{var(\hat{u}_p)var(\hat{u}_p)}}$ (or simply $cor(\mathbf{u}_p, \mathbf{u}_w)$). This has expected value $\frac{acc_p}{acc_w}$ where *acc* means accuracy.

Unselected reliability

$$\text{Unselected reliability, } \widehat{rel}_p = 1 - \frac{\sigma_{u*}^2}{\sigma_u^2} (1 - \widehat{acc}_p^2)$$

Next step

- Model reliabilities $Rel_i = 1 - \frac{PEV_{i,i}}{H_{A_{i,i}}\sigma_u^2}$
- Data editing

Descriptive statistics (updated 2022.11.30)

ADG

Period	First-last date	180-310 days	0-350 days
# animals with phenotype	3037	3108	3281
Mean(sd)	1.41(0.37)	1.38(0.36)	1.36(0.19)

Feed intake

Method	DFI	DMI
# animals with phenotype	2916	2916
Mean(sd)	8.88(3.29)	6.71(1.32)

FCR (=Feed intake_all data/ADG)

Period	First-last date	180-310 days	0-350 days
# animals with phenotype	2358	2358	2887
Mean(sd)	5.69(1.67)	5.79(1.65)	6.55(2.50)

	DFI	DMI	ADG_fl_reg	ADG_chunk_reg	ADG_entire_reg
DFI	1.000	0.615	0.091	0.049	0.004
DMI	0.615	1.000	0.210	0.175	0.333
ADG_fl_reg	0.091	0.210	1.000	0.785	0.367
ADG_chunk_reg	0.049	0.175	0.785	1.000	0.416
ADG_entire_reg	0.004	0.333	0.367	0.416	1.000

Trait	Period	$\sigma_a^2(SE)$		$\sigma_e^2(SE)$		$h^2(SE)$	
		PBLUP	SS-GBLUP	PBLUP	SS-GBLUP	PBLUP	SS-GBLUP
ADG	First-last date (FBC)	0.008(0.004)	0.011(0.004)	0.093(0.004)	0.092(0.004)	0.083(0.037)	0.100(0.037)
DMI	180-310 days chunk	0.156(0.049)	0.164(0.045)	1.001(0.047)	0.994(0.043)	0.135(0.041)	0.141(0.037)
FCR	All	0.205(0.074)	0.171(0.057)	1.202(0.067)	1.235(0.056)	0.145(0.051)	0.121(0.039)

Trait	$\sigma_a^2(SE)$	$\sigma_e^2(SE)$	$h^2(SE)$	Bias	Prediction accuracy
ADG	0.011(0.004)	0.092(0.004)	0.100(0.037)	0.005	0.32
DMI	0.164(0.045)	0.994(0.043)	0.141(0.037)	-0.006	0.41
FCR	0.171(0.057)	1.235(0.056)	0.121(0.039)	-0.04	0.37