Genomic evaluations of carcass traits of young bulls in dual-purpose cattle

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Acknowledgments

Introduction

▸ **Recent development of genetic evaluations for carcass traits of young bull in French dual-purpose breeds**

▸ **Need for a genomic evaluation**

Introduction

- **Recent development of genetic evaluations for carcass traits of young bull in French dual-purpose breeds**

- **Need for a genomic evaluation**

- **Objectives:**
  - Which **evaluation approach** is the most suitable?
  - Find the **optimal setting for SSGBLUP**: which SSGBLUP relationship matrix? How many generations traced back?

Data

- Commercial slaughterhouse data

- Carcass weight, age at slaughter and carcass conformation in the EUROP system

- Young bulls: non castrated males slaughtered between 12 and 24 months

- Genotypes: on 50k SNP-chip or imputed from LD to 50k SNP-chip

Breed	Number of young bulls	Number of sires	Number of genotyped sires
Montbeliarde	118,183	1,452	1,125
Normande	111,789	1,125	925

Genetic evaluation model and genetic parameters

◗ Three-trait (Carcass weight, age at slaughter, carcass conformation) animal model

◗ $y_{ijkl} = \mu + C_i + p_j + s_k + a_l + \varepsilon_{ijkl}$

◗ y_{ijkl}: performance, μ: mean

◗ C_i: fixed effect of contemporary group (finishing herd*season of slaughter*year of slaughter)

◗ p_j: fixed effect of parity*age at calving of dam

◗ s_k: fixed effect of season of birth

◗ a_l: animal genetic effect, ε_{ijkl}: residual error

◗ Low to moderate heritabilities: 0.09 to 0.26

Evaluation approaches tested and comparison

▶ Genomic approaches

    ▶ GBLUP (with or without a residual polygenic effect); univariate

    ▶ BayesC (with a residual polygenic effect); π=0,05; univariate

▶ Single-Step approach; univariate and multivariate

    ▶ Single-Step relationship matrix: $H^{-1} = A^{-1} + \begin{pmatrix} 0 & 0 \\ 0 & G^{-1} - {A_{22}}^{-1} \end{pmatrix}$

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◗ Single-Step approach; univariate and multivariate

  ◗ Single-Step relationship matrix: $H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{-1} - A_{22}^{-1} \end{pmatrix}$

  ◗ Types of $\mathbf{H}^{-1}$ settings: $H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - \omega A_{22}^{-1} \end{pmatrix}$ with $\mathbf{G^*}$=(1-α)$\mathbf{G}$+α$\mathbf{A}_{22}$

  ◗ α: portion of variance not explained by SNP

  ◗ ω: scaling factor of pedigree relationship

Evaluation approaches tested and comparison

◗ Genomic approaches
  ◗ GBLUP (with or without a residual polygenic effect)
  ◗ BayesC (with a residual polygenic effect)

◗ Single-Step approach
  ◗ $H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - 1 * A_{22}^{-1} \end{pmatrix}$ with $G^* = (1\text{-}0.3)G + 0.3^*A_{22}$

◗ Validation population: 20% youngest sires
◗ Accuracy: correlation between EBV and average progeny adjusted performances (DYD)
◗ Bias/inflation: regression coefficient of EBV on DYD

Comparison of approaches in Montbeliarde

Criterion	Trait	BLUP	BayesC	GBLUP
Correlation with DYD	Carcass weight	0.38	0.47 ↗	0.47 ↗
	Age at slaughter	0.28	0.21 ↘	0.21 ↘
	Carcass conformation	0.43	0.52 ↗	0.51 ↗

Criterion	Trait	BLUP	BayesC	GBLUP
Regression coefficient (slope)	Carcass weight	0.81	0.81 →	0.85 ↗
	Age at slaughter	1.06	0.72 ↘	0.76 ↘
	Carcass conformation	0.94	0.95 →	0.95 →

Comparison of approaches in Montbeliarde

Criterion	Trait	BLUP	BayesC	GBLUP	SSGBLUP
Correlation with DYD	Carcass weight	0.38	0.47	0.47	0.45
	Age at slaughter	0.28	0.21	0.21	0.31
	Carcass conformation	0.43	0.52	0.51	0.51
Regression coefficient (slope)	Carcass weight	0.81	0.81	0.85	0.84
	Age at slaughter	1.06	0.72	0.76	0.97
	Carcass conformation	0.94	0.95	0.95	0.97

Setting of the SSGBLUP relationship matrix: ω

$$H^{-1} = A^{-1} + \begin{pmatrix} 0 & 0 \\ 0 & G^{*-1} - \omega A_{22}^{-1} \end{pmatrix}$$ with **G***=0.95**G**+0.05**A**$_{22}$
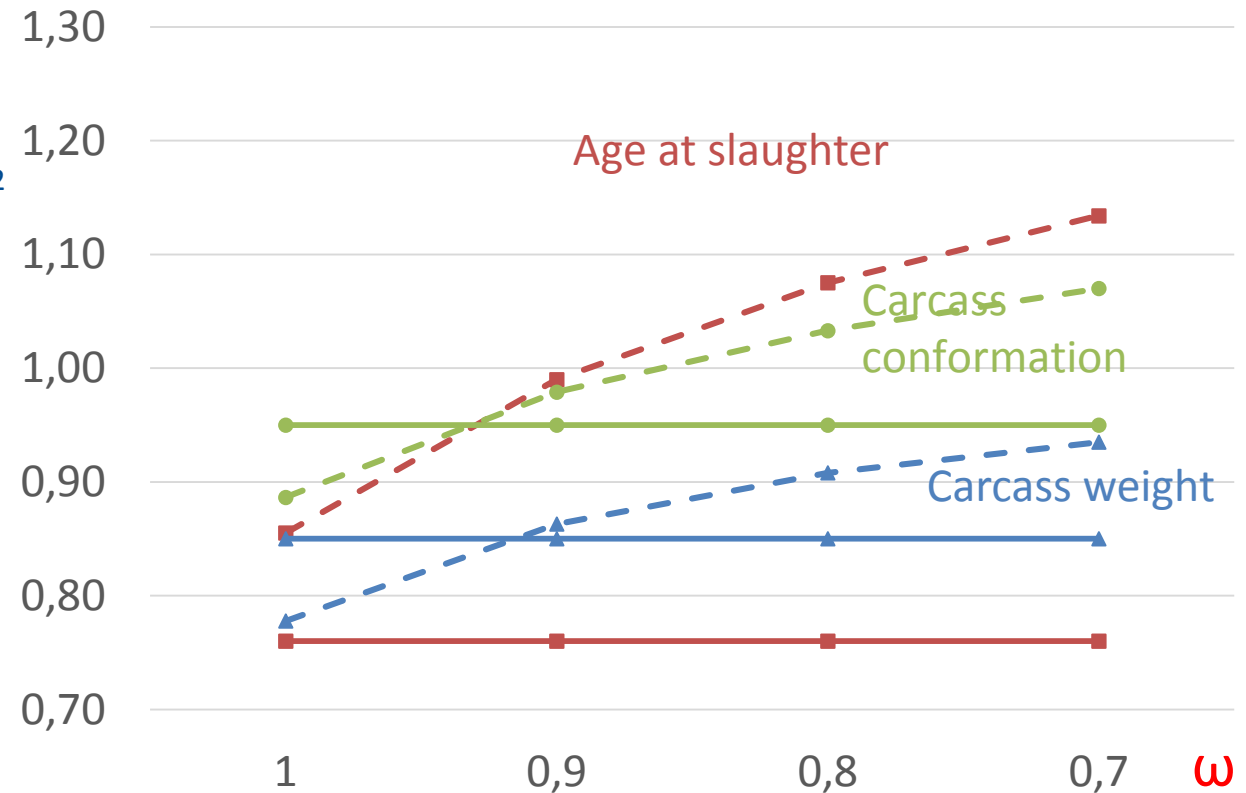
Low impact of ω on accuracy

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Low impact of ω on accuracy

Evolution of the regression coefficient of DYD and EBV depending on the scaling factor ω of the **H** matrix in the Montbeliarde breed
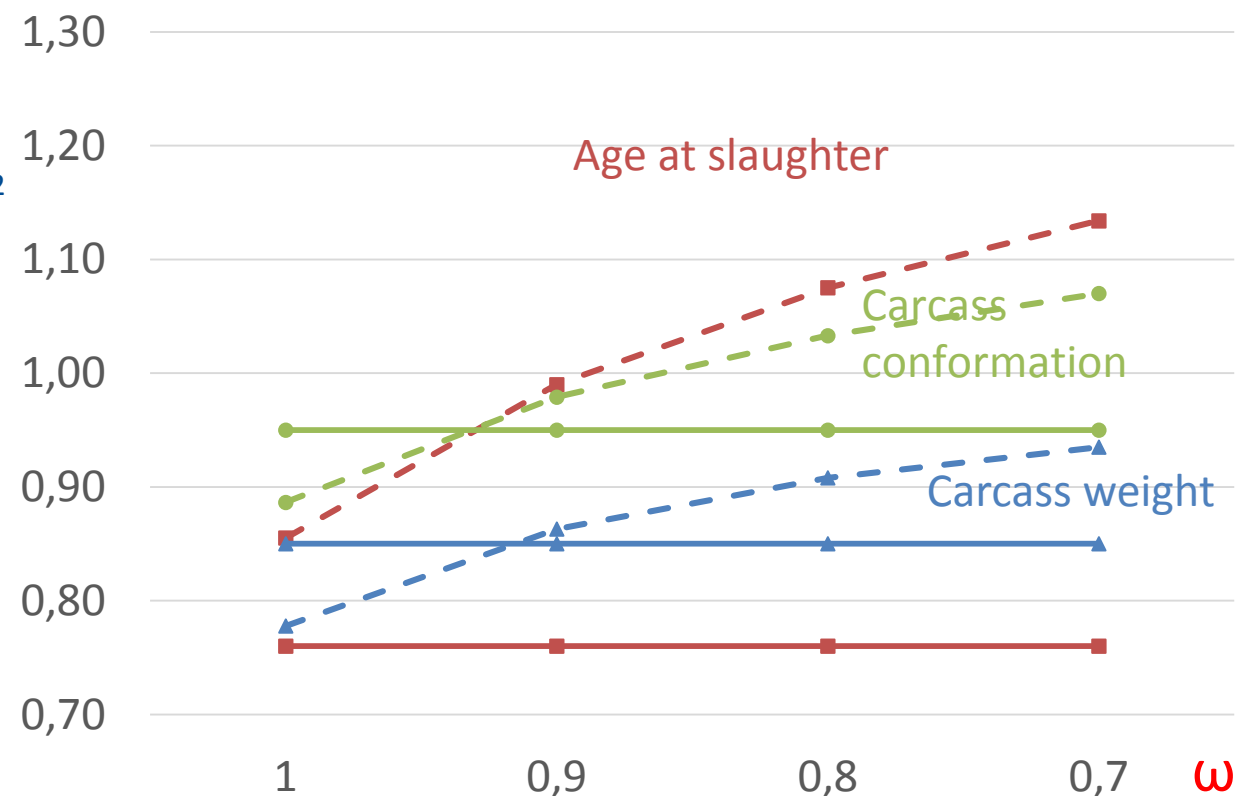
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Low impact of ω on accuracy

Huge impact of ω on bias:
lower ω => lower bias

Evolution of the regression coefficient of DYD and EBV depending on the scaling factor ω of the **H** matrix in the Montbeliarde breed

Setting of the SSGBLUP relationship matrix: α

$$H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - A_{22}^{-1} \end{pmatrix}$$ with **G***=(1-α)**G**+α**A**$_{22}$
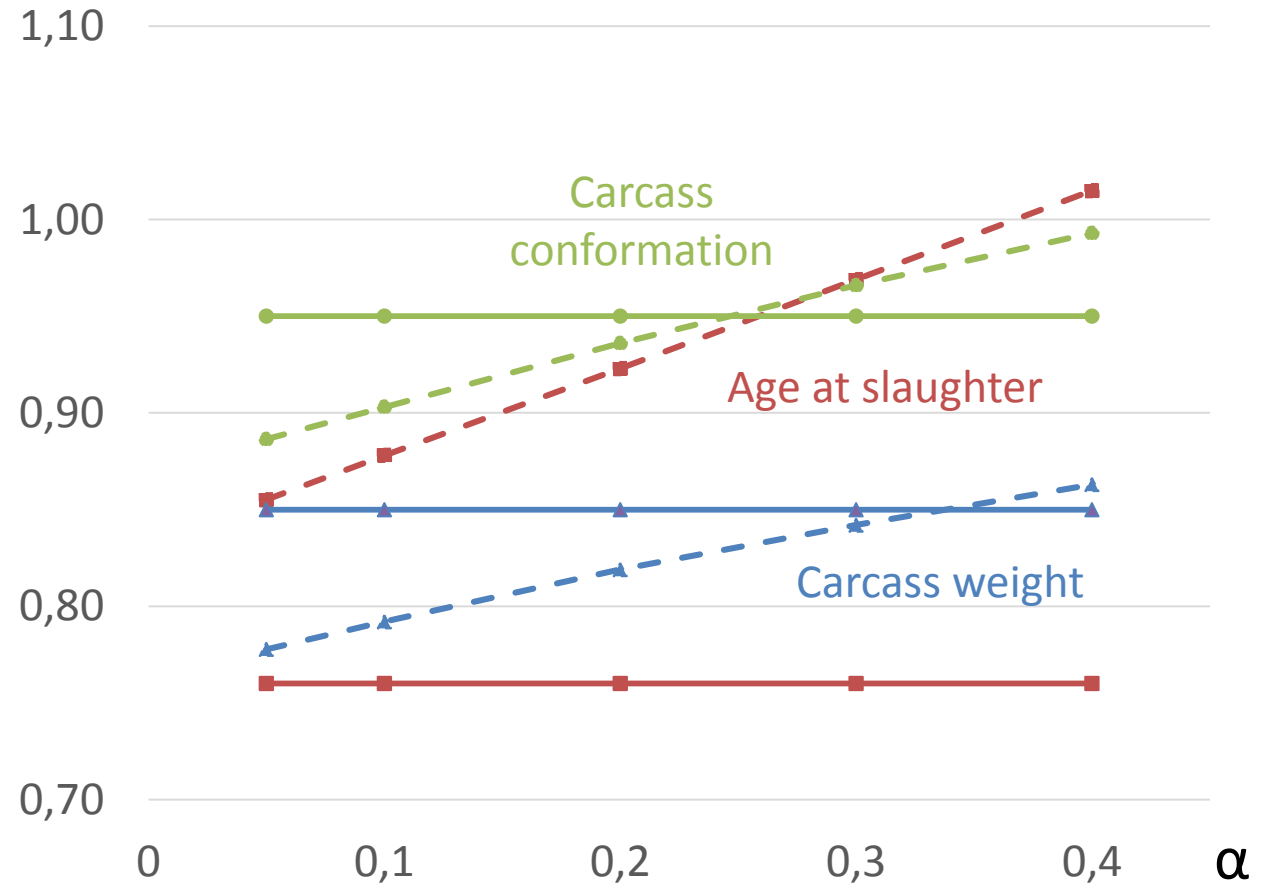
Low impact of α on accuracy; slightly higher
average accuracy with α= 0.2 and α = 0.3

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$$H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - A_{22}^{-1} \end{pmatrix}$$ with **G***=(1-α)**G**+α**A**$_{22}$

Low impact of α on accuracy; slightly higher average accuracy with α= 0.2 and α = 0.3

Carcass conformation

Age at slaughter

Carcass weight

Evolution of the regression coefficient of DYD and EBV depending α in the **H** matrix in the Montbeliarde breed

Setting of the SSGBLUP relationship matrix: α

$$H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - A_{22}^{-1} \end{pmatrix}$$ with $G^* = (1-\alpha)G + \alpha A_{22}$

Low impact of α on accuracy; slightly higher average accuracy with α = 0.2 and α = 0.3

High impact of α on bias:
higher α => lower bias

Evolution of the regression coefficient of DYD and EBV depending α in the **H** matrix in the Montbeliarde breed

Setting of the SSGBLUP relationship matrix: α
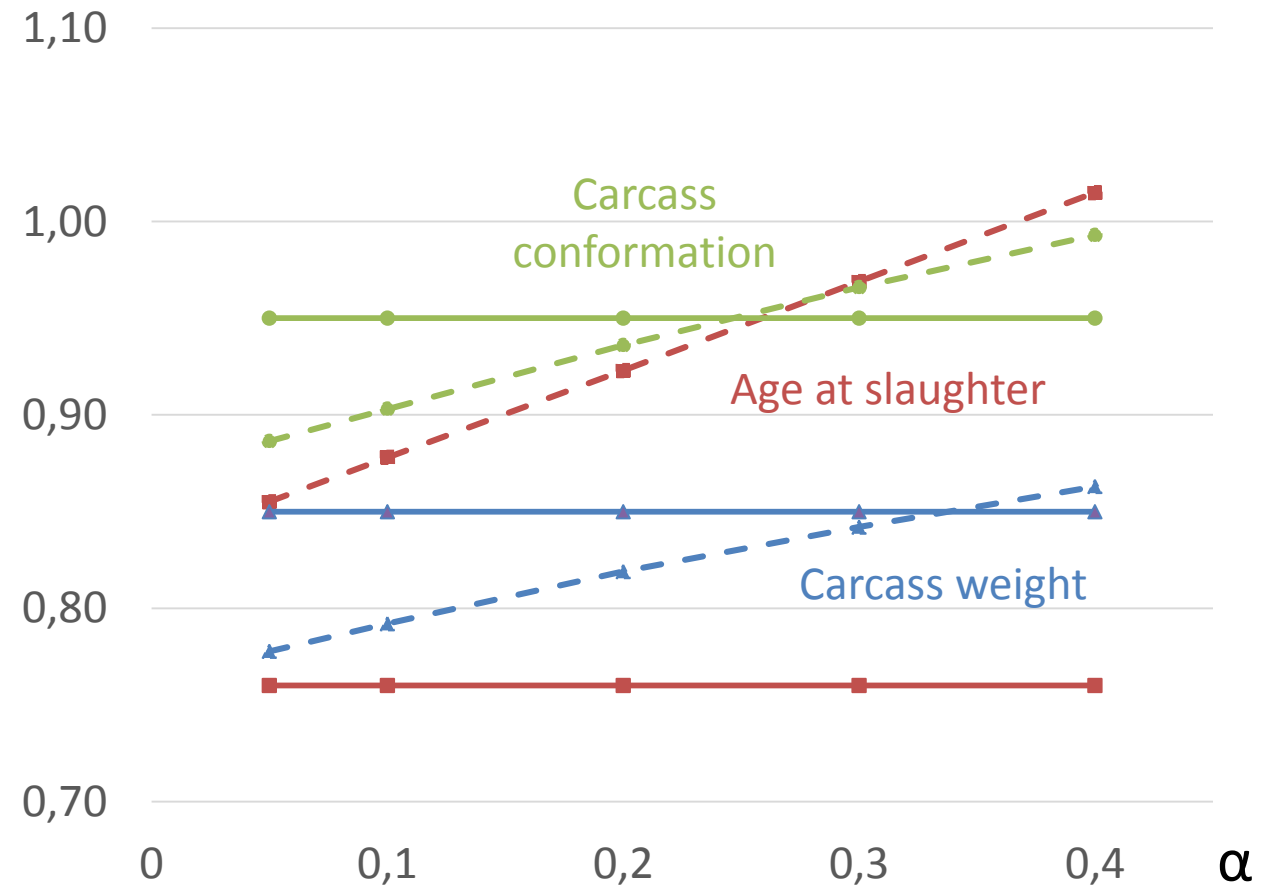
$$H^{-1} = A^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & G^{*-1} - A_{22}{}^{-1} \end{pmatrix}$$ with **G*=(1-α)G+αA$_{22}$**

Low impact of α on accuracy; slightly higher average accuracy with α= 0.2 and α = 0.3

High impact of α on bias:
higher α => lower bias

Highest accuracy with lowest bias without reducing accuracy: α = 0.3

Carcass conformation

Age at slaughter

Carcass weight

Evolution of the regression coefficient of DYD and EBV depending α in the **H** matrix in the Montbeliarde breed

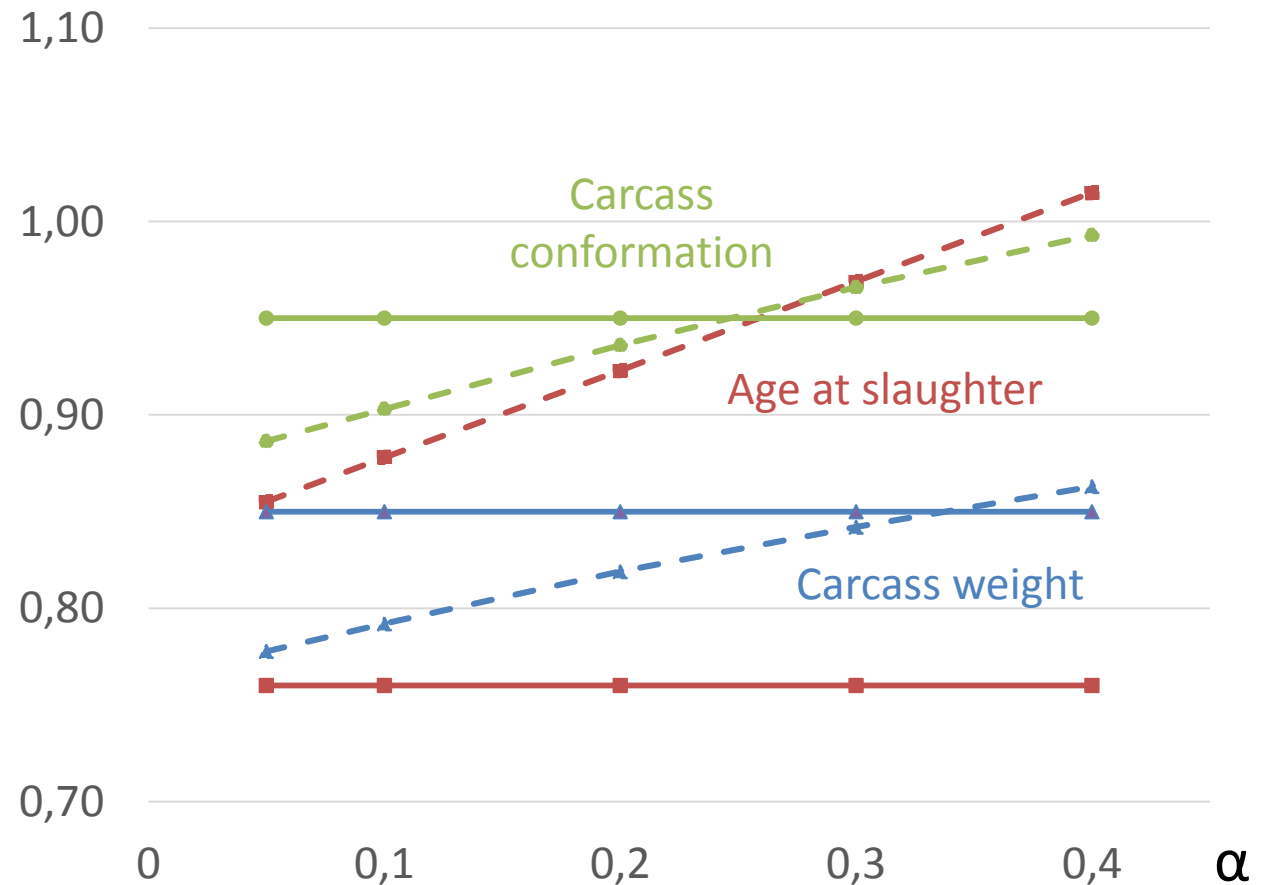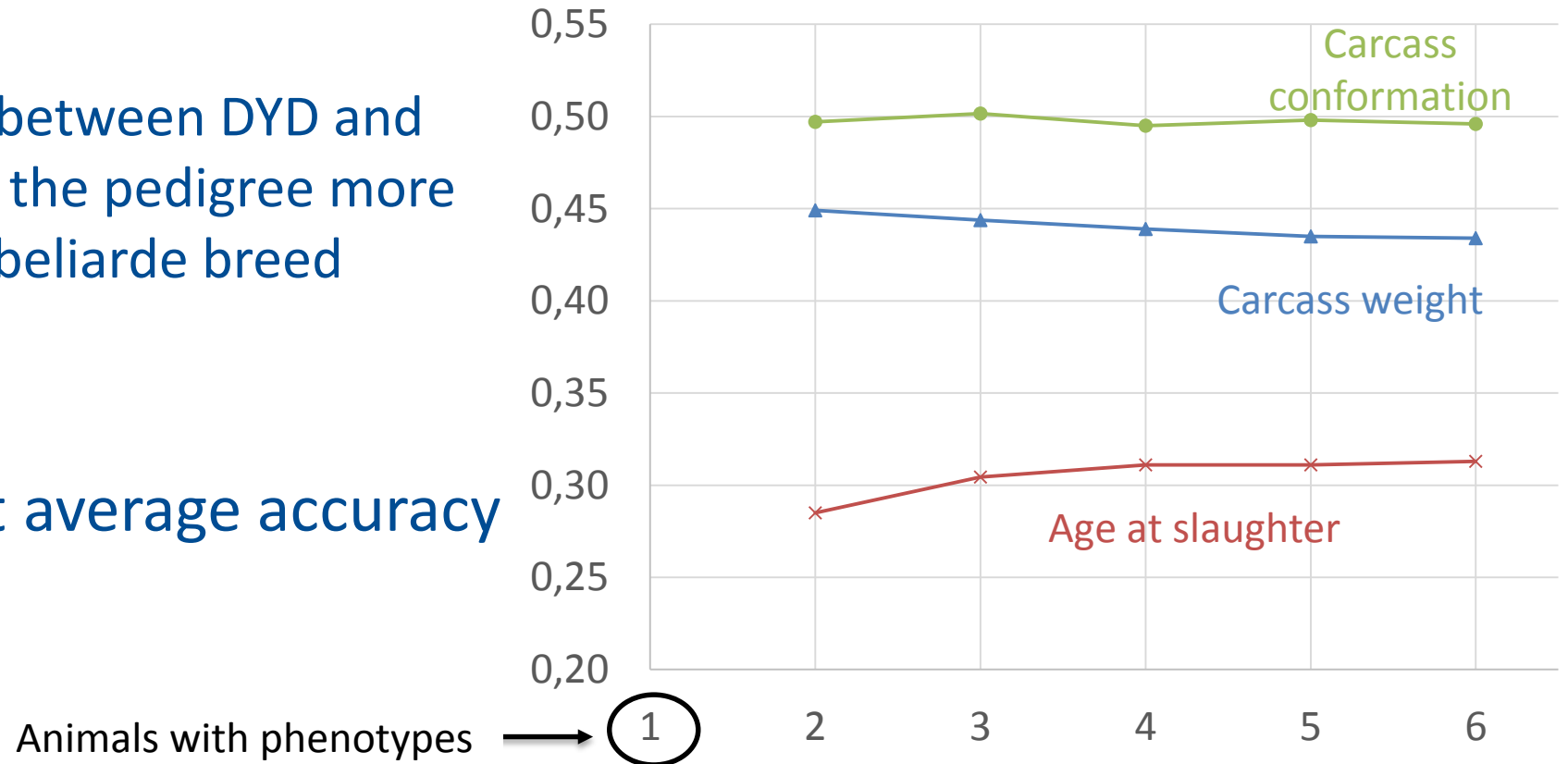# Impact of the number of generations traced back in the pedigree

Evolution of correlations between DYD and EBV when tracing back in the pedigree more generations on the Montbeliarde breed

3 generations: highest average accuracy

Animals with phenotypes →

Carcass conformation
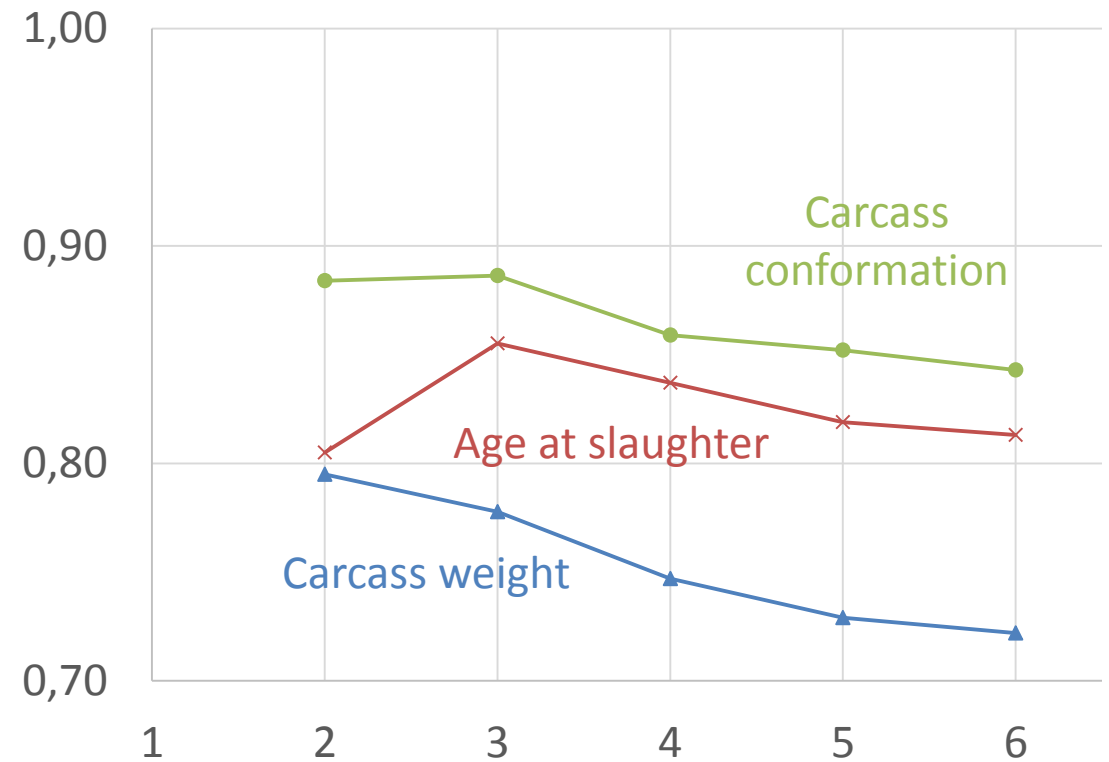
Carcass weight

Age at slaughter

Impact of the number of generations traced back in the pedigree

Evolution of the regression coefficient of DYD on EBV when tracing back in the pedigree more generations in the Montbeliarde breed

3 generations: closest to one average regression coefficient

Carcass conformation

Age at slaughter

Carcass weight

Conclusion

- GBLUP and BayesC equivalent, better than BLUP, except for age at slaughter

- SSGBLUP: most suitable approach

- SSGBLUP requires a trait-dependent setting of the relationship matrix for the control of bias

- More than 3 generations traced back causes higher bias and lower accuracy

Conclusion

- GBLUP and BayesCπ equivalent, better than BLUP, except for age at slaughter
- SSGBLUP: most suitable approach
- SSGBLUP requires a trait-dependent setting of the relationship matrix for the control of bias
- More than 3 generations traced back causes higher bias and lower accuracy

Thank you for your attention!