

# How to improve breeding values prediction for Feed Conversion Ratio in case of incomplete longitudinal body weights A simulation study

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# **Context**

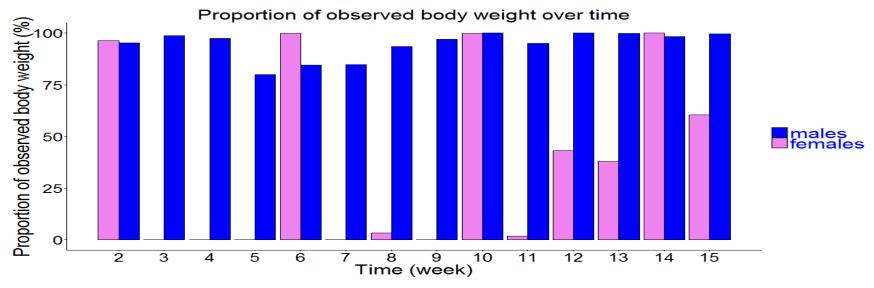
Repeated data over time Feed intake, Body weight, Feed efficiency

= longitudinal data



Improve genetic of feed efficiency

#### Missing body weight records







# The problem

Estimation of variance components becomes erratic when some records are missing (Nobre et al., 2003)

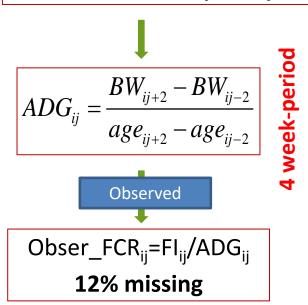
- Do missing BW data have an impact on the estimation of genetic parameters for longitudinal FCR?
- How to improve them?





#### 1286 males i, 14 weeks j of observation

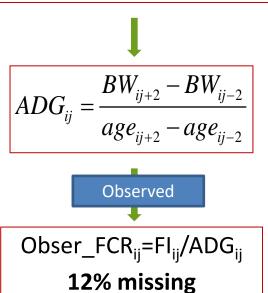
FI<sub>ij</sub>, BW<sub>ij</sub> (missing data was negligible)



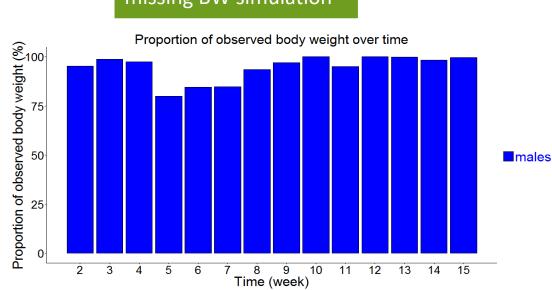


# 1286 males i, 14 weeks j of observation

FI<sub>ii</sub> BW<sub>ii</sub> (missing data was negligible)

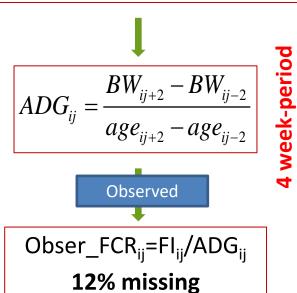


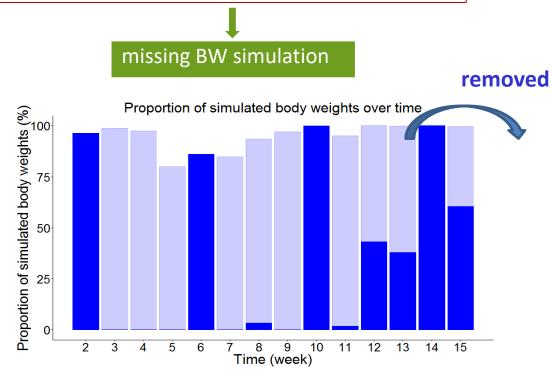
missing BW simulation



# 1286 males i, 14 weeks j of observation

FI<sub>ij</sub>, BW<sub>ij</sub> (missing data was negligible)

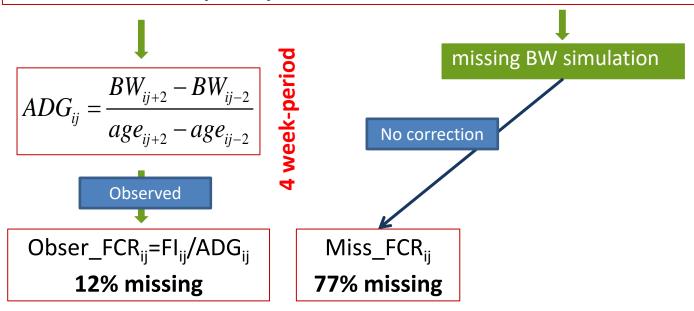






#### 1286 males i, 14 weeks j of observation

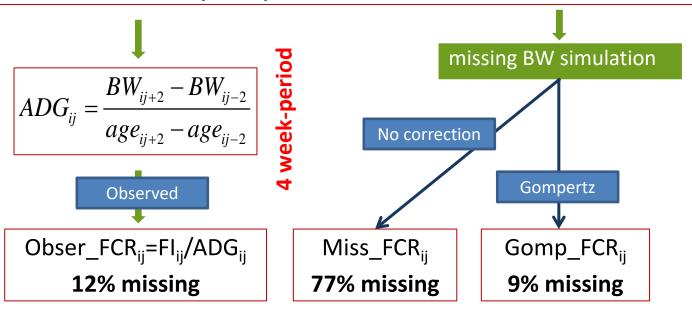
FI<sub>ij</sub>,BW<sub>ij</sub> (missing data was negligible)





# 1286 males i, 14 weeks j of observation

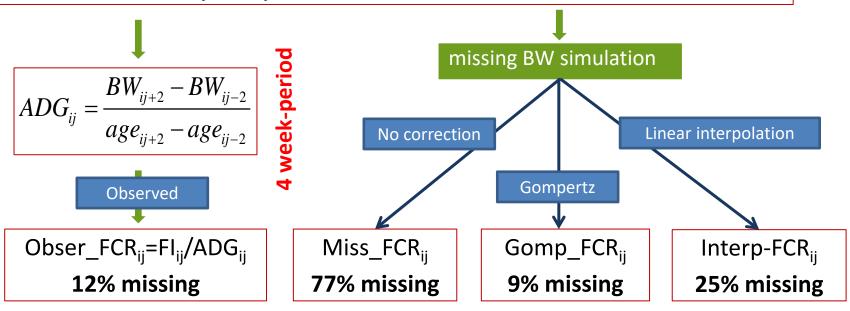
FI<sub>ij</sub>,BW<sub>ij</sub> (missing data was negligible)





#### 1286 males i, 14 weeks j of observation

FI<sub>ij</sub>,BW<sub>ij</sub> (missing data was negligible)



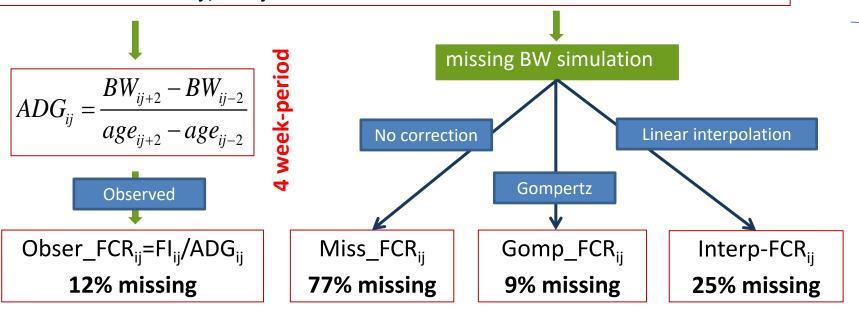


# 100 simulations

# Data analysis

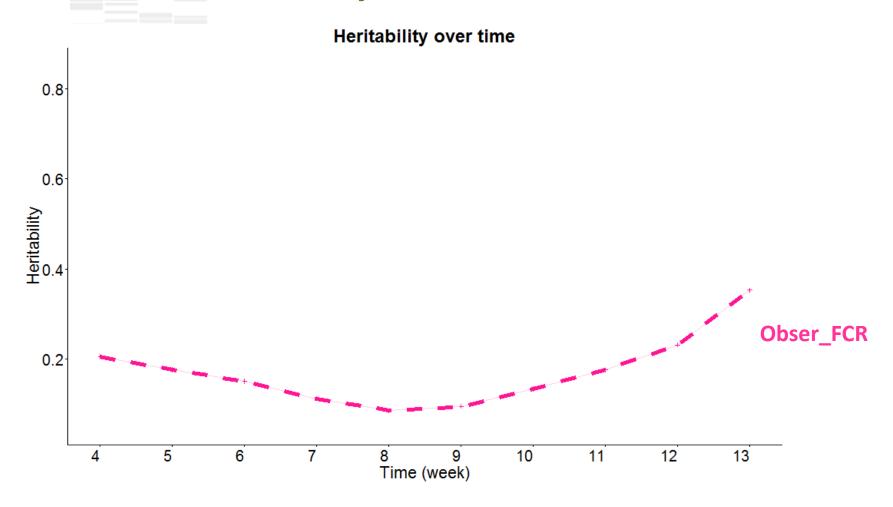
#### 1286 males i, 14 weeks j of observation

FI<sub>ij</sub>, BW<sub>ij</sub> (missing data was negligible)



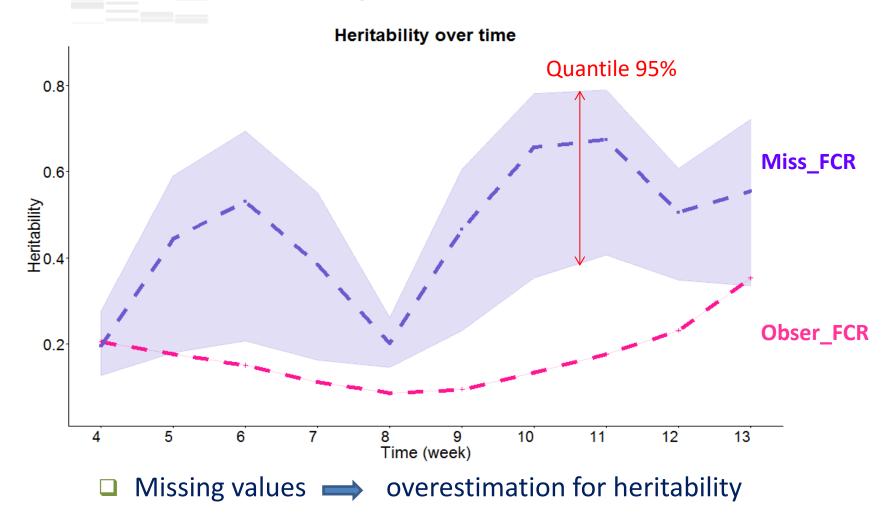
genetic analysis using a random regression model



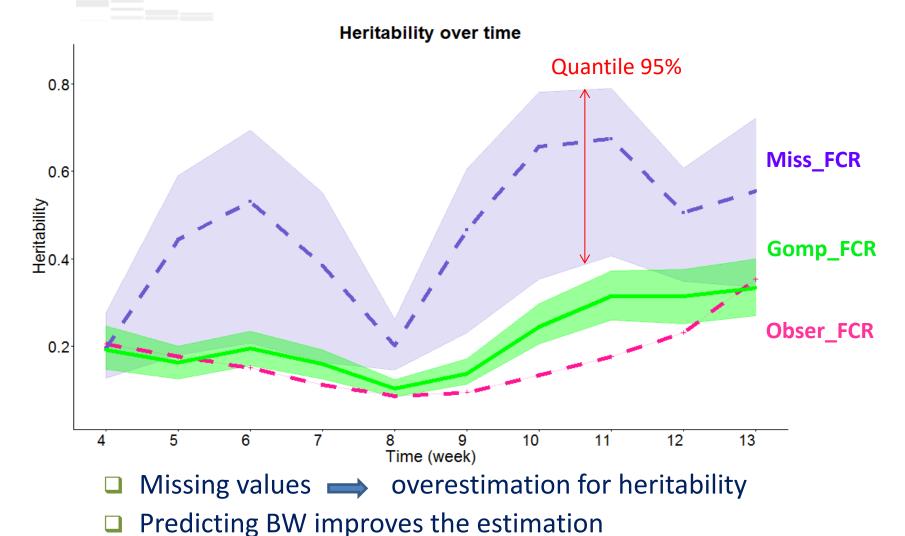


12% = % missing FCR due to : missing BW + outlier values (FCR)

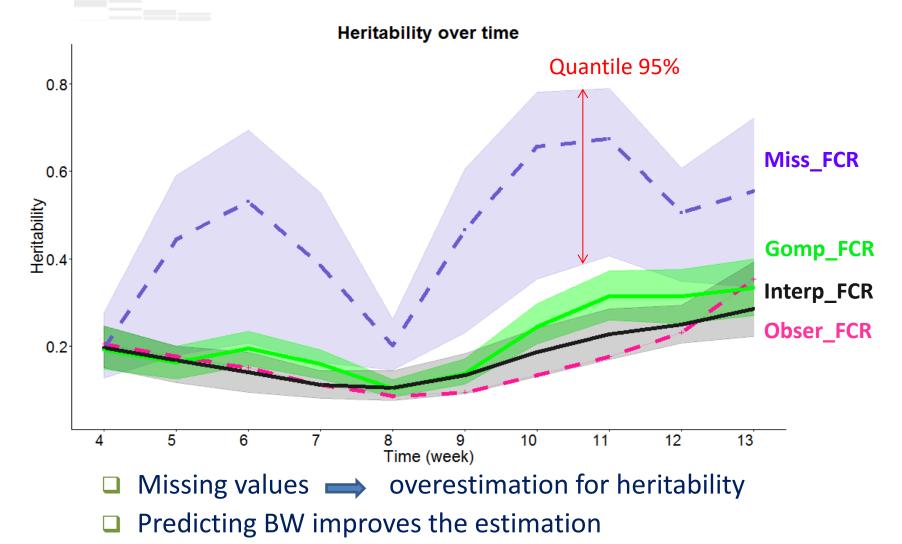






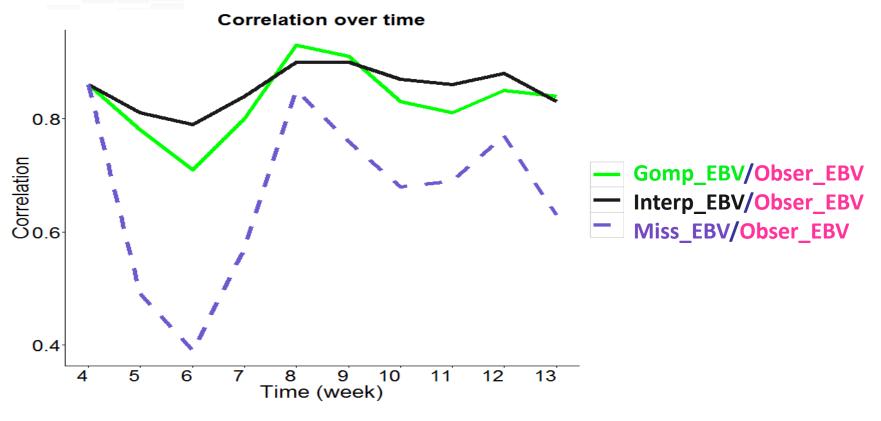








# Results 2: Correlation among EBV for FCR over 10 weeks (week 4 to week 13)

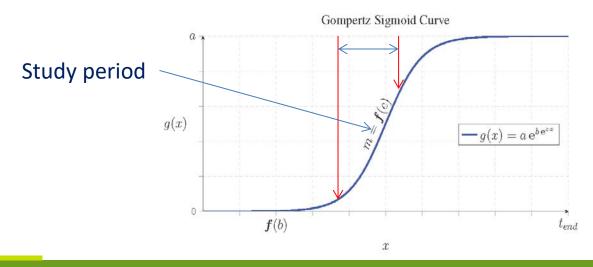


- Missing values poor correlations with obser\_FCR
- Predicting BW improves the correlations



# **Summary and Discussion**

- Missing FCR (due to missing BW)
   ➡ bias h²
   ♣ poor EBV prediction
- Predict BW (Gompertz, quasi linear interpolation)
- improve the estimations of genetic parameters for longitudinal FCR
   Linear interpolation > Gompertz : BW not in the sigmoid part of the curve







# Take home message

It is possible to improve the estimations for longitudinal FCR by predicting the missing BW



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