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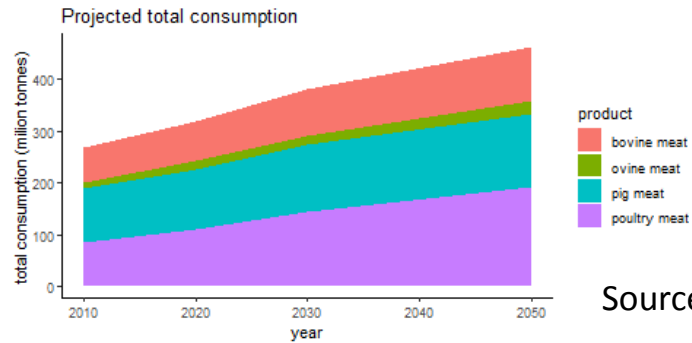
➤ Longitudinal residual feed intake criterion for selection

Ingrid David, Van-Hung Hyunh Tran, H el ene Gilbert



> Context

Forecast : Increase global meat consumption



Needs : Increase in meat production

Solution : Improve feed efficiency

Residual feed intake (RFI)

RFI = **observed FI** corrected by predicted FI based on **production** and **maintenance** requirements

New tools : Development automatic self-feeders



New data : Longitudinal **FI**, **MBW**, **ADG**, **BF**

Longitudinal RFI

➤ Reminder: genetic improvement RFI – single record

RFI = *observed FI* corrected by predicted FI based on **production** and **maintenance** requirements

Traits
FI ADG MBW BF

Method selection

- Index **FI ADG MBW BF**
- Index **RFI (phenotypic regression) ADG MBW BF**
- **RFI (genetic regression)**



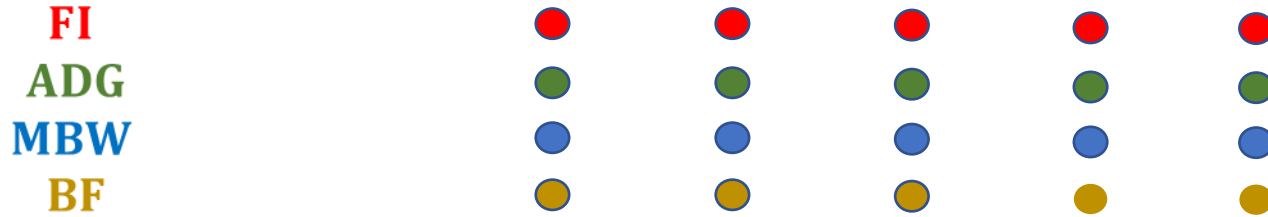
Estimation (4x4) covariance matrices needed



Multiple trait model

➤ The problem – G for longitudinal data

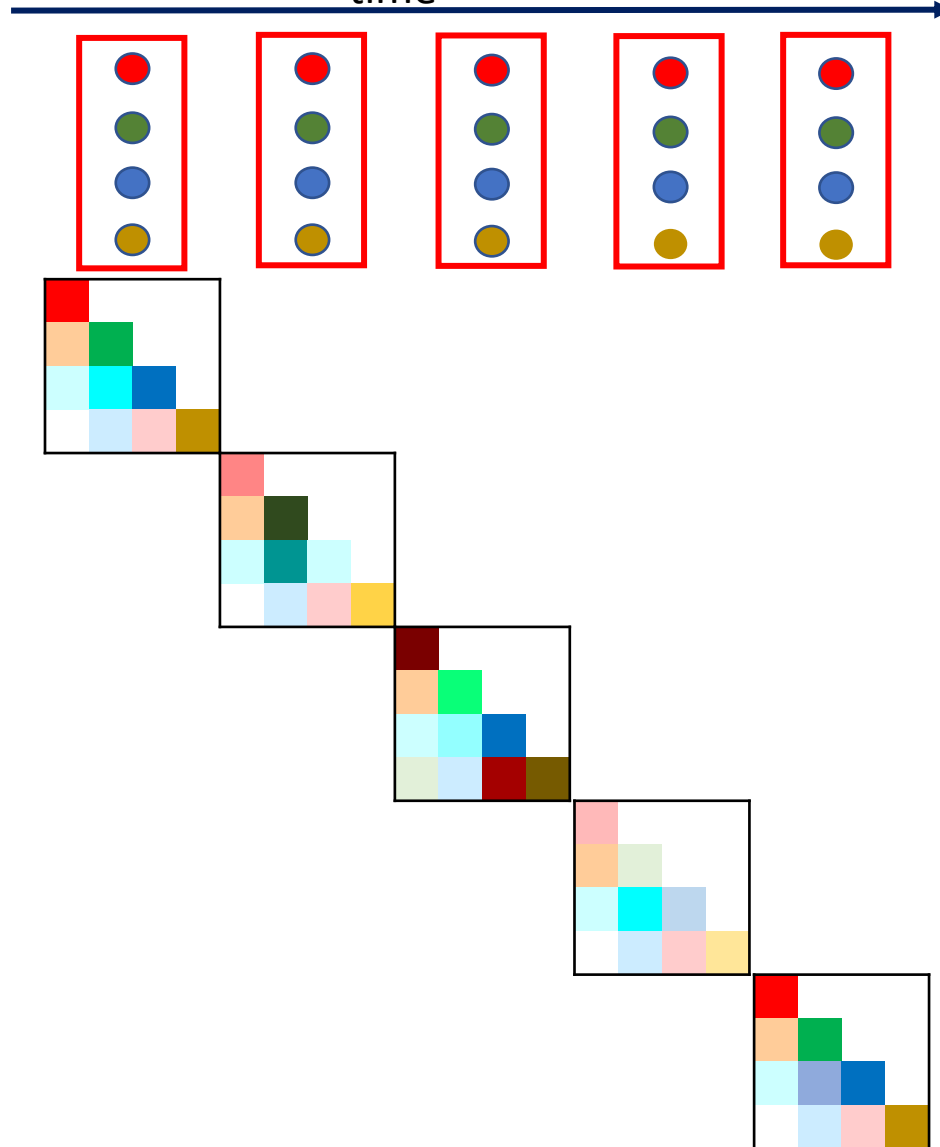
time



➤ The problem – G for longitudinal data

time

FI
ADG
MBW
BF



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Longitudinal RFI criterion
30/08/2021 / David

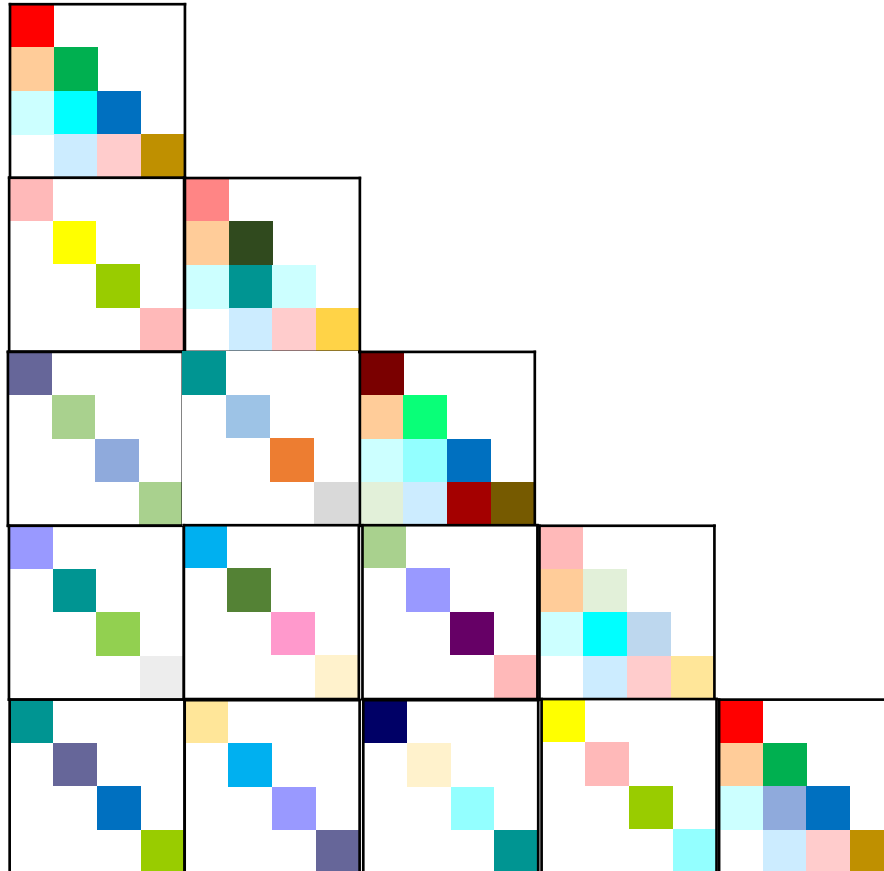
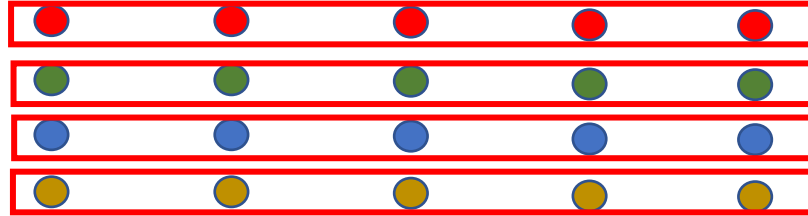


➤ The problem – G for longitudinal data

time



FI
ADG
MBW
BF



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Longitudinal RFI criterion
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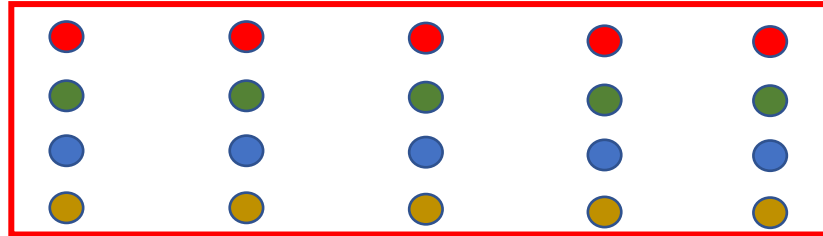


➤ The problem – G for longitudinal data

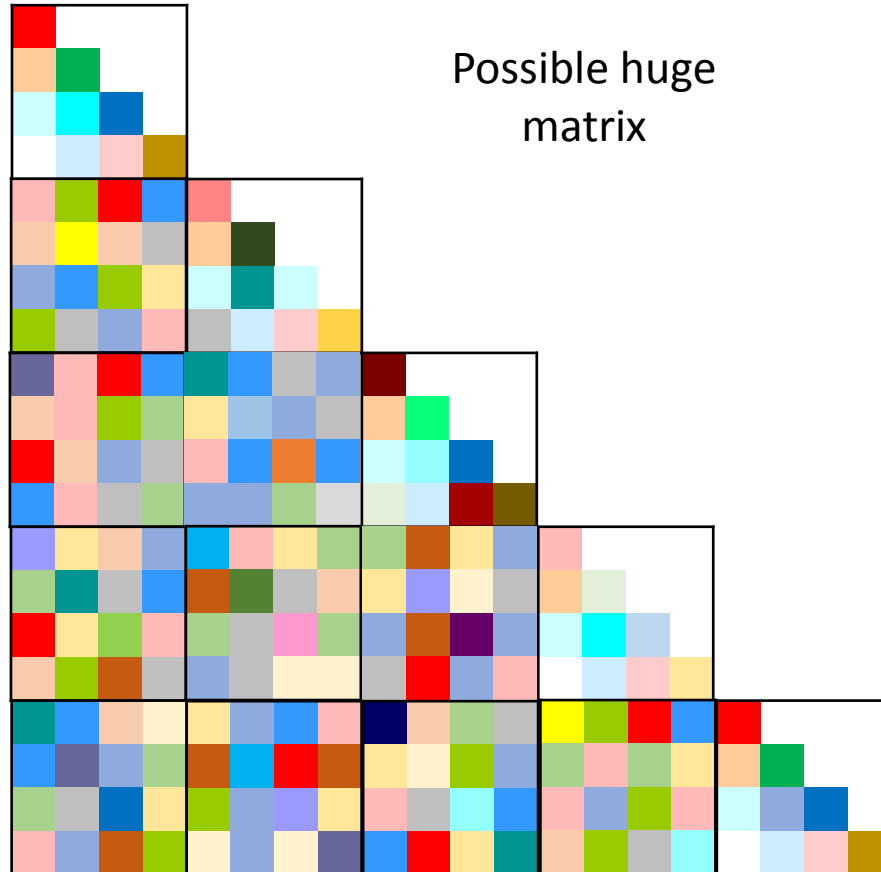
time



FI
ADG
MBW
BF



G



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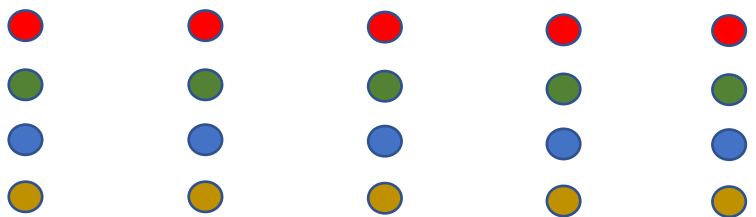
Longitudinal RFI criterion
30/08/2021 / David



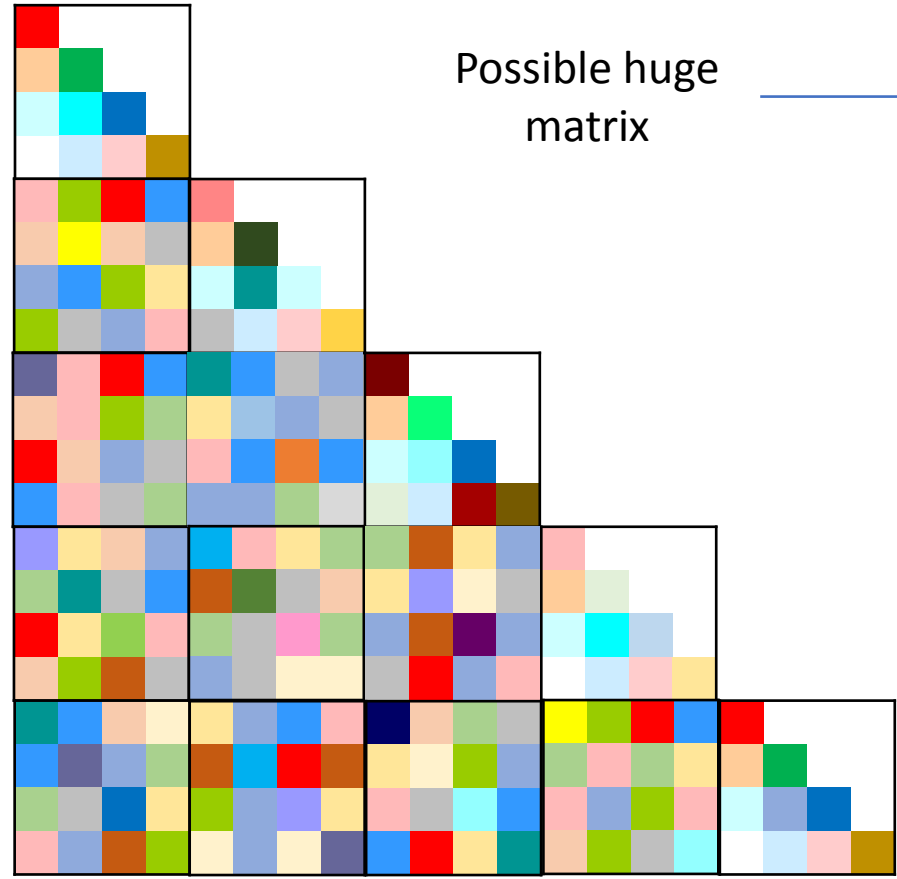
➤ The problem – G for longitudinal data

time →

FI
ADG
MBW
BF



G



Possible huge matrix

Longitudinal models

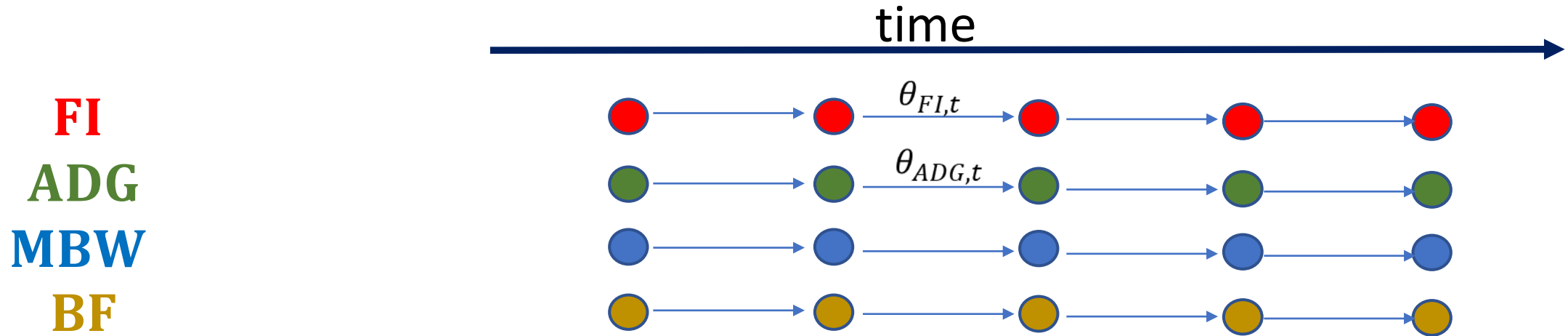
Random regression ?

RR degree 2 → 78 parameters

Convergence issues



➤ The proposed solution: multiple trait structured antedependence model



$$\mathbf{u}_{FI,t} = \theta_{FI,t} \mathbf{u}_{FI,t-1} + \boldsymbol{\varepsilon}_{FI,t}$$

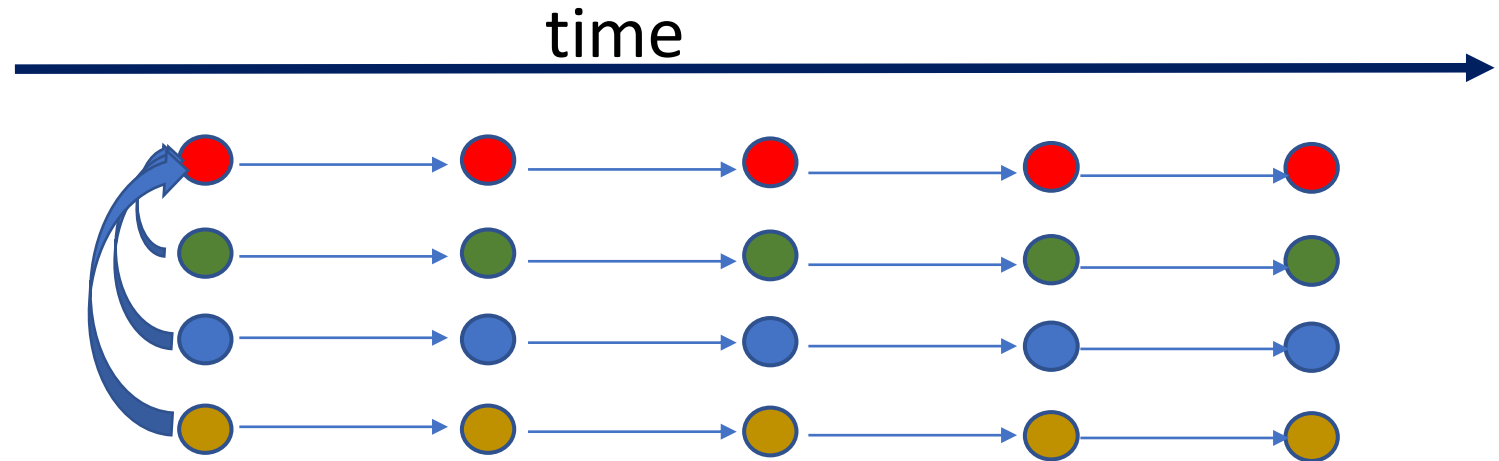
$$\mathbf{u}_{ADG,t} = \theta_{ADG,t} \mathbf{u}_{ADG,t-1} + \boldsymbol{\varepsilon}_{ADG,t}$$

$$\mathbf{u}_{MBW} = \dots$$

$$\mathbf{u}_{BF} = \dots$$

➤ The proposed solution: multiple trait structured antedependence model

FI
ADG
MBW
BF



$$\mathbf{u}_{FI,t} = \theta_{FI,t} \mathbf{u}_{FI,t-1} + \beta_{ADG,t} \mathbf{u}_{ADG,t} + \beta_{MBW,t} \mathbf{u}_{MBW,t} + \beta_{BF,t} \mathbf{u}_{BF,t} + \varepsilon_{FI,t}$$

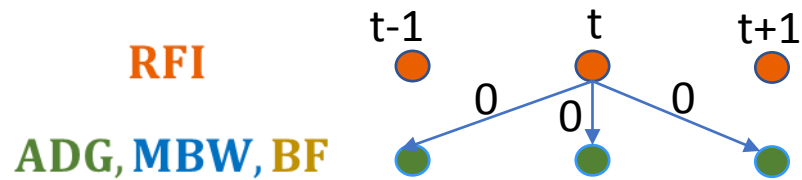
$$\mathbf{u}_{ADG,t} = \theta_{ADG,t} \mathbf{u}_{ADG,t-1} + \varepsilon_{ADG,t}$$

$$\mathbf{u}_{MBW} = \dots$$

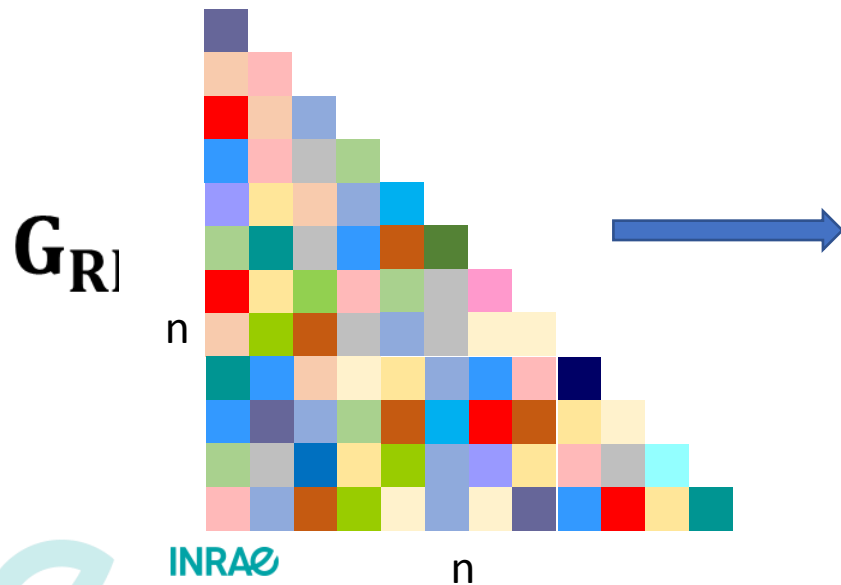
$$\mathbf{u}_{BF} = \dots$$

➤ The proposed solution: multiple trait structured antedependence model

$$\mathbf{u}_{FI,t} = \theta_{FI,t} \mathbf{u}_{FI,t-1} + \beta_{ADG,t} \mathbf{u}_{ADG,t} + \beta_{MBW,t} \mathbf{u}_{MBW,t} + \beta_{BF,t} \mathbf{u}_{BF,t} + \boldsymbol{\varepsilon}_{FI,t}$$



↓
 n $\mathbf{u}_{RFI,t}$ independent from $\mathbf{u}_{ADG}, \mathbf{u}_{MBW}, \mathbf{u}_{BF}$



Eigen decomposition
 $\mathbf{G}_{RFI} \mathbf{L}'_i = \lambda_i \mathbf{L}'_i$

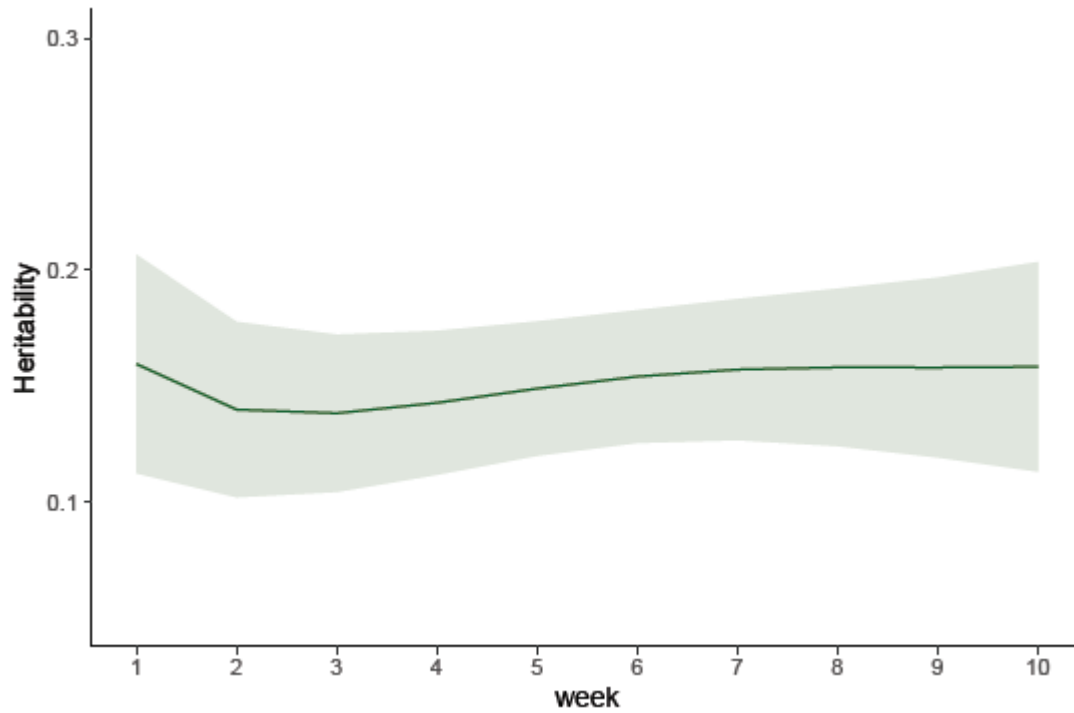
Summarized breeding values
 $\text{SBV}_i = \mathbf{L}_i \mathbf{u}_{RFI}$



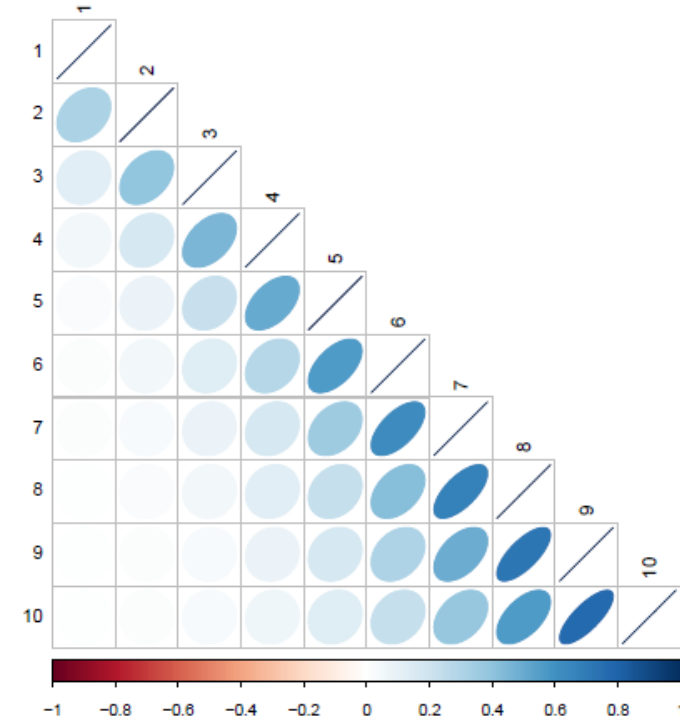
➤ Application to pig data

- 2435 growing french Large White pigs
- 2 lines divergently selected for RFI obtained by phenotypic regression at the test period level (one observation / animal)
- 10 weeks of observation

➤ Results: heritability and genetic correlation for RFI

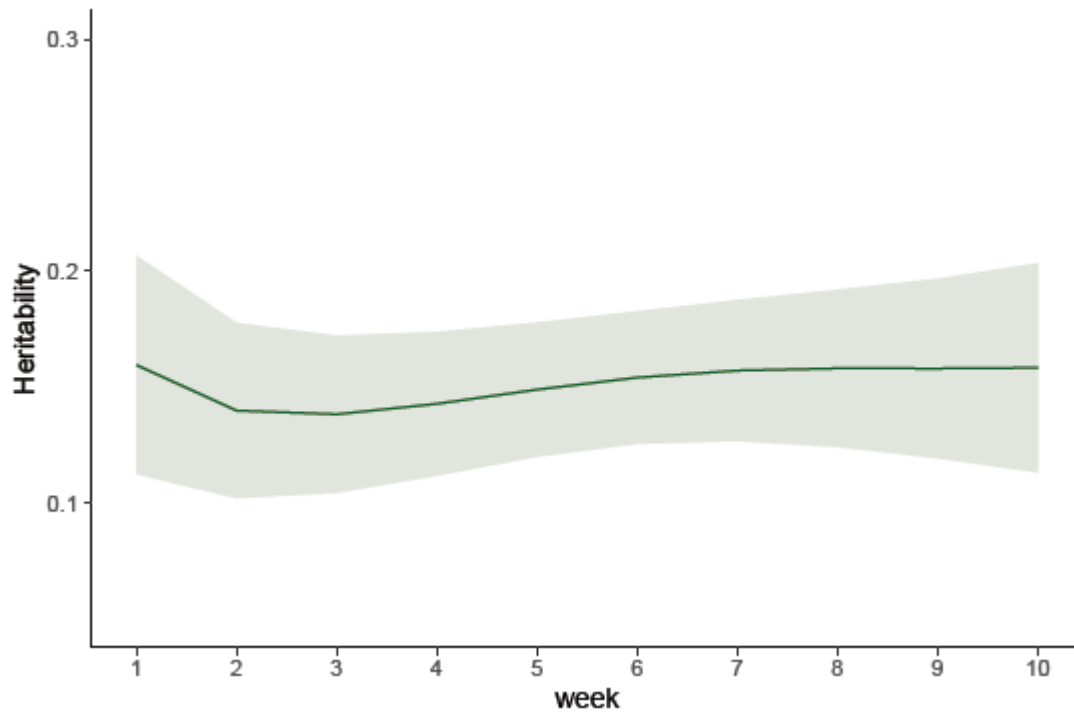


Moderate heritability for RFI

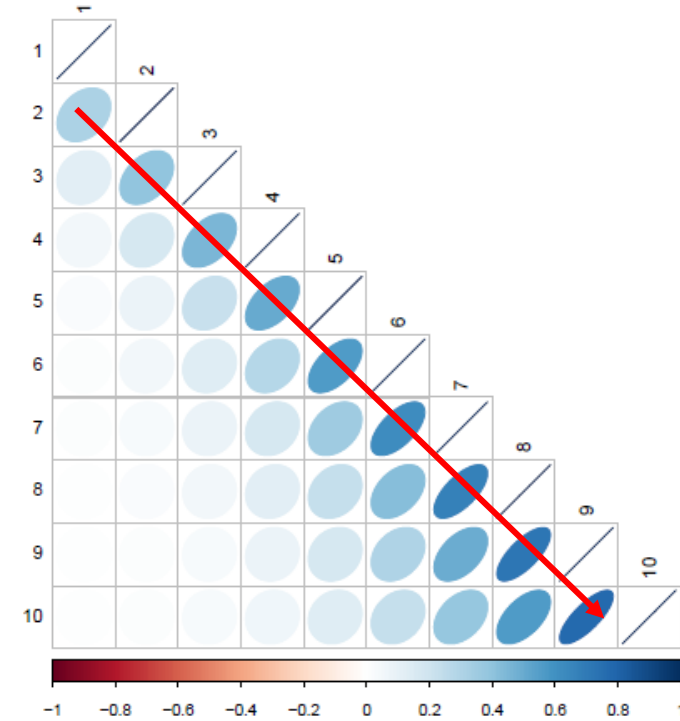


Genetic correlation between RFI that decreased with time interval between measurements

➤ Results: heritability and genetic correlation for RFI

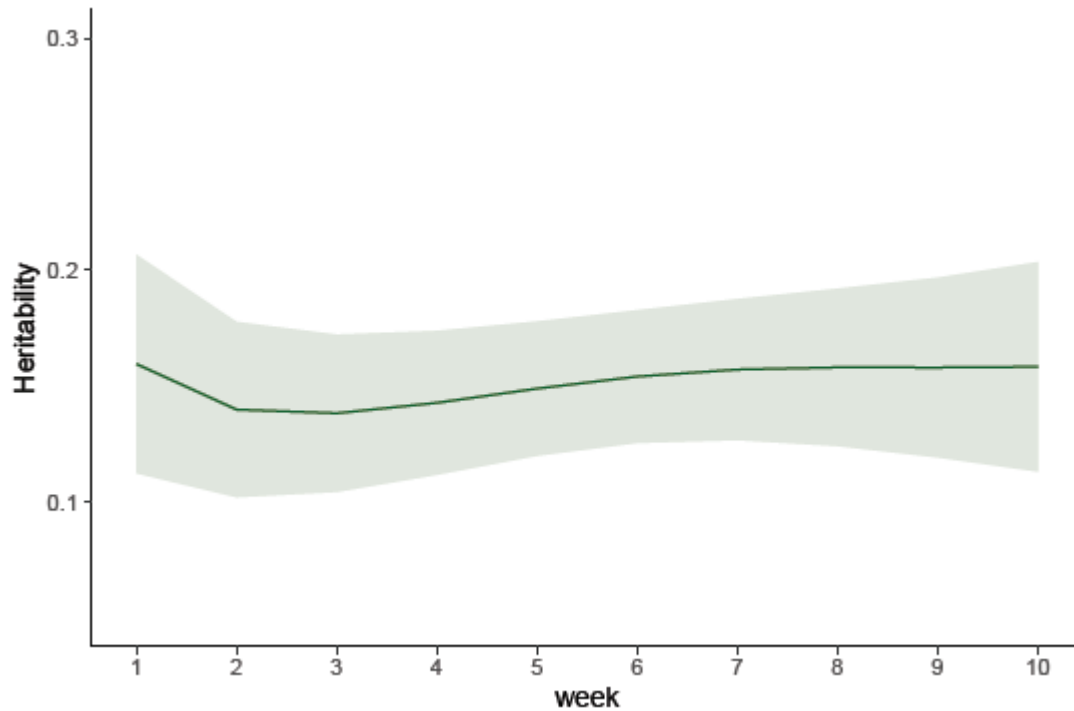


Moderate heritability for RFI

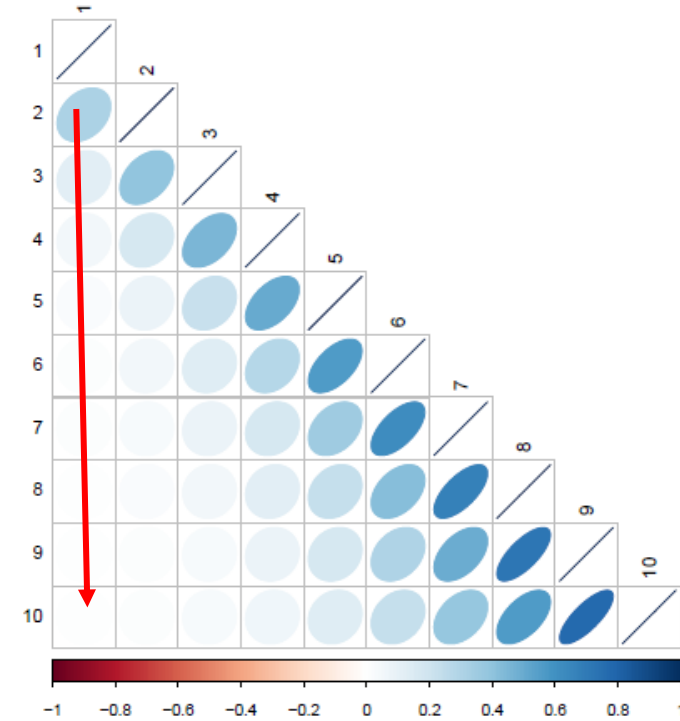


Genetic correlation between RFI that decreased with time interval between measurements

➤ Results: heritability and genetic correlation for RFI

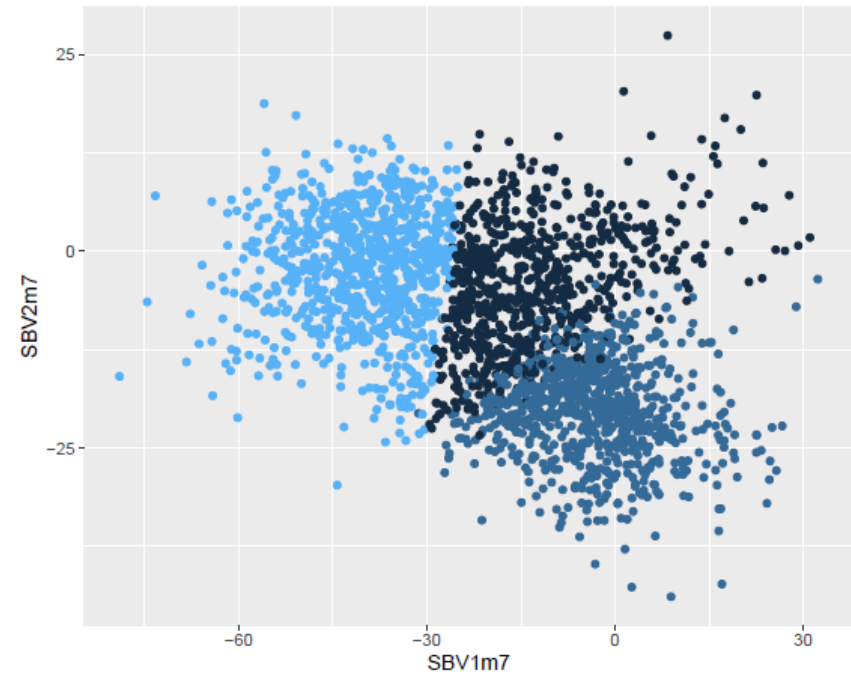
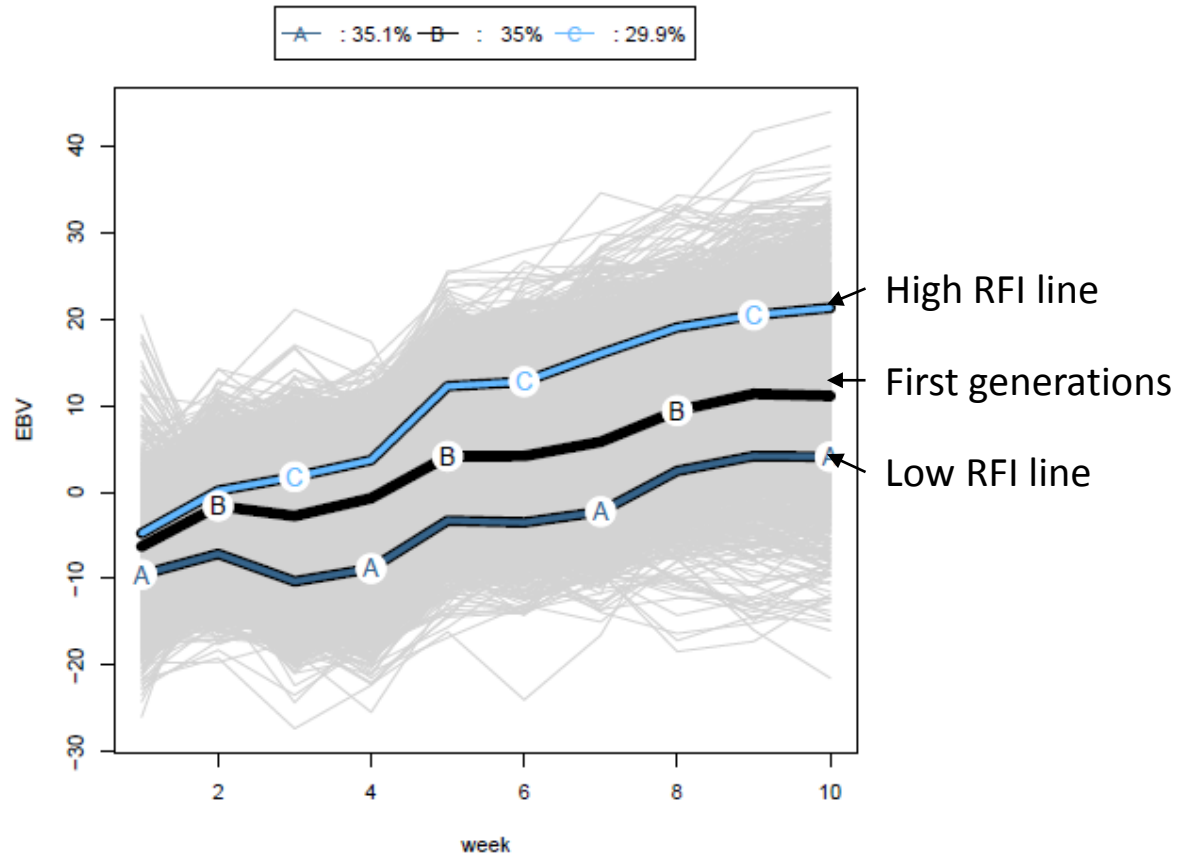


Moderate heritability for RFI



Genetic correlation between RFI that decreased with time interval between measurements

➤ EBV trajectory patterns



➤ Conclusion

- SAD approach permits to model longitudinal RFI
 - ✓ Compute genetic and environmental covariance matrices between traits
 - ✓ RFI genetically independent from production traits at all time points
 - ✓ Trajectory patterns summarized into a limited number of SBV

- Which trajectory is the most interesting?

David, I., Huynh Tran, VH. & Gilbert, H. (2021) New residual feed intake criterion for longitudinal data. Genet Sel Evol 53, 53. <https://doi.org/10.1186/s12711-021-00641-2>

David, I. (2017, September 19). New fortran programs for genetic studies with structured antedependence models (Version V2). Zenodo. <http://doi.org/10.5281/zenodo.1228058>.

