Structured antedependence model for longitudinal analysis of social effects on ADG in rabbits

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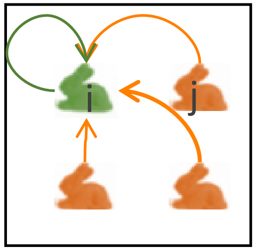
Backgroung

- For animal welfare, group housing is recommended in many species
  - Social genetic effects (SGE) may affect phenotypes of interest

$$\text{Phenotype}_i = \text{direct effects}_i + \sum_{j=1}^{3} \text{indirect effects}_j$$



- SGE may vary over time
  - In group housing conditions, aggressive behavior is generally stronger at mixing and tends to decrease with time

- Few genetic studies have investigated the changes of SGE over time for traits under selection in livestock species.

Goal

- Propose an appropriate model to evaluate changes of SGE (and DGE) over time
- Apply this model to study longitudinal ADG in rabbits
- *Evaluate if it is necessary to account for that phenomenon for selection.*

The model

- For animal *i*, in group *m* with co-mate ϵ K_i at time t_j

$$y_{im}(t_j) = \mu_i(t_j) + DGE_i(t_j) + \sum_{k \in K_i} SGE_k(t_j) + g_m(t_j) + \varepsilon_i(t_j)$$

The problem

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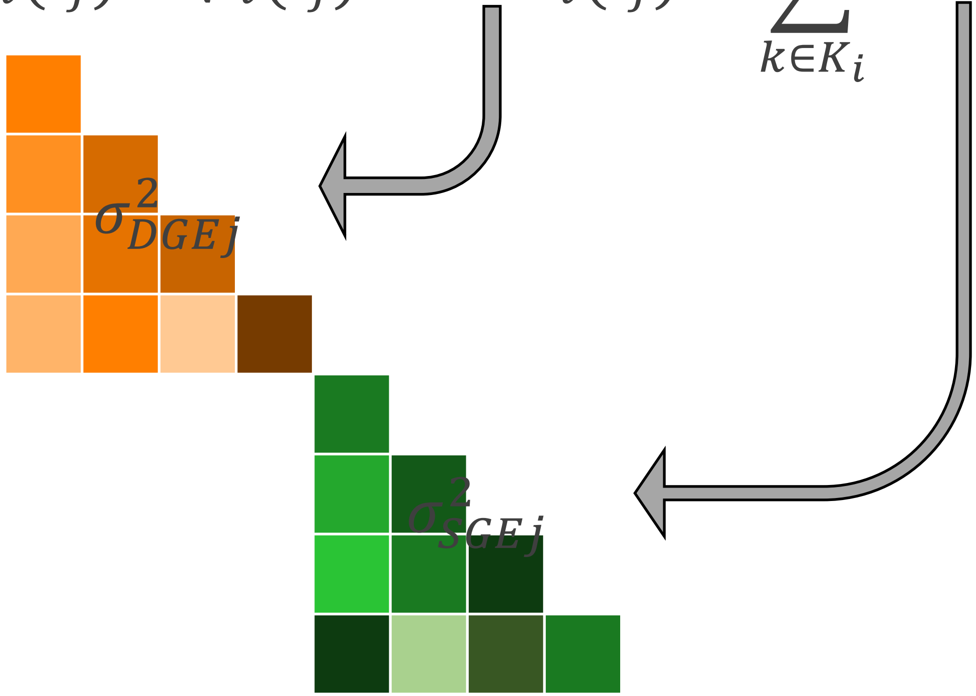

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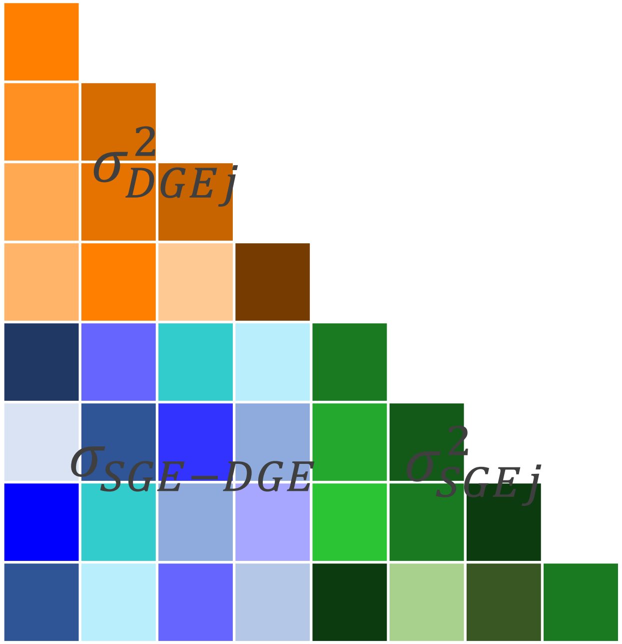


- For n time-points

➔ $\frac{2n(2n+1)}{2}$ genetic parameters

➔ $\frac{n(n+1)}{2}$ parameters other random effects

Large number of parameters

The problem

- For animal *i*, in group *m* with co-mate ϵ K_i at time t_j

$$y_{im}(t_j) = \mu_i(t_j) + DGE_i(t_j) + \sum_{k \in K_i} SGE_k(t_j) + g_m(t_j) + \varepsilon_i(t_j)$$

  - US ➔ too many parameters

  - Character process
  - Random regression

The problem

- For animal *i*, in group *m* with co-mate ϵ K_i at time t_j

$$y_{im}(t_j) = \mu_i(t_j) + DGE_i(t_j) + \sum_{k \in K_i} SGE_k(t_j) + g_m(t_j) + \varepsilon_i(t_j)$$

- US ➔ too many parameters

↓

- ~~Character process~~
- ~~Random regression~~
- Structured antedependence model

Structured antedependence model

- model an observation at time t by regression on the preceding observations.

$$\theta_{s,j} = a_s + b_s t_j + \cdots$$

$$g_i(t_j) = \sum_{s=1}^{\alpha} \theta_{s,j} g_i(t_{j-s}) + e_{g,i}(t_j)$$

$$e_{g,i}(w_j) \sim N(0, {\sigma_j}^2)$$

$${\sigma_j}^2 = \exp(a + b t_j + \cdots)$$

- OWN fortran program for ASReml
- Selection order antedependence and degree polynomial function using LRT

Structured antedependence model

- model an observation at time t by regression on the preceding observations.

$$\theta_{s,j} = a_s + b_s t + \cdots$$

$$g_i(w_j) = \sum_{s=1}^{\alpha} \theta_{s,j} g_i(w_{j-s}) + e_{g,i}(w_j)$$

$$e_{g,i}(w_j) \sim N(0, {\sigma_j}^2)$$

$${\sigma_j}^2 = \exp(a + bt + \cdots)$$

$$SGE_i(w_j) = \sum_{s=1}^{\alpha'} \theta'_{sj} SGE_i(w_{j-s}) + e_{SGE,i}(w_j)$$

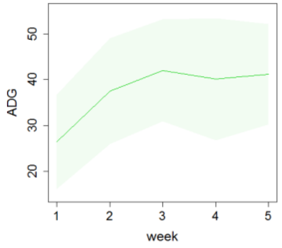
$$DGE_i(w_j) = \sum_{s=1}^{\alpha} \theta_{sj} DGE_i(w_{j-s}) + \delta_j SGE_i(w_j) + e_{DGE,i}(w_j)$$

- extension of the SAD approach to the correlated-effects case is straightforward

Evaluate changes of SGE (and DGE) over time for ADG in rabbit

Data application

- IRTA experiment
  - 3,096  , pen of 8, restricted feeding (75%)
  - weighed at weekly intervals over a 5-week period
  - 5 ADG/ animal



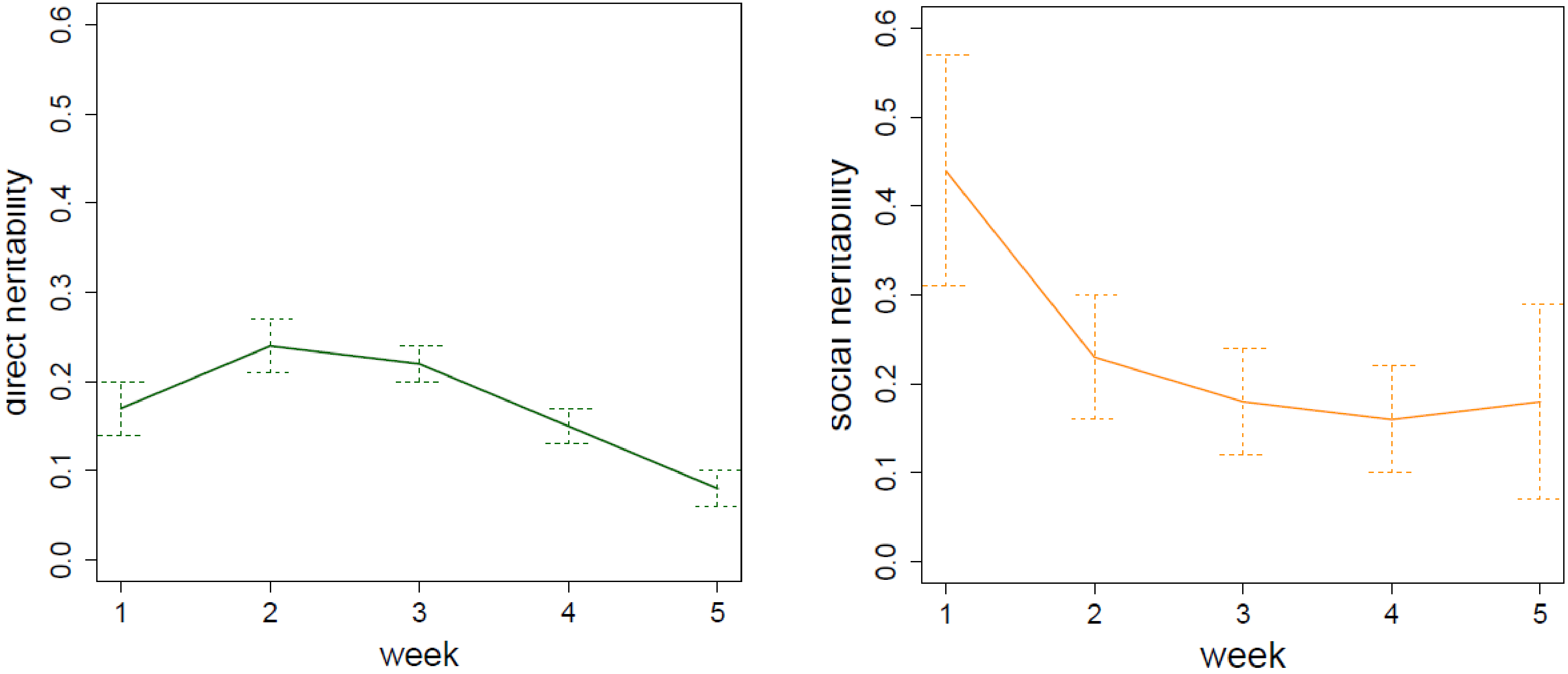
$$ADG_{ilm}(t_j) = \mu_i(t_j) + DGE_i(t_j) + \sum_{k \in K_i} SGE_k(t_j) + g_m(t_j) + l_l(t_j) + \varepsilon_i(t_j)$$

- SAD: 22 parameters instead of 100

Evaluate changes of SGE (and DGE) over time for ADG in rabbit

Result

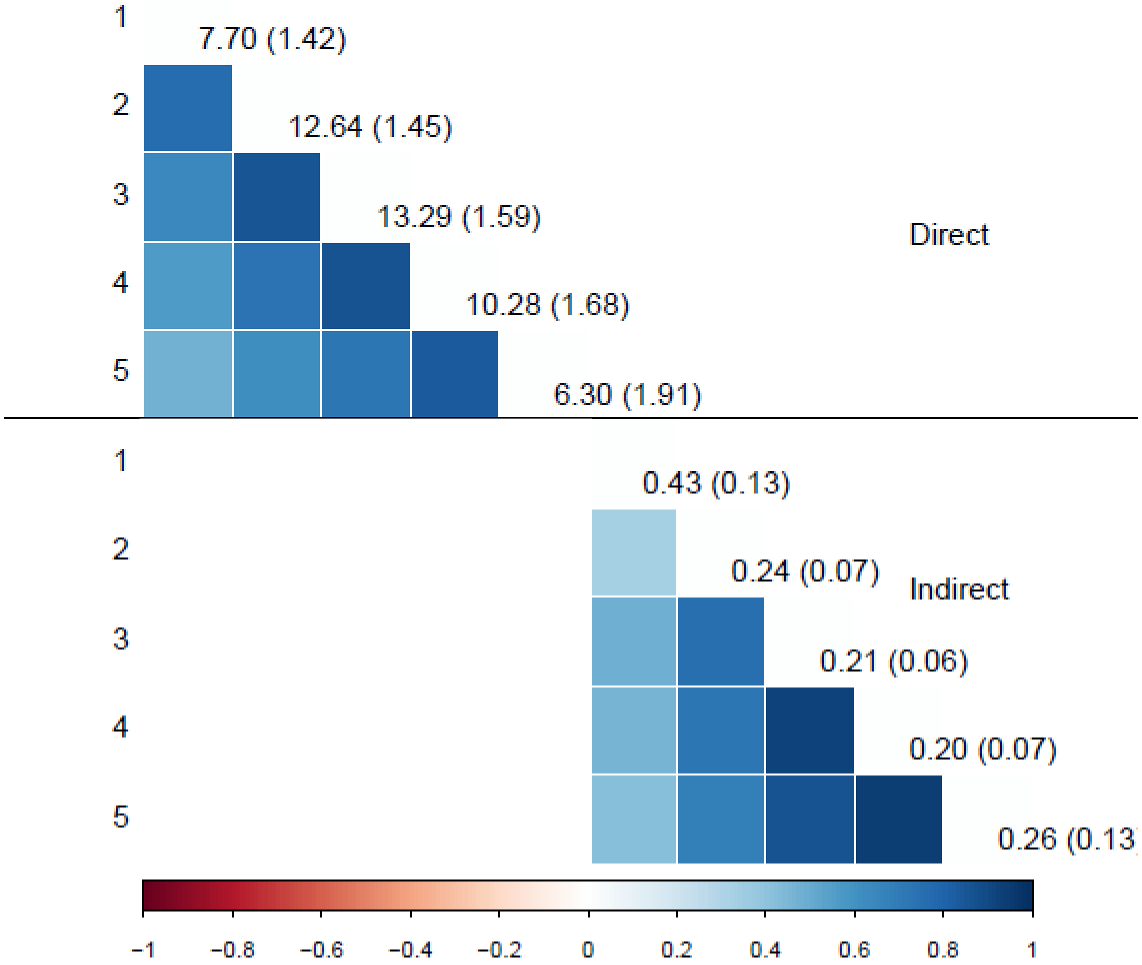
- heritabilities



First week : higher social h^2

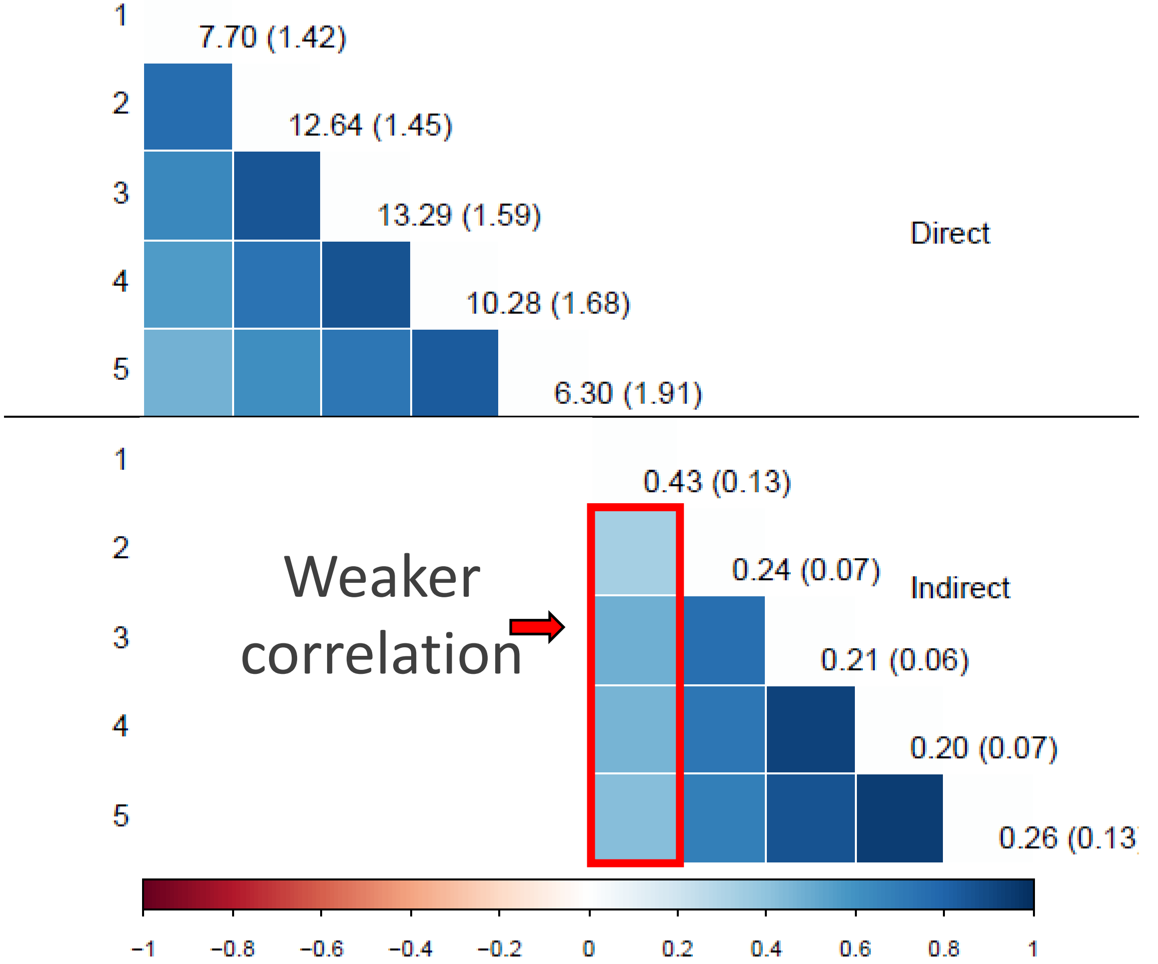
Evaluate changes of SGE (and DGE) over time for ADG in rabbit

Result ◗ Genetic correlations



Evaluate changes of SGE (and DGE) over time for ADG in rabbit

Result ◗ Genetic correlations

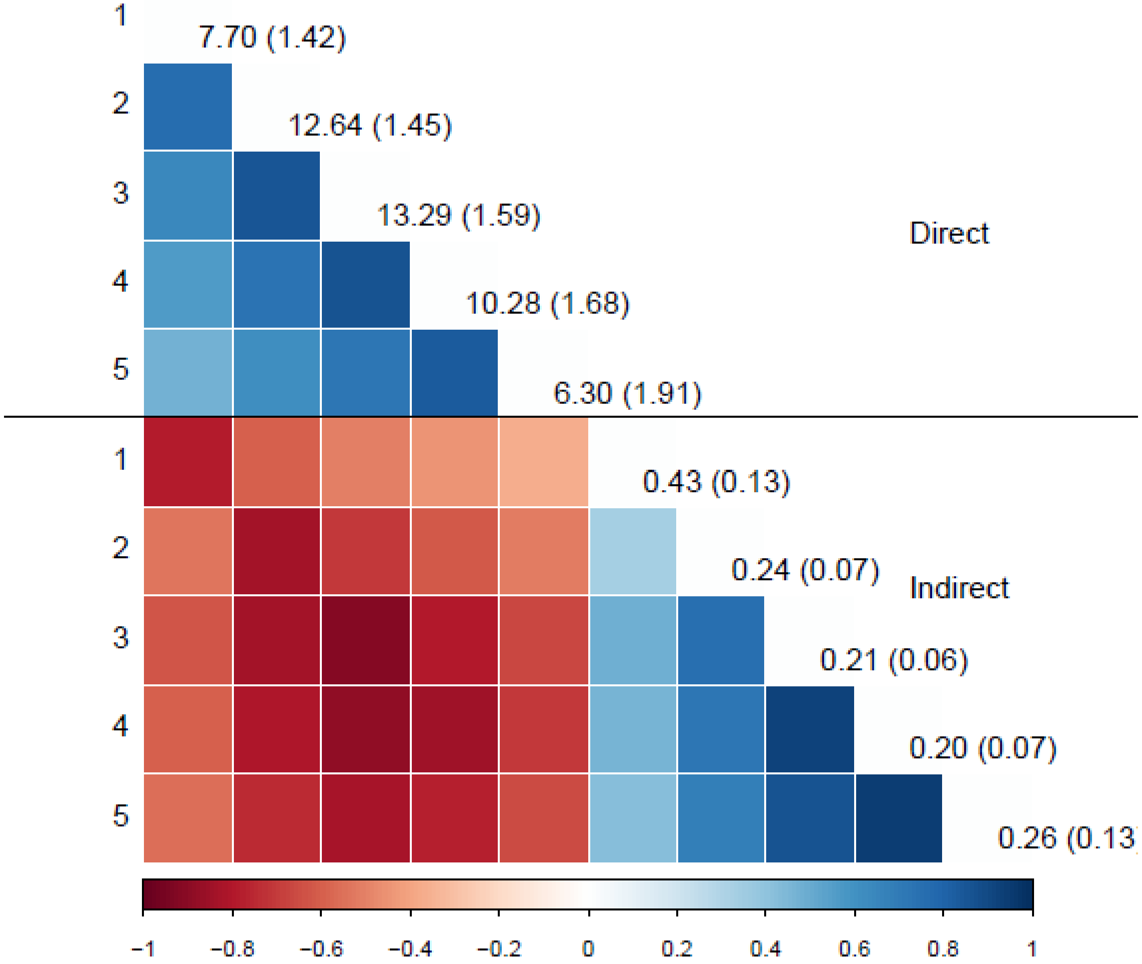


Weaker correlation

SGE first week = different trait

Evaluate changes of SGE (and DGE) over time for ADG in rabbit

Result ◗ Genetic correlations



Genetic antagonism between direct and social genetic effects

Evaluate changes of SGE (and DGE) over time for ADG in rabbits

In summary

- Genetic variances vary over time
- SGE first week is a different trait than SGE of the following weeks
- There is a genetic antagonism between direct and social genetic effects

General conclusion

- This study confirms the hypothesis of changes of SGE over time
- SAD model was appropriate to model these changes
  - SAD programs for correlated random effects are freely available on zenodo https://zenodo.org/record/1228058

account for ΔSGE for selection.

Method

- Simulation study
  - Same design as the experiment
  - SGE, DGE simulated using an unstructured covariance matrix (strong, moderate and weak genetic antagonism)
  - 7 generations of selection
    - Criterion 1: EBV* from a SAD model without SGE
    - Criterion 2: TBV* of the first week (SAD model)
    - Criterion 3: sum of the weekly TBV* (SAD model)

*TBV=EBVd+7*EBVs

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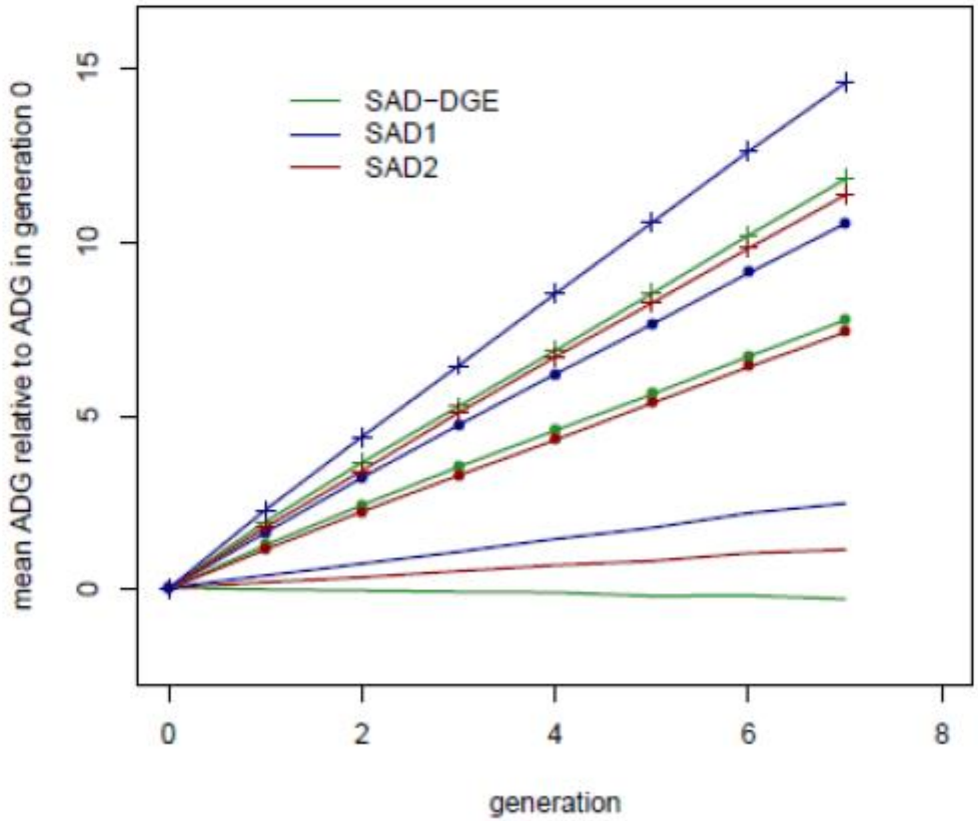
Changes in ADG over generations

account for ΔSGE for selection.

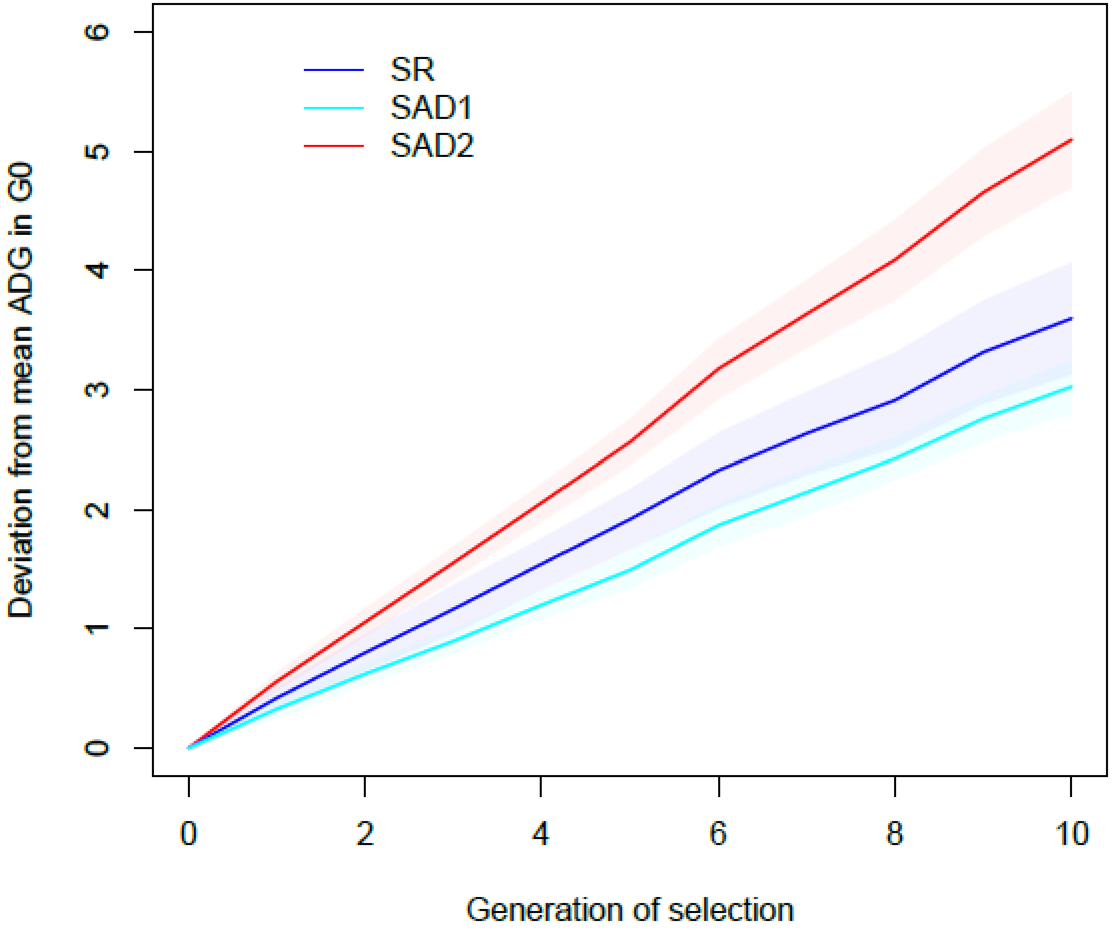
Result



Straight line, line with ● and line with + represent strong, moderate and weak simulated genetic antagonism between direct and indirect effects, respectively.

account for ΔIGE for selection.

Result



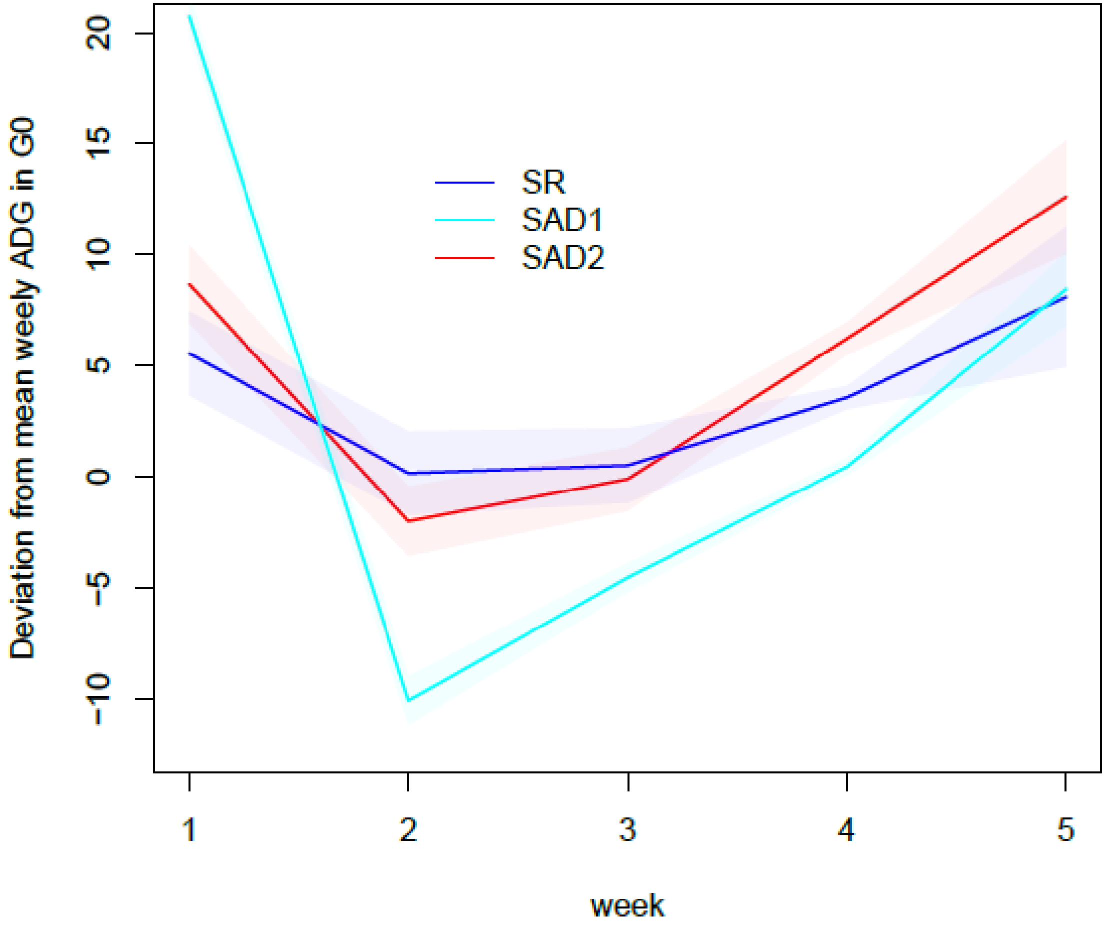
account for ΔIGE for selection.

Conclusion

- Selection is more efficient when changes of SGE over time are taken into account

account for ΔIGE for selection.

Result



$$\boldsymbol{y}(t)=\mu(t)+\boldsymbol{u}(t)+\boldsymbol{p}(t)$$

$$\boldsymbol{p}(t_0)=\boldsymbol{e}(t_0)$$

$$\boldsymbol{p}(t_j)=\sum_{k=1}^{s}\boldsymbol{\theta}_{kj}\,\boldsymbol{p}(t_{j-k})+\boldsymbol{e}(t_j)$$

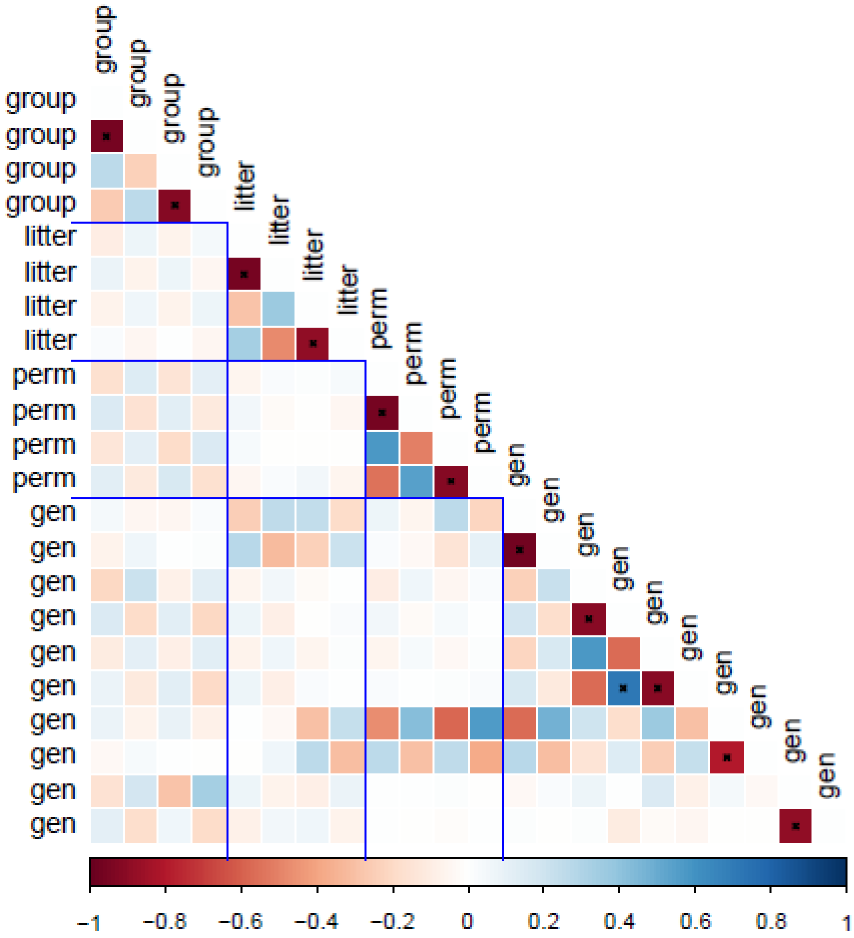
$$\boldsymbol{e}(t_j)\sim N(0,\sigma_{ej}^2),\sigma_{ej}^2=\exp(a+bt+ct^2+\ldots)$$

$$\boldsymbol{\theta}_{jk}=a'+b't+\ldots$$

SAD ordre-degré dep, degré variance Ex: SAD 1-00, SAD2-101

Identifiability

Correlation matrix between parameters estimates



Identifiability

Correlation matrix between variance component estimates