Genetic modeling of feed intake: a case study in growing pigs

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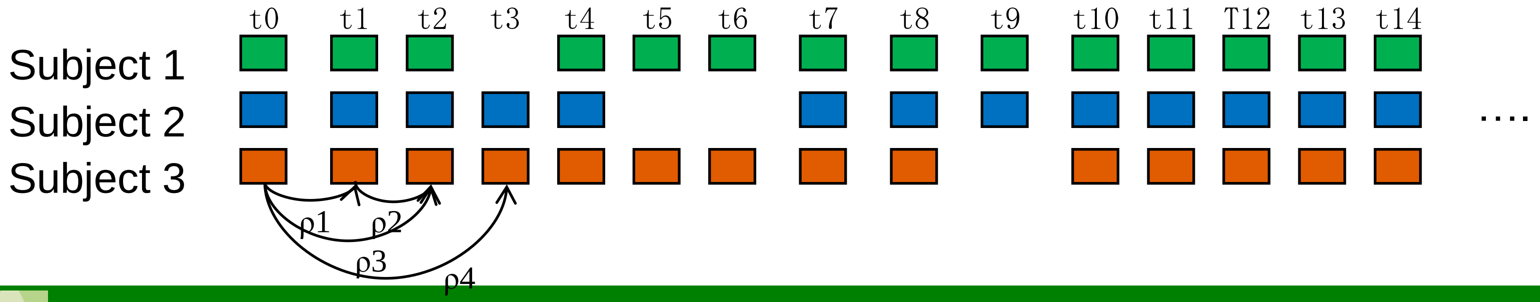
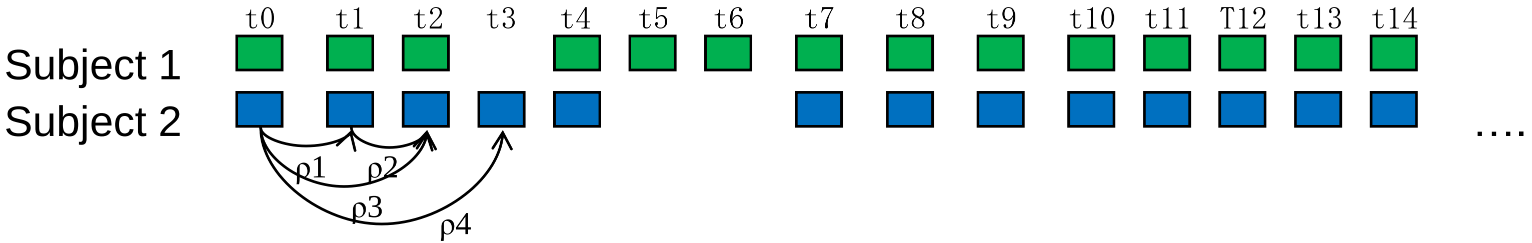
Why new modeling of feed intake is needed?

Development of automatic self-feeder + electronic identification

repeated measurements of
Individual feed intake
Individual weight

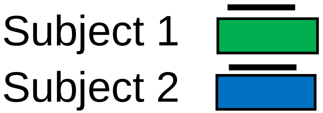


Why new modeling of feed intake is needed?



Most often used approaches:

summarized phenotype



Loss of information

simple repeatability model

$$\rho_1 = \rho_2 = \rho_3 = \rho_4 \cdots$$

$$\sigma^2_{t_i} = \sigma^2_{t_j}$$

Strong assumptions ➔ bias

new modeling needed

Other approaches

$$\boldsymbol{y}(t) = \underbrace{\mu(t)}_{\text{fixed}} + \underbrace{\boldsymbol{u}(t) + \boldsymbol{p}(t)}_{\text{random}}$$

Model

$$\operatorname{cov}(\boldsymbol{u}(t), \boldsymbol{u}(s)) \quad \text{and}$$

$$\operatorname{cov}(\boldsymbol{p}(t), \boldsymbol{p}(s))$$

- Character process model (CP)

Or model $\boldsymbol{u}(t)$ and $\boldsymbol{p}(t)$

- Random regression (RR-OP)
- Spline (RR-SPL)
- Structured antedependence model (SAD)

$$\boldsymbol{p}(t_j) = \sum_{s=1}^{\alpha} \theta_{sj}\, \boldsymbol{p}(t_{j-s}) + \boldsymbol{e}(t_j)$$

Data-analysis

- Weekly averages of daily feed intake
- 17 weeks of observation (67 to 180 d. of age)
- 3096 Large White pigs (9 generations)

1) Selected the best model within approach

   CP, RR-OP, RR-SPL, SAD

2) Compared the 4 best models

   + simple repeatability

⇨

Which model is the best to

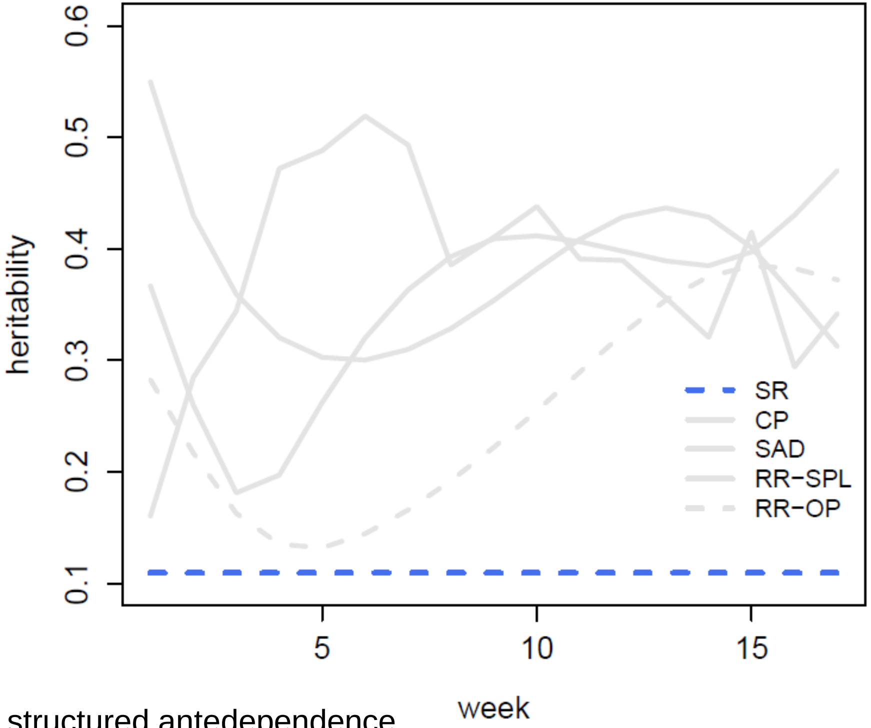
- ❑ Estimate genetic parameters
- ❑ Estimate correlation structures
- ❑ Predict future performances

Approaches comparison: heritability estimates

simple repeatability model

⬇

Low heritability



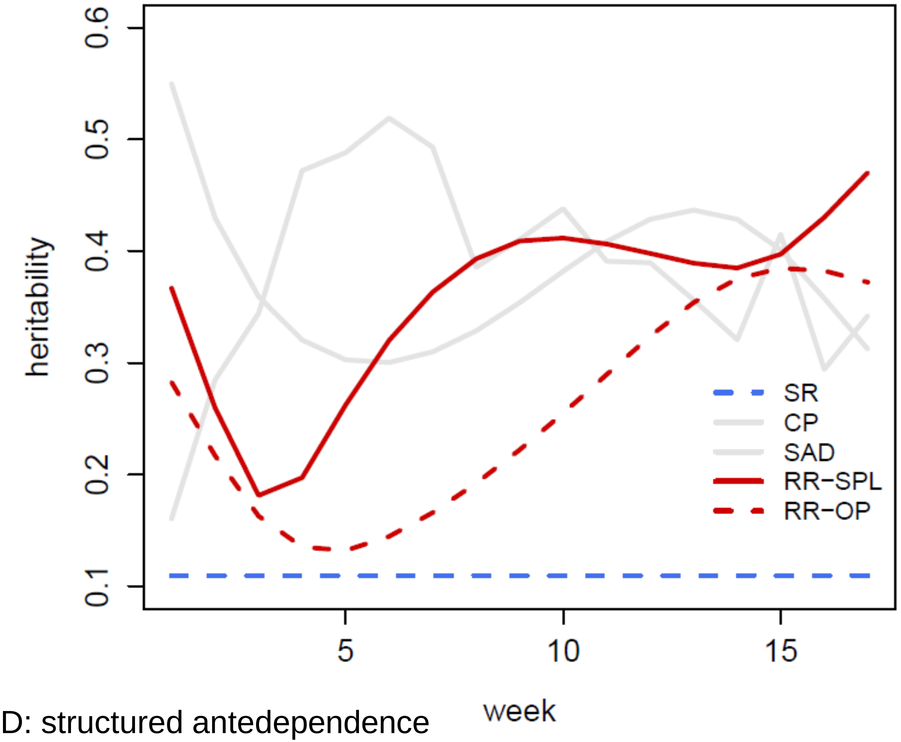
CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: heritability estimates

Random regression
OP or SPL

⬇

Similar pattern of heritabilities



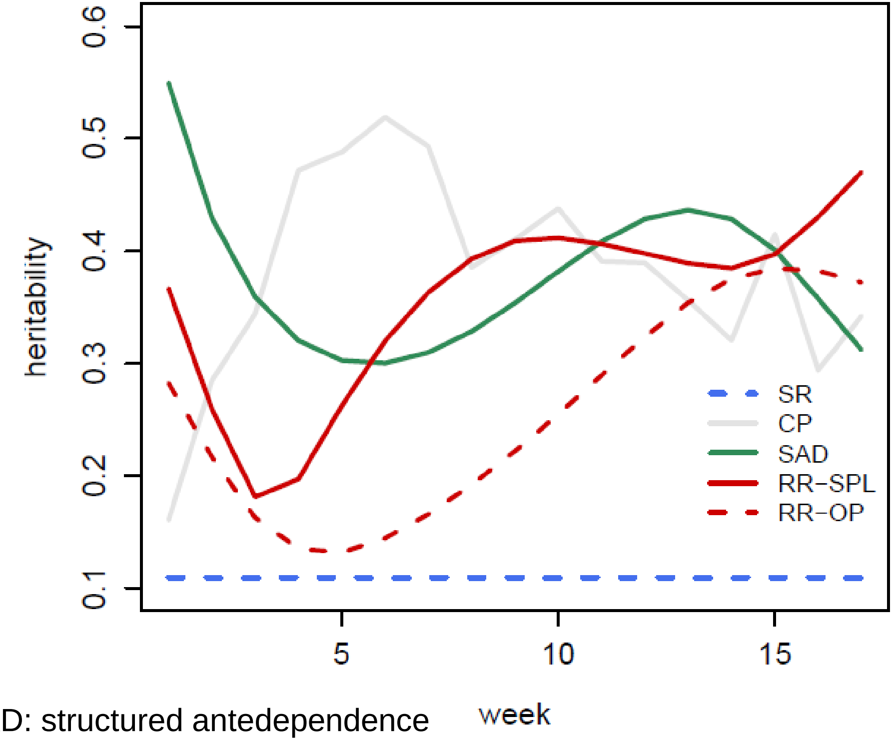
CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: heritability estimates

SAD

⬇

Higher but similar pattern of heritabilities / RR, spline models



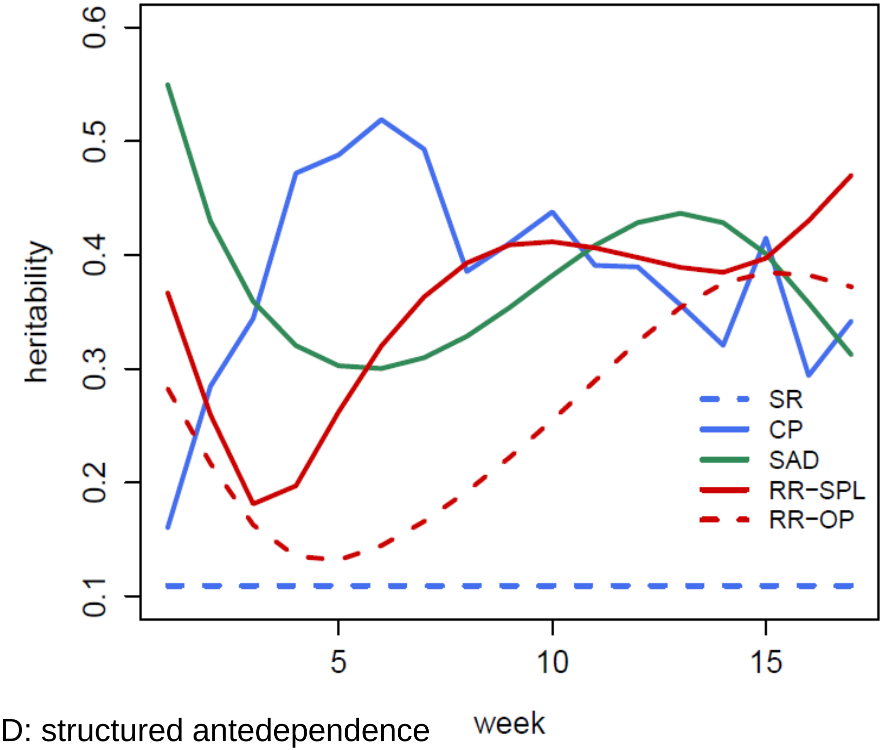
CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: heritability estimates

Character process model

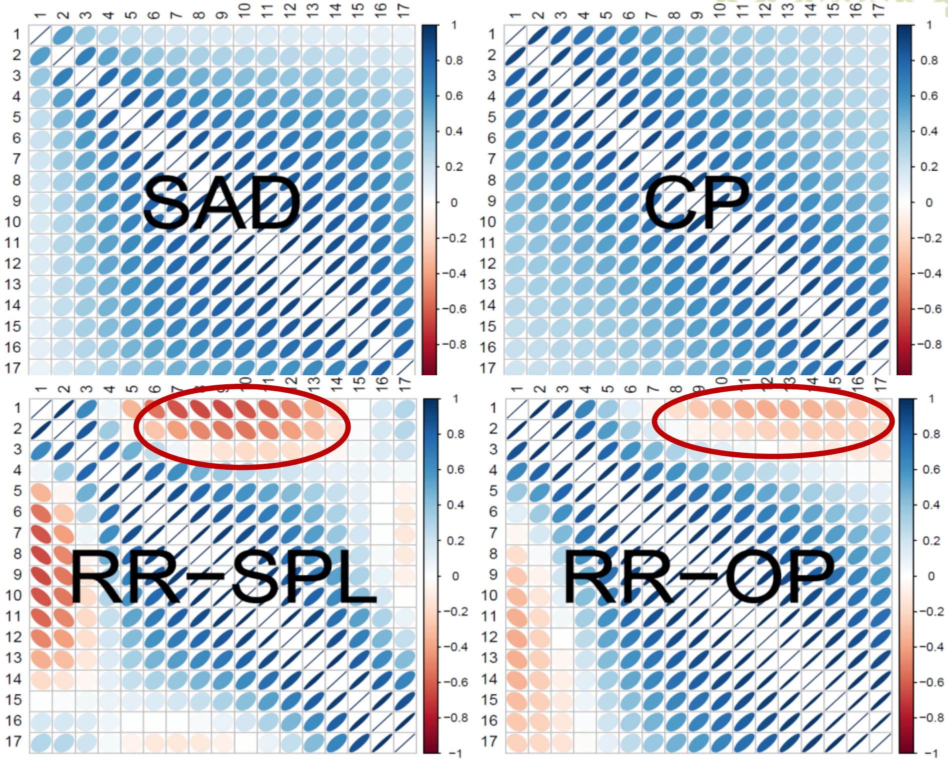
⬇

opposite pattern of heritabilities !



CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: genetic correlation matrices

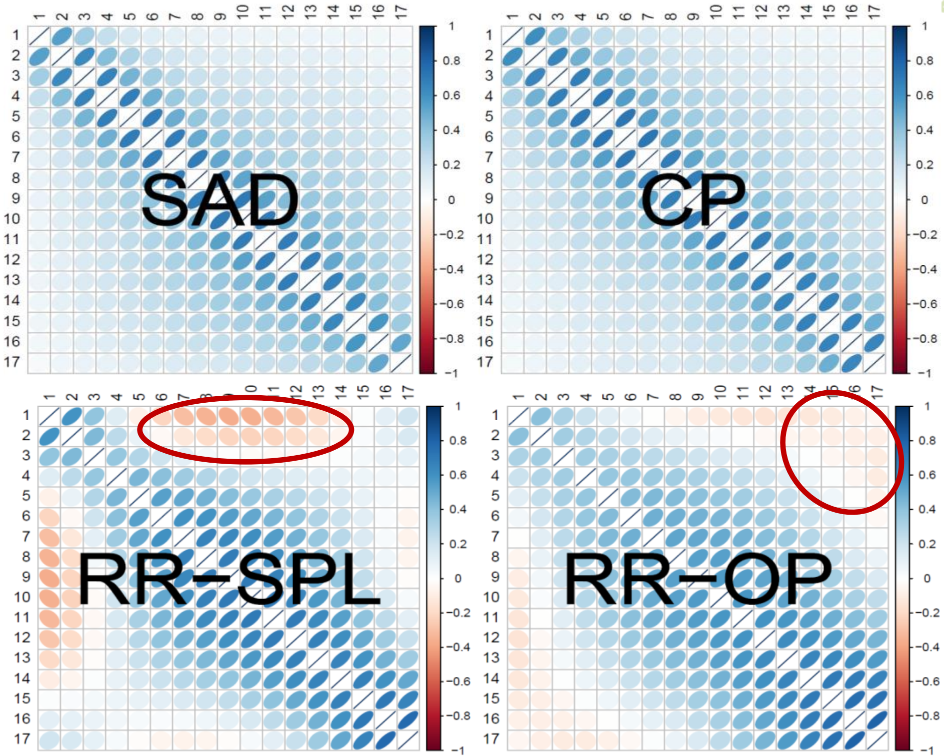


SAD-CP, consistent results

RR models, abnormal negative correlations

CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: phenotypic correlation matrices



SAD-CP, consistent results

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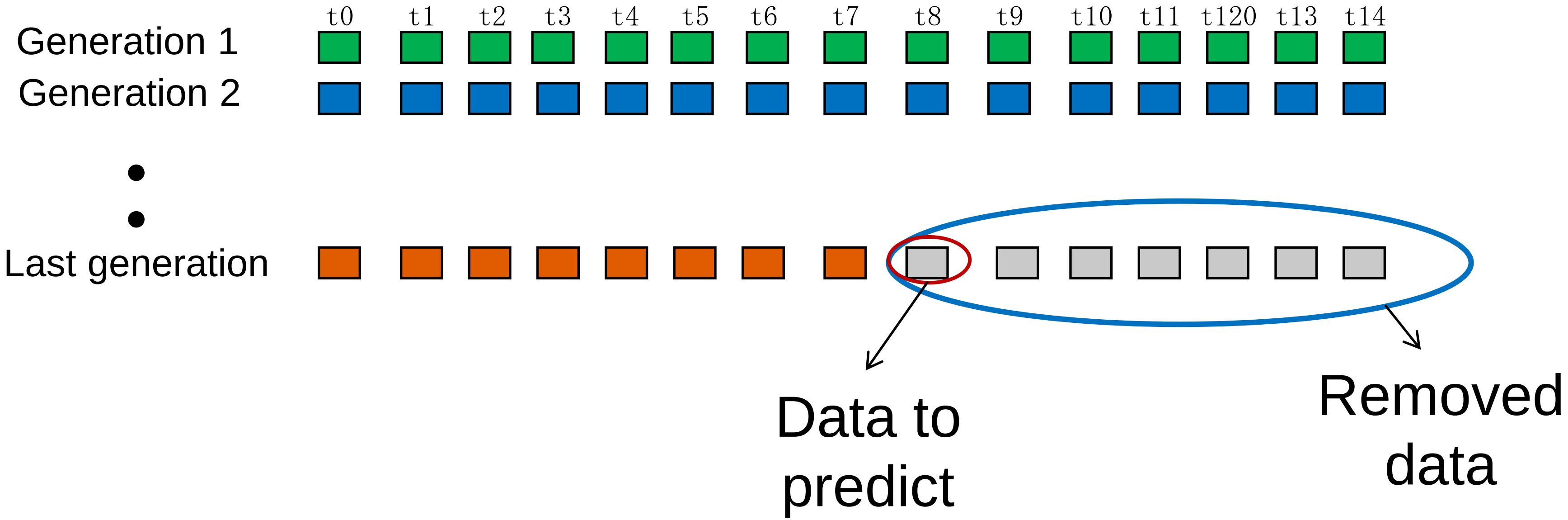
CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Approaches comparison: predictive ability



Generation 1

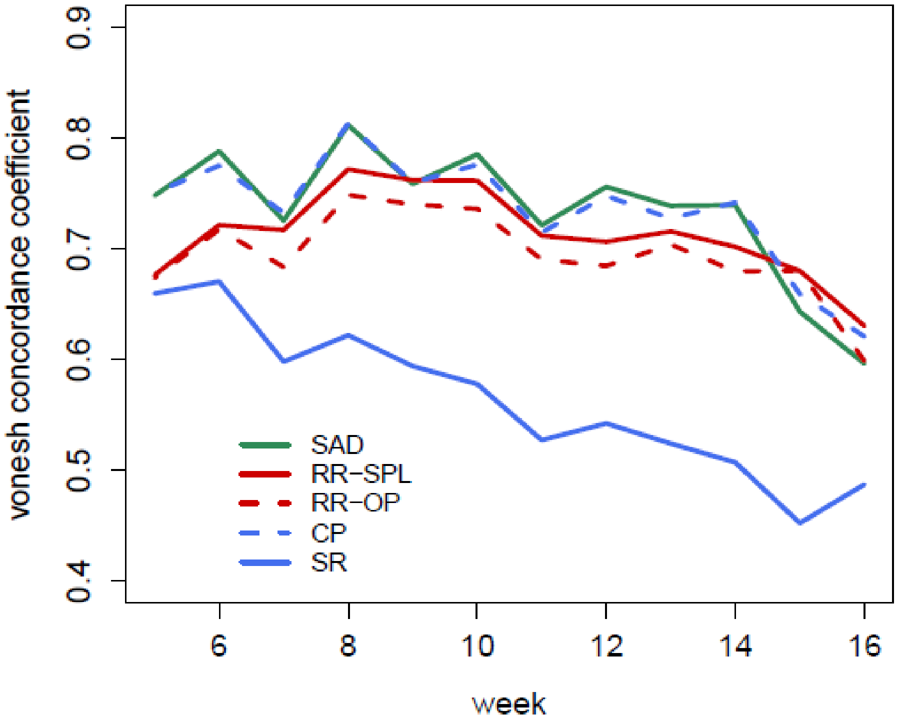
Generation 2

Last generation

Data to predict

Removed data

Approaches comparison: predictive ability



SAD: best predictive ability

CP:character process, RR: random regression, SPL: spline, SAD: structured antedependence

Conclusion

- ❑ Variances / heritability
  - SAD, RR-OP, RR-SPL ≈ similar heritabilities
  - CP very different / other approaches

- ❑ Correlations
  - CP and SAD similar and consistent estimations
  - Bias in RR,SPL models

- ❑ Predictive ability SAD > other approaches

SAD is the most promising approach

- ❑ Similar results obtained for feed intake in rabbits and duck

Best model selection

Approach	**Genetic effect**	**Permanent env. effect**	**ΔBIC**
Simple repeatability			18094
Best CP	AR1H	AR1H	0
Best RR-OP	OP2	OP2	8459
Best RR-SPL	Cubic spline 5 knott points		6303
Best SAD	SAD1-22	SAD1-21	22

CP:character process, RR-OP: random regression, RR-SPL: spline, SAD: structured antedependence

SAD

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

$$\boldsymbol{p} \sim N(0, IP)$$

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

$$\ldots$$

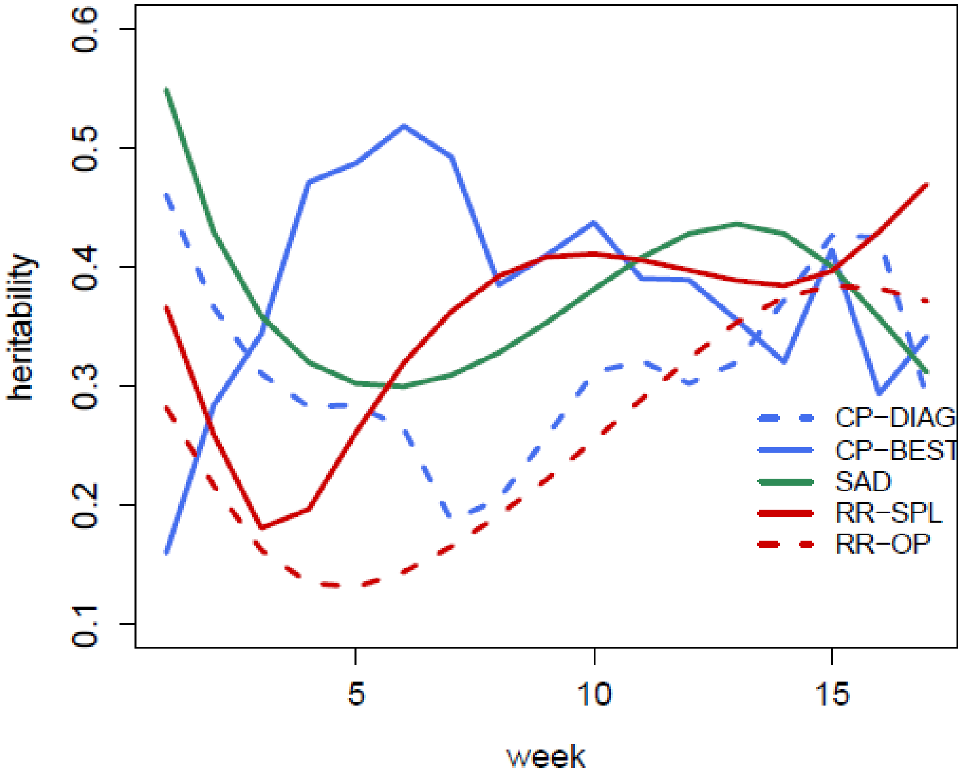
$$\boldsymbol{p}(t_j) = \sum_{k=1}^{s} \boldsymbol{\theta}_{kj}\, \boldsymbol{p}(t_{j-k}) + \boldsymbol{e}(t_j)$$

$$\boldsymbol{e}(t_j) \sim N(0, \sigma_{ej}^2), \sigma_{ej}^2 = \exp\left(\sum_{q=0}^{\gamma} b_q t_j^q\right)$$

$$\boldsymbol{\theta}_{kj} = f_k(t_j) = \sum_{q=0}^{\beta_k} a_{kq} t_j^q$$

Correlations between EBV

	Best RR-SPL	Best RR-OP	Best SAD	Best CP	SR
Best RR-SPL		0.91	0.90	0.90	0.66
Best RR-OP	0.73-0.98		0.92	0.89	0.72
Best SAD	0.81-0.96	0.76-0.97		0.95	0.73
Best CP	0.60-0.96	0.79-0.96	0.72-0.99		0.73
SR	0.35-0.81	0.46-0.96	0.51-0.88	0.65-0.82	


heritability
0.1
0.2
0.3
0.4
0.5
0.6
week
5
10
15
CP−DIAG
CP−BEST
SAD
RR−SPL
RR−OP