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Pedigree *p*-rep Designs:

A class of designs for early stage variety trials

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Overview

Breeders Equation

$$RGG = \frac{i\sigma_g r}{t}$$

- RGG: Rate of Genetic Gain
- i : selection intensity
- σ_g^2 : genetic variance of trait (yield)
- r : accuracy of selection - the correlation between the true and predicted genetic effects. Note that r^2 is the reliability (Mrode 1995)
- t : generation interval

Breeders Equation

$$RGG = \frac{i\sigma_g r}{t}$$

- For fixed i, σ_g^2 and t, an increase in the accuracy of EBLUPs increases the RGG
- This requires implementing procedures that are (and remain) best practice
- We can contribute statistically by
  - Optimal experimental design
  - Appropriate construction of a MET dataset (contemporary groups, co-located trials, etc.)
  - Sophisticated analysis of the dataset (Smith et. al. 2014)
  - Summary and dissemination of results (selection tools (Smith & Cullis 2018), etc.)

p-rep Designs

- Since Cullis et. al. (2006), adoption of *p*-rep designs in plant breeding and crop research has replaced traditional grid-plot designs
- The 25% *p*-rep threshold advocated by Cullis et. al. (2006) was based on the ratio of test plots to grid plots in traditional grid-plot designs
- Cullis et. al. (2006) stated "At present pedigrees are not generally used in routine analyses of EGVTs"
- From 2017 we incorporated pedigree data in MET analysis of PBA breeding programs

Pedigree p-rep designs

- Historically, the design of PBA early generation variety trials (EGVT) were generated in-house using DiGGer (Coombes 2002)
- From 2017 we transitioned to od (Butler & Cullis 2018) and exploited known genetic relationships for the allocation of varieties to both plots and sites
- This gives rise to two areas of research
  - Is the 25% level of p-rep necessary to achieve a given level of accuracy (r)
  - Is there an advantage to using pedigree information in the design of EGVT

Outline of the simulation study

- A simulation study was designed to primarily investigate
  - Various levels of p-rep
  - The advantage (if any) of including pedigree information

  in the design of the PBA Southern Faba Bean S1 trial that consisted of 256 breeding lines and 4 check varieties
- The random component of the linear mixed model for the analysis of a single PBA trial is:
  $\texttt{random} \sim \texttt{vm(Line, A)} + \texttt{ide(Line)} + \texttt{Block} + \texttt{Column} + \texttt{Row}$
  $\texttt{residual} \sim \texttt{ar1(Column)} : \texttt{ar1(Row)}$
- Where $\mathbf{A}$ is the (pedigree derived) relationship matrix
- Variance parameters: $\sigma_g^2 = \bar{a}\sigma_a^2 + \sigma_i^2$, σ_b^2, σ_c^2, σ_r^2, ρ_c and ρ_r

Outline of the simulation study

- Simulation treatment factors
  - 7 levels of p-rep: $p = 0, 5, 10, 15, 25, 50, 100\%$
  - 3 levels of proportion of additive genetic variance to the total: $k = 0.5, 0.7, 0.9$
  - 3 levels of null (baseline) reliability: $r_0^2 = 0.33, 0.5, 0.66$
  - 3 design types $d = od_{od}, od_{gg}, od_{\alpha}$
    - od_{od} *od* design with pedigree information included Butler and Cullis (2018)
    - od_{gg} DiGGer style row-column design Coombes (2002)
    - od_{α} augmented α design for single site Williams et. al. (2011)
- $7 \times 3 \times 3 = 63$ treatments $\{T\} \times 3$ designs

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Outline of the simulation study

- For each $\{T_i\}$ generate n=4000 datasets
- Values of non-genetic variance components chosen from previous analyses of data
- σ_a^2 and σ_i^2 chosen to realise pre-specified values of r_0^2 for a design with no replication and sub-optimal allocation of varieties to plots
- $T_{(id)_j} \rightarrow$ the j^{th} simulation allocated to plots by design strategy d

Outline of the experiment designs

- With reference to the LMM used for analyses, the following indicates a) if a term was fitted and b) whether it was fitted as fixed or random for each of the three design types d

Term	od_{od}	od_{gg}	od_{α}
`Line`		F	F
`Additive`	R		
`Non-Additive`	R		
`Block`	R	R	F
`Column`	R	R	
`Row`	R	R	
`Column:Row (Plot)`	R	R	

Simulations

- The simulated data from each $\{T_{(id)_j}\}$ were analysed in ASReml-R, Butler et. al. (2018).
- For T_i we have

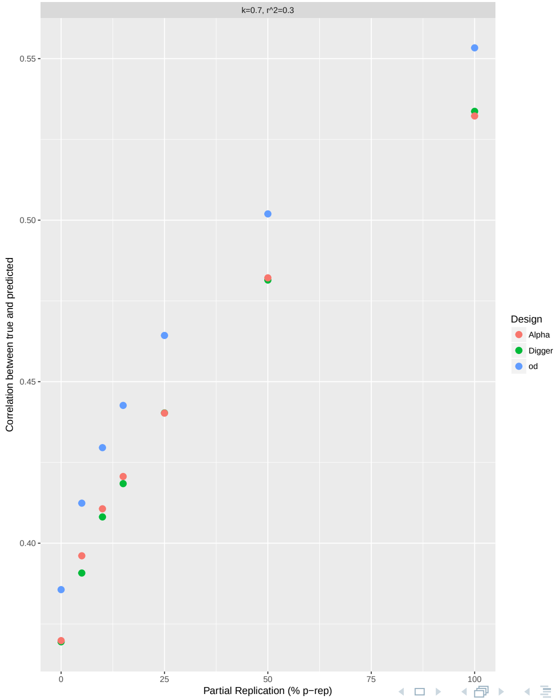
$$\mathbf{u}_g, \mathbf{u}_a, \mathbf{u}_i$$

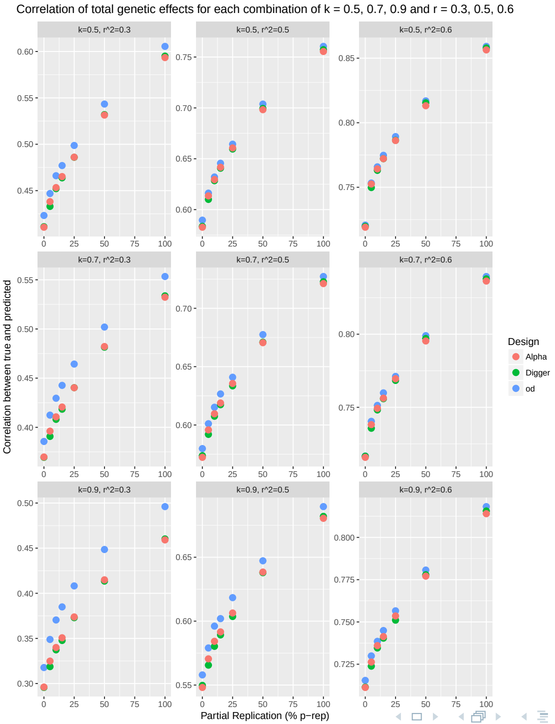
  and for $T_{(id)}$

$$\tilde{\mathbf{u}}_{gd}, \tilde{\mathbf{u}}_{ad}, \tilde{\mathbf{u}}_{id}$$

  For d in $\{od_{od}, od_{gg}, od_{\alpha}\}$, where each $\mathbf{u}$ is of length 260.
- Summarise
  - Bias associated with variance parameter estimates for each design method d for the 63 combinations of p, k and r_0^2
  - Correlation between the "true" (simulated) value and corresponding predicted value for for each design method d and 63 combinations of p, k and r_0^2

Correlation of total genetic effects $k = 0.7$ and $r^2 = 0.3$




Correlation of total genetic effects for each combination of k = 0.5, 0.7, 0.9 and r = 0.3, 0.5, 0.6
k=0.5, r^2=0.3
k=0.5, r^2=0.5
k=0.5, r^2=0.6
k=0.7, r^2=0.3
k=0.7, r^2=0.5
k=0.7, r^2=0.6
k=0.9, r^2=0.3
k=0.9, r^2=0.5
k=0.9, r^2=0.6
Correlation between true and predicted
Partial Replication (% p−rep)
Design
Alpha
Digger
od

Correlation between true and predicted: Total

- There is little to no distinction between the performance of od_{gg} and od_{α} allocations for any level of p, k, and r_0^2 for total correlations
- This suggests that spatial models (i.e. fitting AR1$\times$AR1 to the residual) are not as critical in the design of trials such as these
- As k increases for fixed p and r_0^2 the advantage of od_{od} to od_{gg} and od_{α} designs increases
- For fixed r_0^2 and p, as k increases, the total correlation decreases as the bias associated with the non-additive genetic variance increases

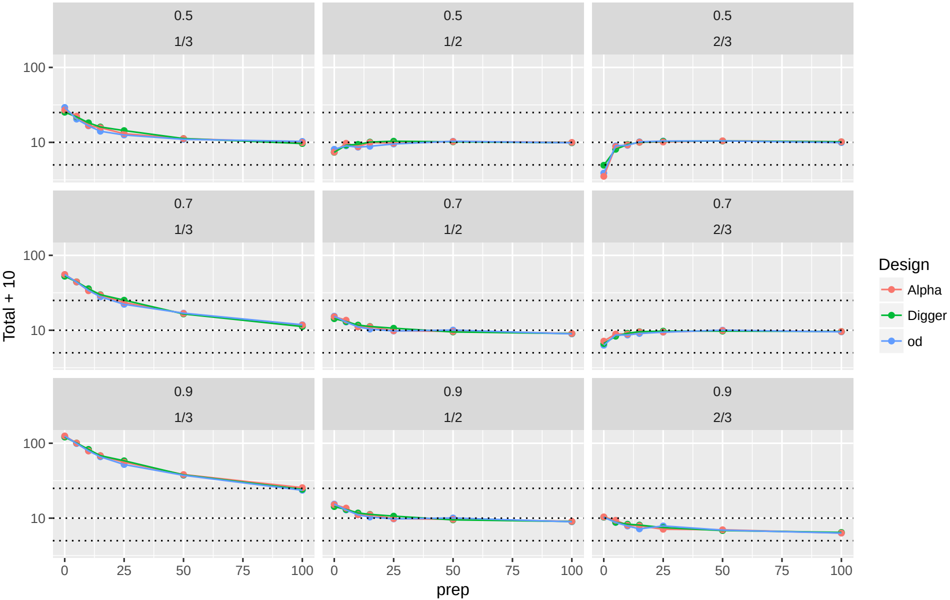
Correlation between true and predicted

- For $k = 0.7$ and $r_0^2 = 0.3$
- Using pedigree information, we can reduce the level of p and still maintain the same level of accuracy as other allocations in this situation.

Design	0	5	10	15	25	50	100
od_α	0.370	0.396	0.411	0.421	0.440	0.482	0.532
od_{gg}	0.369	0.391	0.408	0.418	0.440	0.481	0.534
od_{od}	0.386	0.412	0.430	0.443	0.464	0.502	0.553

Conclusions

- There is still recovery of information for p=0?!
- BUT the bias of variance parameter estimation for low p is large
- Bias associated with σ_i^2 particularly large
- Bias associated with σ_g^2 significantly affected by the bias with σ_i^2 (if it is large) $\forall k$


0.5
1/3
0.5
1/2
0.5
2/3
0.7
1/3
0.7
1/2
0.7
2/3
0.9
1/3
0.9
1/2
0.9
2/3
100
10
Total + 10
0
25
50
75
100
prep
Design
Alpha
Digger
od

Conclusions

- For each level of p and across all levels of k and r_0^2
  - od_{od} achieved the highest accuracy of prediction out of all three design strategies
  - od_{od} had the lowest design criterion (**A**-value) i.e. smallest average pairwise variance of variety contrasts
- For all combinations of p and r_0^2
  - od_{od} achieves a given level of accuracy with smaller p than od_{gg} and od_{α}
- od_{od} is the best design strategy for the true model
- It can be shown the **A** value is proportion to the expected level of accuracy of the predictions in the subsequent analysis

Conclusions

- Is the 25% level of p-rep the gold-standard for EGVTs?
- No... however, this is up to the discretion of the breeder taking into account
  - cost(\$)/plot i.e. how large can the trial be
  - desired level of accuracy
  - population diversity (σ_g^2) and proportion (k) of additive genetic variance
- Is there an advantage to using pedigree data in the design of EGVTs?
- Yes... results indicate for every level of p and all combinations of k and r_0^2
  - the accuracy of the predicted values and
  - relative response to selection (not presented today) are higher for allocations using od_{od} compared to od_{gg} and od_{α} designs (Cullis et. al. in prep.)

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