



**Forest Genetics  
for Productivity Conference**  
**The next generation**

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Handbook



## INVESTIGATING EFFICIENCY OF SELECTION USING UNIVARIATE AND MULTIVARIATE BEST LINEAR UNBIASED PREDICTORS

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Over the last 16 years the Southern Tree Breeding Association (STBA) has developed a dedicated genetic evaluation system (TREEPLAN) for use in forest genetics. It was designed to be useable by operational breeders, tailored for use in rolling front breeding programs, and most importantly, have a massive multivariate capability for integrating all available data generated by a national breeding program. In this study an analysis based on simulated data was run in order to evaluate the benefit of integrated analysis to STBA members and clients. The breeding plan and the quantitative genetic architecture of the simulated species were based on *Pinus radiata*. The 27 traits in the analysis comprised 19 growth traits (growth for three age classes within seven site types), three branch traits, wood density for two age classes, one wood stiffness trait and one disease trait). Several genetic evaluation scenarios were considered: a multi-trait analysis of the 27 traits (MULTI); 27 single-trait analyses (SINGLE); and a multi-trait analysis of the 19 growth traits combined with single-trait analyses for the remaining traits (MULTI/SINGLE). In each case trait EBVs were combined into a \$NPV index score for the objective of improving profitability in an integrated forest growing and structural timber production system. We compared the true \$NPV index score for the top 5% of the population after three generations of breeding and selecting on the basis of the estimated \$NPV score, under each scenario. The main finding is that the gain in \$NPV under the MULTI scenario is significantly greater than in other scenarios.

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R. J. Kerr

Asymptotic rates of response from forest tree breeding strategies using best linear unbiased prediction

“... demonstration of the limited advantage in using multivariate analysis ... “

I forgot to mention!!!

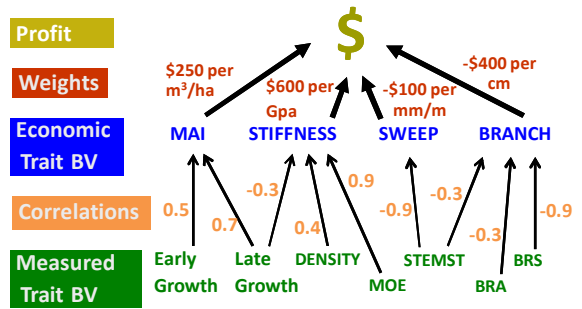
“ under scenarios where all individuals are measured for each trait “

### Structure of the talk

- Summarise the STBA approach to genetic value prediction
- Summarise the STBA *Pinus radiata* breeding population
  - In terms of the numbers of families, genotypes, parents etc
  - In terms of the numbers of measurements
  - Then briefly describe a simulation which resembles the radiata program in Australia
    - Why? → In order to gauge how much additional gain has been realised from using multi-trait analysis
- Results of the simulation
- Conclusion

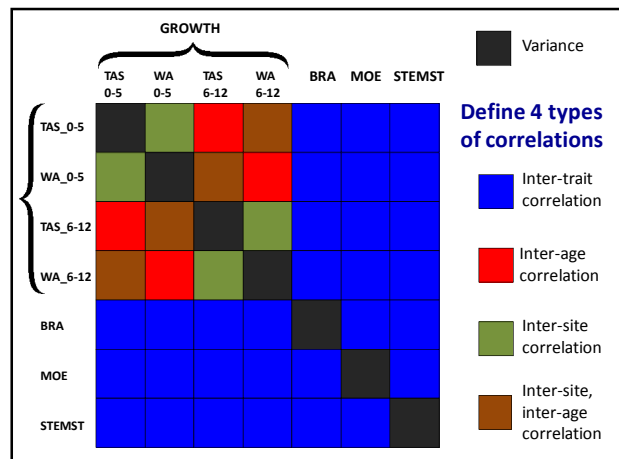
### Genetic improvement - you start with an objective

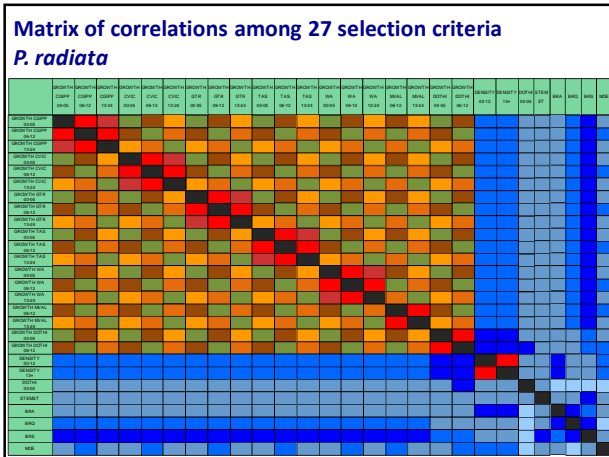
- Genetic value prediction is complicated, so you need a structure



### TREEPLAN philosophy is to maximise gain by using all of the data

- Relationships between measurements
  - Pedigree
  - Genetic correlations
  - Design features and error correlations
- Trial information
  - Design features
  - Different heritabilities
- G X E is accommodated by mapping measured traits to selection criteria (SC)



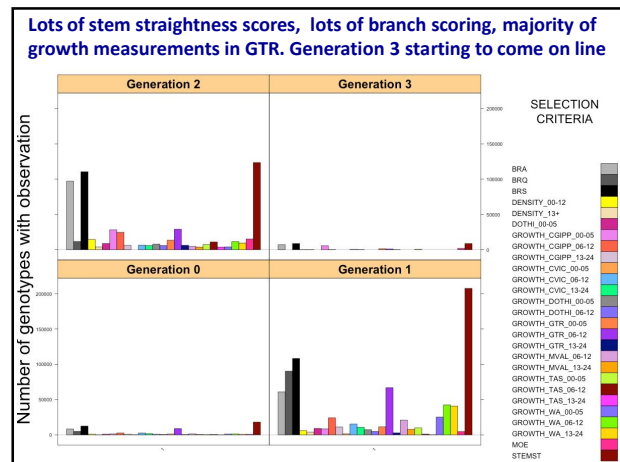


Schneeberger transformation

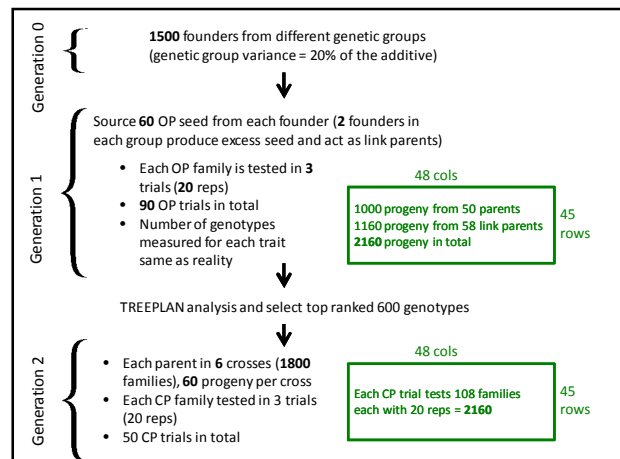
**BOT EBV** 
$$U_{BOT} = G_{BOT,SC} G^{-1}_{SC,SC} U_{SC}$$

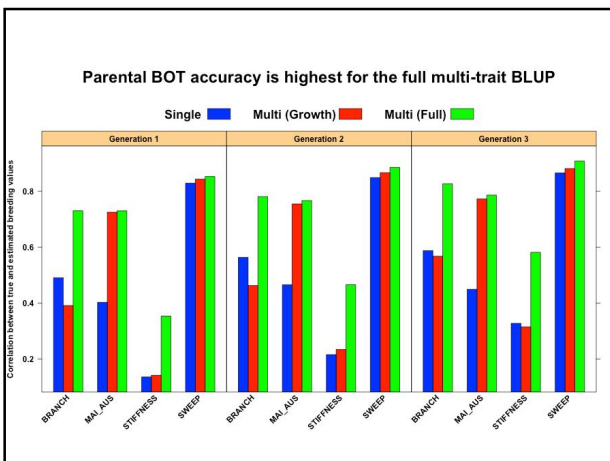
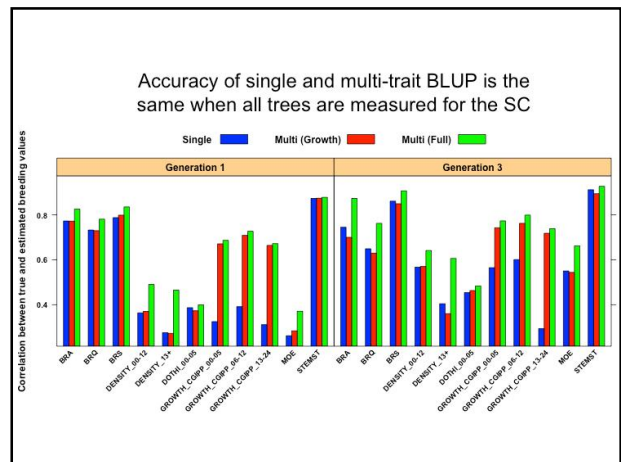
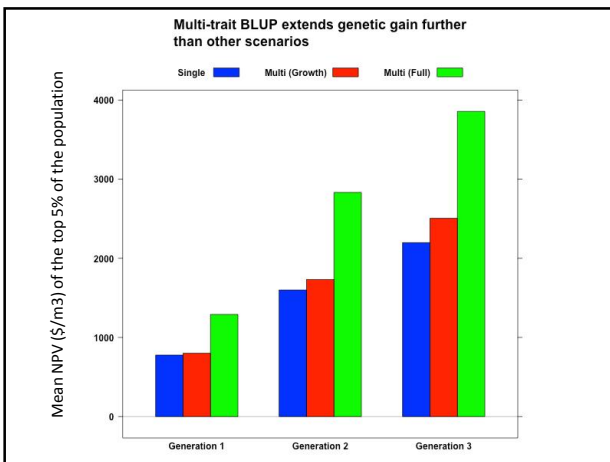
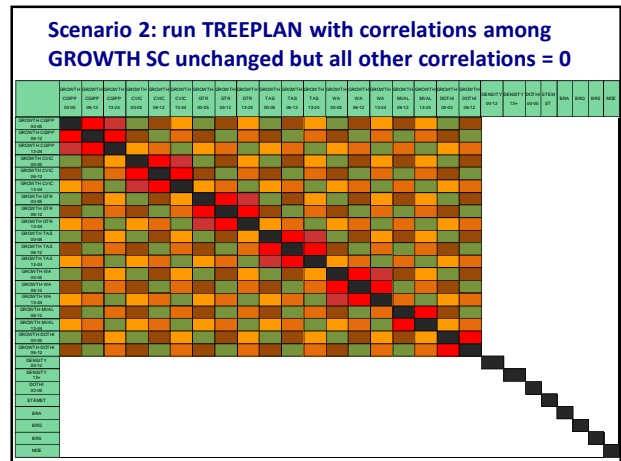
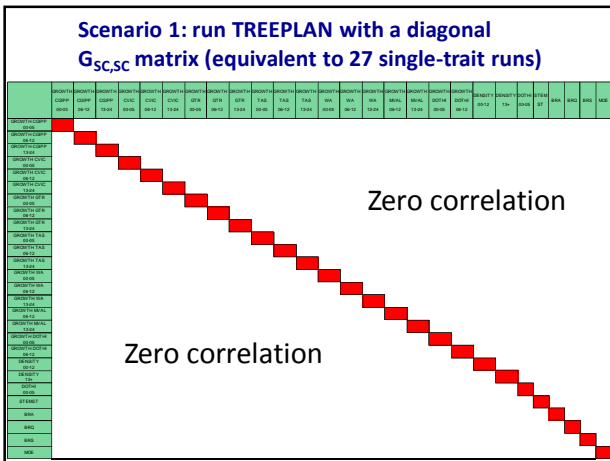
**Radiata breeding was mostly OP in the 1<sup>st</sup> generation, CP in the 2<sup>nd</sup> and 3<sup>rd</sup> generation now coming on line**

Generation	Number of CP families	Average CP family size	Number of CP parents	Average number of mates per CP parent	Number of OP families	Average OP family size	Number of OP parents	Number of genotypes	Number of selections	Select- ion ratio
0								30,000	2200	0.08
1	920	72	284	6	2300	60	2300	250,000	720	0.003
2	1300	72	412	6	400	60	406	147,000	350	0.003
3	278	33	127	4	0	0	0	9,000	0	0



- Simulate the actual program**
- Did not bother simulating non-test material (gen 0)
  - OP to generate 1<sup>st</sup> gen, CP to generate 2<sup>nd</sup> gen
  - Simulated a completed 3<sup>rd</sup> gen (CP, same as 2<sup>nd</sup>)
  - Number of genotypes, parents, mates per parent, family sizes were approximately the same as what has occurred in reality
  - Approximately the same selection intensities
  - Mirrored the true numbers of measurements by trait and by generation
  - Used an average h<sup>2</sup> based on actual trial data
  - Used an average error correlation matrix
  - Used the current SC X SC matrix of correlations





**Conclusions**

- For our situation (important traits measured on a small subset of trees) large multi-variate BLUPs are worth the effort
- We really should be increasing the number of measurements for these traits