Photo: © elPadawan, Flickr
“The future is already here — it's just not very evenly distributed”, William Gibson
The genetic evaluation system of radiata pine in New Zealand

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“Explanation of all my difficulties”
Where we come from (1944)
Where we are now (2014)

Photo: © Horst Kiechle, Flickr
Where we are selecting material for the future

The trees! (not the ferns or cannabis growing in between)
Clearly there has been progress

but

Has it been enough for 50 years?

How far from our potential?
The tools we use to study a problem condition our understanding of the problem
As breeders, our **genetic evaluation system** is the main tool we use to understand the world

Genotypes (what) → Environments (where)

Techniques & models (how)

Have an effect on our conclusions
Genotypes

3,000 parents under testing

325,000+ progeny in trials

Multiple experimental designs

Multiple mating designs

(OP, CP, clonal)
The aim of improving intrinsic properties like spiral-grain and stiffness, and matched to sites where they were likely to be of most value.

Part of the RPBC’s programme involved the establishment and measurement (mostly between the ages of 7-10 years old) of more than seventy progeny trials across the length of New Zealand (Figure 1 and Appendix A). These trials were populated by more than 2,500 genotypes, making available stem growth and form data for approximately 0.3 million trees. In addition, wood quality data has been collected for a subset of those trees.

Figure 1: Location of RPBC progeny trials in New Zealand.

Techniques & models (how)

Two extreme naive models for genetic evaluation:

Univariate analysis, homogeneous variance, equal correlation between all sites

Generic understanding of GxE interaction

Ideally our model would be in between

Multivariate analysis, unstructured heterogeneous variances, all sites highly interacting with different correlations

Every site is highly interacting
Plant breeding

- Emphasis on experimental design (including spatial trends)
- Few genotypes under testing

Animal breeding

- Emphasis on pedigree
- Large number of genotypes under testing

Tree breeding is special
This creates 2 big problems in tree breeding

(Remember that gold standard is single-stage evaluations)

We have too many traits  \rightarrow \text{Factor analytic models}

We have too many genotypes  \rightarrow \text{Reduced animal models}

We use both \textit{simultaneously} in the New Zealand Radiata Pine evaluation.

Therefore we can run a single-stage evaluation
Number of $G$ parameters to estimate

Projecting sites on 1 (FA1) or 2 (FA2) latent variables:

1) Is often enough to represent the correlation structure for 80 sites.
2) Reduces estimation problems

https://en.wikipedia.org/wiki/Factor_analysis
Reduced Animal Model*

Makes a distinction between trees with progeny (roughly 3,000 in our problem) and trees without progeny (>300,000), greatly reducing the size of the problem.

$A_{pp}^{-1}$ is diagonal for parents, ignores Mendelian sampling for non-parents, produces breeding values only for parents. If required, model can be modified to obtain forward selections, by expanding $A_{pp}$

On top of that, the NZRPBC uses a Factor Analytic structure to model the reduced animal model**.

*Pollak and Quaas (1980)

**Cullis, Smith, Jefferson & Thompson 2013. Implementation strategy for RPBC breeding values incorporating GxE
Jefferson & Cullis 2012. Prediction of breeding values maximizing data from trials over 76 sites.
(dis)connectedness

• Lack of/poor connectedness between trials is our largest problem in genetic evaluation.
• It means we can’t compare some genotypes to each other.
• It also means that many genotypes have been tested under a small subset of environments
• One of the priorities of the RPBC breeding plan is to expand coverage and connectedness. We have ramped up trial installation for the last 5 years.
Additive genetic correlation matrix

Cullis, Smith, Jefferson & Thompson 2013. Implementation strategy for RPBC breeding values incorporating GxE
HOW DO WE EXPLAIN THESE CORRELATIONS?
Some times we have simple explanations for GxE; for example, scale effect of temperature on basic density

![Graph showing the relationship between annual average temperature and basic density](image)

- Site means based on 23,000+ increment cores in 18 sites
- \( R^2 = 0.75 \)

Apiolaza 2012 Basic density of radiata pine in New Zealand: genetic and environmental factors. TGG 8: 87-96
In contrast, for growth we don’t know the drivers of GxE. Several attempts:

McDonald & Apiolaza 2008-9
Raymond 2010
Ivkovic et al 2012-14
Cullis & Jefferson 2013-14

One probable cause: we have soil and climate data at the wrong scale (both in space and time)
Example of 5 x 5 km grid
Red crosses indicate **actual** weather stations used in the interpolation
On top of that, climate will be different in our next rotation.
And, even worse, very poor resolution for soils
In summary, we have no first-hand, reliable information on environmental variables that drive GxE interaction for growth
An understanding of deployment environments permits adjusting our approach to risk

Final remarks

• Today we can run a single-stage multivariate national evaluation (with Factor Analytic & Reduced Animal models) using ASReml-R.

• We are not yet able to explain the environmental factors driving GxE for growth.

• Probable cause: *wrong scale* environmental data.

• One of our priorities should be to invest in high resolution descriptions of the environment for our best, better-connected trials (*moving from G to E*).
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