Sampling tree breeding trials

Luis Apiolaza & Elena Moltchanova
University of Canterbury
Private Bag 4800, Christchurch, New Zealand

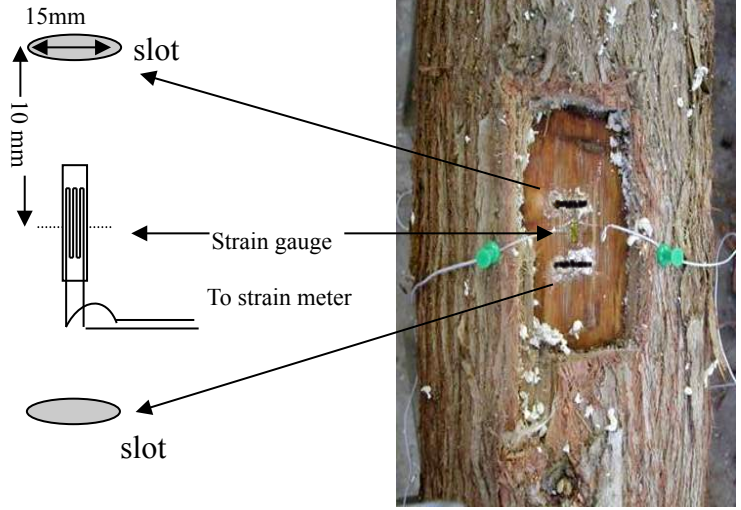
This presentation is based on work for the New Zealand Dryland Forests Initiative, and connects with projects and discussions with Clemens Altaner, Nicholas Davies, John Walker, Ruth McConnochie, Paul Millen and Shaf van Ballekom.
http://www.nzdfi.org.nz

UC
UNIVERSITY OF CANTERBURY
Te Whare Wānanga o Waitaha
CHRISTCHURCH NEW ZEALAND

Motivation

- We are domesticating *Eucalyptus bosistoana* for the production of durable and high performance timber.
- Pretty much any tree breeding program involves quantity & quality of wood + adaptation traits.
- Some traits cheap and easy to assess, while the rest are very expensive -> sampling.

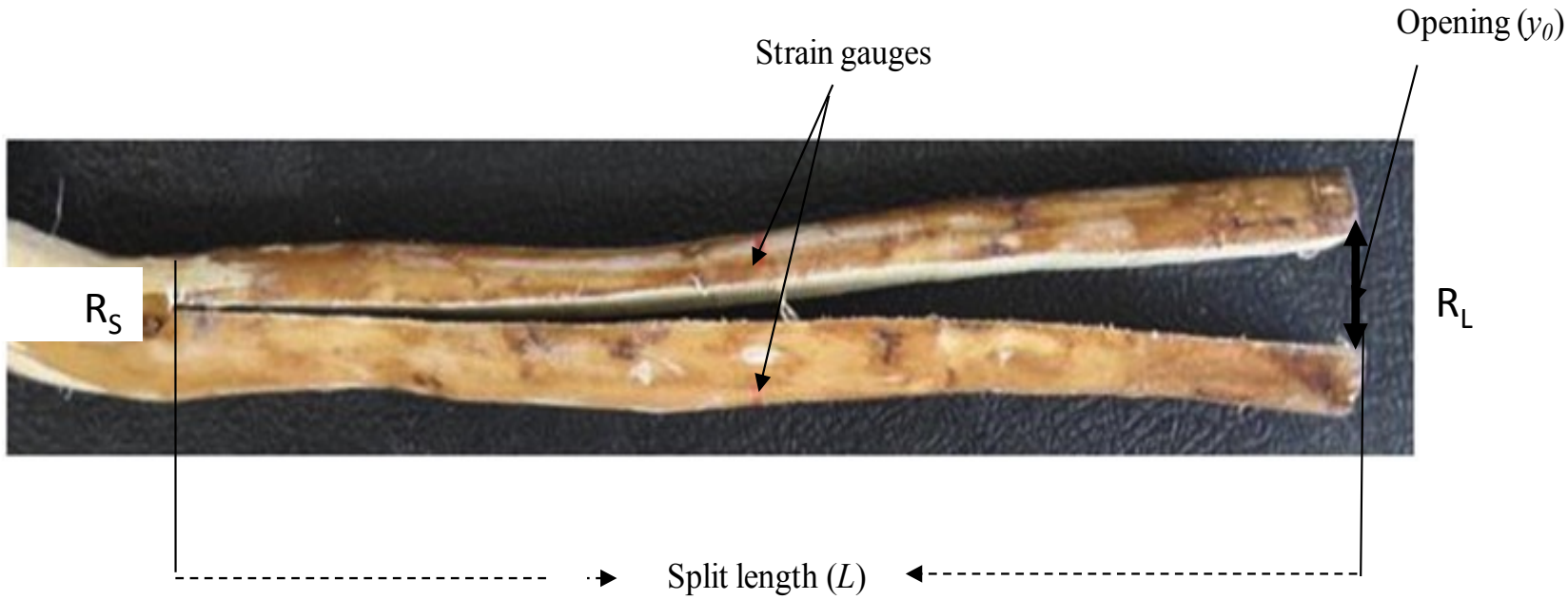
Measuring longitudinal growth strain in standing trees



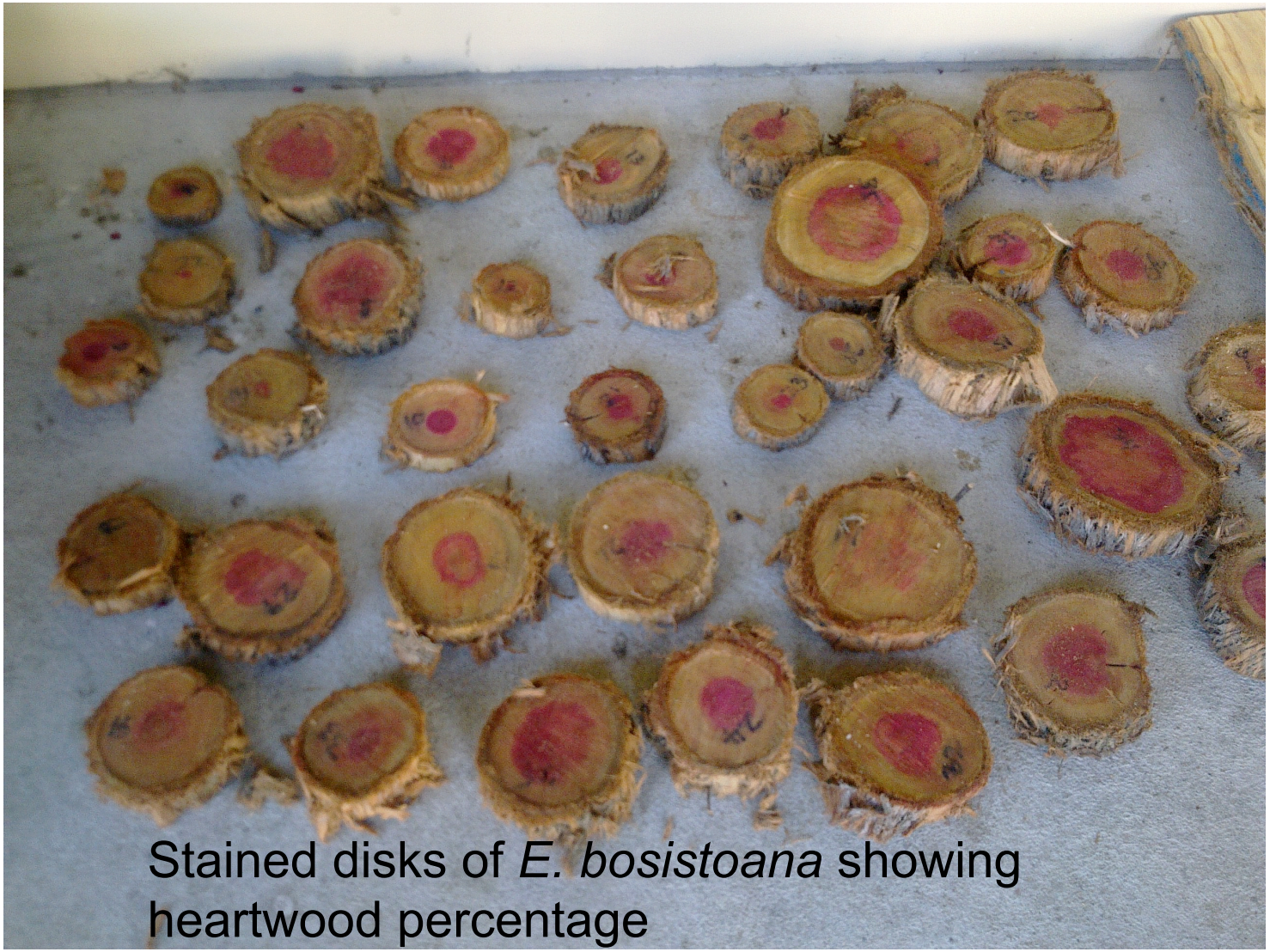
Strain is measured with a resistance or a CIRAD tool

We need 8-10 measures/tree to get a proper description of strain.

From (very slowly) assessing trees to (slowly) assessing 1-2 year old plants

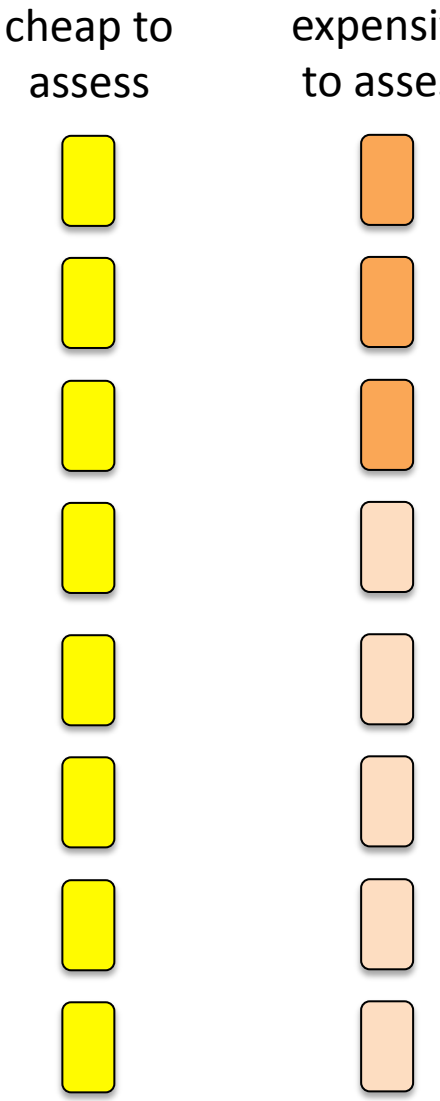


Another example: Heartwood variability



Stained disks of *E. bosistoana* showing heartwood percentage

In the old days: truncation sampling

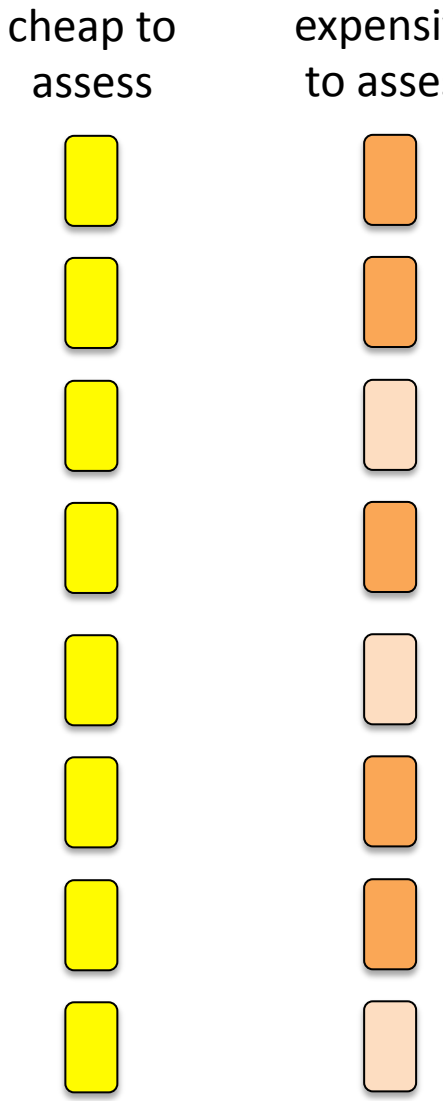


h^2 of cheap trait: no bias, increasing precision with larger samples

h^2 of expensive trait: bias, increasing precision with larger samples

r_g between traits: Large bias, poor precision

Better: random sampling

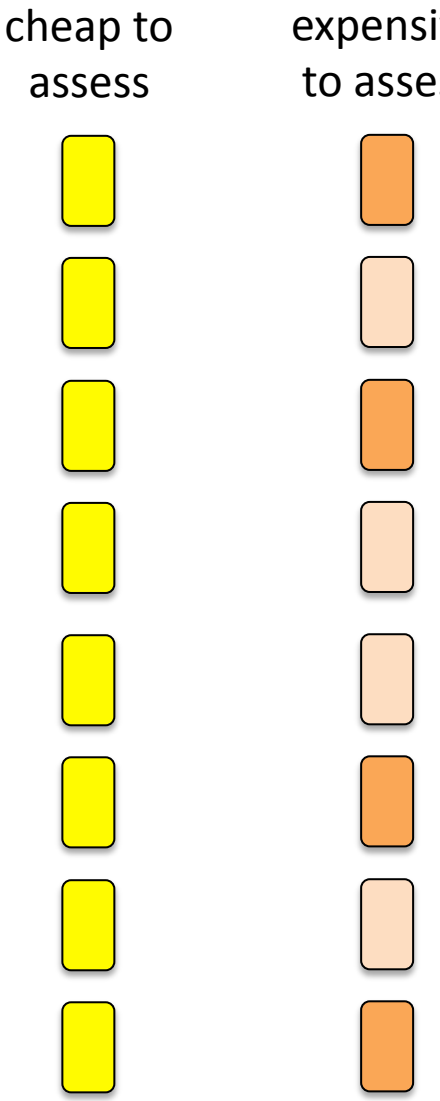


h^2 of cheap trait: no bias, increasing precision with larger samples

h^2 of expensive trait: decreasing bias and increasing precision with larger samples

r_g between traits: decreasing bias and increasing precision with larger samples

Sometimes random is too random: Ranked Set Sampling



Using additional info (cheap trait) we can improve representativeness of sample, increasing precision

1. Choose multiple ‘sets’ of observations

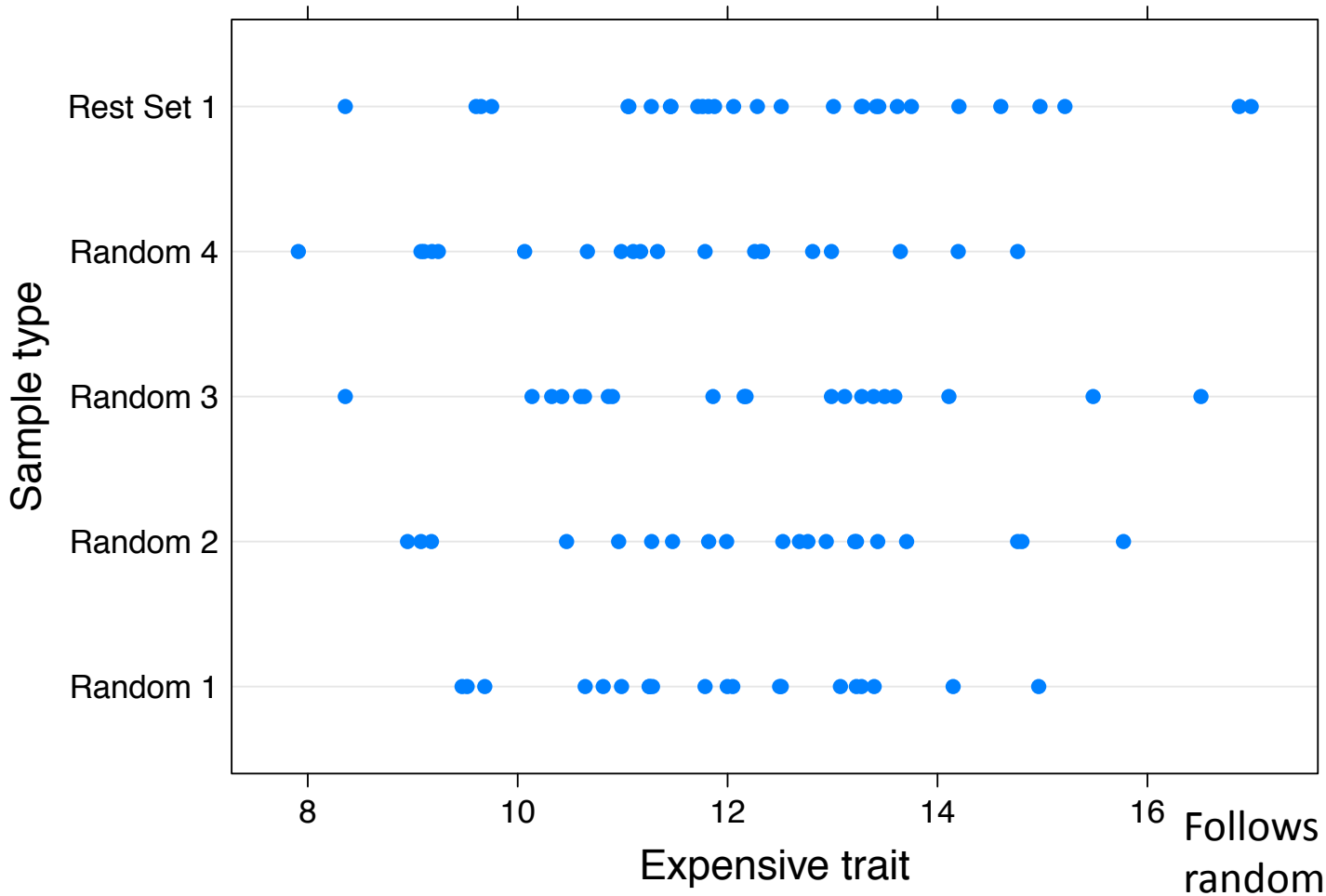
2. Within each set rank observations based on cheap trait

3. Choose smallest unit in first set, second smallest in second set, etc.

4. You have a sample.

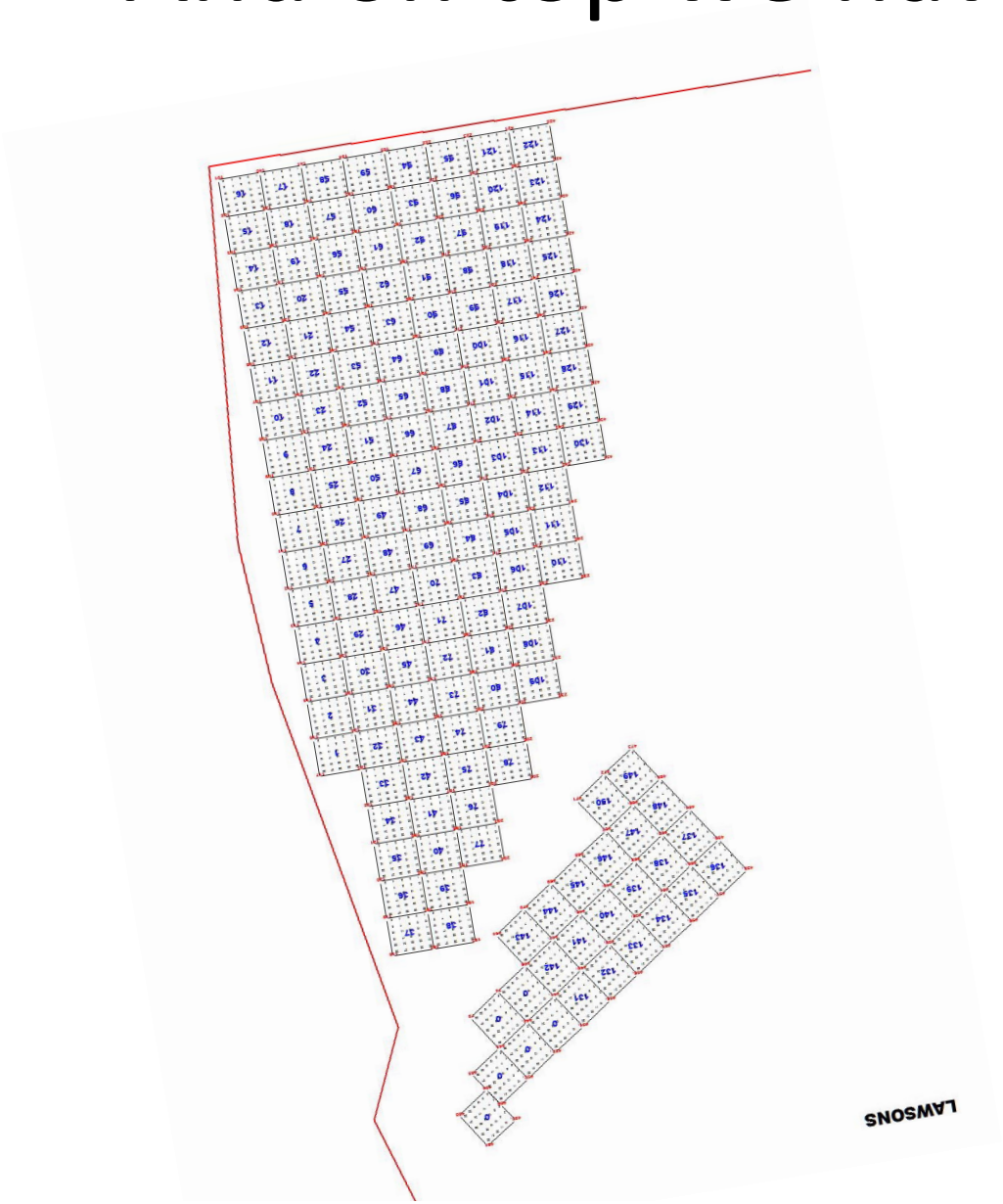
Goes back to 1950s, current revival in environmental monitoring

Example of coverage



Follows performance of random sampling, but more precise

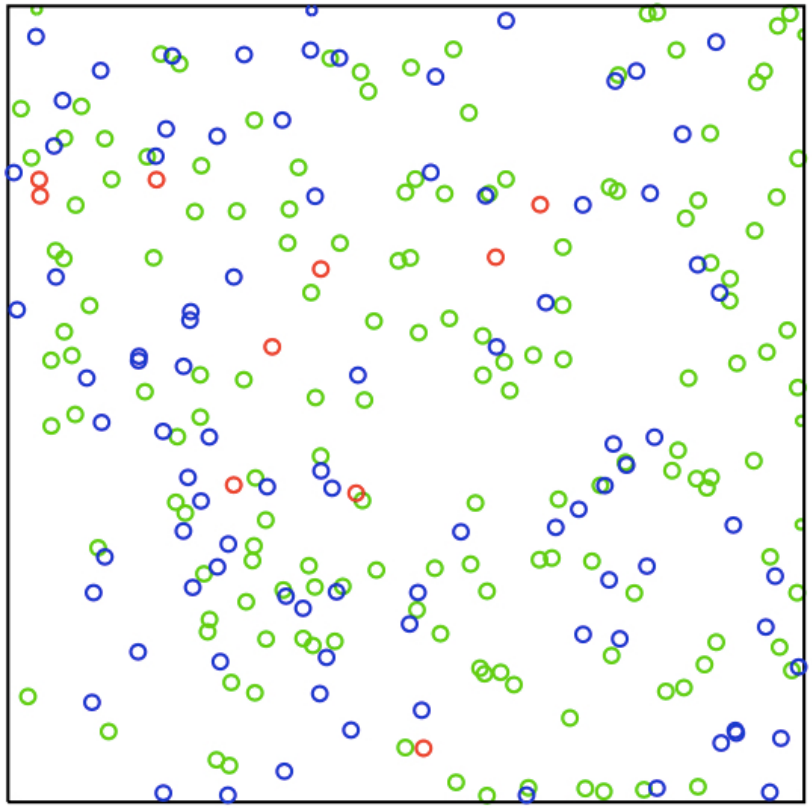
And on top we have spatial trends



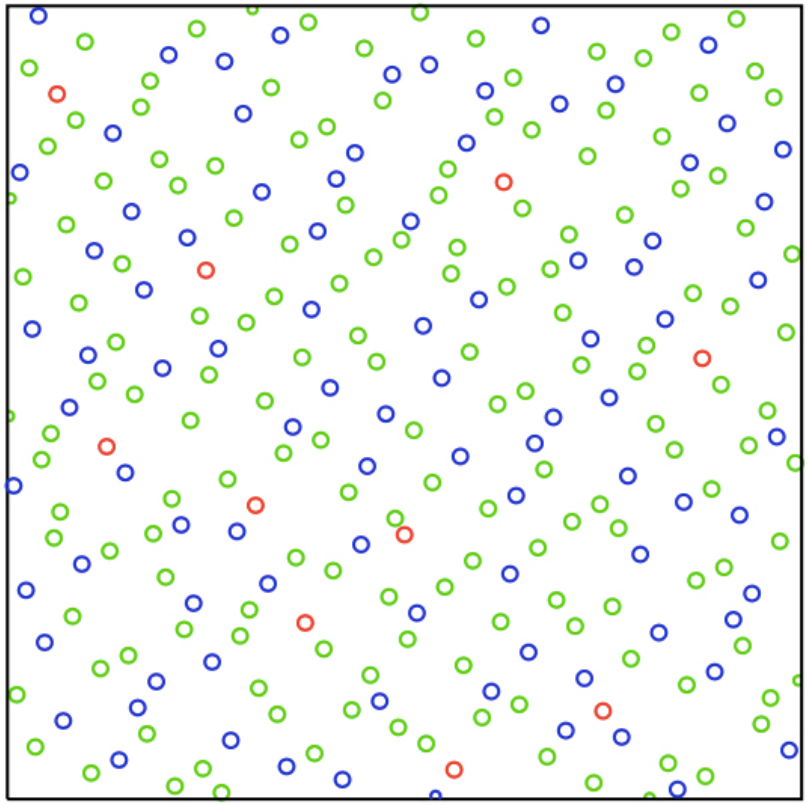
Balanced Acceptance Sampling

- Based on Halton sequences, which are deterministic but appear random for many purposes, generating well-spread positions.
- In general, evenly spatially balanced designs are more precise.
- This can be adapted to consider additional information from multiple covariates (e.g. cheap trait) and groupings (e.g. families)

Example spatial sampling



Random sample



Balanced Acceptance Sampling

In summary

- Sampling is a necessity in tree breeding programs
- A poor sampling scheme will deliver misleading, poor or unusable data
- Good sampling schemes will increase precision (or maintain it for smaller samples)
- Explicit spatial constraints to sampling are needed to make the most of our trials