What is needed to perform joint genetic testing and analysis of trees across countries?

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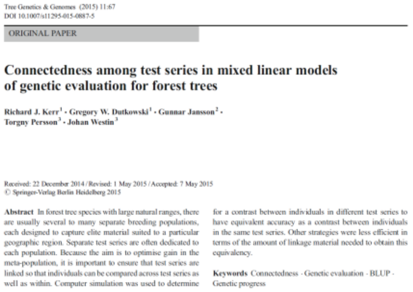
Content

- How should trials be connected when we establish progeny tests in different countries?
- What kind of data is needed? Pedigree? Measurements?
- What tools are needed for genetic analysis of data?

How should test series be linked?

- Routine progeny testing
- Separate test series are often dedicated to each population
- Aim is to optimize gain in meta-population
- Important that test series are linked so that individuals can be compared across test serie as well as within



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ORIGINAL PAPER

Connectedness among test series in mixed linear models of genetic evaluation for forest trees

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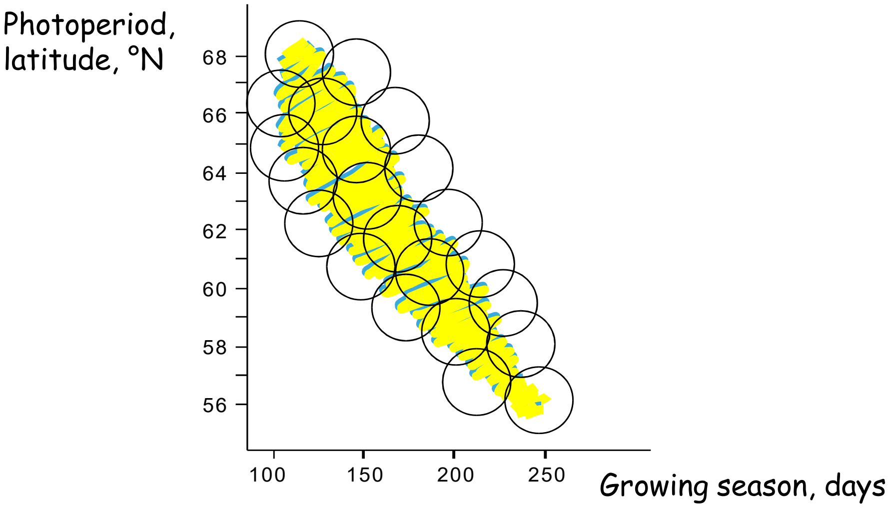
Abstract In forest tree species with large natural ranges, there are usually several to many separate breeding populations, each designed to capture elite material suited to a particular geographic region. Separate test series are often dedicated to each population. Because the aim is to optimise gain in the meta-population, it is important to ensure that test series are linked so that individuals can be compared across test series as well as within. Computer simulation was used to determine for a contrast between individuals in different test series to have equivalent accuracy as a contrast between individuals in the same test series. Other strategies were less efficient in terms of the amount of linkage material needed to obtain this equivalency.

Keywords Connectedness · Genetic evaluation · BLUP · Genetic progress

Distribution of breeding populations in Sweden



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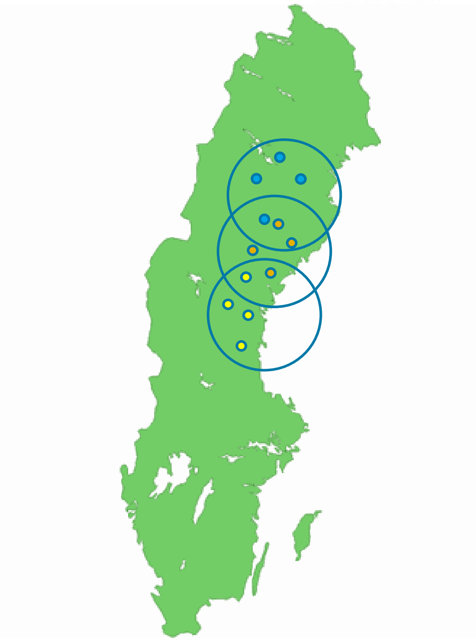
Testing strategy

- Field tests 4-5 per population
- Progeny or clone tests
- Measured at ages 10-15 yrs (growth, survival, damage, quality)



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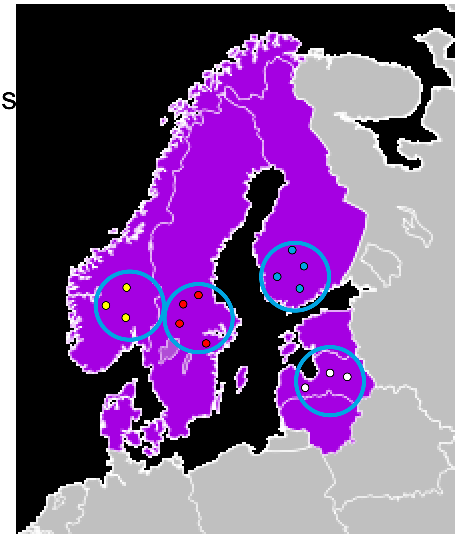
Joint testing strategy

Link test series across countries



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Link material

- Common test families (full-sibs)
- Common check-lots
- Seed orchards
- Families generated from inter-crossing parents from different test series

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Methods

- Data simulations used to compare strategies
- Average accuracy of genetic value contrast between individuals was used as criterion for assessing optimal level of linkage
- 50 parents crossed to produce 50 families in each of three populations
- GxE not considered

Results

- Use of common test families most efficient
- For low-heritability (h^2=0.1) scenario needed link material was
  8% for progeny and,
  12% for parents

Joint or separate database and analysis tool?

TREEPLAN-system as a joint tool

- Database with pedigree (DATAPLAN)
- Database with measured data from the trials (DATAPLAN)
- Tool for calculation of breeding values (TREEPLAN)

Selection criteria (SC) and breeding objective traits (BOT)

SC

- Height
- Diameter
- Survival
- Straightness
- Branch angle
- Branch diameter
- Branch number
- Branchiness
- Vitality
- Damage
- Number of ramicorns
- Freeze testing

BOT

- Volume per ha
- Survival
- Vitality - healthy trees
- Straightness
- Branch angle
- Number of ramicorns

Define SC in the same way so they can be evaluated acoss countries

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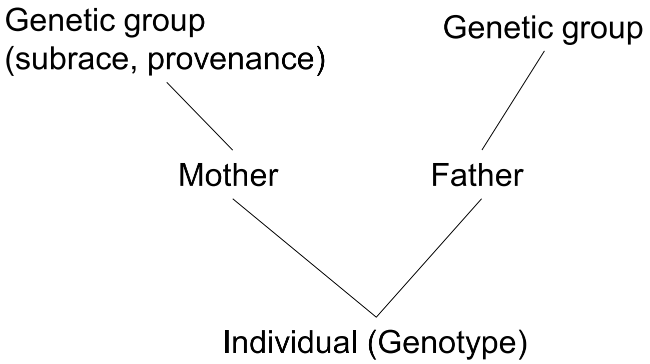
Analysis procedure

- Establish pedigree
- Enter trial data
- Single-site analysis
  - Spatial analysis
  - Multivariate analysis
- Define harvest age traits and indices
- Define site types – e.g. harsh or mild
- Predict multi-variate breeding values (TREEPLAN)
- Review breeding values
- Make selections for deployment or for breeding

Establish pedigree


Genetic group
(subrace, provenance)

Genetic group

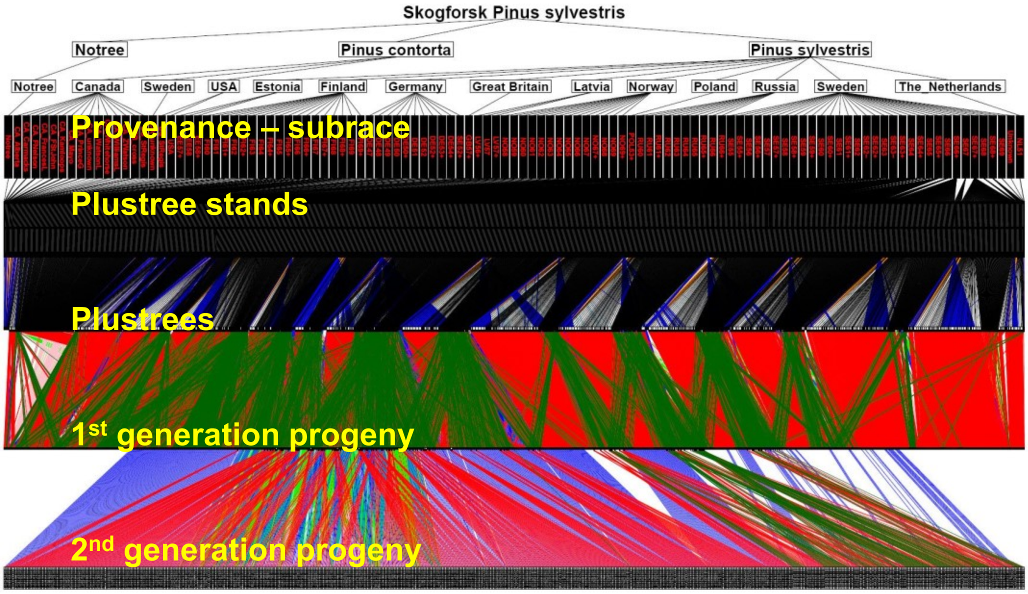
Mother

Father

Individual (Genotype)

Pedigree must be defined with the same identity across countries

Pedigree for Scots pine



Spatial analysis improves h^2

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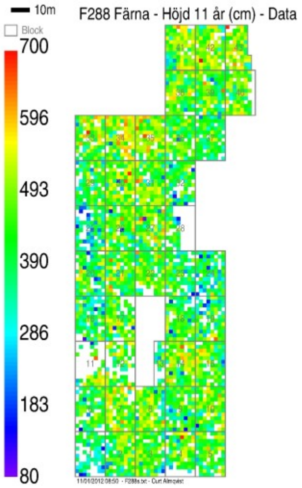
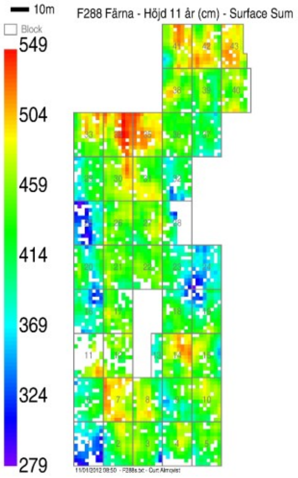
Height age 11 yrs (cm) –
Raw data



Height age 11 yrs (cm) –
Spatial adjusted



Single-site and trial series parameters calculated

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Parameters from single-site and site-site analysis are stored in a database

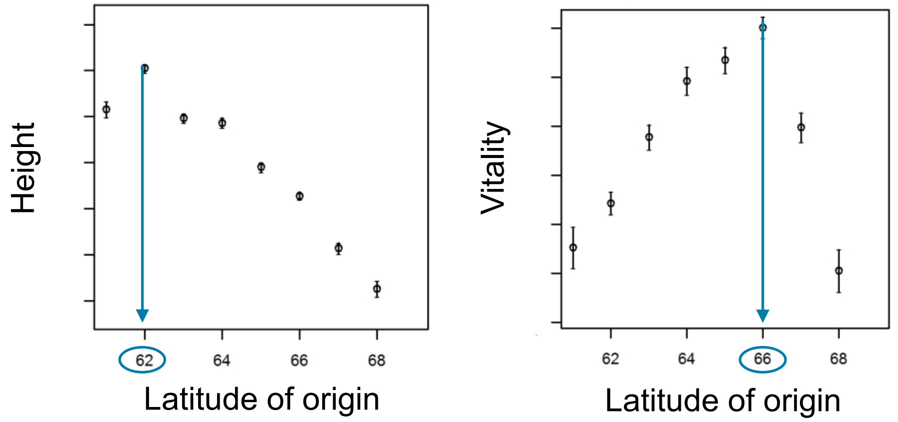
- Heritability
- Correlations between traits calculated
- Correlations between sites calculated
- Correlations between ages calculated
- ”Average” values are calculated to be used in mulitvariate analysis with TREEPLAN

TREEPLAN analysis procedure

- Measured traits
  - Defined by trait, site-type and age
- Multivariate anlysis
  - Uses trial design
  - Scales data into unit additive variance
  - Allows for heterogenous heritability
  - Uses age-age, trait-trait and site-site correlations
- Harvest age traits
  - Predicted by trait at harvest age
- Indices
  - Traits are weighted into an index

Strong provenance cline in Northern Sweden

Scots pine, mild sites, latitude 62 at age 20 yrs



Index selection increases volume and improves branch angle

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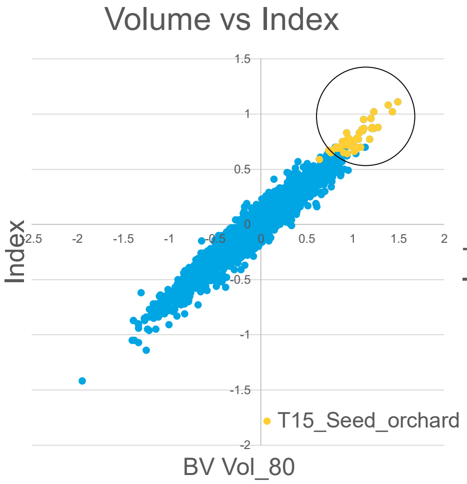

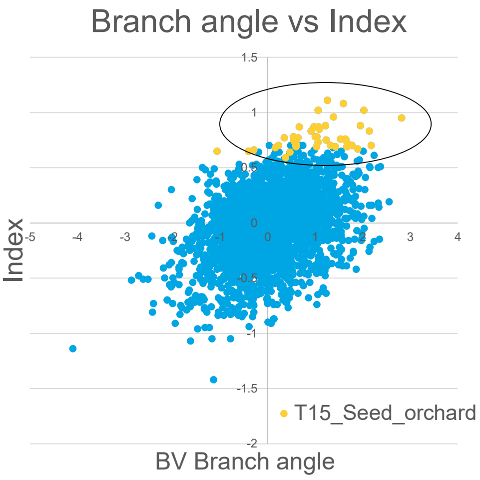

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Conclusions

- Common families most efficent to link trial series for routine progeny testing
- Standardization of pedigree and measurements needed to perform joint analysis
- Multivariate analysis handles unbalanced measurements, i.e. different traits and different age at measurement