Incorporating genetic gain into stand level modeling: a forest genetics perspective

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Overview: a forest genetics perspective

• Deployment policy/guidelines of selected material must consider:
  – future unknown risk (e.g., exotic pests)
  – known risks / pests (e.g., weevils, MPB)
  – growth potential, yield & stability

• Breeding Values (BV) > Genetic Worth (GW) > stand level projections

• Future research issues
Loblolly pine in the southern US

**Full or half sib forestry**

- nursery advantages real
- silviculture handling, also ‘real’
- growth and yield advantages?
- no ‘value added’ as of yet?
Eucalyptus in Brazil

All clones still mixed at the mill!
Reforestation ‘Landscapes’ in B.C.
Deployment for Unknown Risks

Past models of deployment, e.g., Libby (1982), Roberds et al (1990), etc.

- Largely ‘single gene-for-gene’ models,
- Plantation ‘failure’ at an arbitrary value (e.g., 50% mortality), show;
  - more than 30 clones does not provide any advantages
  - sometimes 1 is best
  - Incredibly sensitive to gene frequencies of resistant genes in natural populations
Probability of plantation failure at 50 years for 3 gene frequencies for recessive susceptible allele

Adapted from Bishir and Roberds (1997)
Probability of plantation failure at 50 years for 3 gene frequencies for recessive susceptible allele

Adapted from Bishir and Roberds (1997)
Probability of plantation failure at 50 years for 3 gene frequencies for recessive susceptible allele

Adapted from Bishir and Roberds (1997)
Deployment for Unknown Risks…cont.

Recent work:

- **Spruce Growth & Yield** with an insect population dynamics model
  - Spruce terminal weevil model
- **Tree and Stand Simulator** (TASS - B.C. For.Ser.)
  - Individual trees, competition-driven model
Key elements of the Tree and Stand Simulator (TASS) (Mitchell, 1975)

Dead tree

Live trees, 

Critical distance

Dead tree
Key elements of the Tree and Stand Simulator (TASS)...cont.
Spruce weevil resistance mechanisms

- ATR - attractiveness (volatiles)
- RES - rate of resin flow rate
- TOX - toxicity of resin
- GRW - tree ‘vigour’

- $h^2 < 1.0$ for ATR, RES, TOX
- $h^2 = 0.5$ for GRW
- GRW correlated with RES ($r_g = 0.5$)
BC TASS / Pest Dynamics Model

- Spruce weevil movements and site characteristics
  - temperature
  - plantation size
  - weevil distribution
  - site index
BC TASS/Pest Dynamics Model

- **Numbers of clones**
  - 2
  - 6
  - 18
  - 30

- **Deployment strategies**
  - Random Mix (RM)
  - Single Clonal Blocks (SCB)
  - Mosaic of Clonal Blocks (MCB)
### ‘Random’ Mixes – 2 clones

| 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 |
| 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 |
| 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 |
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| 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 |
| 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 | 1 | 2 |

The table above represents the checkerboard pattern for two clones in a ‘random’ mix.
Random Mixes – 2 clones
## Single Clone Blocks – 2 clones

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This diagram illustrates the arrangement of single clone blocks in a 2x2 grid, with alternating blocks marked as '1' and '2' respectively.
Mosaic of Clonal Blocks - 2 clones
Mosaic of Clonal Blocks - 6 clones

| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |

| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | 5 | 5 | 5 | 5 | 5 | 6 | 6 | 6 | 6 | 6 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
| 6 | 6 | 6 | 6 | 6 | 5 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 4 | 4 | 4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 |
Random Clones (WD=1, TMP=11, SI=30)

from Yanchuk et al. 2006 (Silvae Genetica)
RANDOM CLONES (WD=1, SI=30, Ha = 1)

Top 50% clones = ~85% volume

Ne reduction 20%
Random mixes versus single clonal blocks for 6 fixed clones: Western redcedar at 100 years

- Volume random mixes
- Volume single clonal blocks
- # trees random mixes
- # trees single clonal blocks
Conclusions from Modelling

For a well-characterized pest behaviour and polygenic resistance model:

- **for unknown risks,**
  - ‘acceptable’ numbers of clones is around 5-25

- **for both unknown risks and known pest behaviour,**
  - random mix was always the best
  - G&Y predictions can be highly variable and driven by site variations
  - the best genotype(s) do most of the work
  - effective pop. size change only by ~20%
    
    *(however, surviving #'s of stems is misleading)*

  - still need to factor in pest/disease ‘evolution’ potential
Policy for B.C.

- Vast, variable landscapes
- still addressing extensive management; long rotation ages
- Current research was policy-driven
  - supports our minimum Ne of 10
  - most ‘responsible’ approach is random mixes
  - first ‘bullet proof’ stands genetically
  - landscape diversity accomplished at seed zone level
Additional Research

• single gene effects
• blister rust / MPB >> mortality
• orchard families vs clones?
• variable genotypic representation in stands?
• climate change
  • moving and modelling population growth functions in space and time?
  • seed planning units?
• build in empirical results into our ‘theoretical’ models
Breeding Values and Genetic Worth

• breeding value (BV) – predicted genetic ‘value’ of a parent

• BV – measured as the mean of a parents offspring relative to the mean of wild stand progenies (e.g., %)

• after competition sets in, progeny tests cannot predict unit area yields!

Genetic worth = average BV of parents making up a seed orchard seedlot, adjusted for gain at rotation age
Two examples of the relationship between numbers of parents in an orchard and genetic gain for spruce and WK-low and SA-high

- BV's individually have errors of +/- 4-8%
- seed orchards have unbalanced matings
Estimating the effects of genetics on stand-level yields in B.C.

- **Historical approach** was a direct lift to site index (e.g., 5, 10, 15%, etc) by orchard ‘category’

- **Mid-90’s** changed to have Genetic Worth (GW) of a seed orchard lot (%) lift site index (SI)
  - GW is a volume estimate at ‘rotation/ index age’ at max MAI
  - so we adjusted SI at an index age, by GW / 2 (a general rule of thumb)
  - however, there are problems with magnitudes of gain before and after ‘index age’

- **New approach**
  - users input GW of seedlots directly into TIPSY
  - now adjusts for GW from ‘age of selection’ to anticipated ‘harvest age’ (Xie and Yanchuk, 2003)
‘TIPSY’
Table Interpolation Program for Stand Yield
AGENCY: MOF Research Branch
PROJECT: Experimental

STAND
GEOGRAPHY: Prince George/Prince George/SBS/10% Slope
ESTABLISHMENT: Regen delay = 0; Target Density = 1500 trees/ha (Planted)

SPECIES
100% WHITE SPRUCE; Site Index = 17.50
Site curve: *Goudie (1984ac) (plantation)
Top Ht @ 100 age 50 (m) = 17.50 (base); 19.42 (incl. GW)
Stock ht = 21cm
Genetic Worth: 18.0% (total vol. gain 80 years after planting: 15.8%)

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<th>Top Gross Merch</th>
<th>Merch 12.5+</th>
<th>Merch 12.5+</th>
<th>Merch 0.0+</th>
<th>Merch 0.0+</th>
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<td>599</td>
<td>5.44</td>
<td>65</td>
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Vol. Merch 12.5+ (m3/ha)

- Gw = 0
- GW = 18
CLOSED TO MOTOR VEHICLES
3 DAYS PRIOR TO FIRST RIFLE BULL THROUGH LAST DAY OF THE SECOND RIFLE BULL SEASON
OREGON DEPARTMENT OF FISH AND WILDLIFE
Gain and Breeding Value ‘Math’

- Gain (Gₘ) for selections at maturity:
  \[ Gₘ = iₘ hₘ² \sigma_P² \]
  where:
  - \( iₘ \) = selection intensity
  - \( hₘ² \) = heritability = \( \sigma_G² / \sigma_P² \)
  - \( \sigma_P² \) = phenotypic variance
  - \( \sigma_G² \) = additive genetic variance

- Correlated Gain (CGₘ) for selections < rotation age:
  \[ CGₘ = iₘ hᵢ hₘ r_{Gᵢₘ} \]
  where:
  - \( r_{Gᵢₘ} \) = genetic correlation between the juvenile and mature traits
Genetic Worth ‘math’

Where:

\[ R_i = 1.02 + 0.308 \times \ln\left(\frac{a_s}{a_i}\right) \]  
(Lambeth model (For. Sci. 1980), e.g. Age-age correlation between selection age and index age)

\[ R_y = 1.02 + 0.308 \times \ln\left(\frac{a_s}{a_y}\right) \]  
(Age-age correlation between selection and yield age)

\[ a_s = \text{selection age} \]
\[ a_i = \text{index age} \text{ (60 or 80 years)} \]
\[ a_y = \text{age of yield estimate} \]
Genetic Worth example

Let:

\[ a_s = 12 \text{ years (selection age)} \]
\[ a_i = 60 \text{ years (index rotation age)} \]
\[ a_y = 100 \text{ years (harvest age)} \]
\[ GW = 20\% \text{ (genetic worth)} \]
\[ GH_i = 20/2 = 10 \]

Then

\[ R_i = 1.02 + 0.308 \cdot \ln(12/60) = 0.524 \]
\[ R_y = 1.02 + 0.308 \cdot \ln(12/100) = 0.367 \]
\[ GH_{100} = GH_i \cdot (R_i/R_y) \]
\[ = 10 \cdot (0.367/0.524) \]
\[ = 10 \cdot (0.700) = 7.00\% \]

Additionally,

\[ GH_{10} = 20\% \]
\[ GH_{60} = 10\% \]
\[ GH_{100} = 7\% \]
\[ GH_{150} = 8\% \]
\[ GH_{300} = 3\% \]

Effects of GW on yield as modelled in TIPSY

Site index=30
Species=coastal Douglas-fir
Planted 1000/ha
Selection age=12
Index rotation age=60
GW=10%

Green - up
Realized Gain Trials

• Realized gain trials needed to validate juvenile age selections in single-tree plots
  • (everything up to now is model based!)
  • established realized gain trials for most commercial species, starting in 1991
  • trials include:
    • 3-4 genetic entries
    • 4 spacings
    • 4 sites per series
    • 4 replications /site
    • 144-tree square plots

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<th>Height @ age 7</th>
<th>Actual</th>
<th>Predicted</th>
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<tr>
<td>Mid Gain (+10%)</td>
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<tr>
<td>Top Cross (+18%)</td>
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Realised gain early results
(Douglas-fir Norrish site, Spacing=1.6m)
Spatially Explicit Genetic Gain Estimates in Timber Supply Analyses for the “Arrow” and “Golden” Timber Supply Areas

Figure 2.1 Harvest forecasts, Arrow genetics analysis

Figure 2.2 Harvest forecasts, Golden genetics analysis
Conclusions

- genetic theory has served us well in most areas of predicting genetic gain across many organisms
- while we can be ‘out’ on any individual stand, the mean of many stands will likely be very close to our predictions
  - e.g., loblolly pine (B.D. Shiver and S. Logan)
  - theory and models can only provide general guidance to managers dealing with a system driven by great variability
- with climate change / more pest disease epidemics likely, future research may be best focussed on inter- and intra-specific performance of select populations over wider environments
Thank you!
Effects of genetic worth on discounted stand value

Site index=30
Species=coastal Douglas-fir
Planted 1000/ha
Selection age=12
Index rotation age=60
GW=10%
4% interest rate
Port Alberni costs
Lumber market
Extra cost for improved seed=$30
Increase in maximum site value: $414/ha

3 years