Incorporating Genetic Gain into Growth Models

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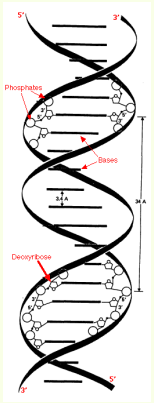
The authors:

- Randy Johnson
  - A geneticist
  - I think in linear terms

P = G + E

Phenotype = Genotype + Environment

=



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The authors:

- Randy Johnson
- David Marshall
  - A growth modeler
  - He thinks in non-linear terms

$$\Delta DBH = e^{\left[\beta_0 + \beta_1 \ln(DBH_0 + 1) + \beta_2 DBH_0^{\,2} + \beta_3 \left(\frac{BACL^2}{\ln(DBH_0 + 5)} \right) + \beta_4 \sqrt{BA} \right]}$$

The authors:

- Randy Johnson
- David Marshall
- Greg Johnson
  - Another growth modeler, but he has “played” geneticist for over 15 years
  - He can think in both languages

Talk Objectives:

- Provide background on the methods used to incorporate genetic gain into growth models

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- Provide background on the methods used to incorporate genetic gain into growth models
- Present preliminary results of a study using Douglas-fir progeny test data to incorporate genetics into regional growth models.

How Should Gain Be Measured?

- Geneticist:
  - Heritable difference between a selected genotype and a control.
- Modeler:
  - Difference in the components of tree and stand growth attributable to a genotype.

How Should Gain Be Measured?

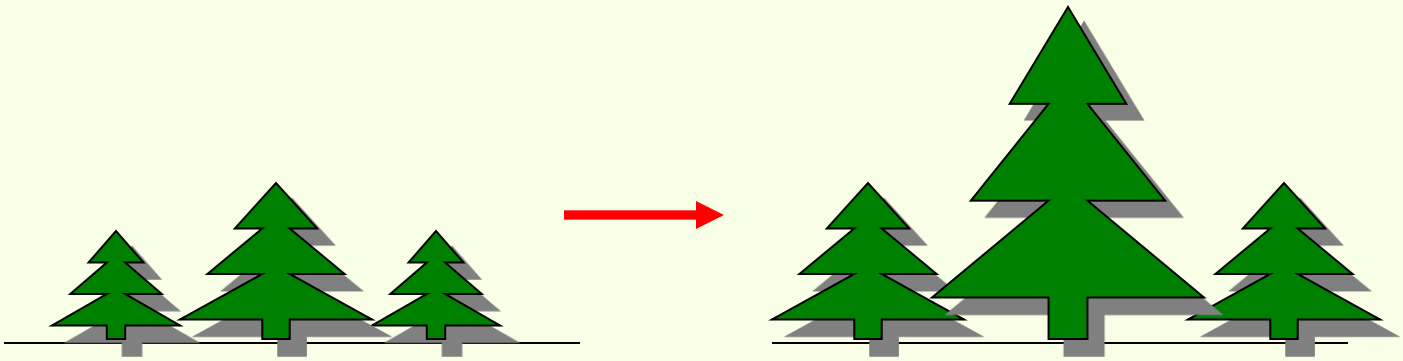
- Geneticist:
  - Heritable difference between a selected genotype and a control.
    - Typically a measure of ***individual*** tree performance.
    - Accounts for both *genetic* and *environmental* variation in the calculation of heritability.

Genetic tests

- Typically small plots
  (single-tree or rows)
- Test 10’s to 100’s of families
- Families tested on 3 to 5 sites
- Selection age (test life) is ¼ rotation
  (maximizes gain per year)

The problem with small plot sizes

After among-tree competition sets in, larger trees suppress neighbors and have better environments

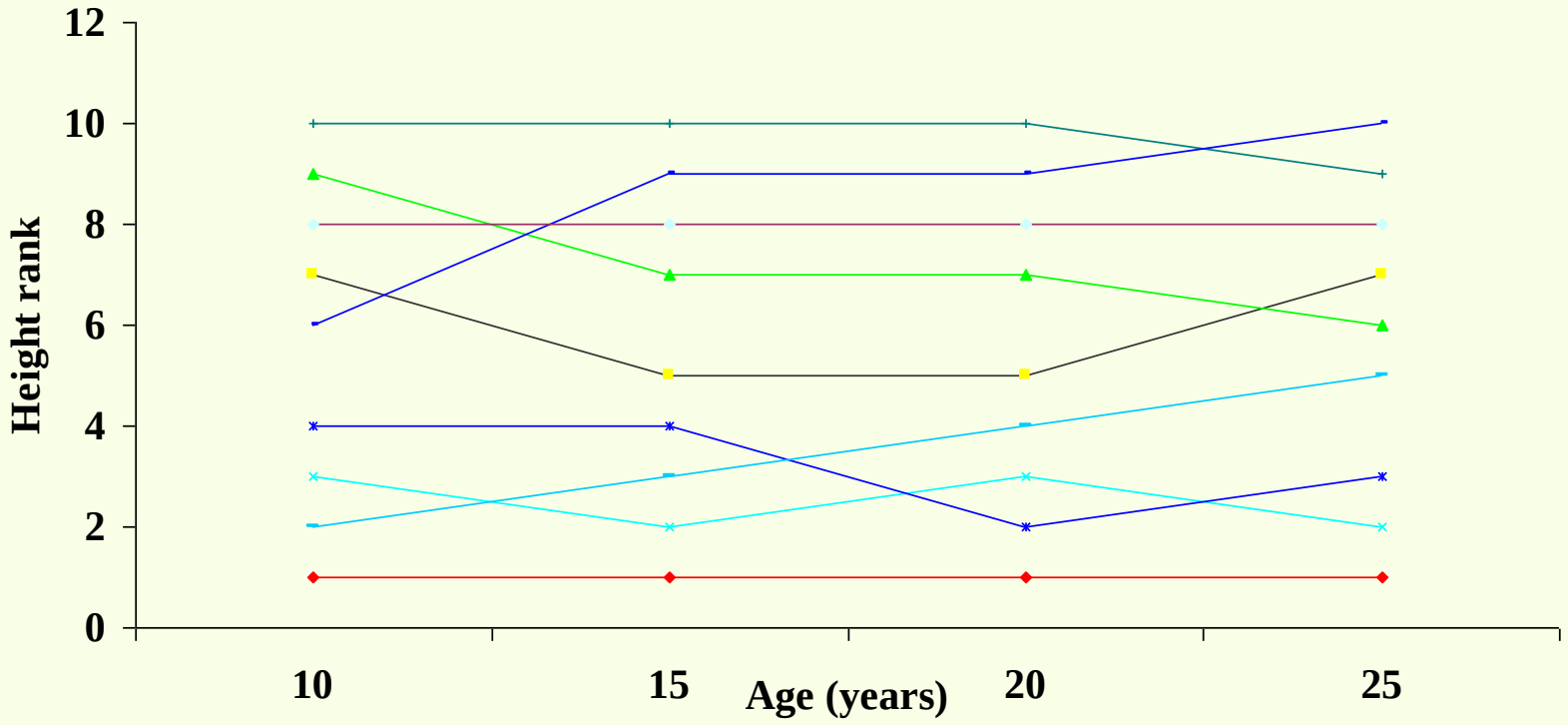


Therefore, we can't distinguish whether older trees are big because of genetics alone or whether the altered environment is, in part, the reason for later improved growth

Selection age – Juvenile-Mature Correlations

- I’m impatient and don’t want to wait 40 years to decide which family is best at rotation.
- But, the genes that influence early growth aren’t necessarily the same as those that influence later growth

Family ranks change over time



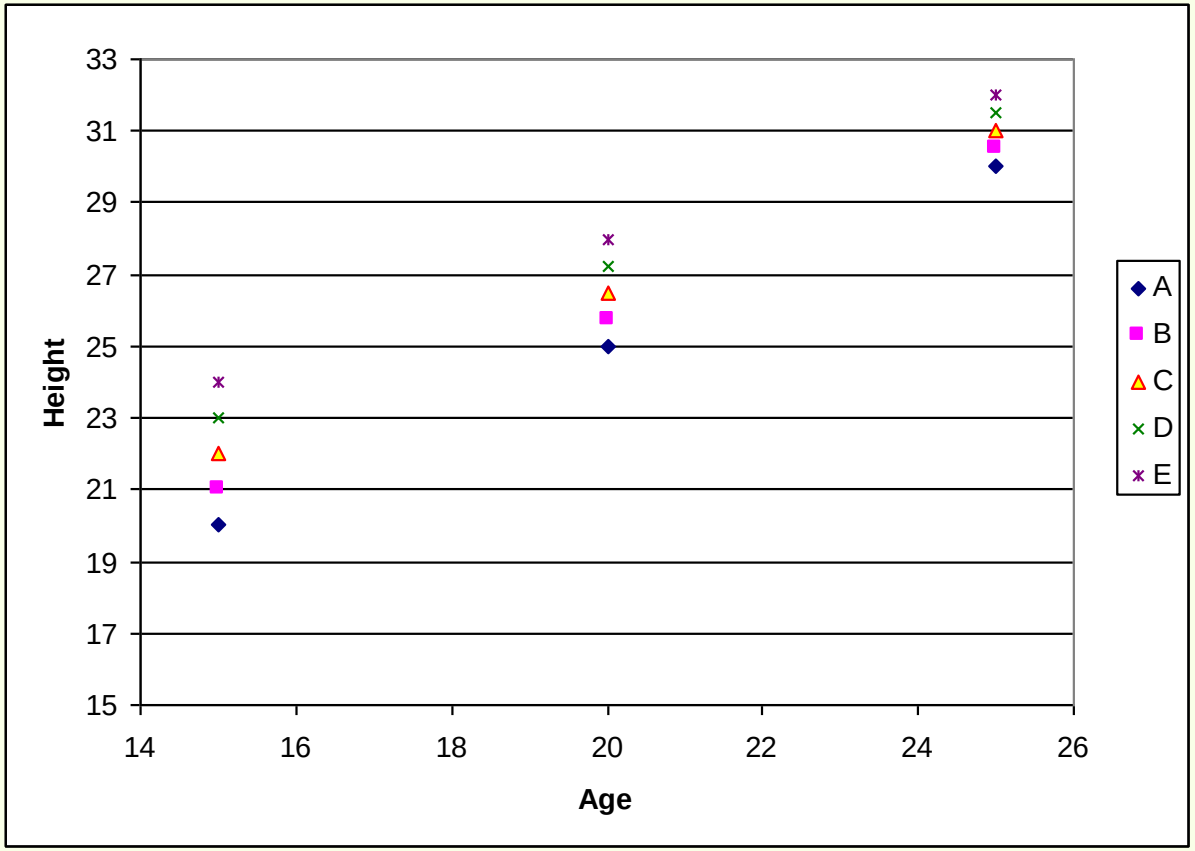
Age-age genetic correlations
(Douglas-fir example)

AGE	10	15	20	25
7	0.97	0.85	0.79	0.64
10		0.94	0.90	0.74
15			0.99	0.93
20				0.97

Lambeth's equation: $r = 1.03 + 0.306 \times \log(\text{age ratio})$

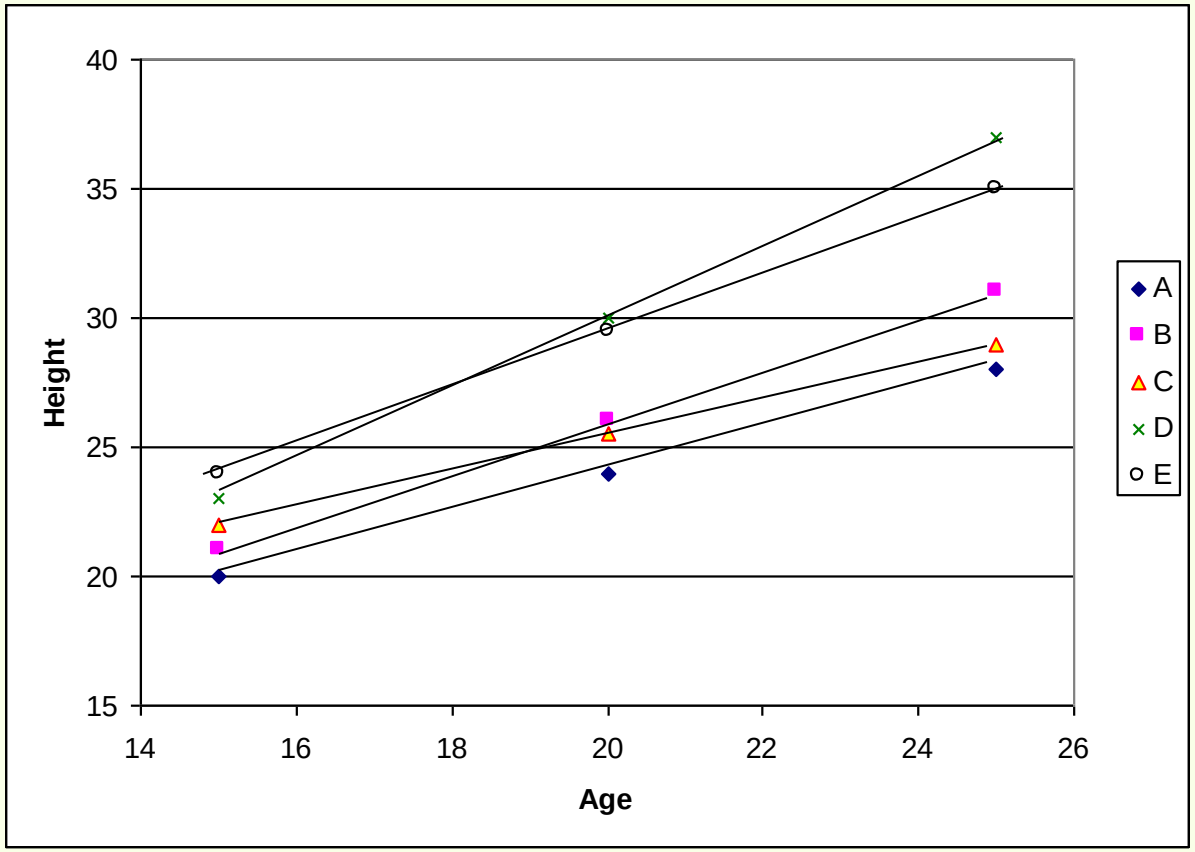
$\log(\text{age ratio}) = \ln(\text{age}_{young} / \text{age}_{old})$

But... correlation is not directly associated with future gain



An example of r = 1.0,
but both absolute and percentage gain decreases with time

Correlation is not directly associated with future gain



An example of r = 0.8,
but both absolute and percentage gain increases with time

Geneticists pick winners

Growth Modelers predict growth

(**They're NOT the same thing**)

How Should Gain Be Measured?

- Modeler:
  - Difference in the components of tree and stand growth attributable to a genotype.
    - What is the:
      - magnitude,
      - form, and
      - duration

      of changes to the components of growth?

How Should Gain Be Measured?

- Magnitude: $\Delta HT = \beta_0 HT_0^{\beta_1} e^{-\beta_2 HT_0 - \beta_3 CCH}$
- Form: $\Delta DBH = \beta_0 e^{\left[\beta_1 DBH_0 + \beta_2 DBH_0^2 + \beta_3 \left(\frac{BACL^2}{\ln(DBH_0 + 5)}\right)\right]}$
- Duration:
  - $B_0 = f$ (Gain, Age, ???)

Growth Modeling plots

- Typically large plots

  (> 64 trees)
- Test limited number of seed lots
- Tens to hundreds of locations
- Keep until rotation

These are not appropriate genetic tests

Growth Modeling plots

- It would be nice to have large plots of rotation-age genetically-improved growing stock to formulate new growth models.
- But older growth plots will always have less gain than provided by current seed orchards.
- So we need to figure out how to modify existing growth models.

Gain modeling in the past

- Reviewed during the workshop in Nov 2003

http://www.fsl.orst.edu/pnwtirc/publications/Electronic version of some pubs/Growth Modeling Proceedings - PNWTIRC.pdf

Scientific literature reporting growth and yield models that incorporate genetic effects into the calculation of stand volume. Information supplied by G.S. Foster and presented in Cherry and Howe 2004.

Species	Approach	Reference
Chamaecyparis obtusa	Modeled improved populations	Kurinobu and Shingai 1987
Pinus monticola	Modeled improved populations vs unimproved populations	Rehfeldt et al. 1991
Pinus ponderosa	Modeled improved populations	Hamilton and Rehfeldt 1994
Pinus radiata	Derived growth rate multipliers for height, basal area, and calculated volume increase	Carson, Garcia, and Hayes 1999
Pinus radiata	Modeled growth of seedlots	Goulding 1994
Pinus radiata	Modeled seedling vs rooted cutting stands	Holden et al. 1995
Pinus taeda	Modeled pure family stands	Knowe and Foster 1989
Pinus taeda	Simulation modeling of pure family and mixed family stands	Nance 1982
Pinus taeda	Simulation modeling of improved vs woods run seedlots	Nance and Bey 1979
Pinus taeda	Modeled pure provenance stands	Nance and Wells a&b 1981
Populus deltoides	Modeled pure clone and mixed clone stands	Foster and Knowe 1995
Populus deltoides	Modeled improved clonal stands	Cao and Durand 1991

Gain modeling in the past

- Reviewed during the workshop in Nov 2003
- Three basic ways used to incorporate genetics into growth models

Genetic Modeling Methods

- Site index adjustment
- Effective age computation
- Growth modifiers

Genetic Modeling Methods

- **<u>Site index adjustment</u>**
  - Compute site index for the heights observed at a given age.

Our model will be the height growth trajectory for the hypothetical species *Pseudopinus johnsonii*

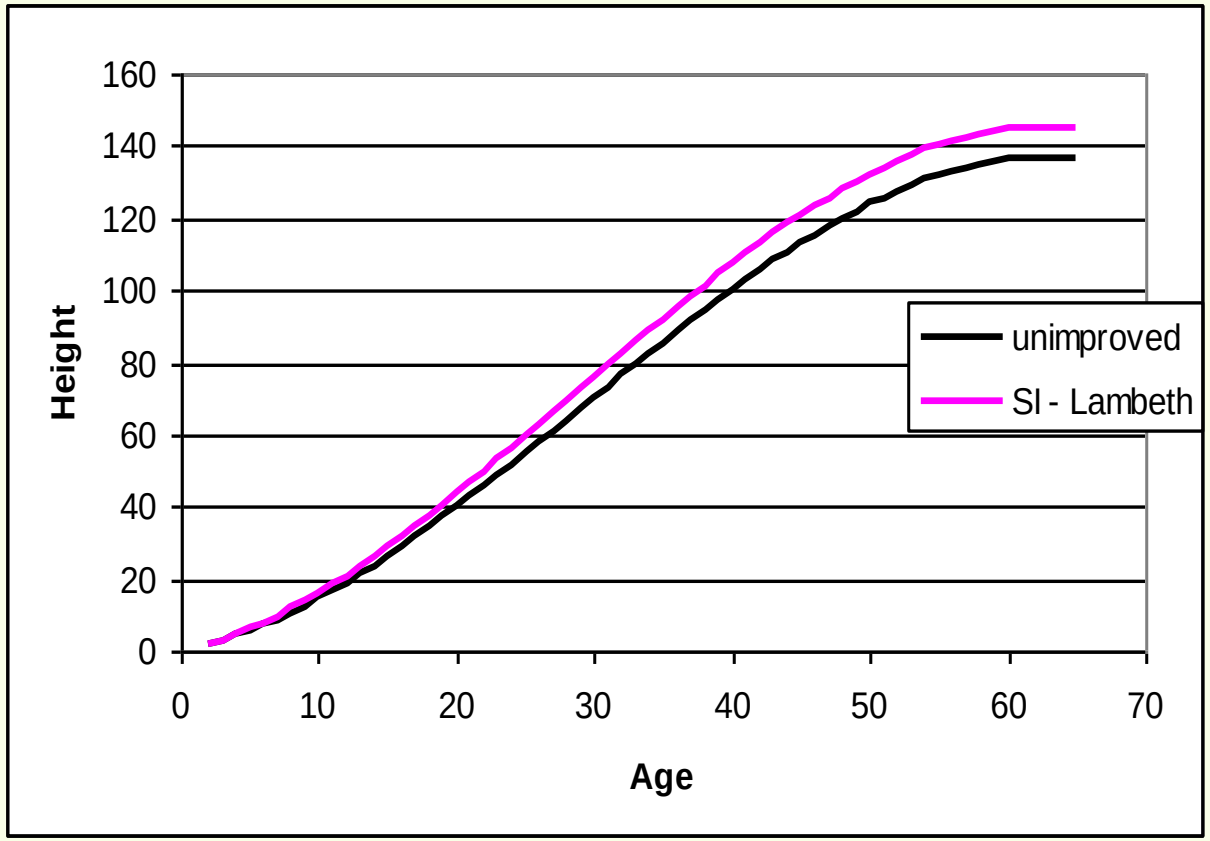
An example using King's SI curves; a percentage increase in height at selection age (age-15 in my examples) is the same as that at the index age

SI adjustment

a structural change

Note increase in both slope and asymtote

An example that assumes the percentage gain decreases according to the Lambeth relationship



SI adjustment

Both these adjustments assume some level of “site” improvement (*i.e. a change in the asymptote*). That is, one now assumes the site has become more productive.

Should we expect a “site” improvement?

- No difference if photosynthesis found among families of the same species.
- Possibly a change in:
  - Growing season
  - Soil exploitation
  - Biomass partitioning

- The literature has cases of changes and no changes in the asymptote.

Genetic Modeling Methods

- Site index adjustment
- **Effective age computation**
  - Estimate height/age curves for the two populations
  - Then calculate increased volume based on the increase in height at rotation or index age

(Now I'm going to use real data from Douglas-fir as an example)

Age-15 selections - height over time

Age	Population average	Top 10% of the families	Height difference	% increase
7	1.8	2.0	0.2	8.2
10	4.4	4.7	0.3	7.0
15	9.0	9.5	0.5	5.5
20	13.8	14.4	0.6	4.4

Data from 3 NWTIC breeding units

Age-15 selections - height over time

Age	Population average	Top 10% of the families	**Height difference**	**% increase**
7	1.8	2.0	**0.2**	**8.2**
10	4.4	4.7	**0.3**	**7.0**
15	9.0	9.5	**0.5**	**5.5**
20	13.8	14.4	**0.6**	**4.4**

Increasing **Decreasing**

Height-Age Equations

- Total population

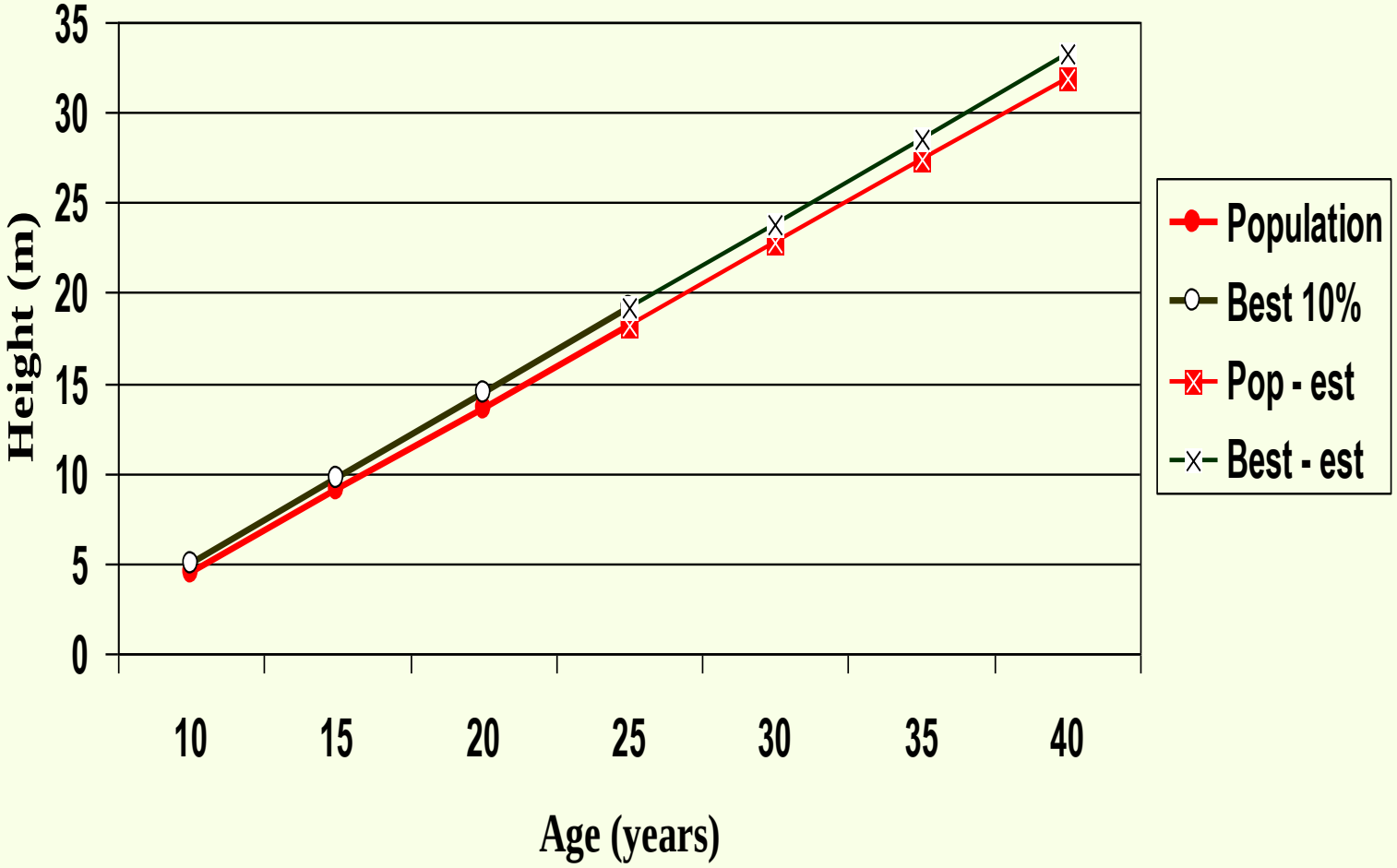
  Height (m) = (0.915 * age) – 4.7

- Top 10% of the families

  Height (m) = (0.944*age) – 4.5

For Douglas-fir our ht-age lines are on the linear-like portion of the growth curve

Douglas-fir projected height growth



How much better?

- 1.6 m at 50
  - Increase SI by 1.6 m

- 1.4 m at rotation age of 40 years

  1.4 / (0.915 m/yr) = 1.5 years more advanced
  - DF-Sim estimates for SI=125

    Age 40 = 186 m^3

    Age 41 = 194 m^3

    --- *Age 41.5* = 198 m^3

    Age 42 = 202 m^3

Genetic Modeling Methods

- Site index adjustment
- Effective age computation
- **Growth modifiers**
  - Go into the model and insert a multiplier

Basal area change = *f* (starting ht, ba, stems/ha)

becomes

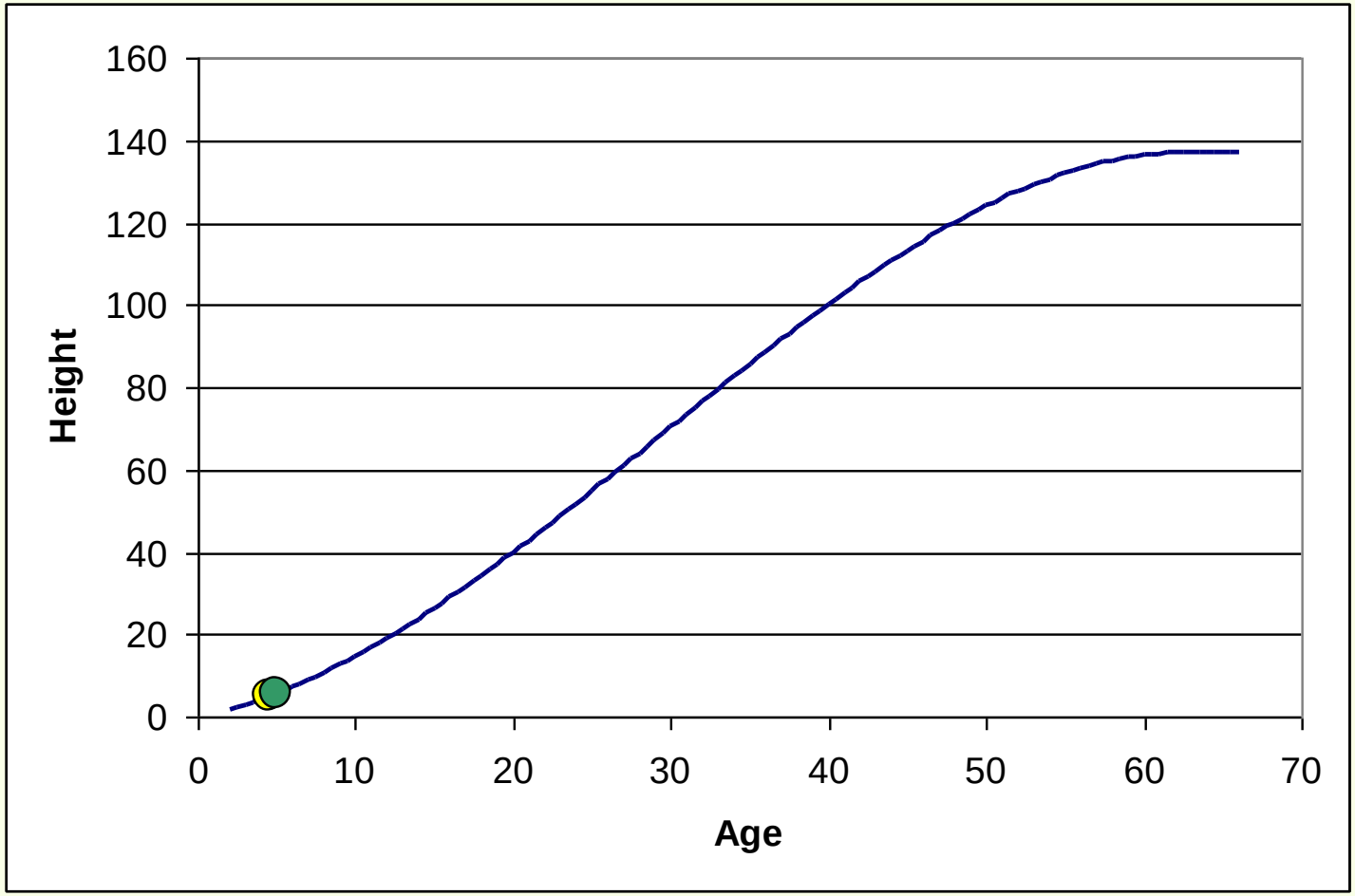
Basal area change = *m f* (starting ht, ba, stems/ha)

The improved population progresses through the same growth curve, but at a faster rate.

Carson, Garcia and Hayes (1999). Realized gain and prediction of yield with genetically improved *Pinus radiata* in New Zealand. Forest Science 45: 186-200.

Concurrent Session A – at: 15:30

Same growth trajectory, but moving faster



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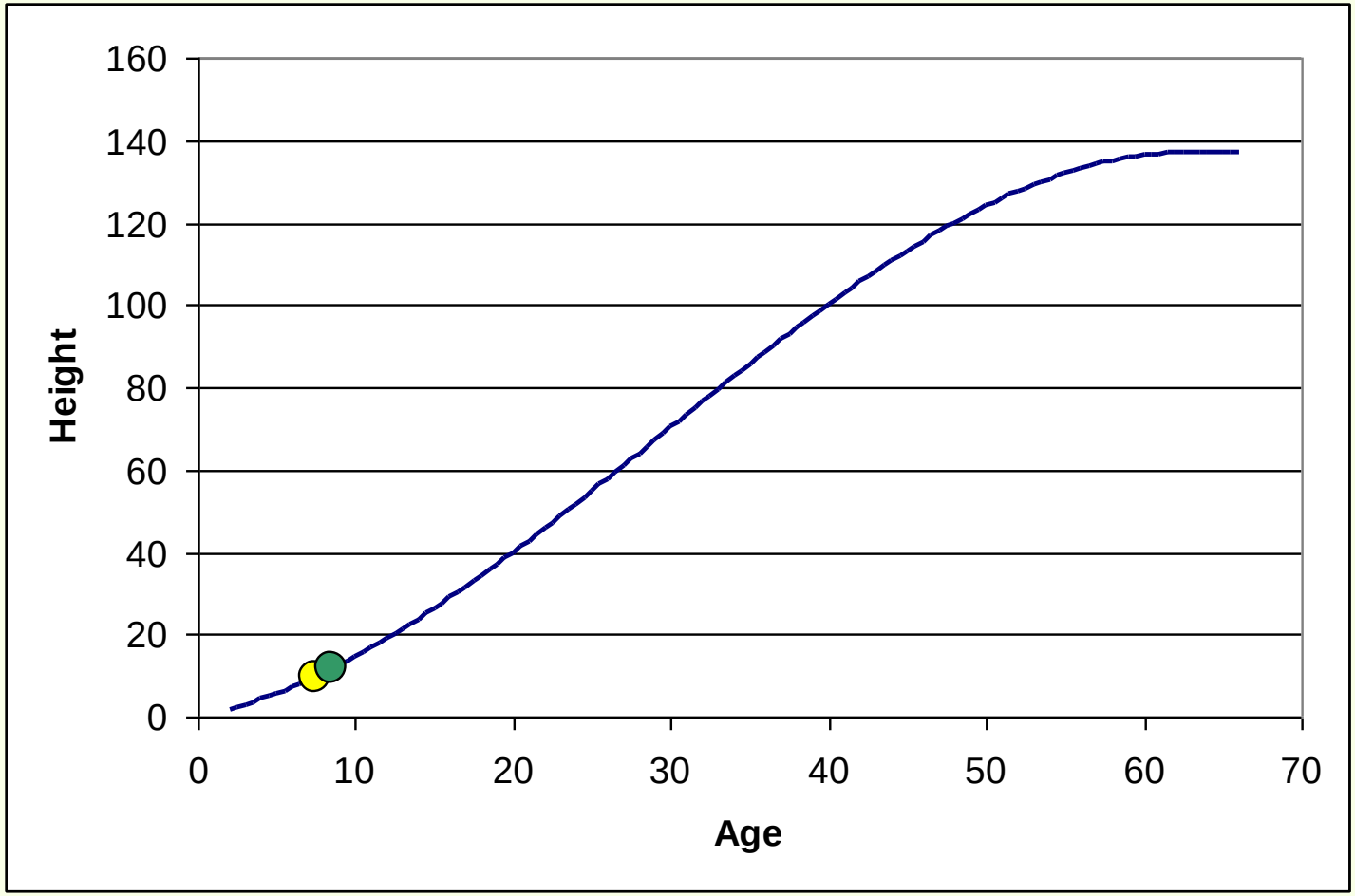

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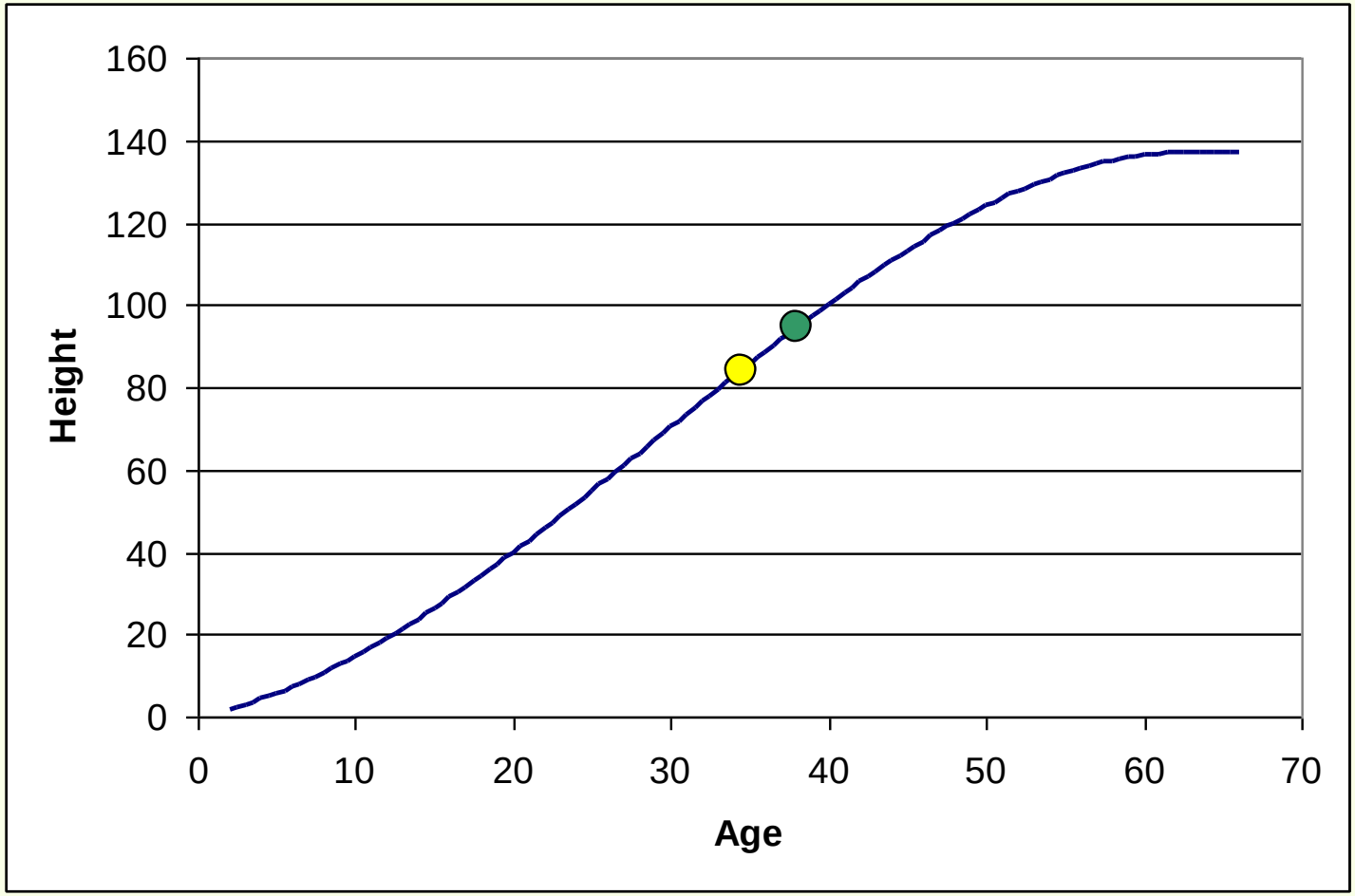

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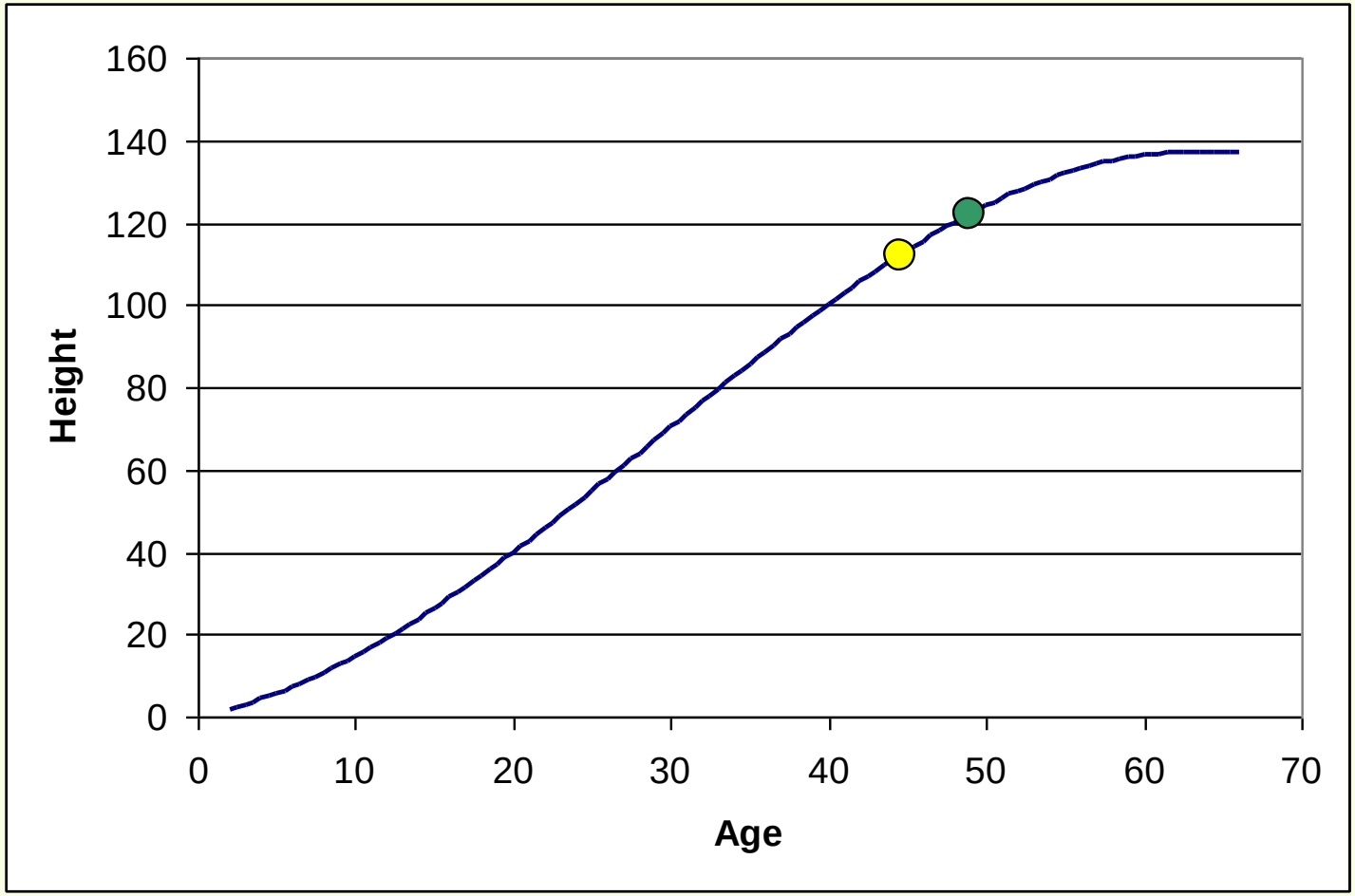

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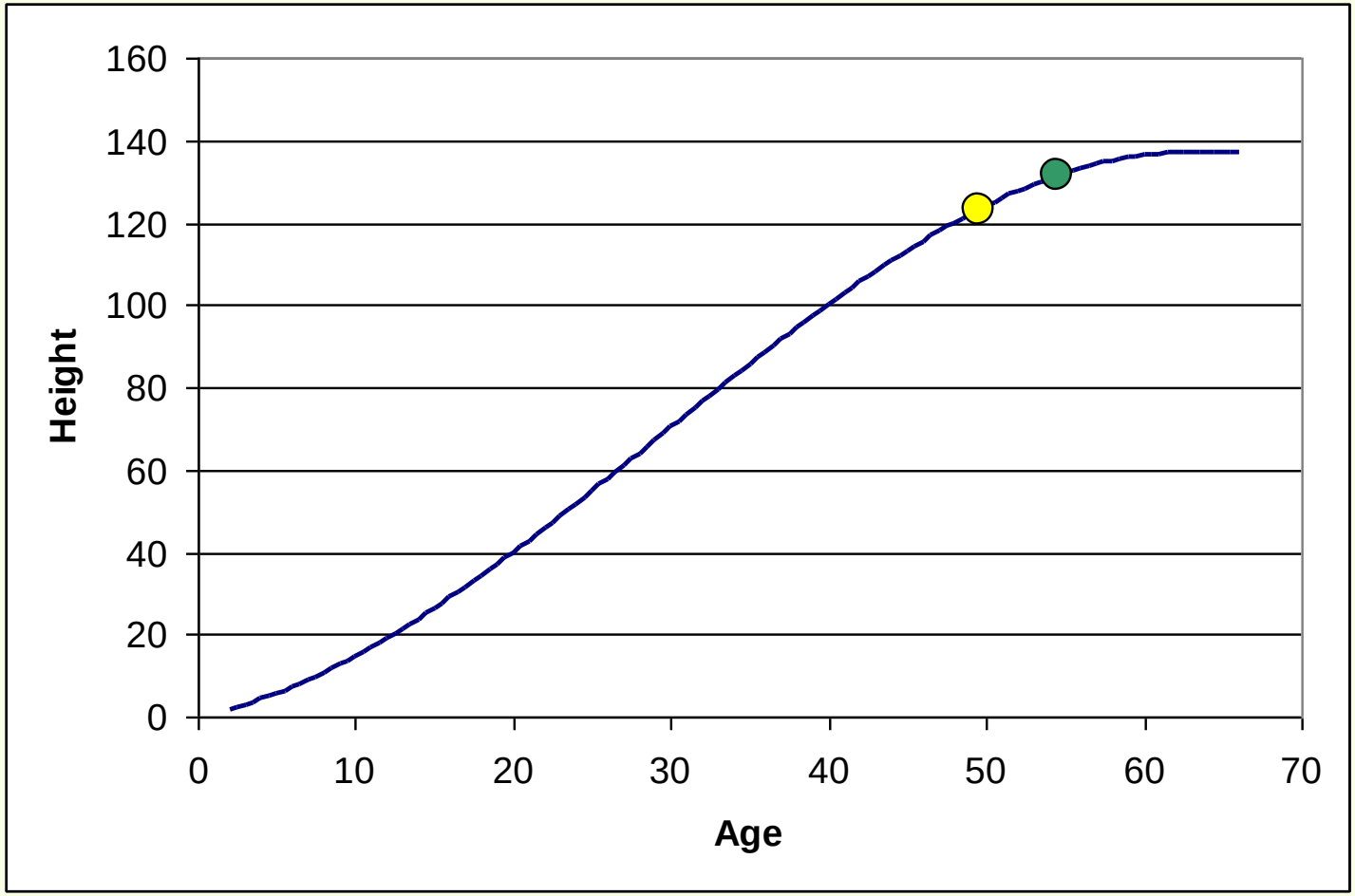
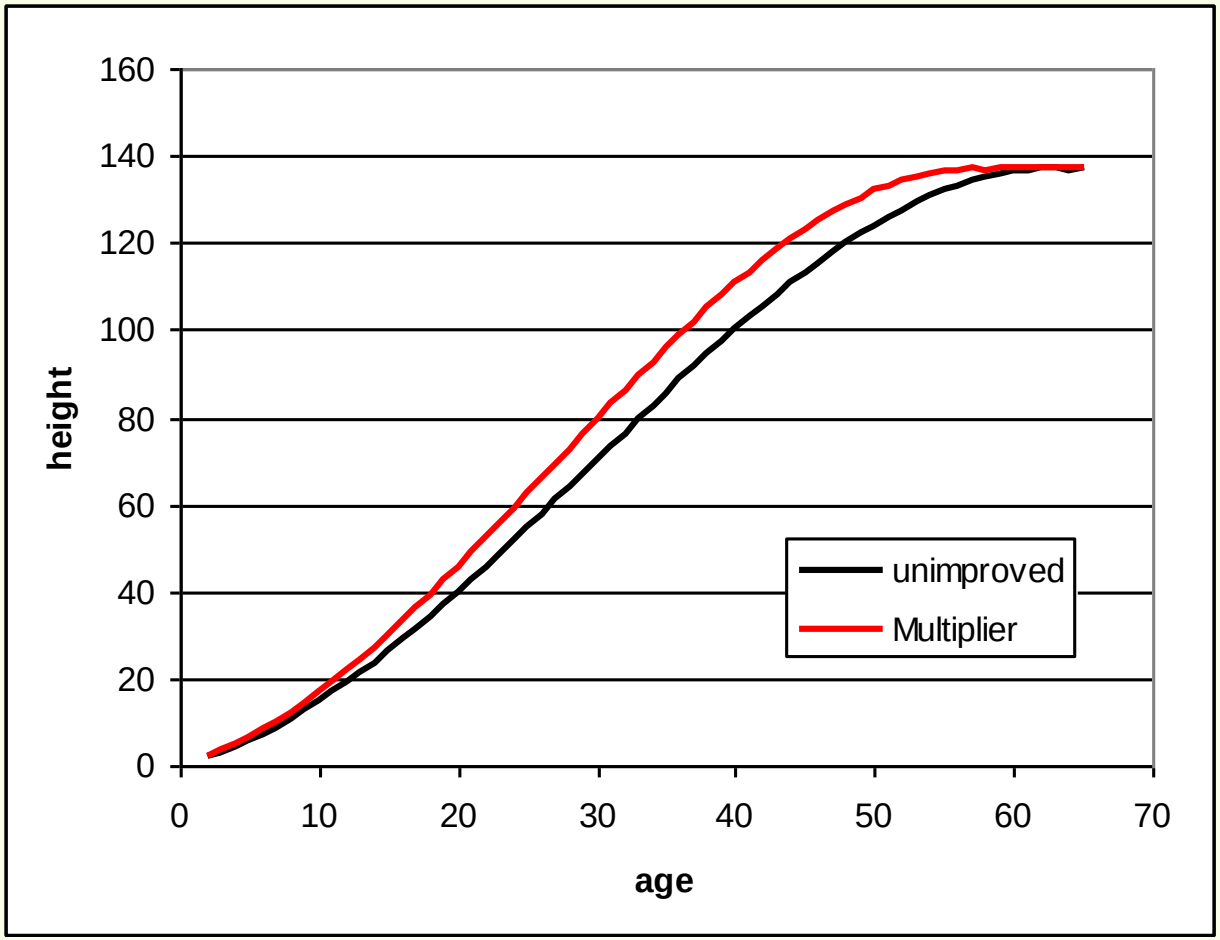


Same growth trajectory, but moving faster

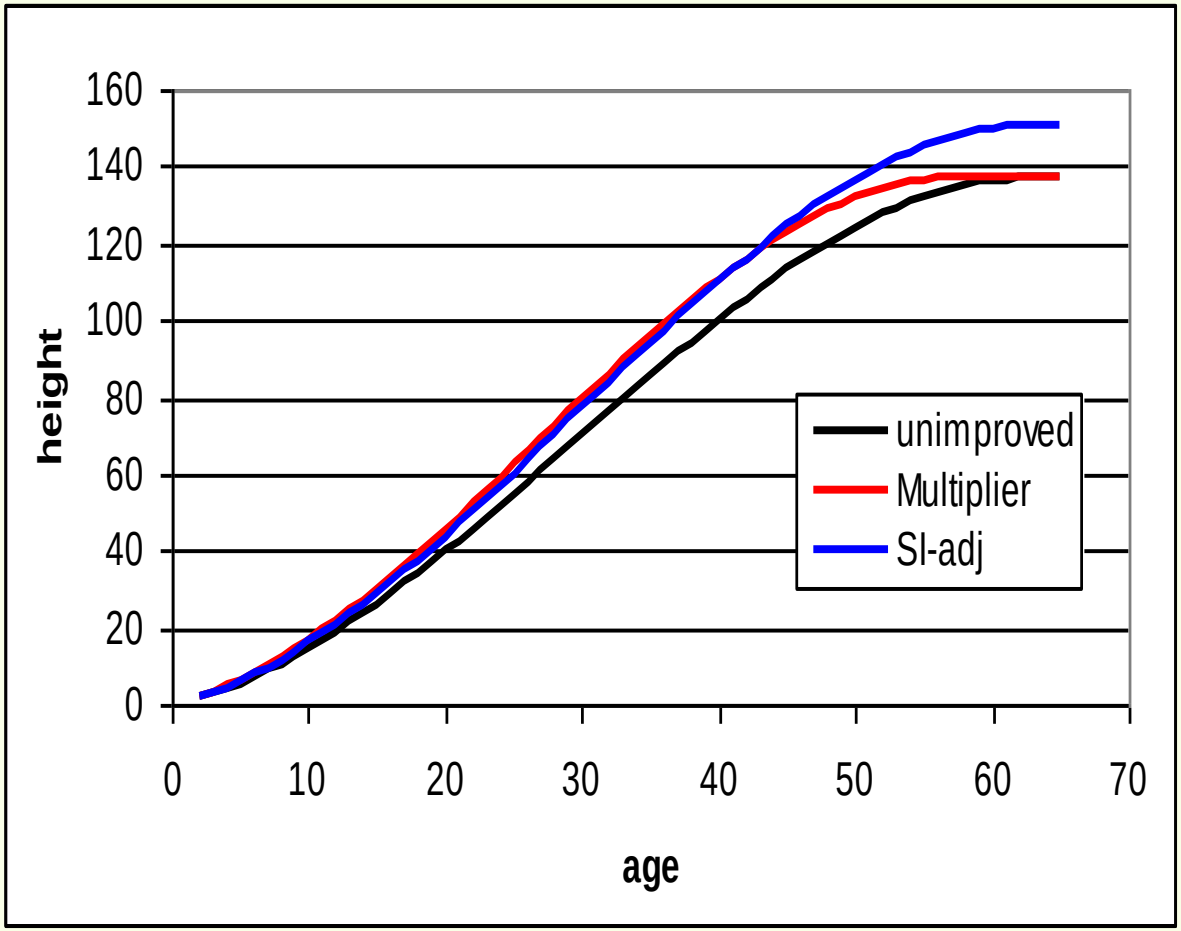
Same growth trajectory, but moving faster

This resulting growth curve:

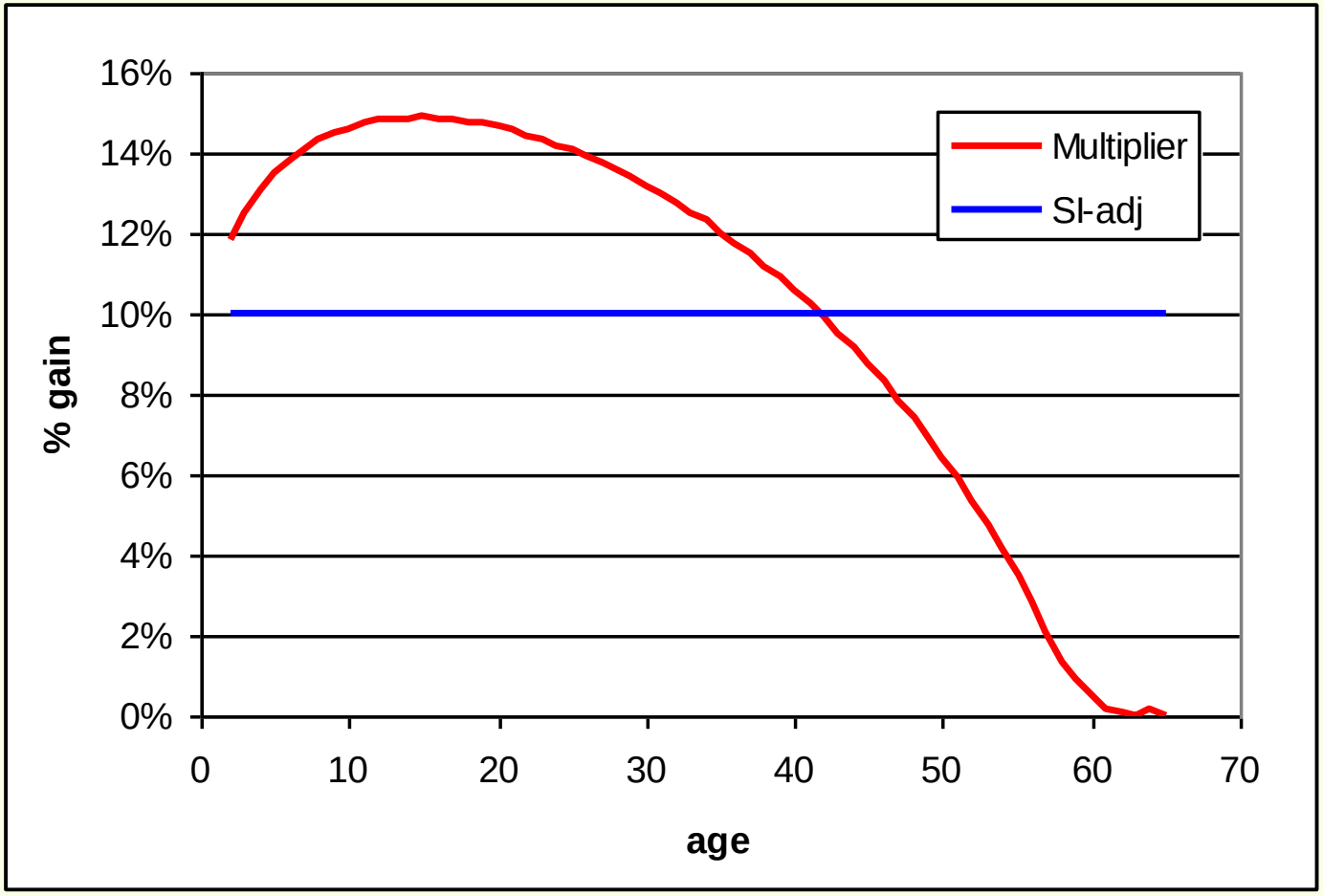


Multiplier

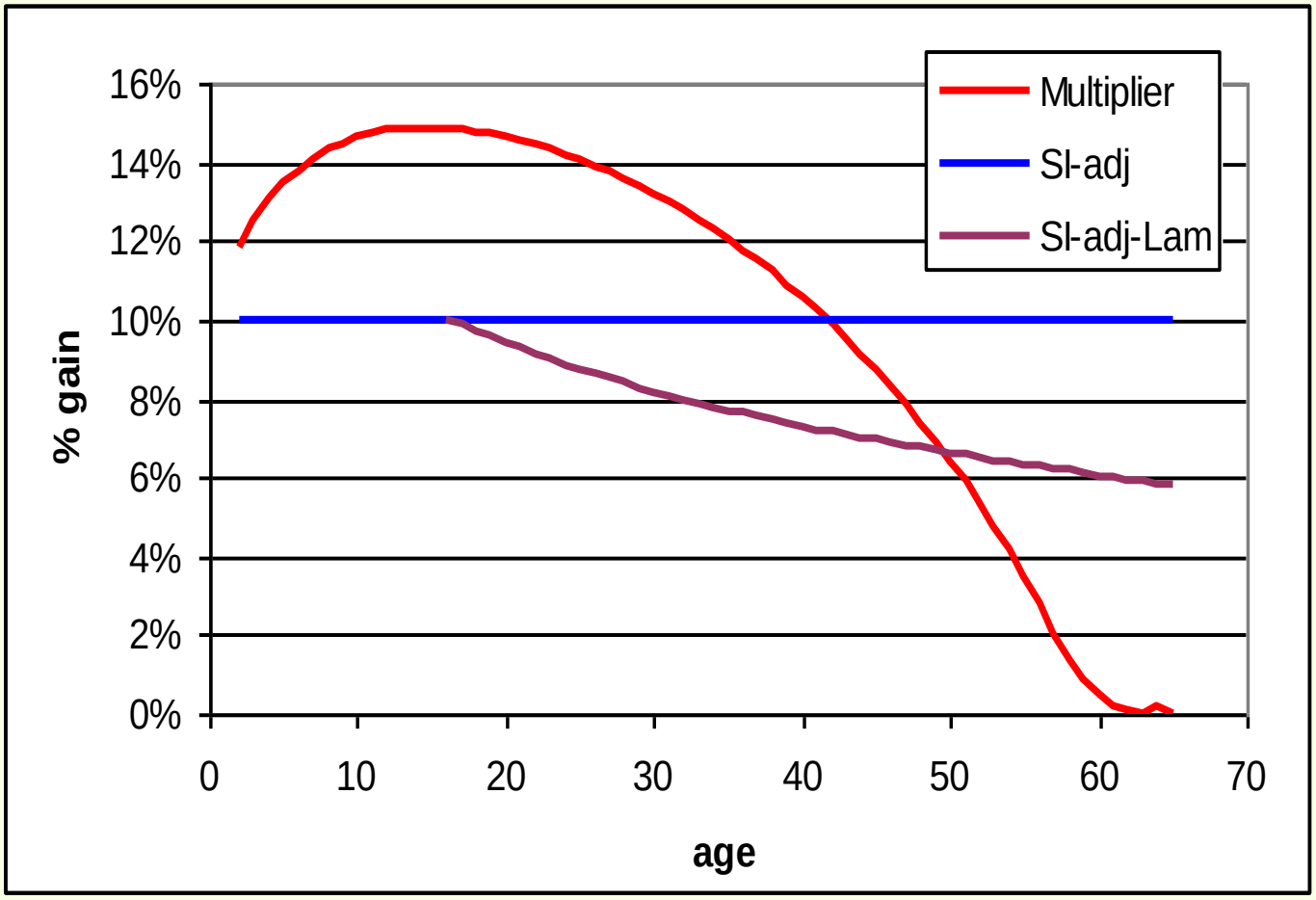
Both the *growth multiplier* and the *site index adjustment* look alike for much of the timeline, but..



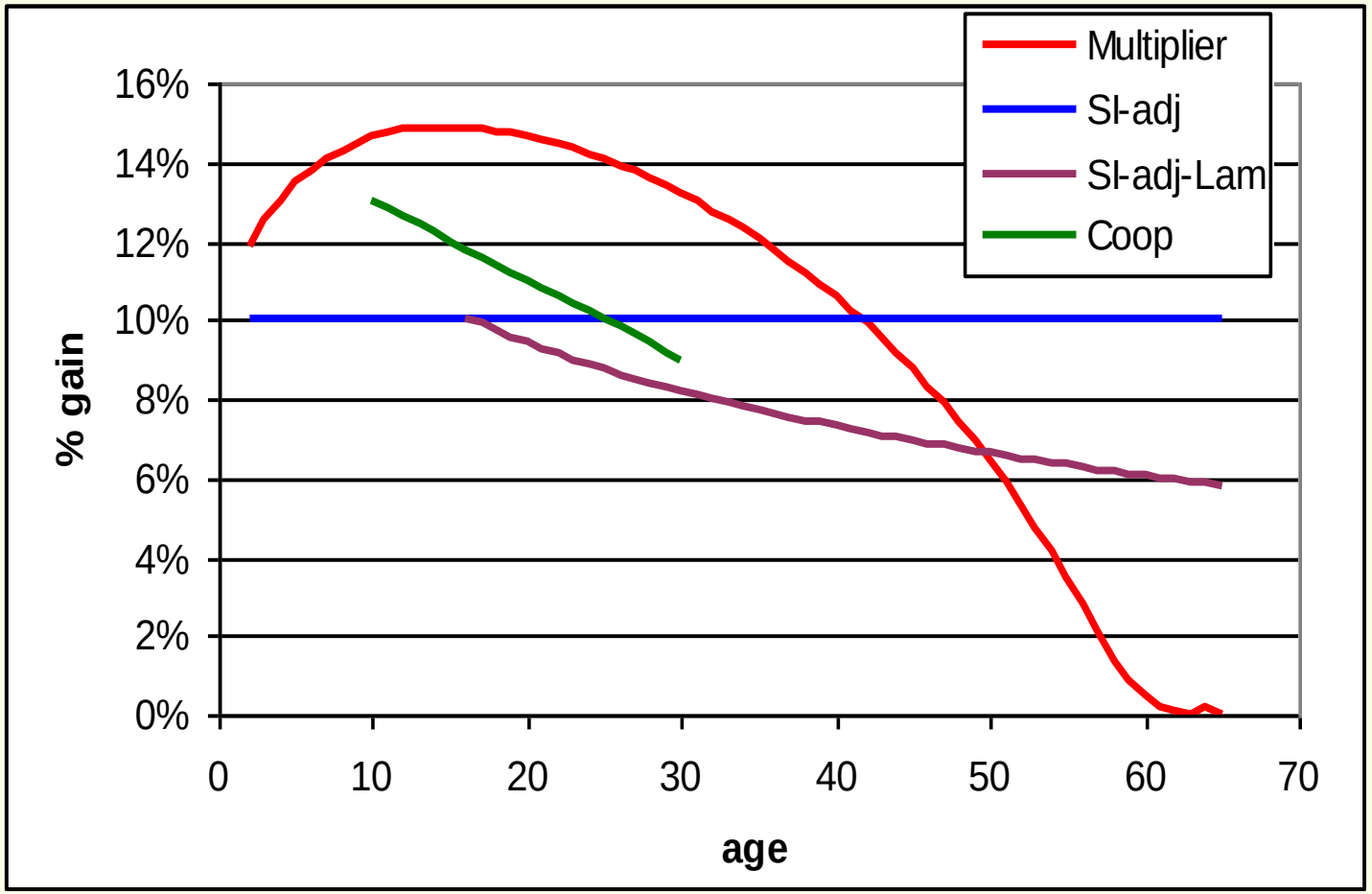
the gain estimates for both scenarios are not all that similar



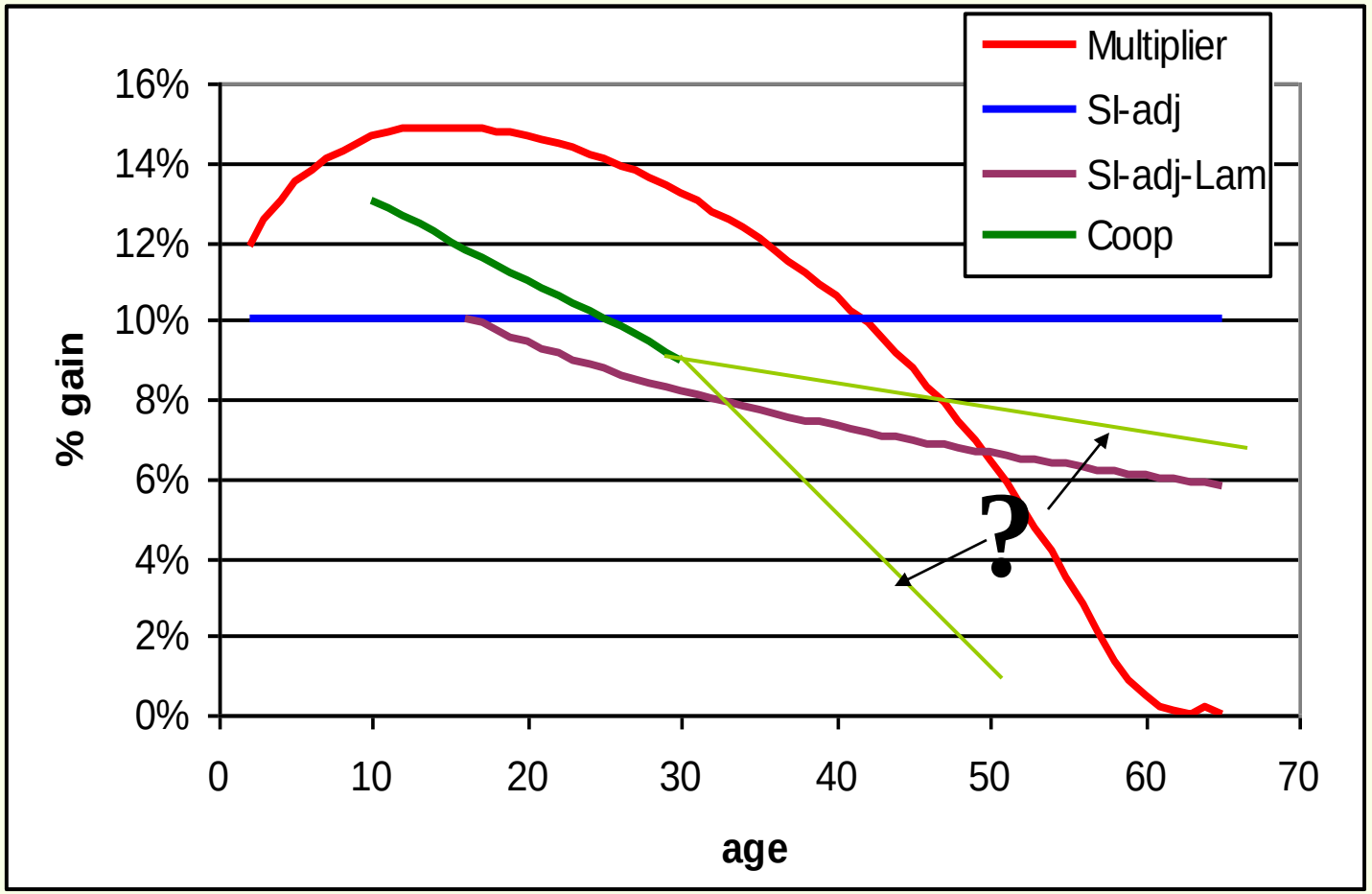
Although the trends are more similar for the Lambeth adjustment and the multipler



Now what we've found with Douglas-fir data

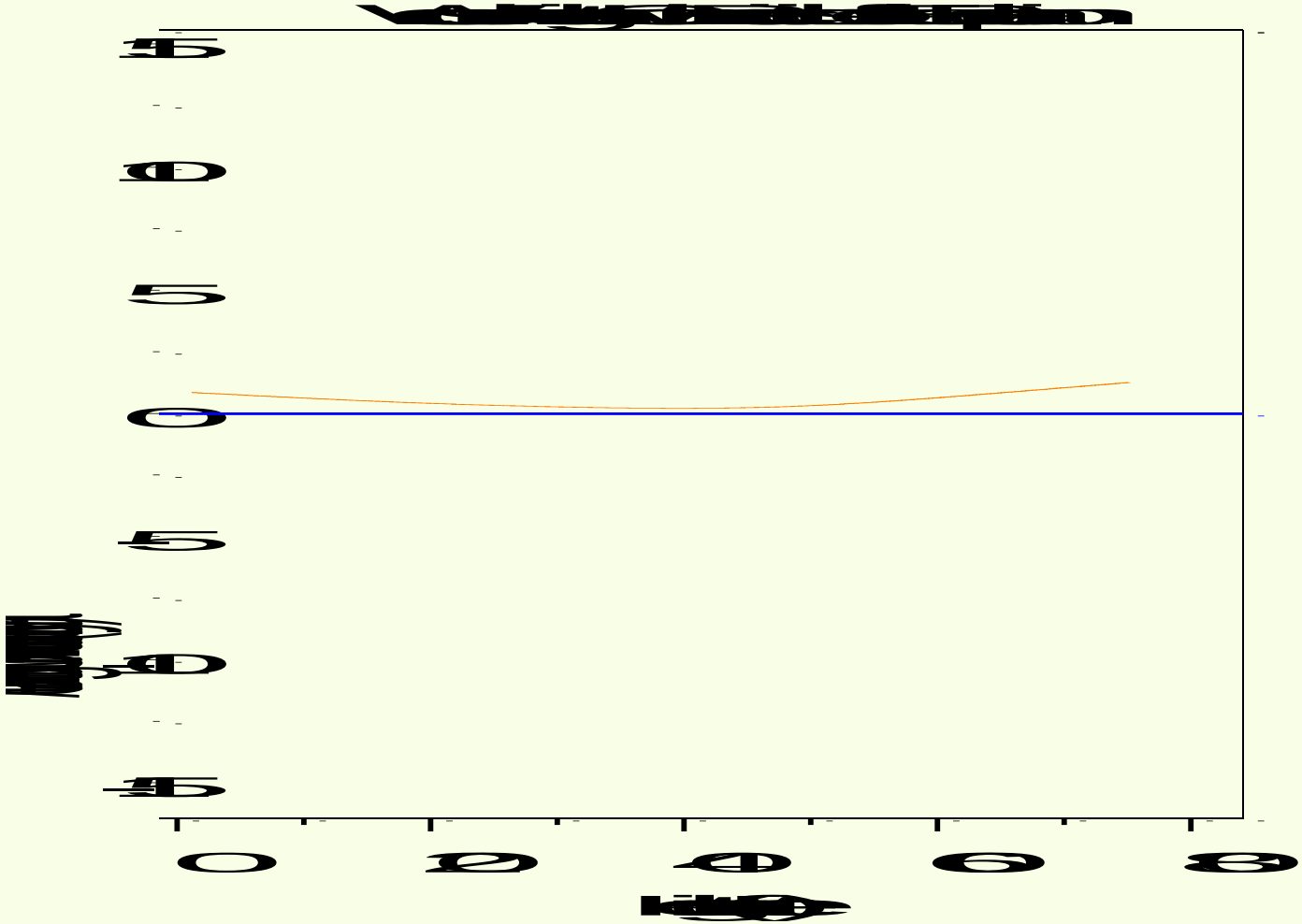


….. and what we don't know



Evidence for growth multipliers in Douglas-fir

Greg Johnson (2003) found evidence for a height growth multiplier in the Vernonia tree breeding cooperative

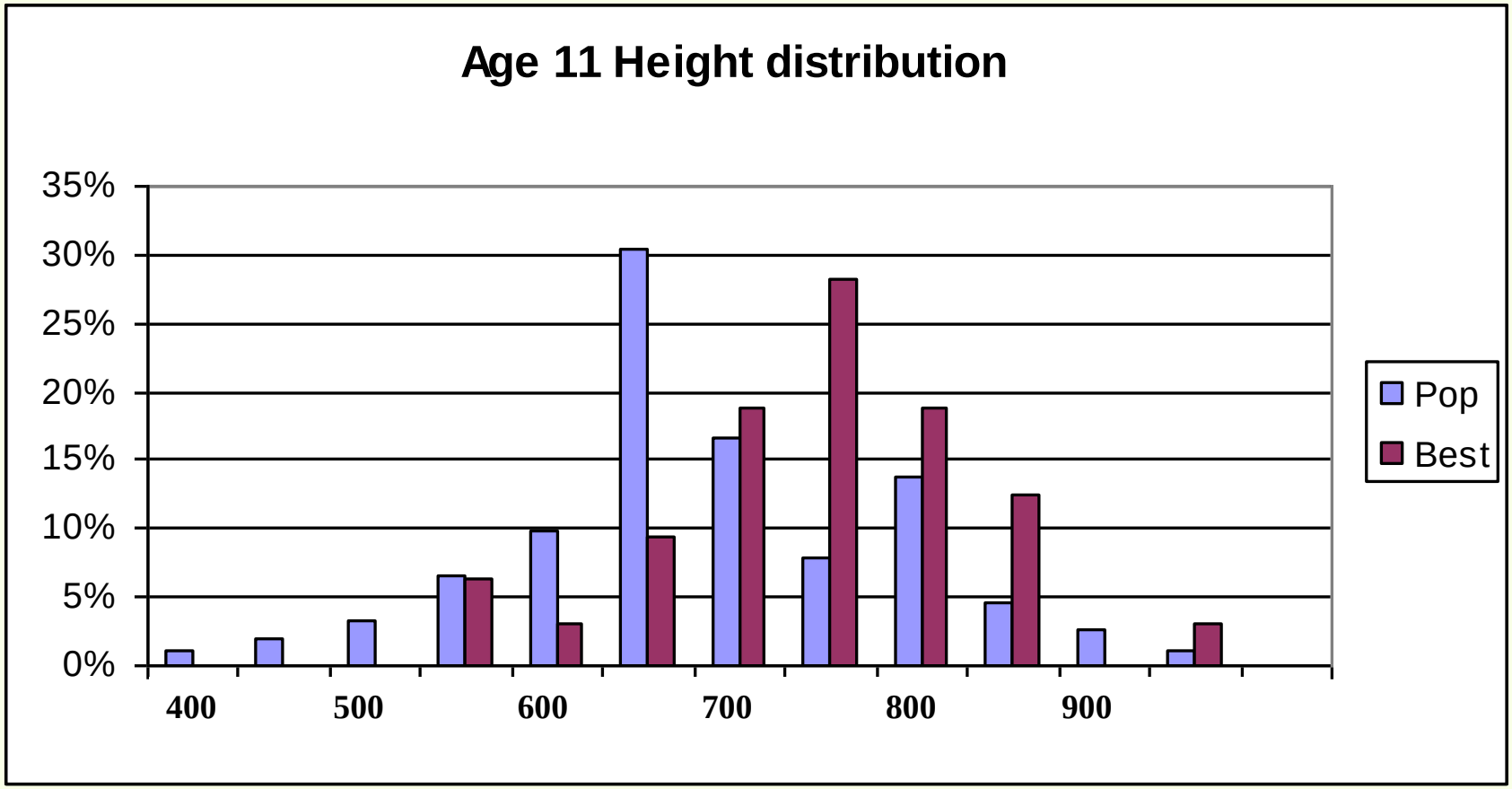


Our Present Study Proposal

- Start with age 10 and 15 height data from 20 Northwest Tree Improvement Cooperative 1st-generation breeding unit to investigate the possibility of using growth multipliers in regional growth models (e.g. ORGANON)

Individual tree growth model using single-tree plots

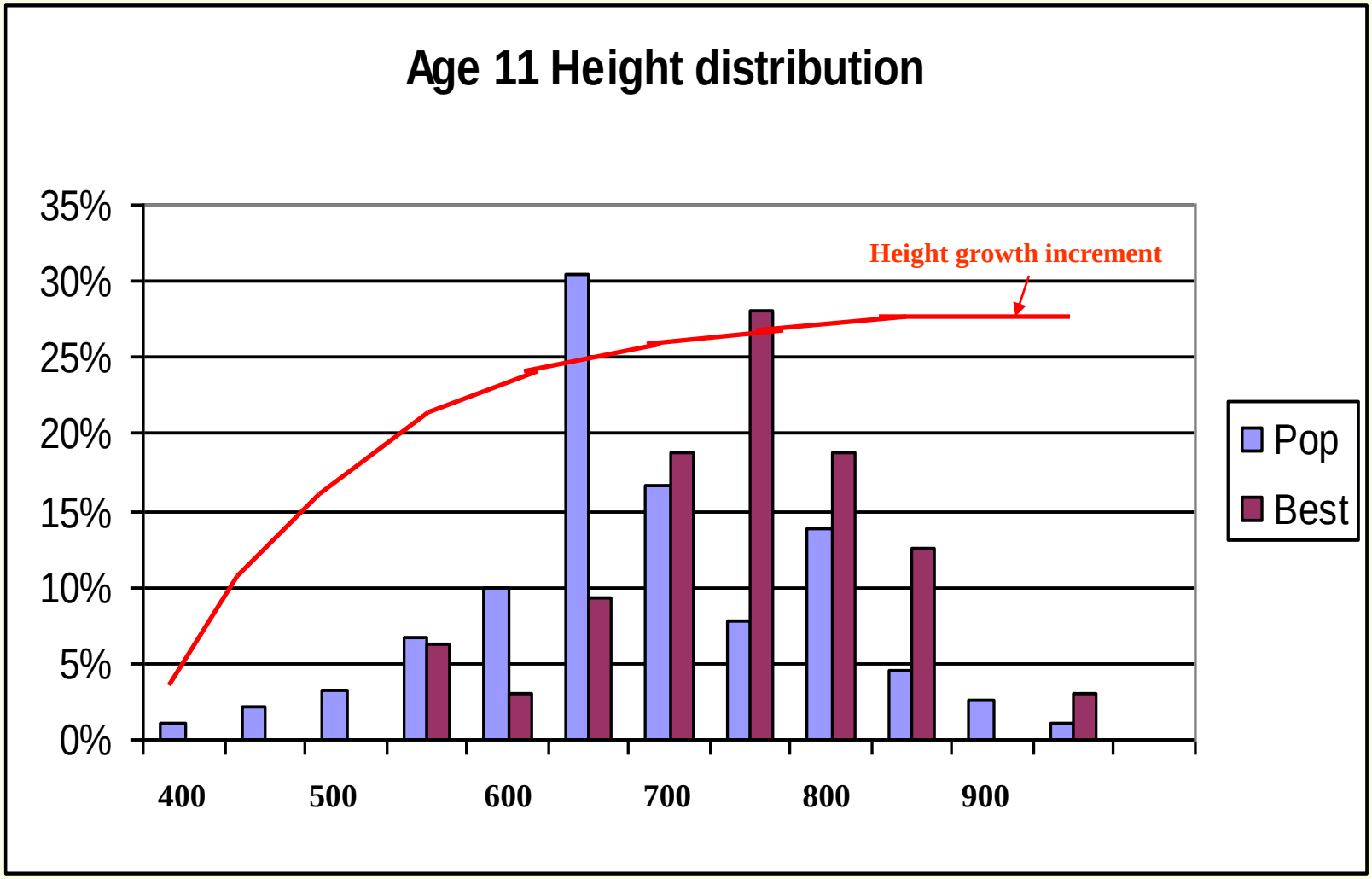
Individual tree model is needed because of STPs: Most variation can be found within a family



Distribution of the best family (n=32) vs. the population (n=1309)

Our Proposal

- Use data from 20 NWTIC 1st-gen coops
- Develop an individual tree growth model using all available trees as the baseline "unimproved" model



Distribution of the best family (n=32) vs. the population (n=1309)

Our Proposal

- Use data from 20 NWTIC 1st-gen coops
- Develop individual tree growth models using all available trees
- Determine if a growth multiplier associated with breeding values will improve the model

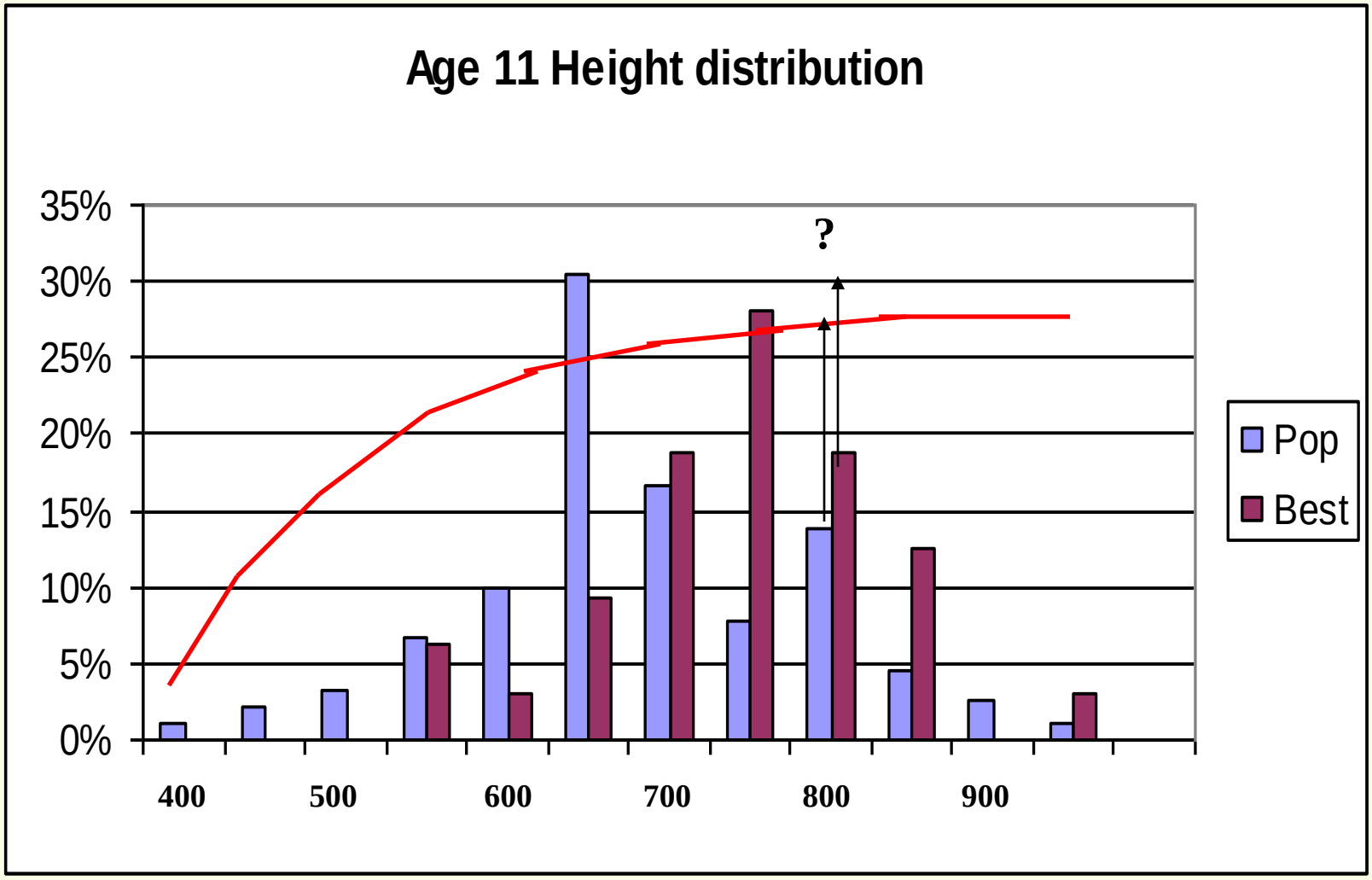
Actual increment = $(m \times BV)$ × predicted increment

Actual increment = (m) × predicted increment

(for an elite subset)

Breeding values are BLUP estimates of genetic gain from the progeny tests

For a given tree size, do better families grow more increment?



Distribution of the best family (n=32) vs. the population (n=1309)

If it appears that multipliers work for height increment from 10 to 15 yrs:

- Check that multipliers are constant over time
- Look for DBH multipliers

(limited data for these analyses)

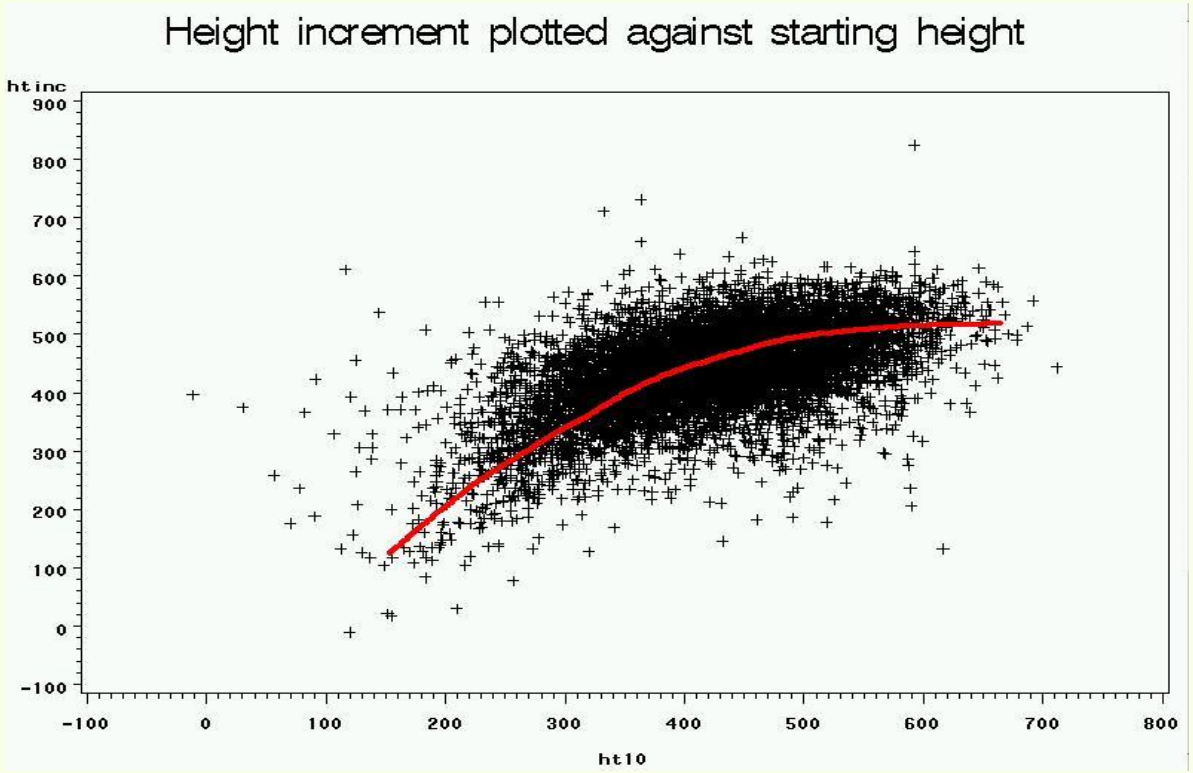
Preliminary Analyses

- 4 Breeding Units
  - 26 Progeny test sites
  - 45,500 trees

(Final analysis will use ~¼ million trees)

Preliminary Analyses

- 4 breeding units
- Develop a general growth model predicting the height increment from age 10 to 15.



Preliminary Analyses

- 4 breeding units
- Develop a general growth model predicting the height increment from age 10 to 15.

Height growth increment

$$\Delta H = b_1 * (1.0 - EXP[-b_2 * HT])^{b_3}$$

Age-10 starting height

Unique to a site – represents site growth potential

Preliminary Analyses

- Add a variable representing the breeding value of the family from which the tree belongs:

$$\Delta H = EXP(a * Gain) * \{b_1 * (1.0 - EXP[-b_2 * HT])^{b_3}\}$$

Preliminary Analyses

- Add a variable representing the breeding value of the family from which the tree belongs:

$$\Delta H = EXP(a * Gain) * \{b_1 * (1.0 - EXP[-b_2 * HT])^{b_3}\}$$

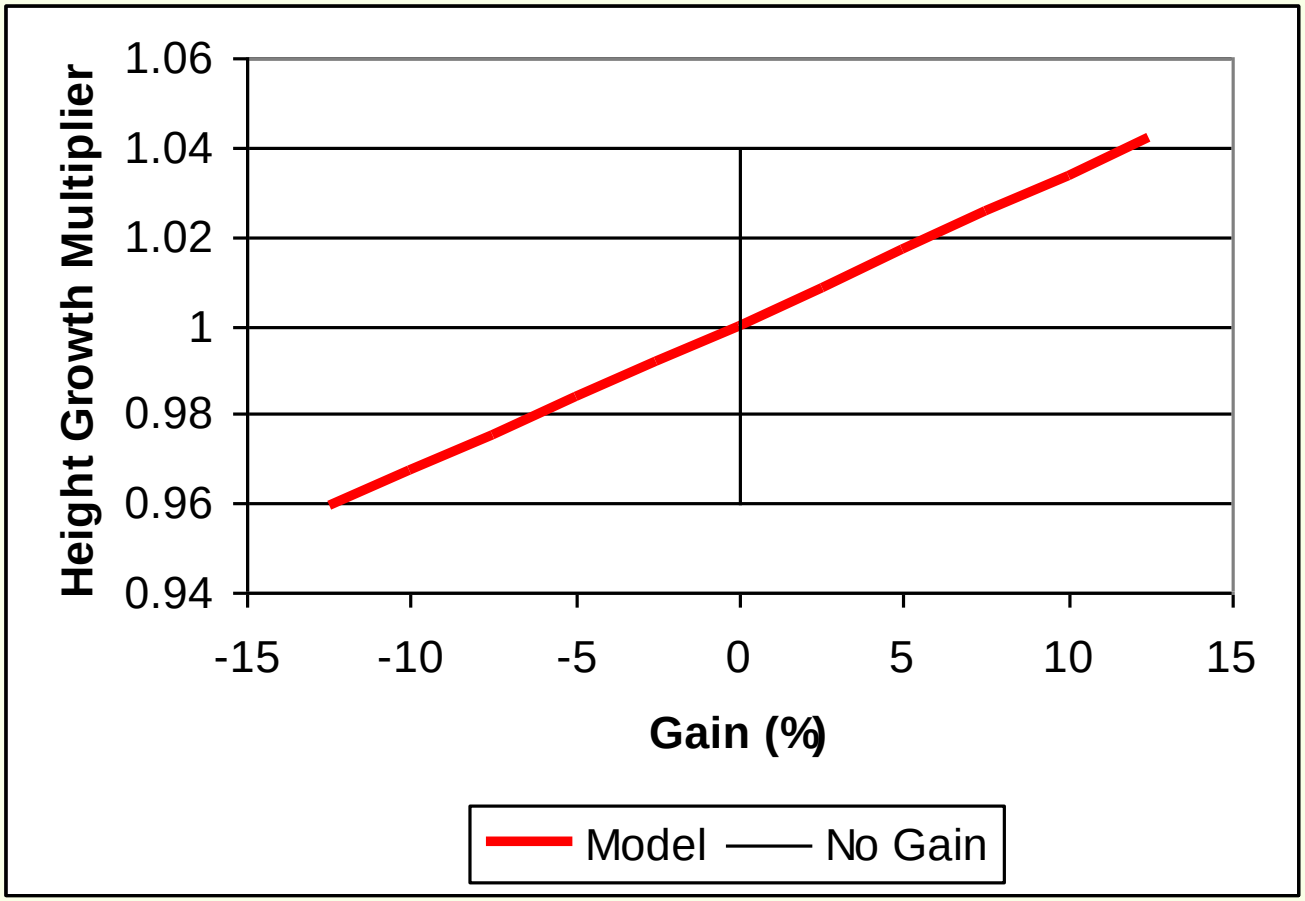
But we took a 2-step approach to ease some difficulties

$$\Delta H = EXP(a * Gain) * \{b_1 * (1.0 - EXP[-b_2 * HT])^{b_3}\}$$

$$\Delta H \Big/ \{b_1 * (1.0 - EXP[-b_2 * HT])^{b_3}\} = EXP(a * Gain)$$

We examined the ratio of observed increment divided by predicted

Observed / Predicted = $e^{(0.0017 \times \text{Gain})}$



Randy's simple approach (the preliminary preliminary analysis)

- By individual breeding unit (5 units examined)
- Simple linear regression (with a quadratic)

  Ht inc.= f (site, height-10, height position)
- Ran a regression to see if trees from the top 10 families differed from their predicted height increments

  Actual height inc = $m \times$ predicted height inc.

- Randy's approach
  - 6.5% gain yielded an average multiplier of 1.015
- David's approach
  - 6.5% gain yielded an average multiplier of 1.021
- **Two different approaches, with very similar answers**

Preliminary Conclusion

- Growth multipliers can be developed for our regional growth models.
- Large plot data will be needed to verify our estimates

A point to remember

- Changes must be modeled separately for each part of the growth model:
- Height
- Diameter
- Mortality

Height:diameter ratio is heritable, it will change if you select differently on height and diameter.

Example:

- *Pinus radiata* in New Zealand selects on DBH, Carson et al. found a diameter multiplier (height multipler found, but not statistically significant)
- *Pseudotsuga menziesii* in Oregon selects on height, Johnson found a height multiplier (DBH not statistically significant)

Acknowledgements

- Funding is provided by a Sustainable Forestry component of Agenda 2020, a joint effort of the USDA Forest Service Research & Development and the American Forest and Paper Association
- Northwest Tree Improvement Cooperative provided the data and breeding value estimates