Unshackling FVS

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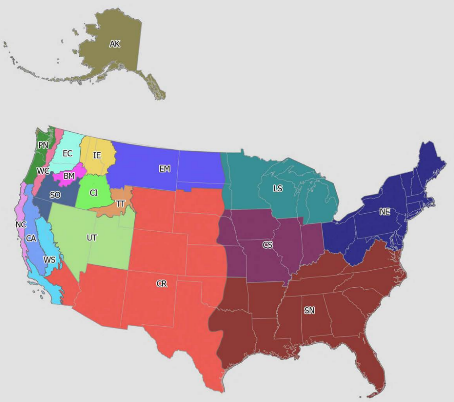
Motivation

- FVS has around 25 variants.
- Variants vary in basic model design and function.
- Species behave differently depending on the variant.
- Some equations have not been updated to make use of new data.
- Site productivity is handled differently among variants.
- Some variants validate poorly.

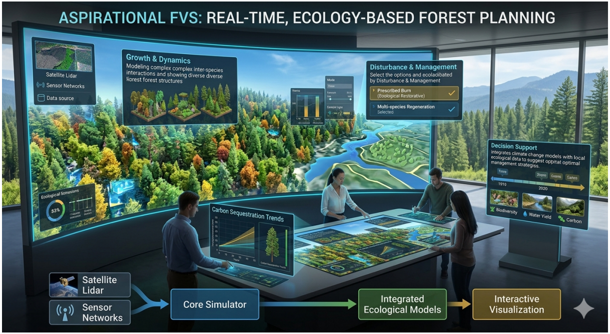


Questions

- Do we need variants?
- Can we build a accurate and precise model without site index?
- Can we use Forest Inventory and Analysis (FIA) remeasurement data?
  - Multiple condition plots
  - Age determination
  - Variable remeasurement intervals
  - Site index

Goals

- Use FIA remeasurement data as the source for fitting and testing growth and imputation equations.
- Develop biologically consistent, parsimonious growth increment equations that can be used across the continental United States (CONUS) and species.
- A single growth module that is capable of projecting tree growth for any species in CONUS.
- Verified unbiasedness at the tree and stand level.



Open Invitation

Anyone who is interested can join in the fun. We are setting up a Git Repository https://github.com/gregjohnsonbiometrics/fvs_remodeling to manage the project and have a private (for now) Google Drive to house the data files.

Contact one of the authors for more information!

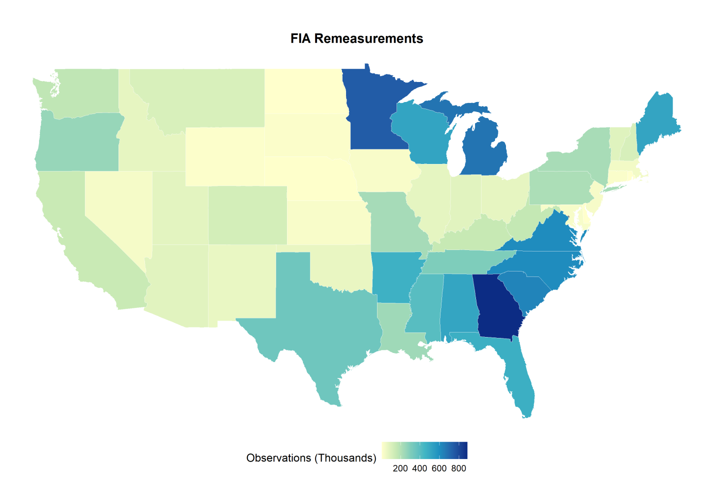
Challenges using FIA Data for Modeling

- Multiple Condition Plots
  - Insures unbiased for sample estimates (a good thing).
  - Conditions can be a small area with too few trees to summarize (“plot” size).
  - Very different conditions can give poor stand estimates (e.g., basal area per acre (ba), height of 40 largest trees (ht_{40}), basal area per acre in larger trees (bal)).
- Growth Periods
  - 5- or 10-year (and others) intervals for same species (standardize or annualize?).
  - Measurements throughout the year (may not match a growth year).
- Treatment Histories
  - Identifies recent (measurement period) thinned but no description of intensity.
  - No information on genetics, fertilization, and other treatments.
  - Identifies recent tree damage (e.g., insects and weather) but not historic.
- Measurements
  - 1-inch minimum dbh.
- Productivity
  - Multiple definitions of site index (si) across a species range (e.g., base age).
  - Site tree selection may not match site curve definition.
  - Ages on older stands.

Progress

Data Retrieval and Screening

We have pulled FIA remeasurement data for CONUS. This resulted in 10870980 records before screening for errors and missing data.



Progress

Data Retrieval and Screening

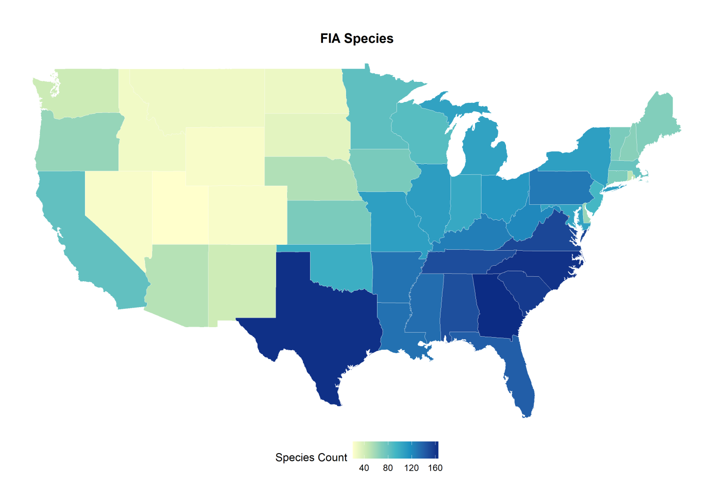


Figure 2: Map of US States scaled by FIA Species

The Site Productivity Condundrum

Site index is a mess. For example, plots with Douglas-fir have 36 site tree species using 36 site index equations, and 3 base ages.

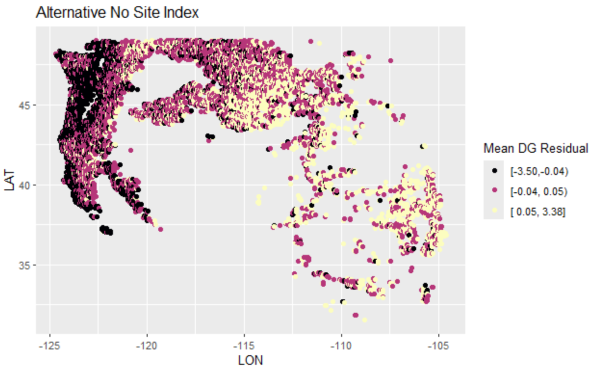
Other, less frequent species are in worse shape.

We began to search for alternatives:

- ClimateSI
- Climate and environmental variables (e.g. precipitation, temperature, growing degree days)
- Embedded variables (primary and secondary principal components of climate and environment variables)
- Asymptotic Above Ground Biomass
- Remote Sensing Metrics

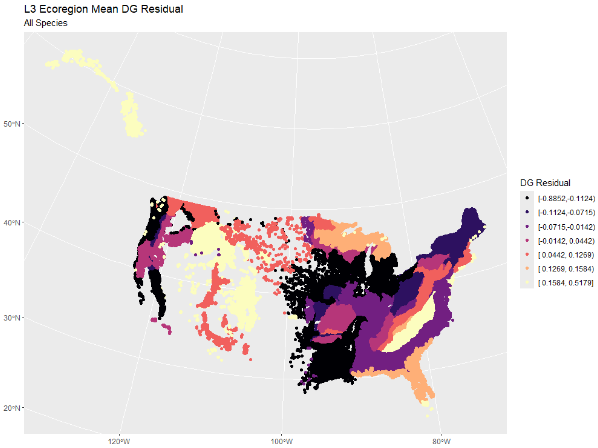
The Site Productivity Condundrum

A productivity (or location) variable is needed. Below are Douglas-fir diameter growth residuals from a model without a site or location effect. The points are the mean residual for an FIA condition. Darker colors are under-predictions, light colors over-predictions. Productivity gradients are apparent.



The Site Productivity Condundrum

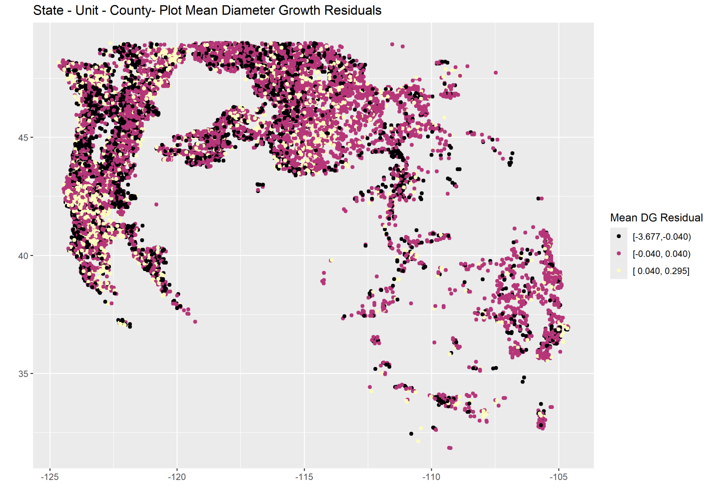
Across all species in CONUS:



The Site Productivity Condundrum

Diameter Growth Residuals

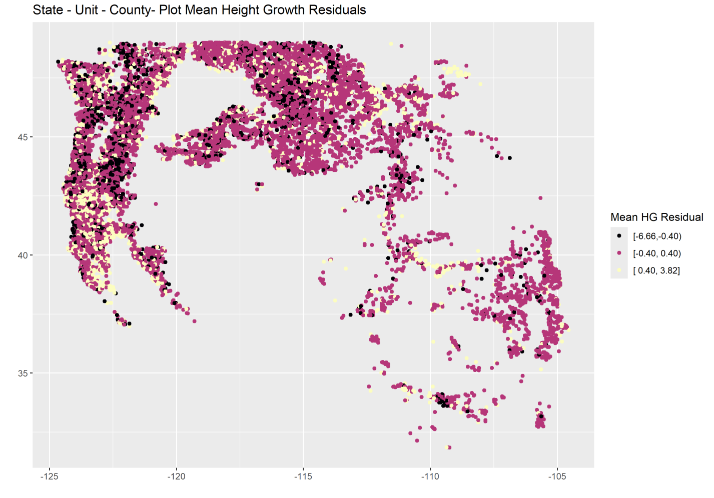
Incorporating elevation and extreme minimum temperature does help, but it does not completely account for the spatial effects.



The Site Productivity Condundrum

Height Growth Residuals

Incorporating elevation, min/max temperature difference, and extreme minimum temperature does help, but as with diameter growth it does not adequately account for the spatial effects.



Biologically Consistent, Parsimonious Diameter Growth Equations

We have had good success with ORGANON's diameter growth equation[1], however, we wanted to attempt to streamline the equation and alleviate an issue where proper behavior over diameter at breast height (dbh) is problematic for many species.

Currently we have:

$$\Delta dbh = e^{(\beta_0 + \beta_1 log(\frac{(dbh+1)^2}{(cr*ht+1)^{\beta_3}}) + \beta_2 \frac{bal^{\beta_4}}{dbh+2.7} + \beta_5 elev + \beta_6 EMT)} \quad (1)$$

where:

- dbh = diameter at breast height (inches)
- cr = crown ratio (fraction of total height)
- ht = total height (feet)
- bal = basal area in larger trees ($feet^2/acre$)
- $elev$ = elevation above sea level (feet)
- EMT = extreme minimum temperature ($^{\circ}C$)

[1] Zumrawi, A.A. and D.W. Hann. 1993. Diameter growth equations for Douglas-fir and Grand Fir in the Western

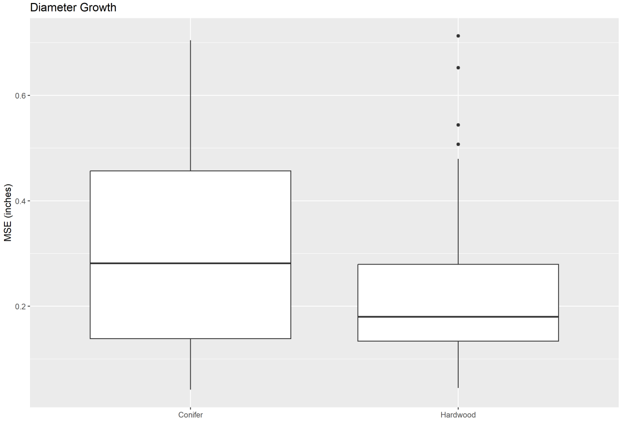
Diameter Growth Equations

We fit Equation 1 to 84 species in CONUS (limited to species with $\geq$ 5000 growth observations) resulting in 3481225 observations. The top ten species in terms of observations are:

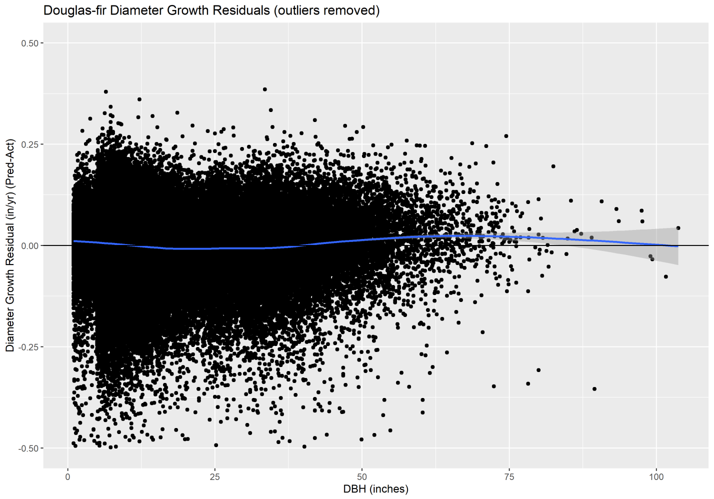
FIA SPCD	Name	Observations
316	red maple	283321
131	loblolly pine	269719
318	sugar maple	170961
202	Douglas-fir	156486
12	balsam fir	150407
746	quaking aspen	149764
802	white oak	103638
241	northern white-cedar	98956
611	sweetgum	78754
122	ponderosa pine	74938

Diameter Growth Equations

With the broad range of species and geography embodied in the data set, we can look at patterns in the diameter growth equation's parameters – something often not available to us.

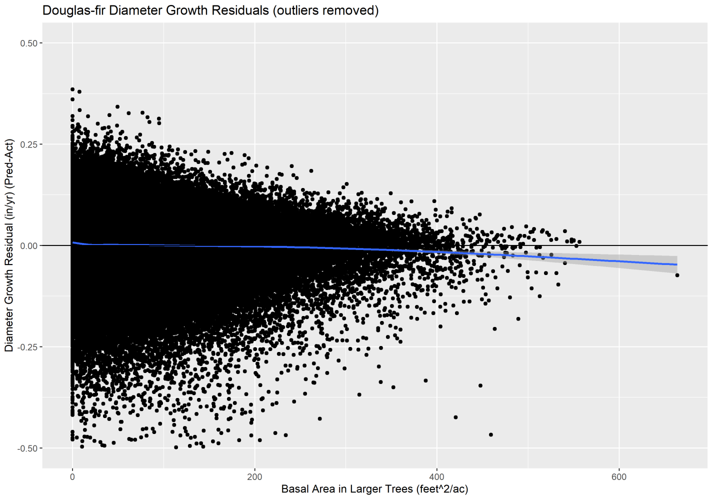


Residual Analysis – Initial Diameter



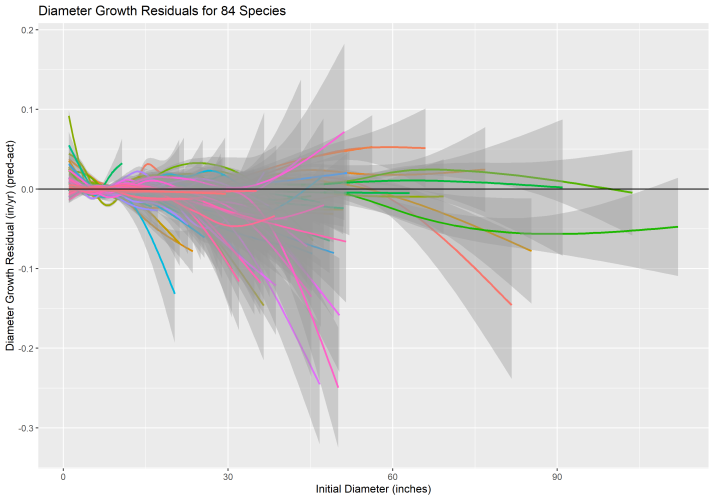
Diameter Growth Equations

Residual Analysis – Basal Area in Larger Trees



Diameter Growth Equations

Residual Analysis – All Species



Diameter Growth Equations

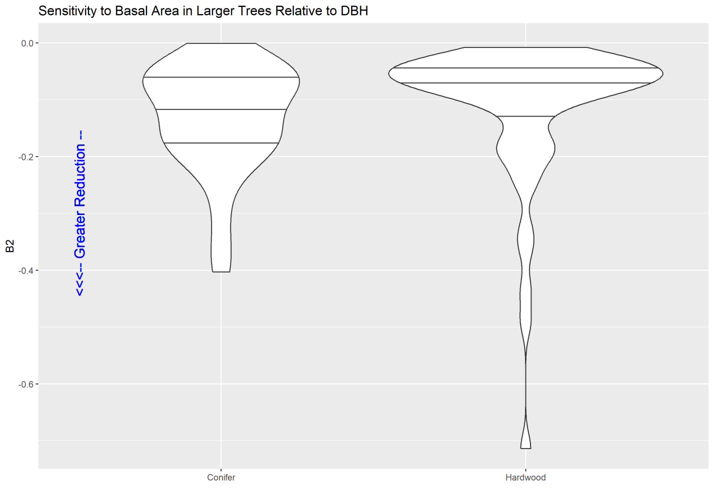
β_0

Diameter Growth Equations

β_1

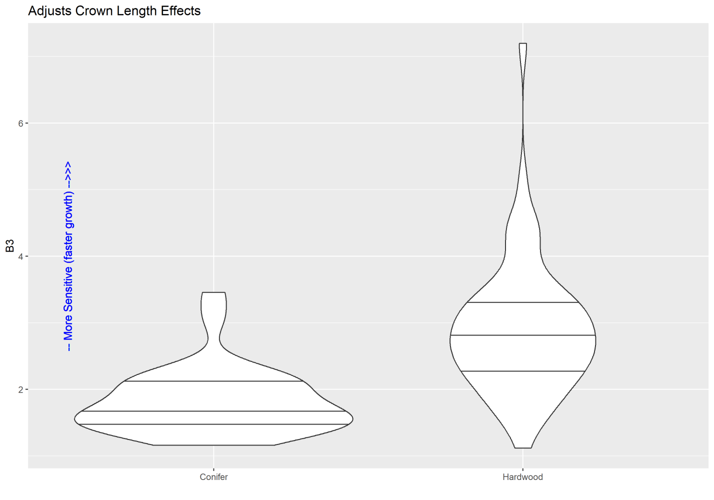
Diameter Growth Equations

β_2

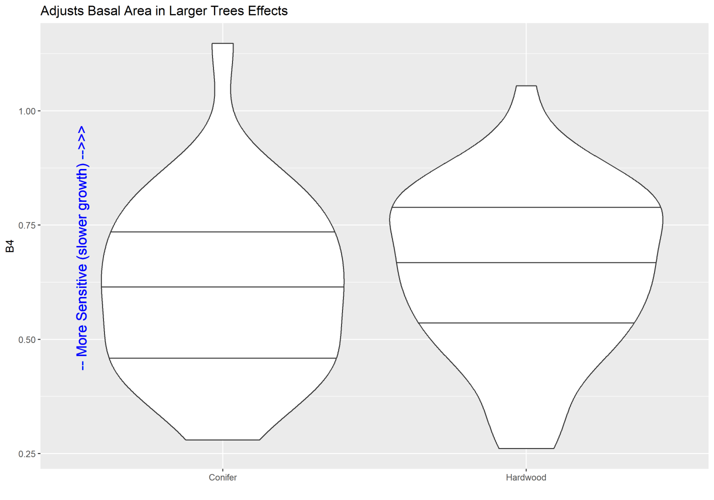


Diameter Growth Equations

β_3



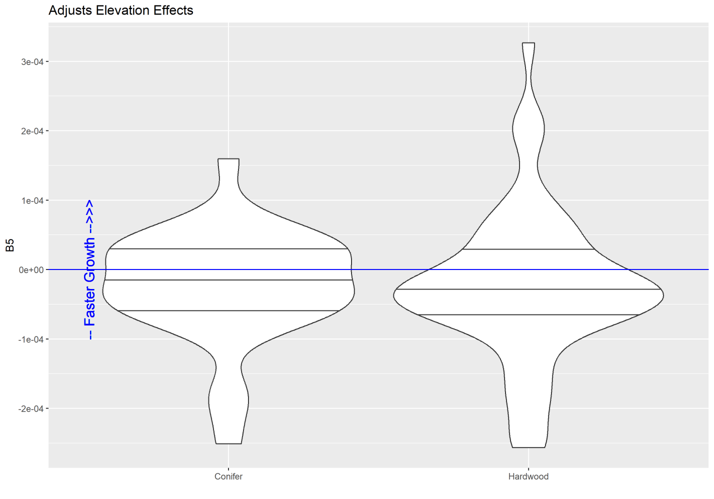
β_4



Adjusts Basal Area in Larger Trees Effects
B4
1.00
0.75
0.50
0.25
-- More Sensitive (slower growth) -->>>
Conifer
Hardwood

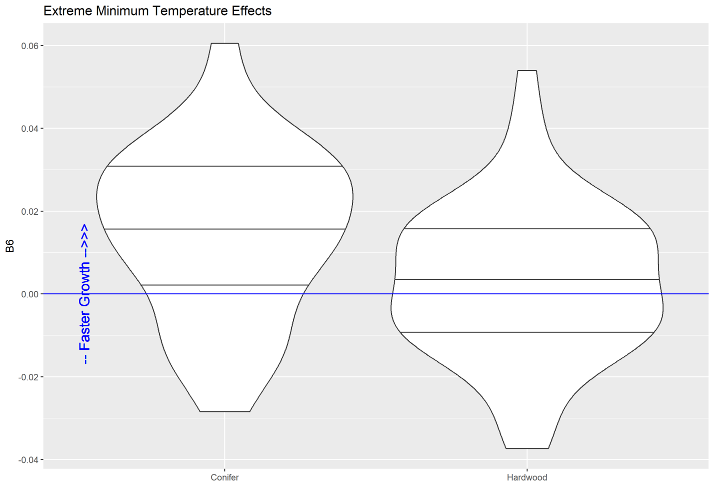
Diameter Growth Equations

β_5



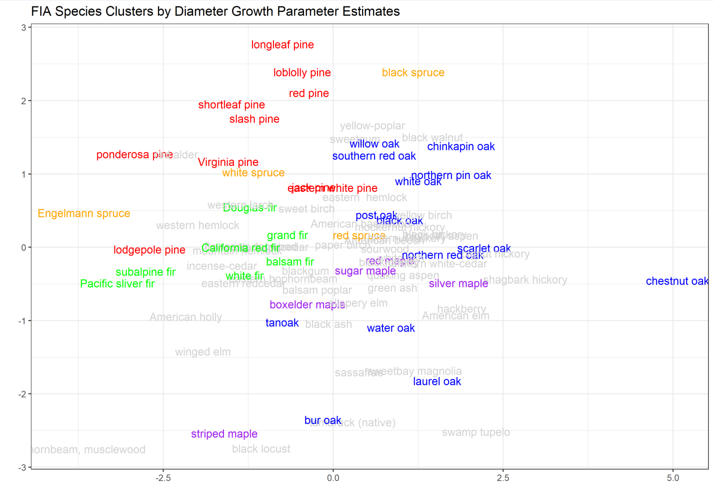
Diameter Growth Equations

β_6



Diameter Growth Equations

Diameter Growth Parameter Clusters



Biologically Consistent, Parsimonious Height Growth Equations

It is common to use growth effective age (geage) [2] [3] to guide height growth predictions via a differentiated site index curve to estimate potential height growth.

Given our reluctance to use site index, we had to abandon geage. We started with the Chapman Richards[4] model form for height (`ht`):

$$ht = \beta_0(1 - e^{(-\beta_1 age)})^{\beta_2} \tag{2}$$

where β_0 can be interpreted as the asymptotic (maximum) height (ht_{max}).

[2] Peet, R.K. 1976. Successional patterns and tree population structure in Rocky Mountain forests. Bull. Ecol. Soc. Am. 57:60

[3] Hann, D.W., M.W. Ritchie. 1988. Height Growth Rate of Douglas-Fir: A Comparison of Model Forms. Forest Science,Vol. 34, No. 1, pp. 165-175.

[4] Chapman, D.G. 1961. Statistical problems in population dynamics. In: Neyman, J., ed. Proceedings of the fourth Berkeley symposium on mathematical statistics and probability. Vol. 4. Berkeley, CA: University of California Press: 153-186.

Height Growth Equations

Differentiated with respect to age and substituting current `ht` for age:

$$\Delta ht = \beta_0 \beta_1 \beta_2 e^{(-\beta_1 ht)}) e^{(-\beta_1 ht})^{(\beta_2 - 1)} \quad (3)$$

Equation 3 forms a sigmoidal growth curve with an asymptote at β_0.

Using Equation 3 as the foundation, we added competition and environmental/climate variables to the model.

Height Growth Equations

Currently we have fit:

$$\Delta ht = ht_{max}\beta_1\beta_2 cr^{\beta_3} e^{(-\beta_1 ht - \beta_4 ccfl - \beta_8 cch^{0.5} - \beta_5 elev + \beta_6 TD^{0.5} + \beta_7 EMT)} (1 - e^{-\beta_1 ht})^{(\beta_2 - 1)} \quad (4)$$

to the all 3069754 growth observations, estimating β_0 through β_8. Where:

- ht = total height (feet)
- cr = crown ratio (fraction of total height)
- $ccfl$ = crown competition factor in larger trees ($feet^2/acre$)
- cch = crown closure at tree tip (fraction of acre)
- $elev$ = elevation above sea level (feet)
- TD = temperature difference ($^\circ C$)
- EMT = extreme minimum temperature ($^\circ C$)

ht_{max} was estimated by finding the maximum height observed in the FIA data set for each species.

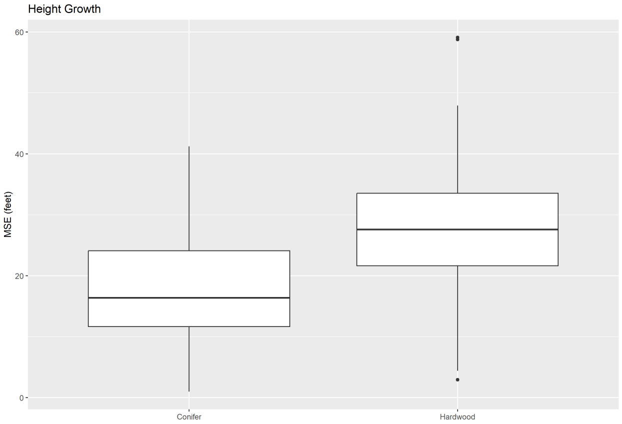
Height Growth Equations

We fit Equation 4 to 96 species in CONUS (limited to species with $\geq$ 5000 growth observations). The top ten species in terms of observations are:

FIA SPCD	Name	Observations
131	loblolly pine	383322
316	red maple	209090
202	Douglas-fir	141678
318	sugar maple	111277
611	sweetgum	96180
746	quaking aspen	91010
802	white oak	80327
12	balsam fir	78494
122	ponderosa pine	68350
108	lodgepole pine	63142

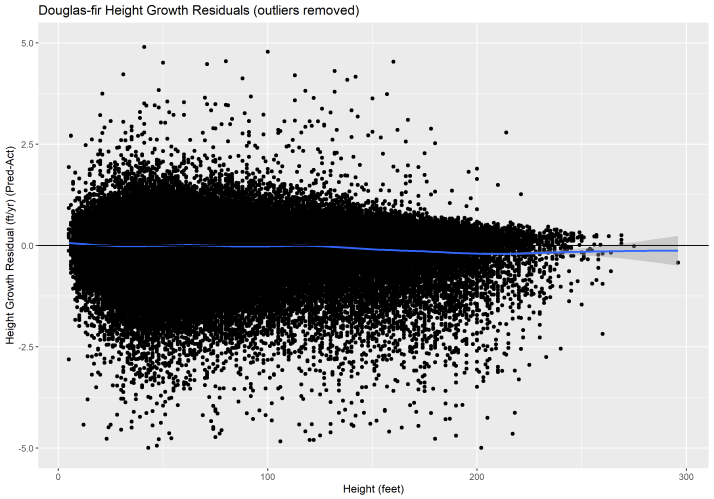
Height Growth Equations

As with diameter growth, the broad range of species and geography embodied in the data set lets us look at patterns in the height growth equation's parameters – something often not available to us.



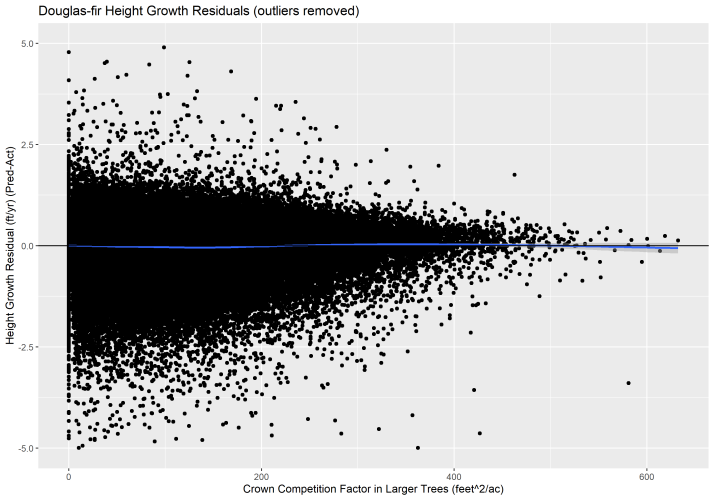
Height Growth Equations

Residual Analysis – Initial Height

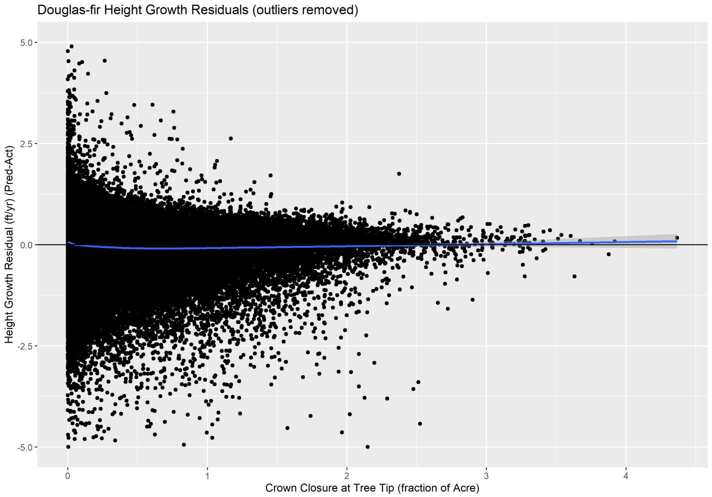


Height Growth Equations

Residual Analysis – Crown Competition Factor in Larger Trees

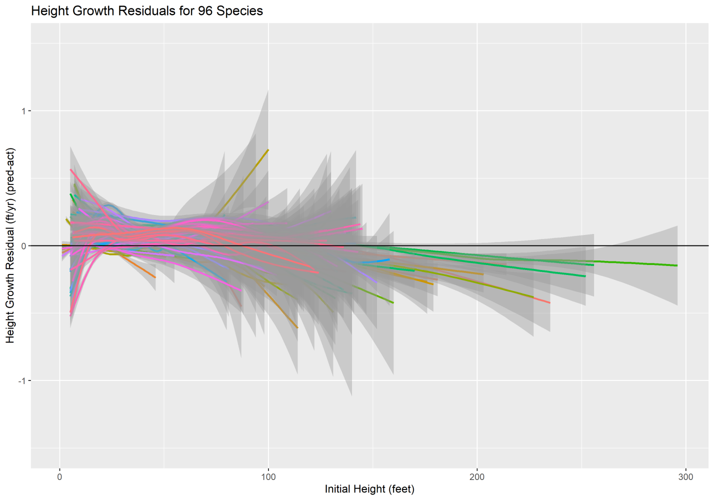


Residual Analysis – Crown Closure at Tree Tip



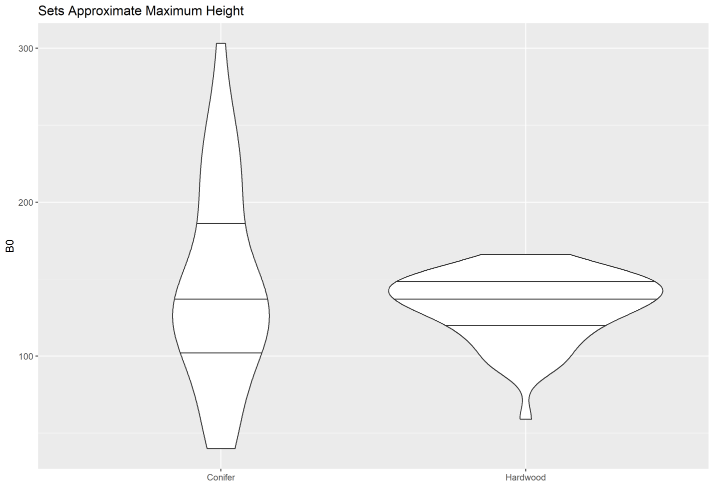
Height Growth Equations

Residual Analysis – All Species



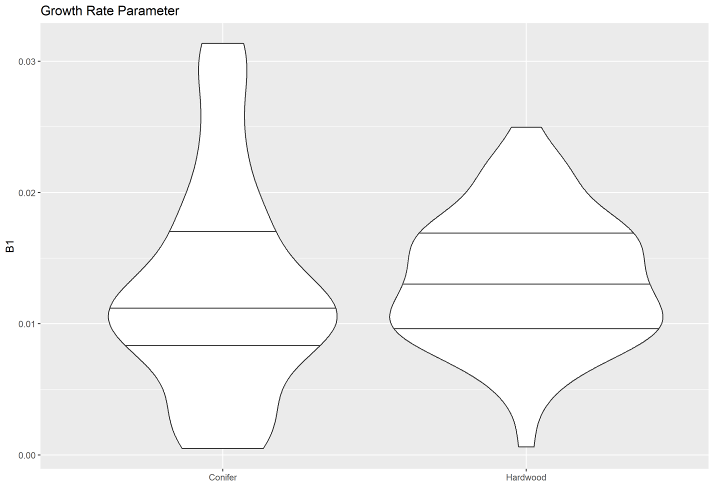
Height Growth Equations

β_0



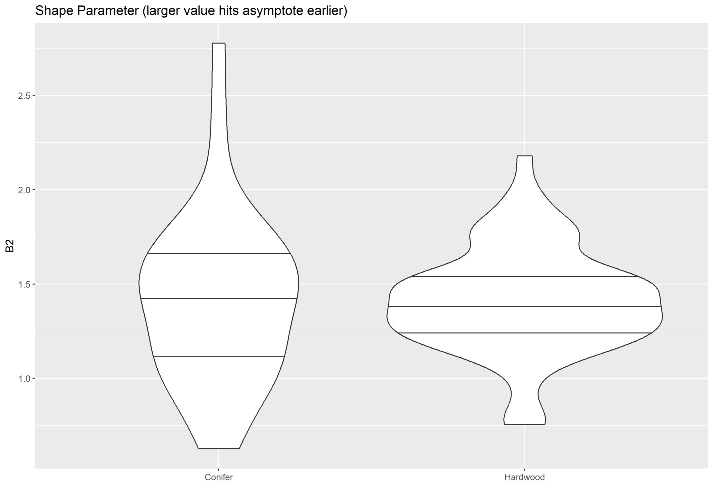
Height Growth Equations

β_1



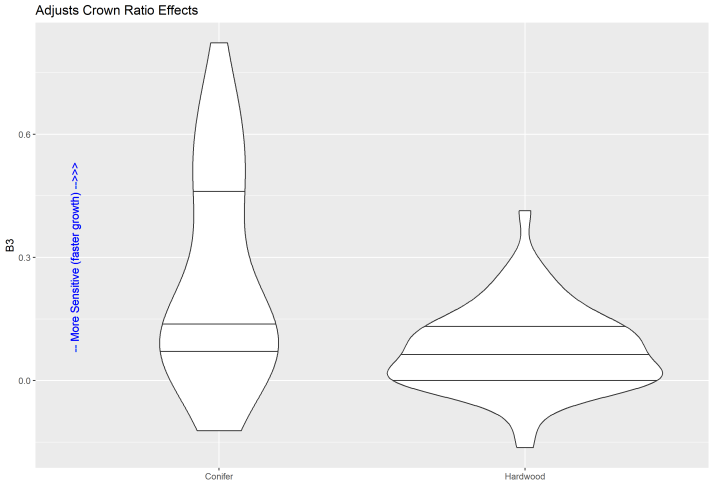
Height Growth Equations

β_2



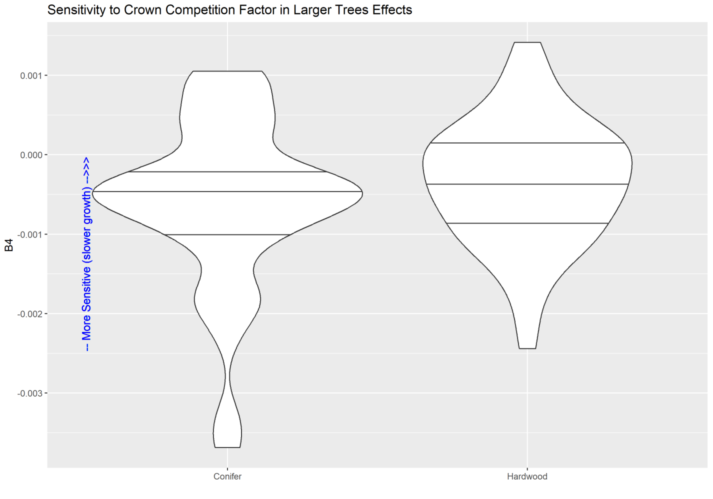
Height Growth Equations

β_3



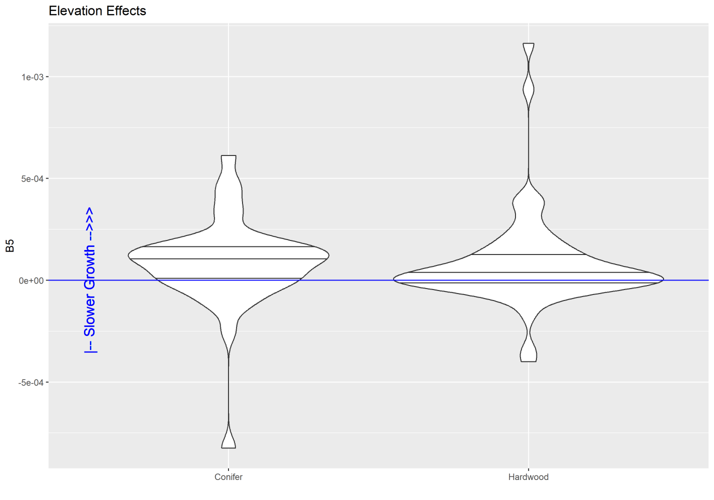
Height Growth Equations

β_4

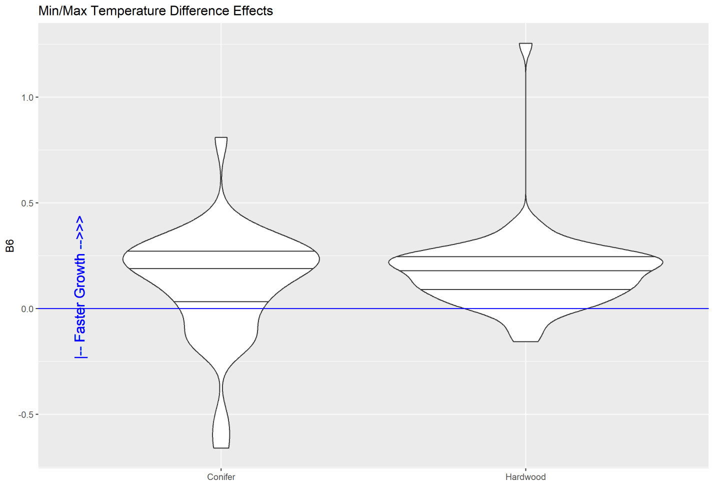


Diameter Growth Equations

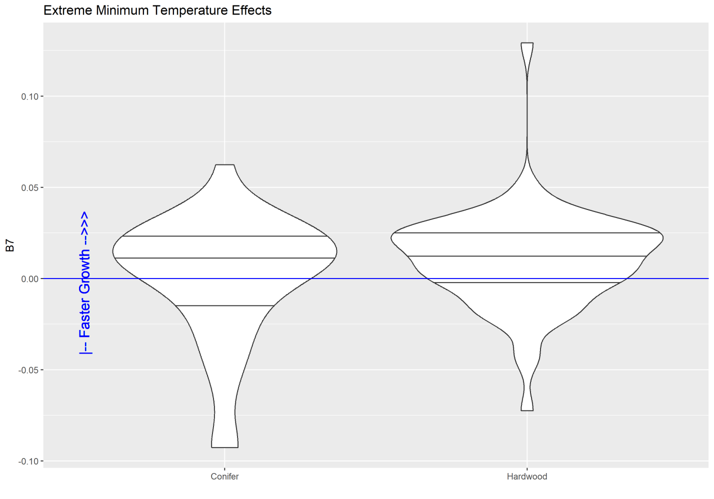
β_5



β_6

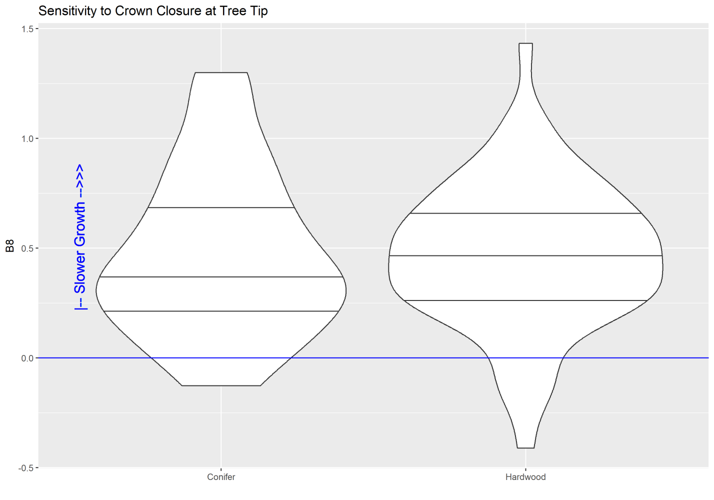

Min/Max Temperature Difference Effects
1.0
0.5
0.0
-0.5
B6
|-- Faster Growth -->>
Conifer
Hardwood

β_7


Extreme Minimum Temperature Effects
B7
0.10
0.05
0.00
-0.05
-0.10
|-- Faster Growth -->>
Conifer
Hardwood

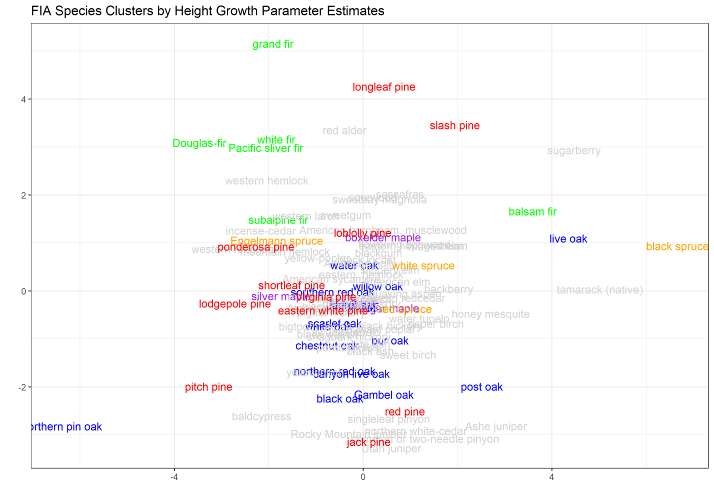
Height Growth Equations

β_8



Height Growth Equations

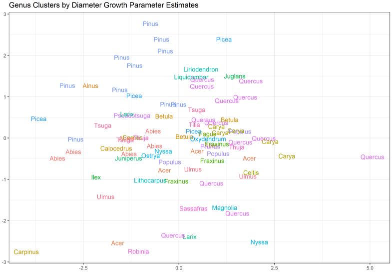
Height Growth Parameter Clusters



Work to be Done

- Improvement in site (location) effects
- Modeling will continue as we explore robust equations that explain change in:
  - Crown Length (height to crown base (`htlc`))
  - Trees per acre or mortality (`tpa`)
- Continue to refine height growth equation for consistency across species.
- We are planning to explore parameter clustering techniques (perhaps at the genus level) to build species mappings for species with growth observations below our threshold (currently 5000).
- Additionally, we recognize the need to build (or rebuild) imputation equations for:
  - `ht`
  - `htlc`
  - `dbh???`
- Build a testing simulation framework and a growth verification system to evaluate bias and precision.

Will genus clustering work?



Thanks!

GROWTH MODEL USERS' GROUP
– NETWORKING & LEARNING –
GROWTH MODEL USERS' GROUP 2024:
UNSHACKLING FVS
(Forest Vegetation Simulator)
Greg Johnson | 12:45 PM
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