

Alternative Loblolly Pine Diameter Growth

Greg Johnson and David Marshall

2026-01-27

Data

We extracted and processed Forest Inventory and Analysis (FIA) data from 14 states listed in the native range of Loblolly Pine in the Silvics of North America.¹

After subsetting the data to censor observations with missing data, limiting the species to Loblolly Pine (FIA species code 131), and remeasurement intervals ≥ 5 years we get the observations in Table 1.

Table 1: Loblolly Pine Growth Observations by State

State	Observations
AL	44564
AR	23710
DE	888
FL	3962
GA	59591
LA	19885
MD	2743
MS	43005
NC	30776
NJ	16
OK	3354
SC	49561
TX	39929
VA	20792

¹Burns, Russell M., and Barbara H. Honkala, tech. coords. 1990. Silvics of North America: 1. Conifers; 2. Hardwoods. Agriculture Handbook 654. U.S. Department of Agriculture, Forest Service, Washington, DC. vol.2, 877 p.

Alternative Model Formulation

An alternative to the ORGANON diameter growth equation² which reduces parameter count while retaining key features of the original model is shown below. The key change is the term with a ratio of a transformation of diameter at breast height (**dbh**) squared to crown length. Since β_1 is expected to be negative, this tends to slow growth as more basal area accumulates in the tree while moderating that decline by the amount of productive crown capacity as measured by crown length. Basal area in larger trees (**bal**) serves as the inter-tree competition factor, and site index (**si**) as the inherent productivity scaling factor.

Site index is flawed for a number of reasons:

1. It is not consistently obtained for each plot due to missing Loblolly Pine site trees,
2. It is estimated using a number of different and not necessarily compatible **si** equations, and
3. The available **si** equations do not all use the same base age.

In the data set **si** is derived from 22 different site index equations for 22 species. Loblolly Pine site index comprises 91% of the observations. There are 1 base ages used. Preliminary graphical analysis revealed that base age was most correlated with residual bias. Thus in the following, we fit two equations: one where **SIBASE** and **SISP** are treated as a random effects in a mixed model framework, and a second leaving site index out.

$$\Delta dbh = e^{(\beta_0 + \beta_1 \log(\frac{(dbh+1)^2}{(cr*ht+1)^{\beta_4}}) + \beta_2 \frac{bal^{\beta_5}}{dbh+2.7} + \beta_3 \log(si_{s,b} + 4.5))} \quad (1)$$

and

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

where:

- **dbh** = diameter at breast height (inches),
- **bal** = basal area per acre in larger trees ($feet^2/ac$),
- **cr** = crown ratio (fraction of total height),
- **ht** = total height (feet), and
- $si_{s,b}$ = site index (feet) for species **s** and base age **b**.
- $\beta_0 - \beta_5$ are parameters to be estimated.

²Hann, D.W., Marshall, D.D., and Hanus, M.L. 2006. Reanalysis of the SMC-ORGANON equations for diameter-growth rate, height-growth rate, and mortality rate of Douglas-fir. Forest Research Laboratory Research Contribution 49.

Nonlinear regression was used with an integrated fitting approach such that individual observations can have differing remeasurement intervals. The error to be minimized is ending dbh. Since this effectively minimizes diameter growth it can weight observations with longer remeasurement intervals more heavily. The effect of this needs to be evaluated, but putting more emphasis on longer periods may be beneficial.

The fit statistics for Equation 1 are:

Nonlinear mixed-effects model fit by maximum likelihood

Model: endDIA ~ est_dg(B0, B1, B2, B3, B4, B5, startDIA, startBAL, endBAL, startCR, endCR)

Data: tree_subset %>% mutate(SIINT = interaction(as.factor(tree_subset\$SIBASE), as.factor(tree_subset\$SIINT)))

	AIC	BIC	logLik
	810815.5	810901.4	-405399.7

Random effects:

Formula: B3 ~ 1 | SIINT

	B3	Residual
--	----	----------

StdDev: 0.00092019 0.7895843

Fixed effects: B0 + B1 + B2 + B3 + B4 + B5 ~ 1

	Value	Std.Error	DF	t-value	p-value
B0	-1.6667227	0.027115045	342769	-61.46856	0
B1	-0.6276905	0.002428813	342769	-258.43507	0
B2	-0.0386252	0.001265804	342769	-30.51436	0
B3	0.1664421	0.006048101	342769	27.51973	0
B4	1.5952328	0.005769258	342769	276.50572	0
B5	0.9002310	0.006733521	342769	133.69394	0

Correlation:

	B0	B1	B2	B3	B4
B1	-0.021				
B2	-0.225	0.351			
B3	-0.884	-0.070	-0.018		
B4	-0.241	0.165	0.368	-0.216	
B5	-0.217	0.324	0.994	-0.001	0.320

Standardized Within-Group Residuals:

	Min	Q1	Med	Q3	Max
	-18.5101042	-0.6326443	-0.1107581	0.5169780	79.6303013

Number of Observations: 342776

Number of Groups: 2

\$SIINT

B3
50.FALSE -0.0008253978
50.TRUE 0.0008253978

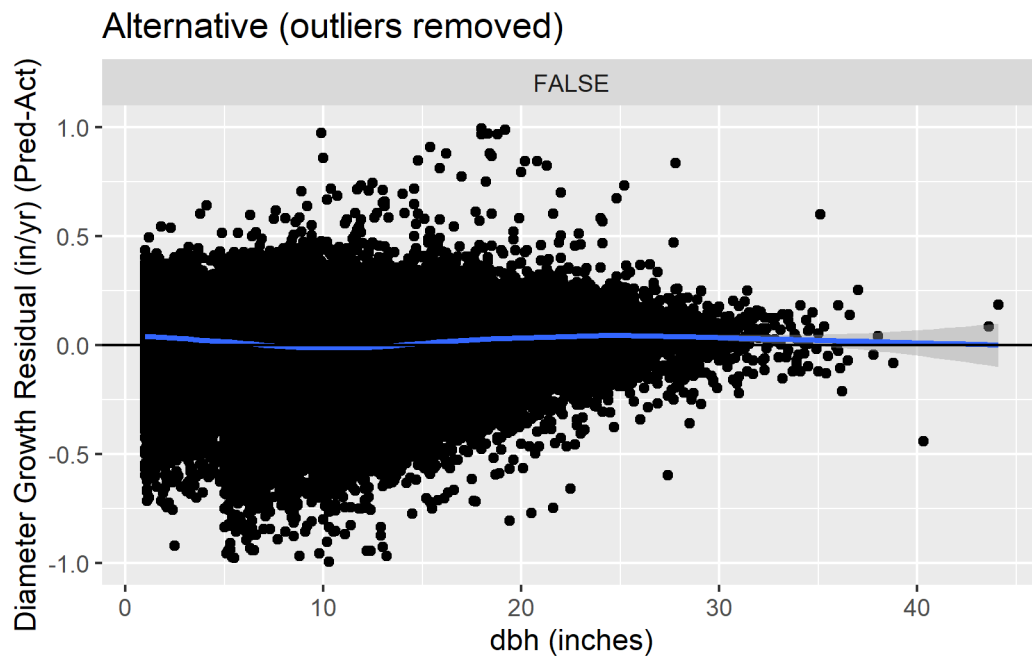
Residual Standard Error: 0.78958431908179 on 342769 degrees of freedom, AIC: 810815.5

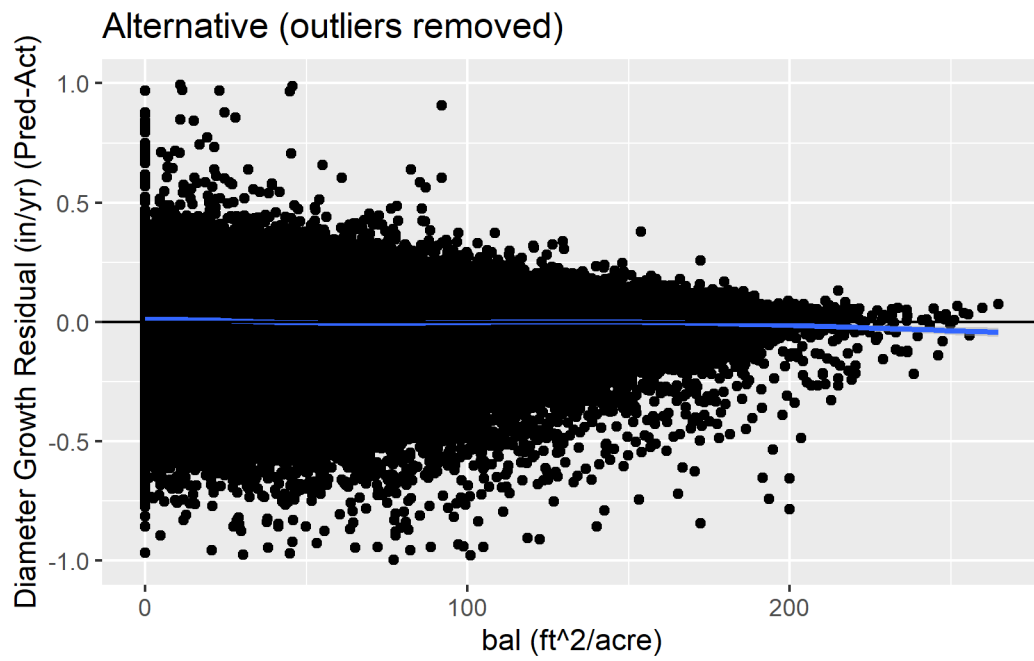
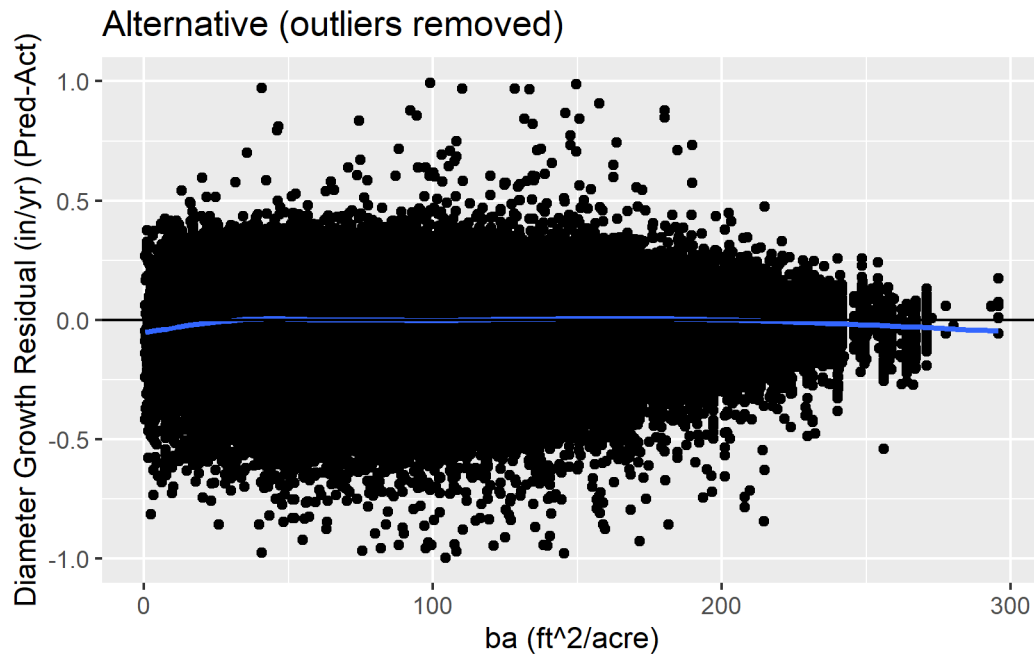
and for Equation 2:

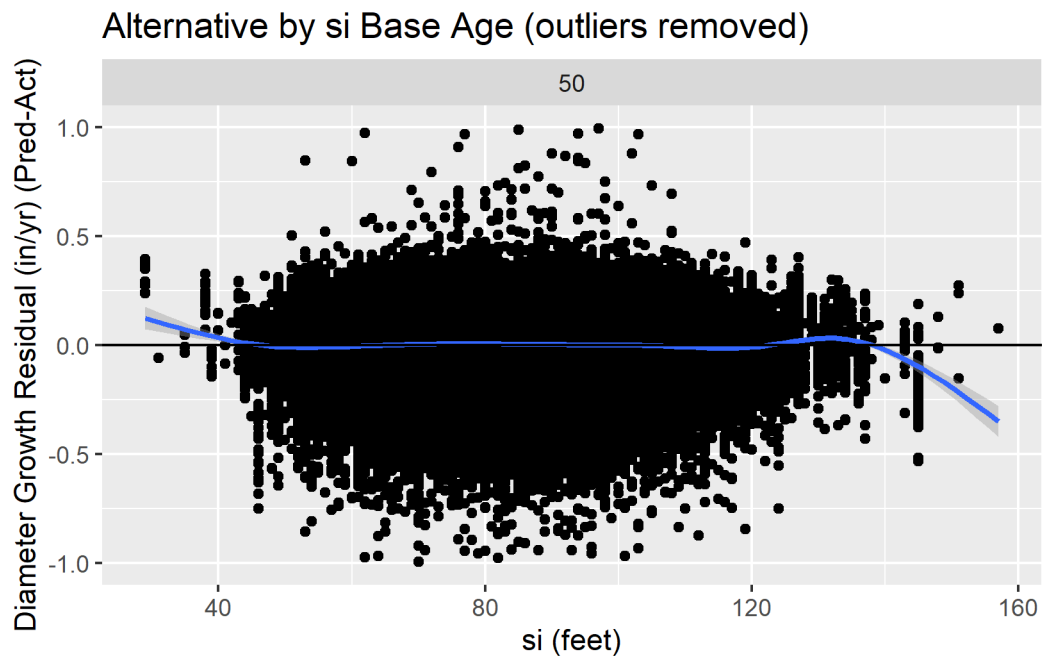
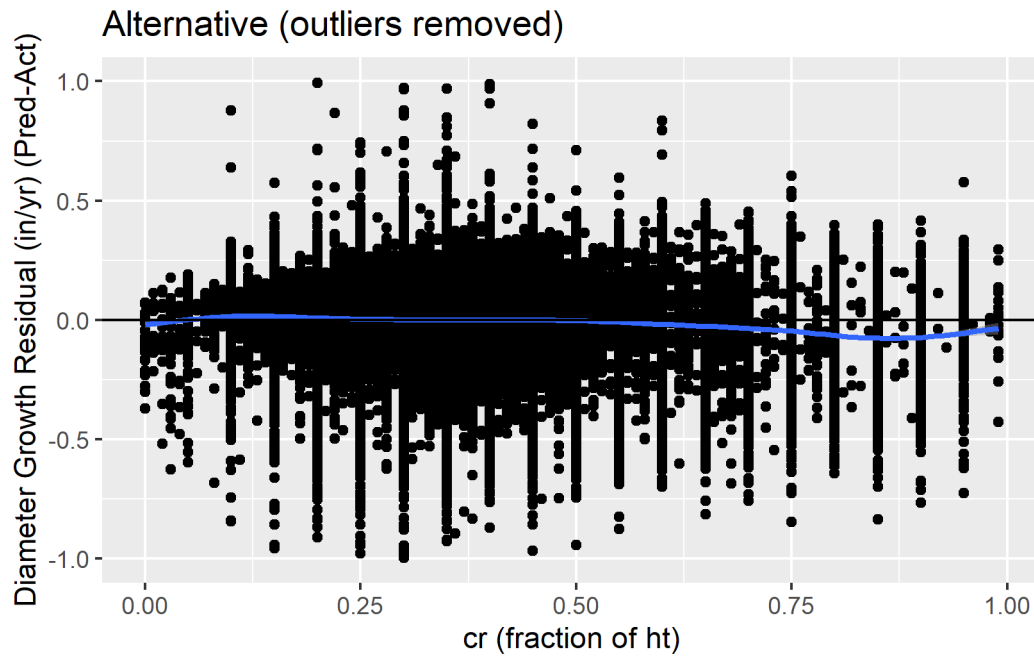
	Coef.	Std. error	t-stat.	p
B0	-1.0015318	0.0124239	-80.61301	0
B1	-0.6223743	0.0024177	-257.41892	0
B2	-0.0378570	0.0012636	-29.96024	0
B4	1.6346829	0.0057049	286.54079	0
B5	0.9006825	0.0068591	131.31161	0

Residual Standard Error: 0.790522481994518 on 342771 degrees of freedom, AIC: 811616.5

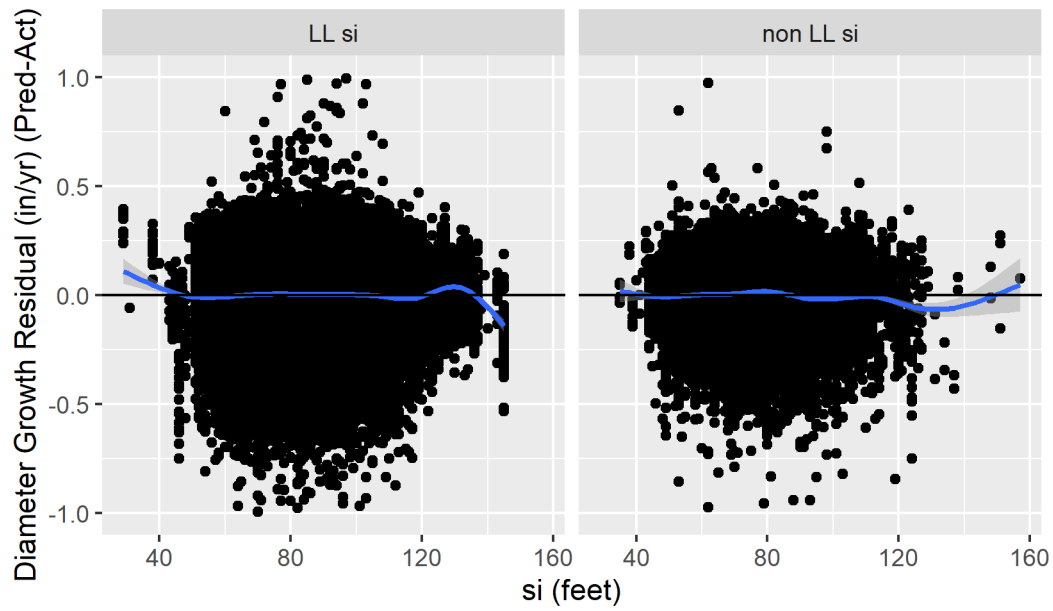
Residual Analysis for Equation 1



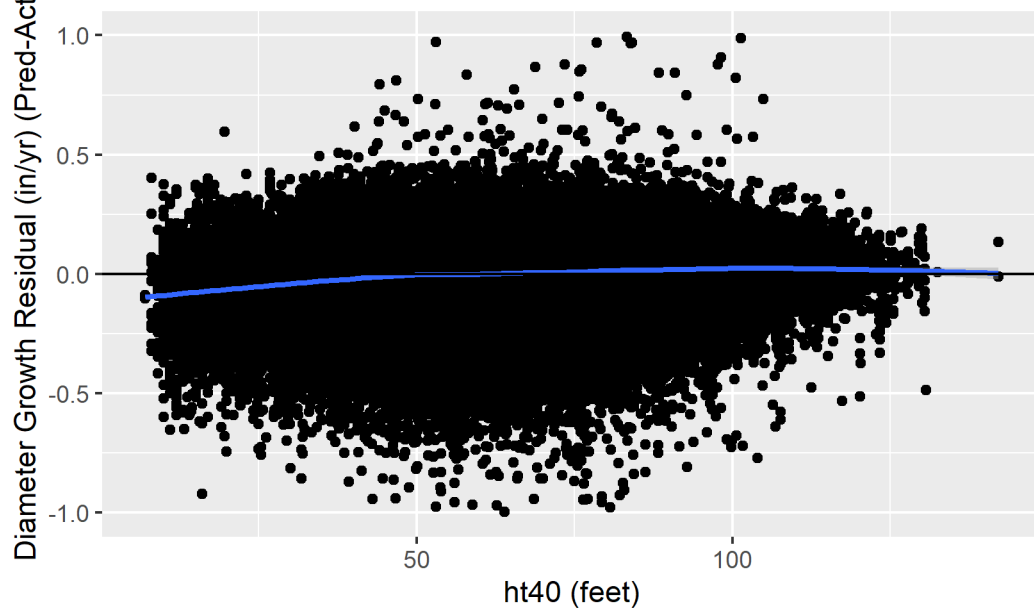


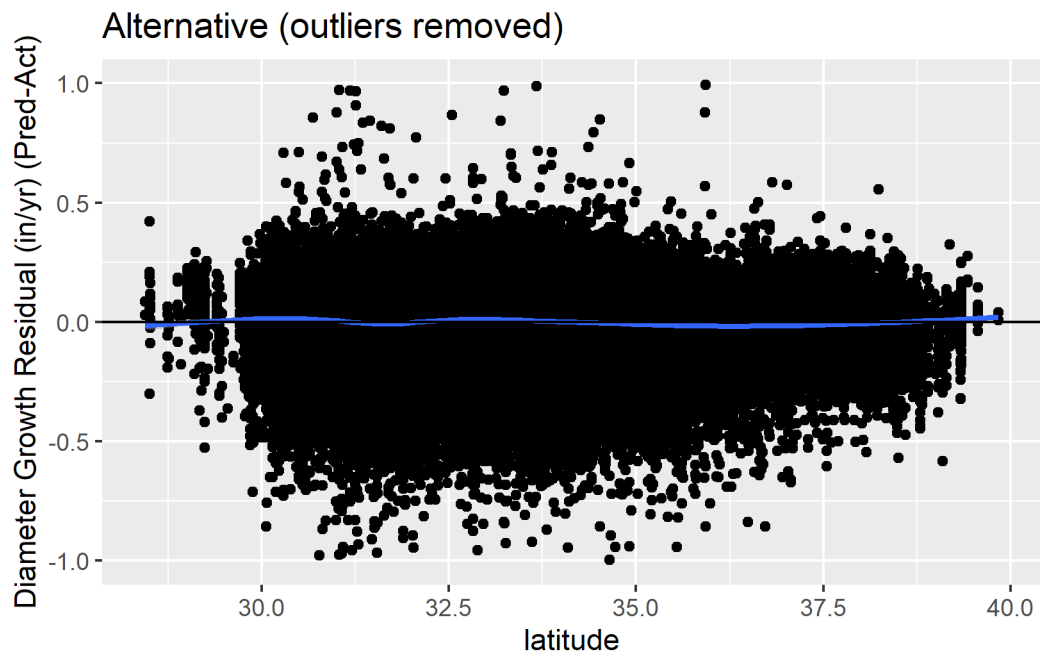
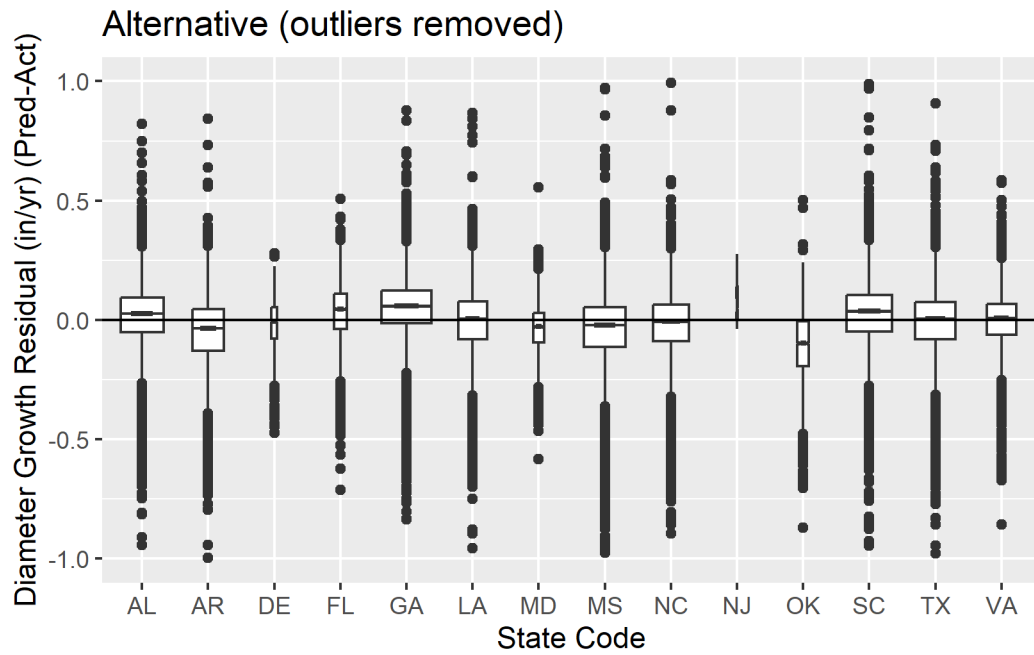


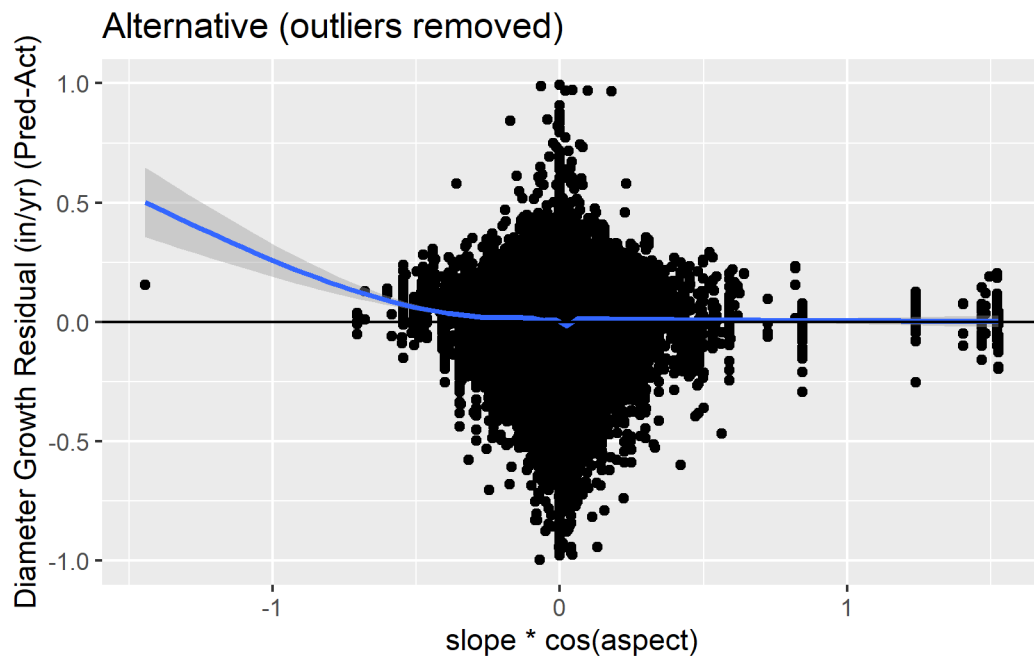
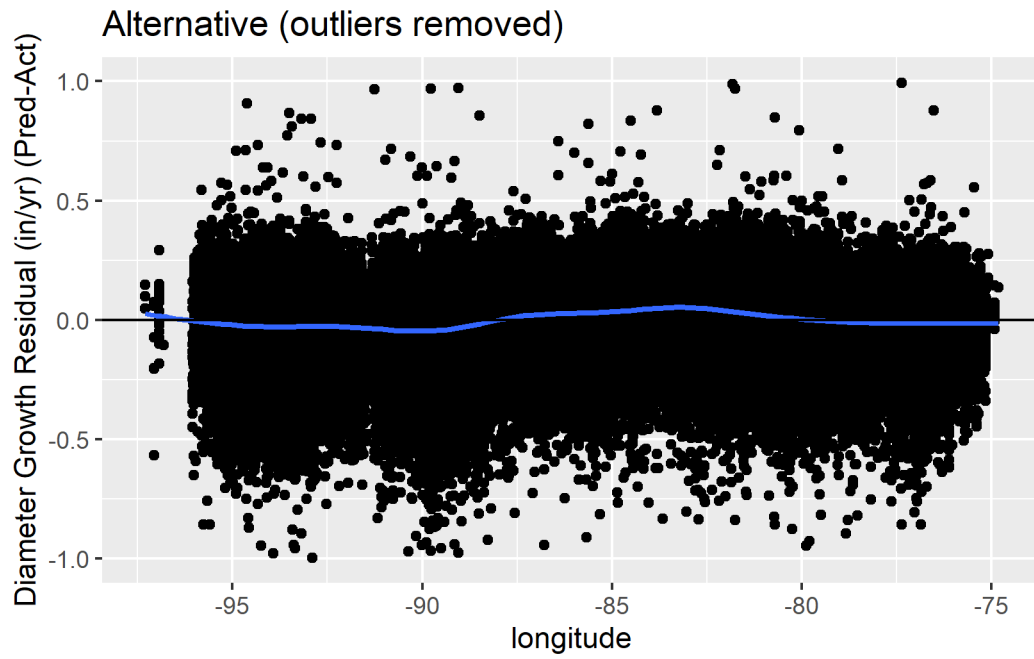
Alternative by si Species (outliers removed)

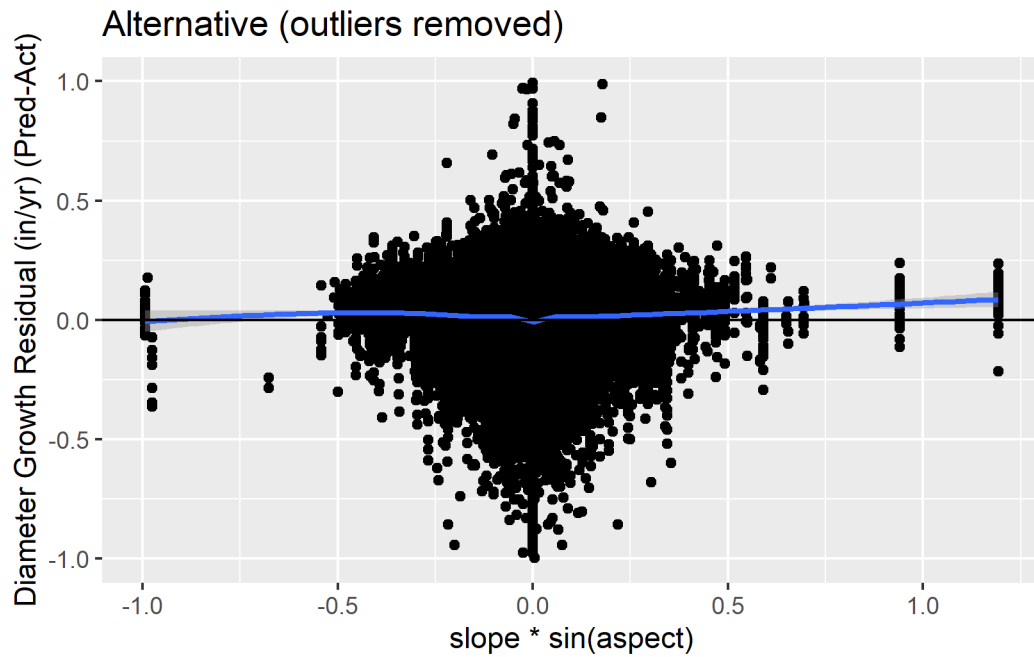


Alternative (outliers removed)

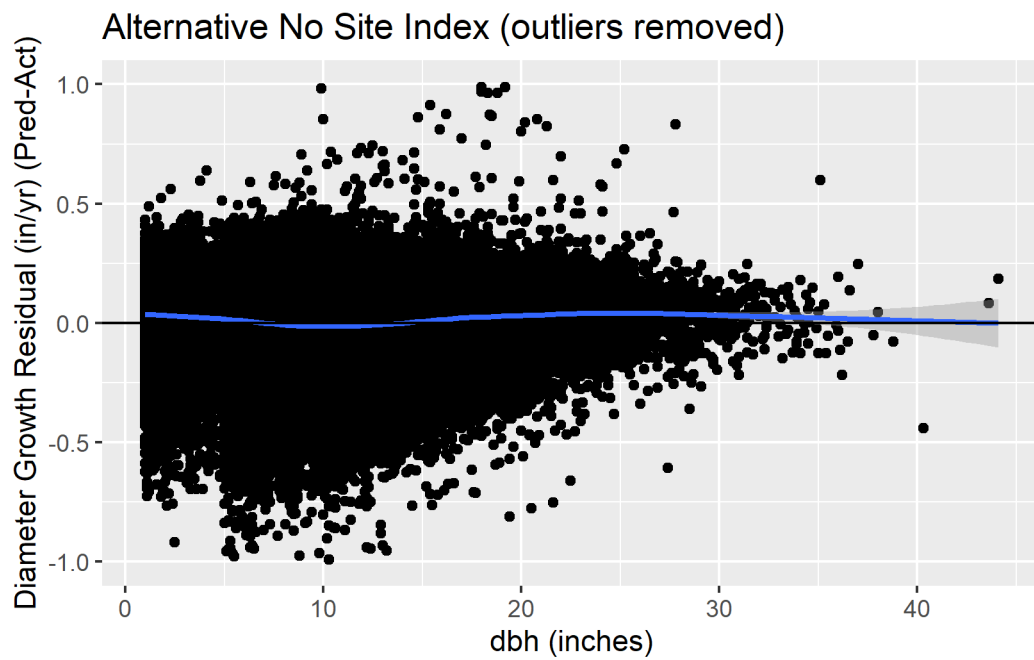


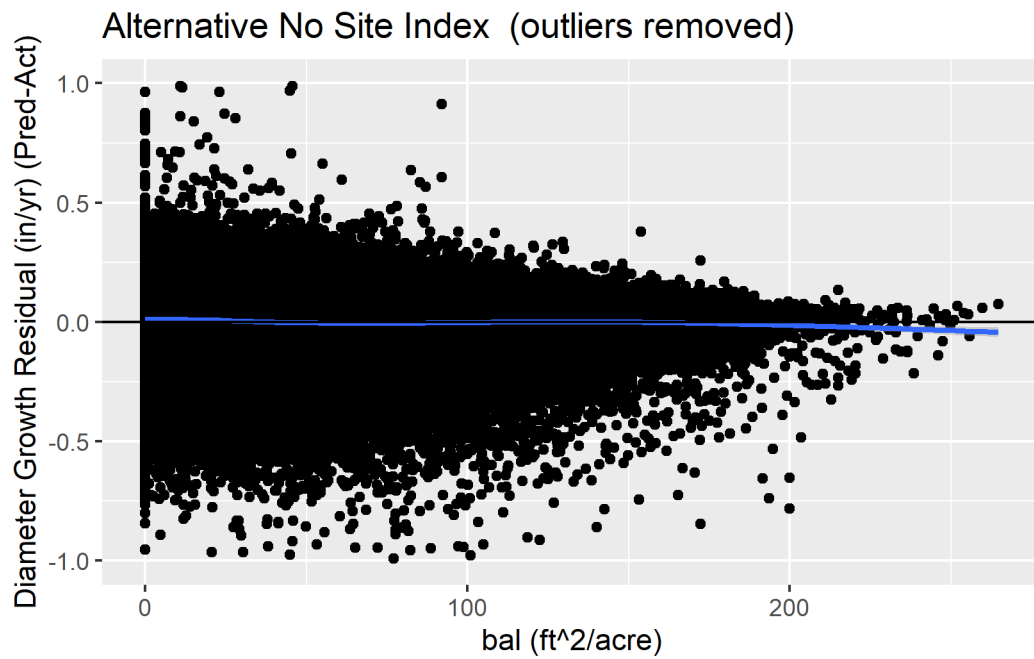
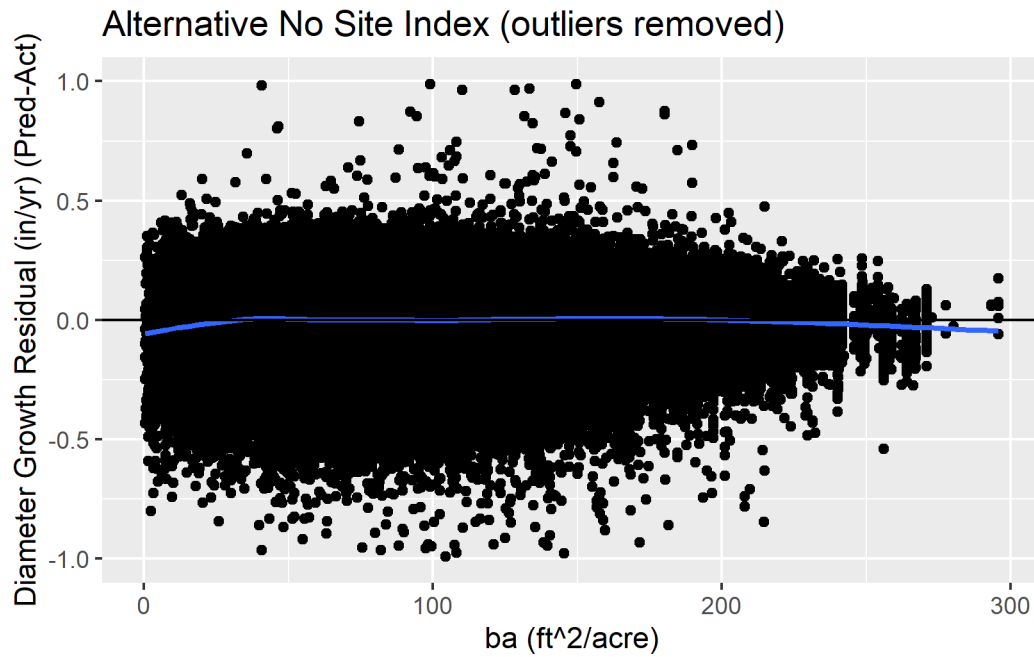


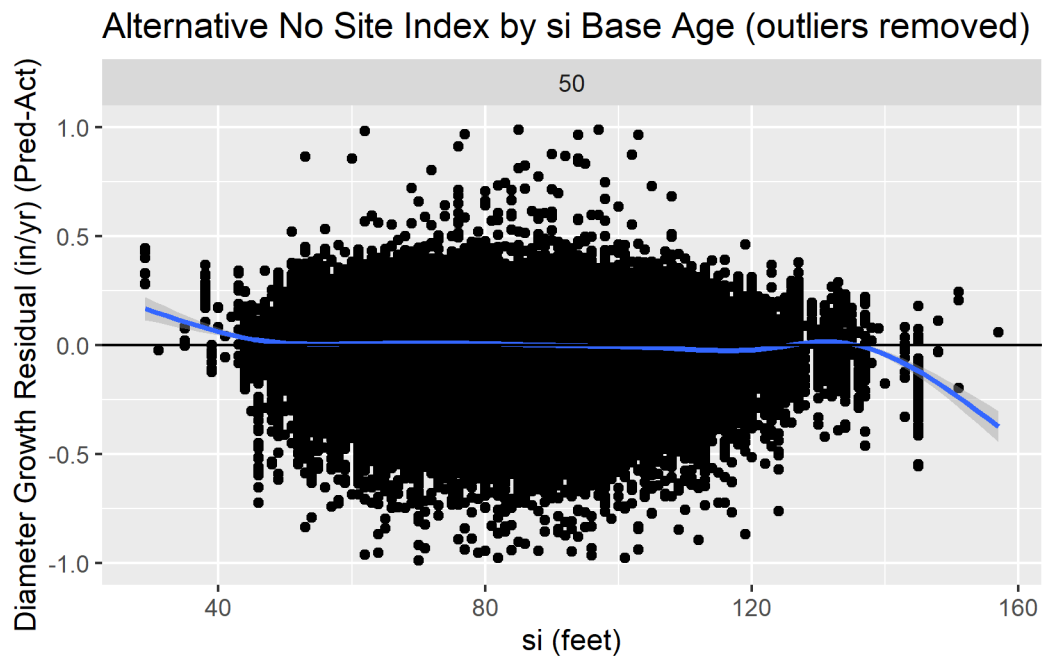
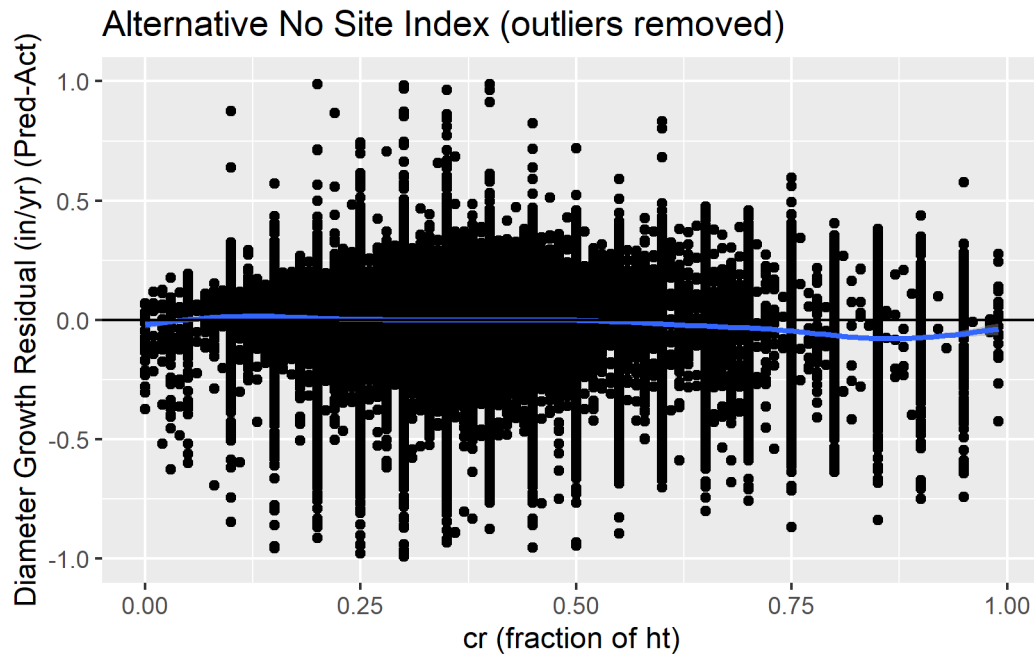




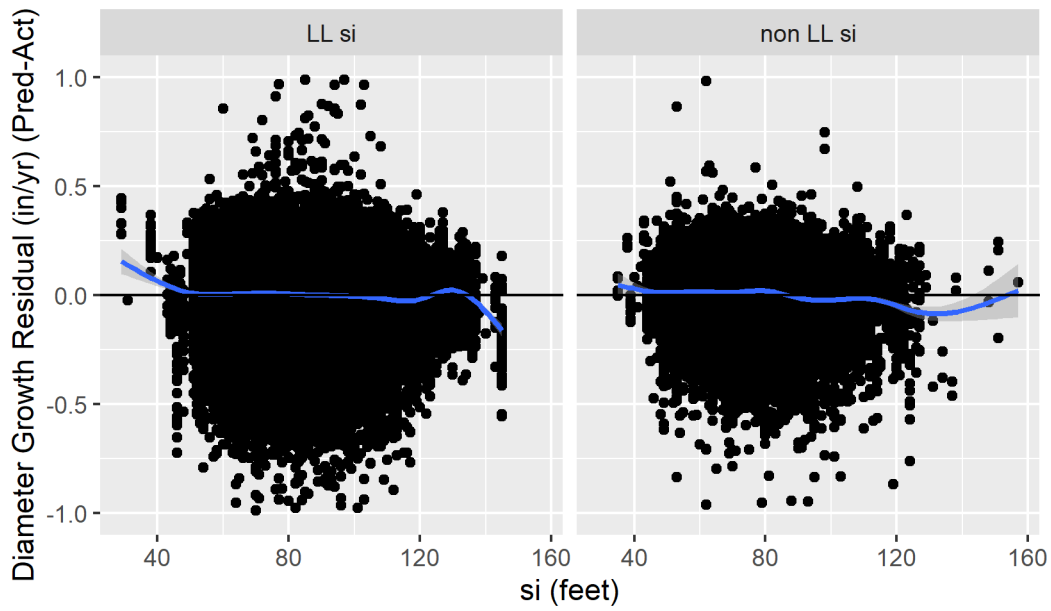
Residual Analysis for Equation 2



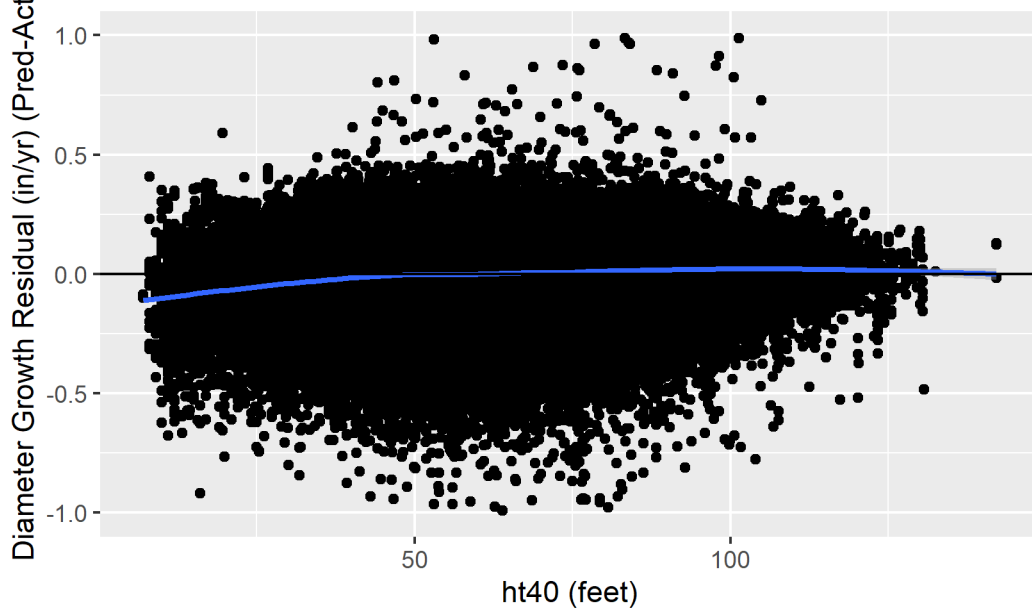


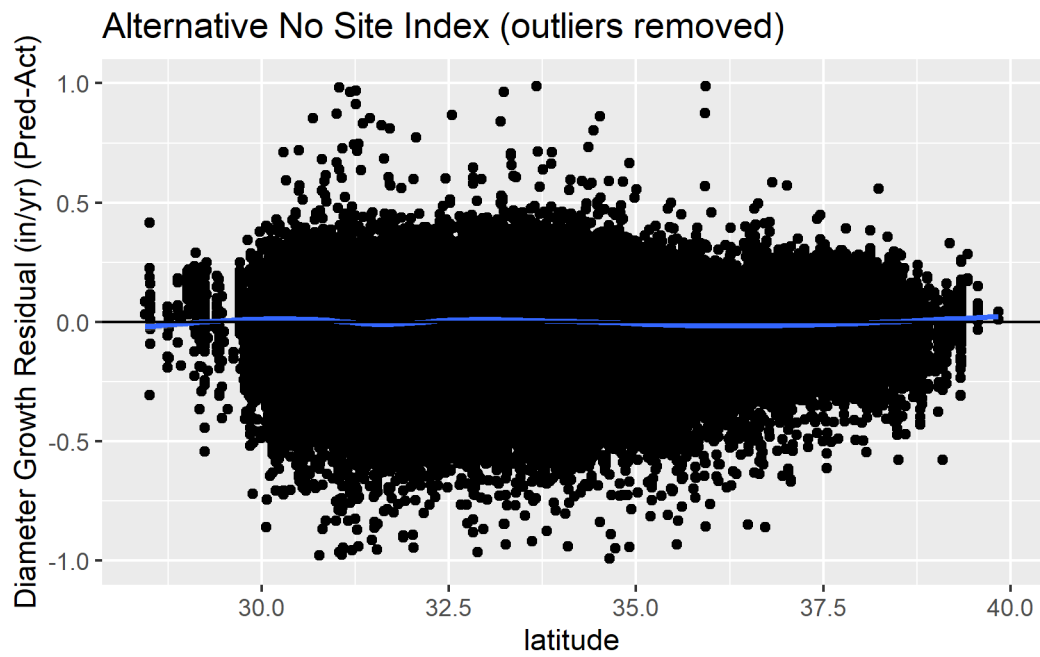
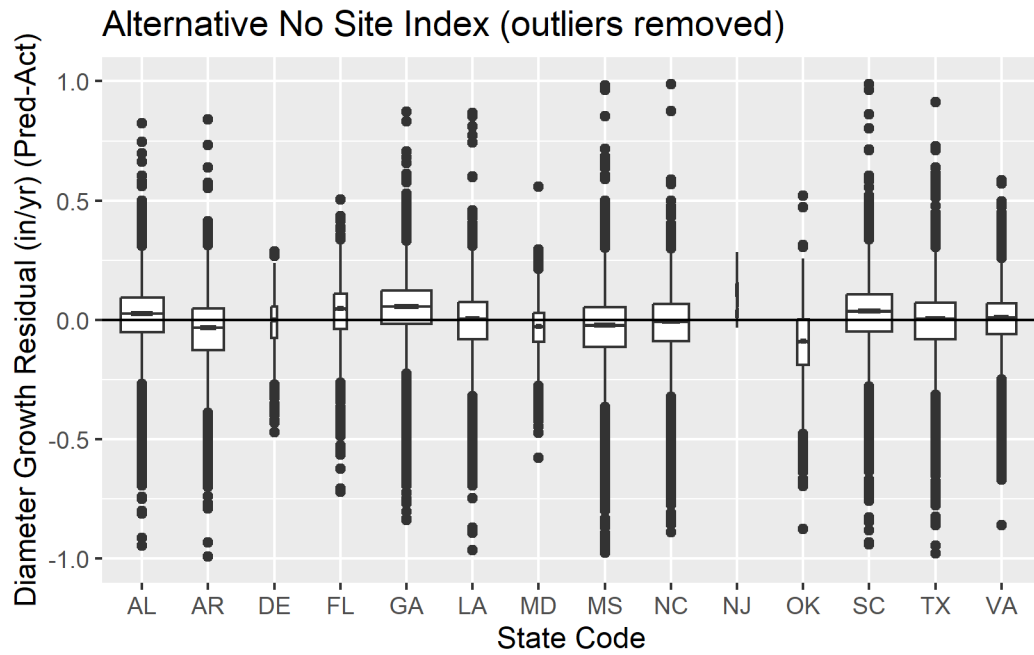


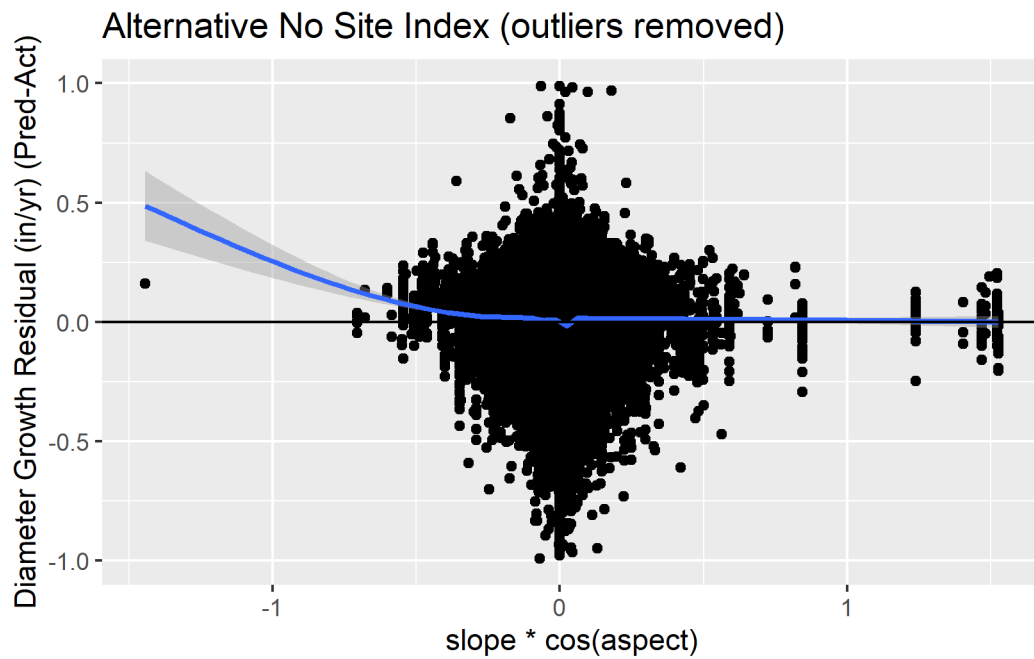
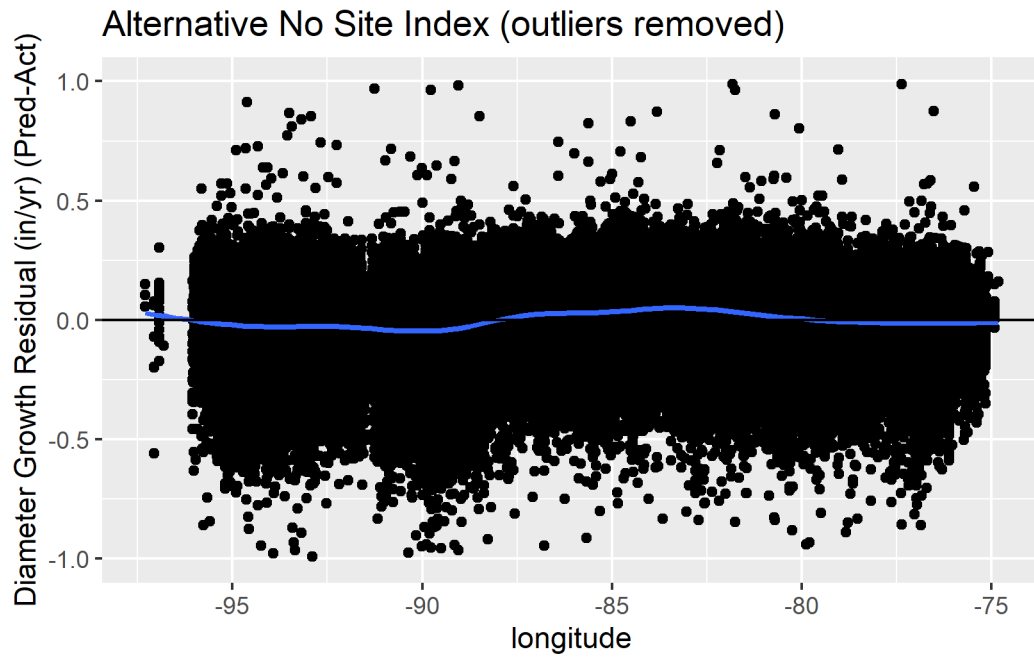
Alternative No Site Index by si Species (outliers removed)



Alternative No Site Index (outliers removed)







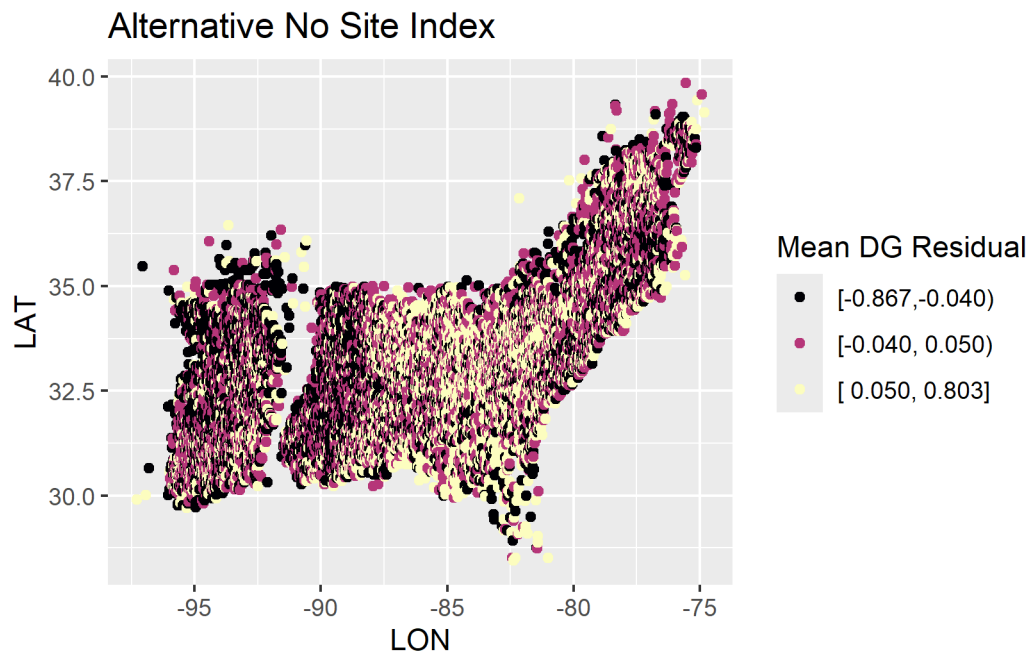
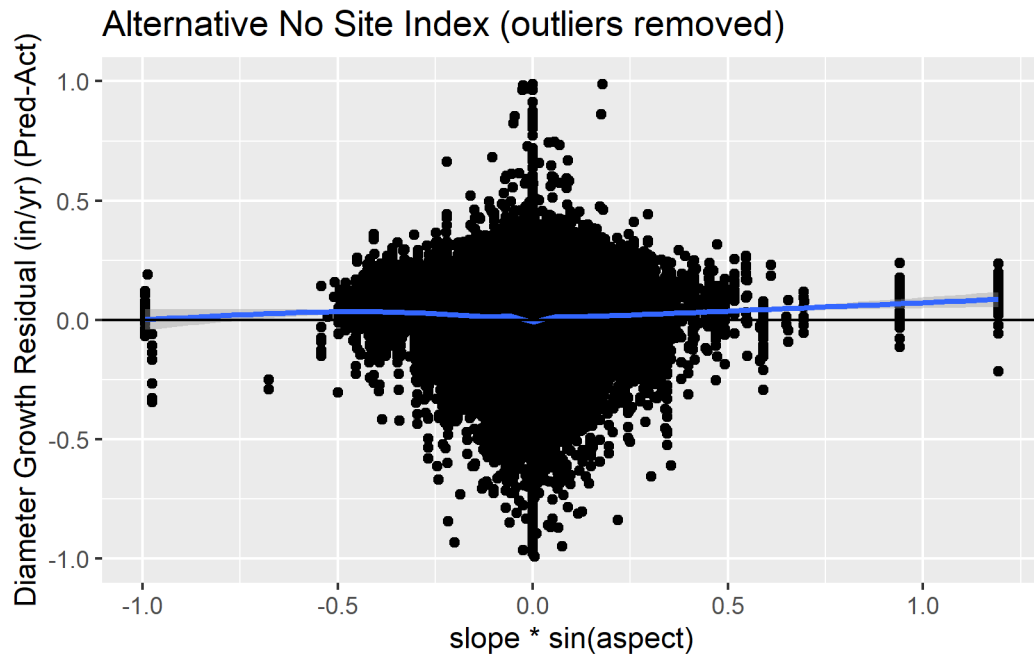


Table 3: Independent Variables for One Inch dbh Trees

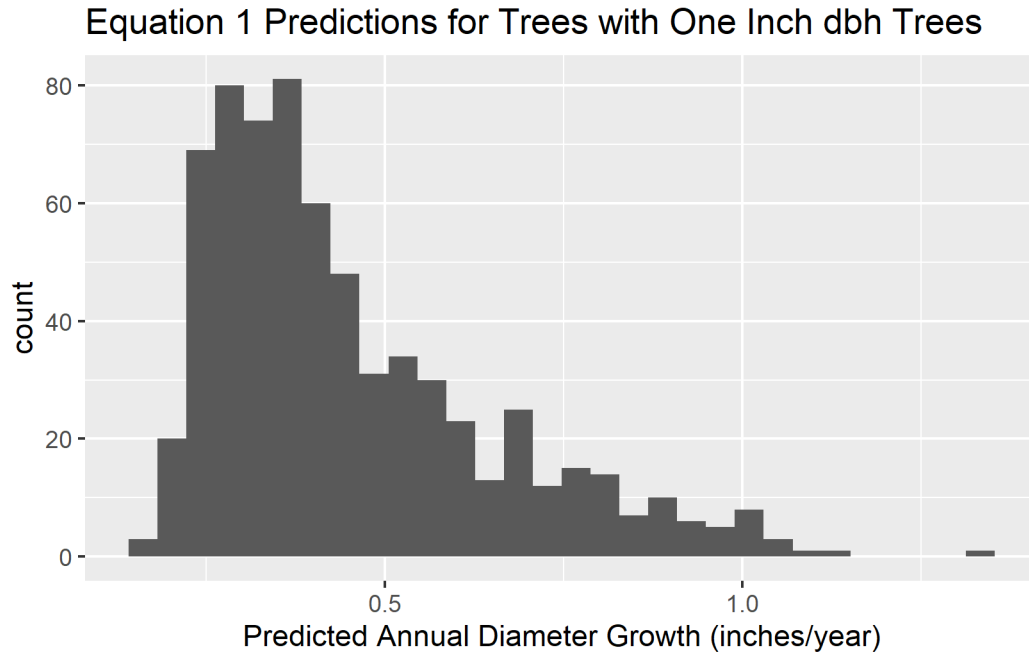
Variable	N	Mean	Std. Dev.	Min	Pctl. 25	Pctl. 75	Max
ba	674	64	43	0.41	30	91	210
bal	674	63	43	0	29	90	210
ht	674	11	2.3	6	10	13	23
cr	674	0.46	0.21	0.05	0.3	0.6	0.99
si	674	81	14	45	72	90	131

Discussion

Removing **si** do not degrade the fit significantly. There appears to be an under-prediction bias for low HT40 values. A few states (notably GA, AL, and SC) are over-predicted even with the flawed **si** values.

Equation 1 residual graphs show that there are clear residual trends spatially.

Equation Behavior for Very Small Trees



Equation 2 Predictions for Trees with One Inch dbh Trees

