

Linear models

Example dataset: forest trees

- ▶ Download this dataset (or the entire [zip file](#))

```
trees <- read.csv("data/trees.csv")
head(trees)
```

	site	dbh	height	sex	dead
1	4	29.68	36.1	male	0
2	5	33.29	42.3	male	0
3	2	28.03	41.9	female	0
4	5	39.86	46.5	female	0
5	1	47.94	43.9	female	0
6	1	10.82	26.2	male	0

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- ▶ Import:

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Questions

- ▶ What is the relationship between DBH and height?

Questions

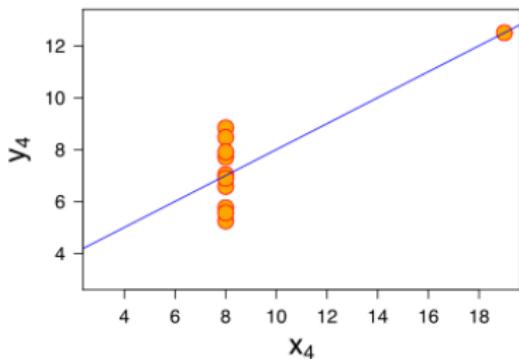
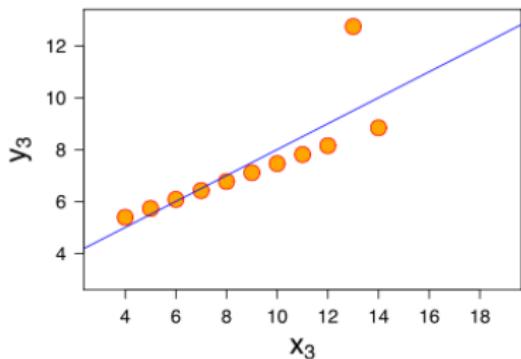
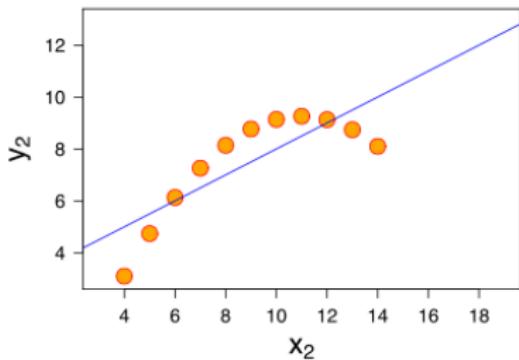
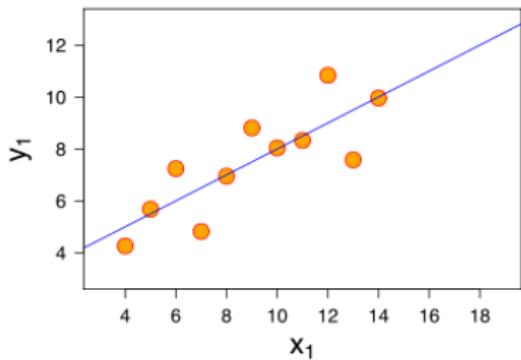
- ▶ What is the relationship between DBH and height?
- ▶ Do taller trees have bigger trunks?

Questions

- ▶ What is the relationship between DBH and height?
- ▶ Do taller trees have bigger trunks?
- ▶ Can we predict height from DBH? How well?

Always plot your data first!

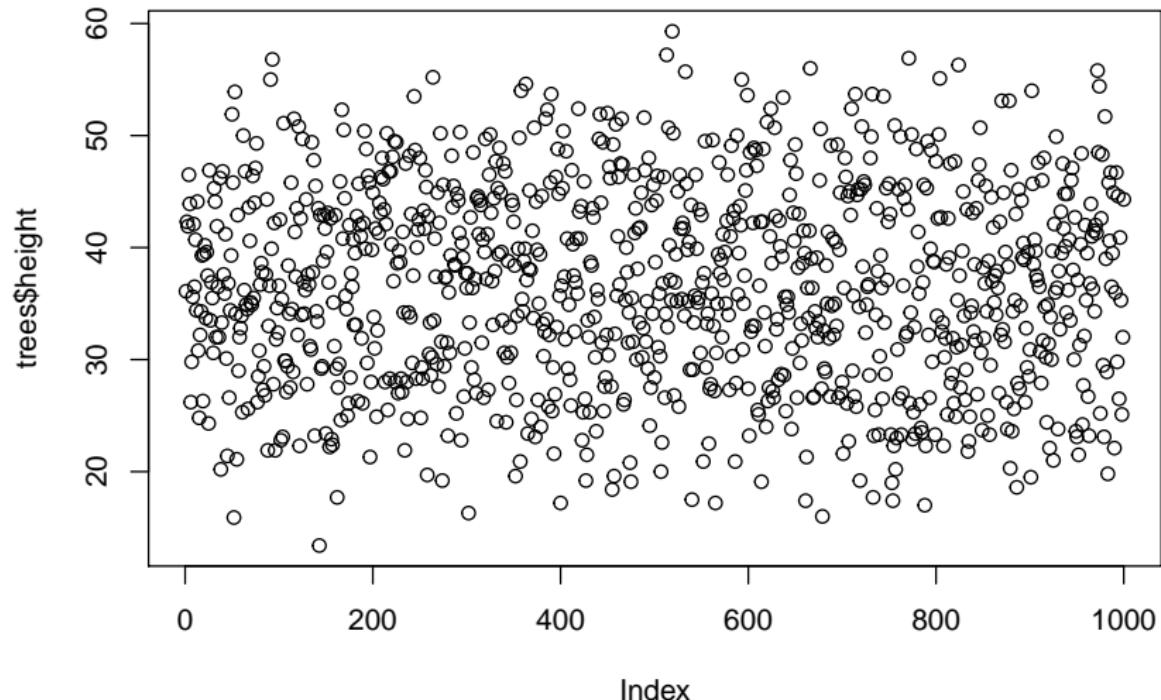
Always plot your data first!



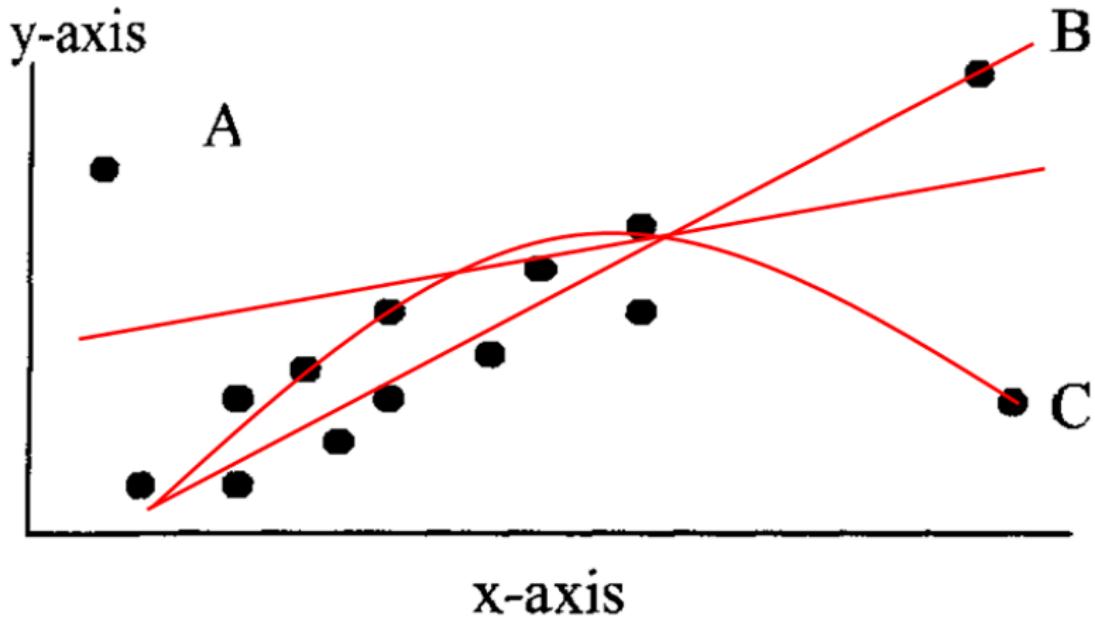
Exploratory Data Analysis (EDA)

Outliers

```
plot(trees$height)
```



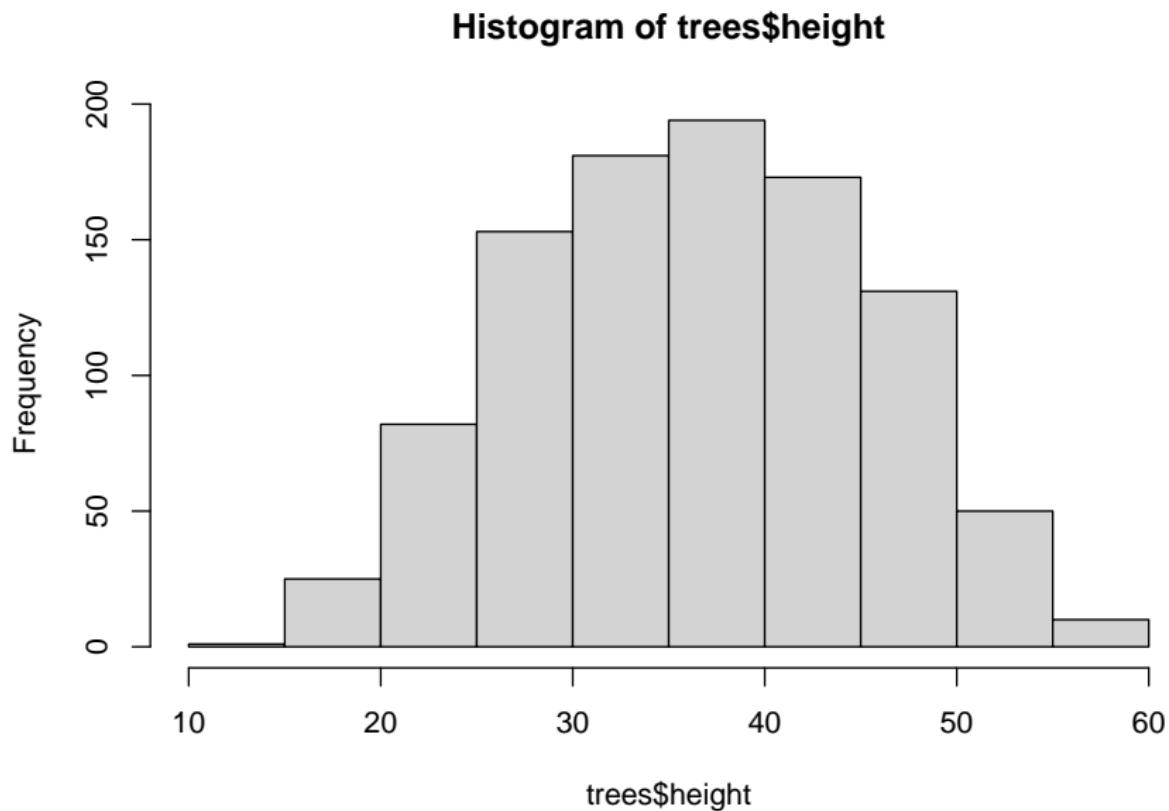
Outliers impact on regression



See <http://rpsychologist.com/d3/correlation/>

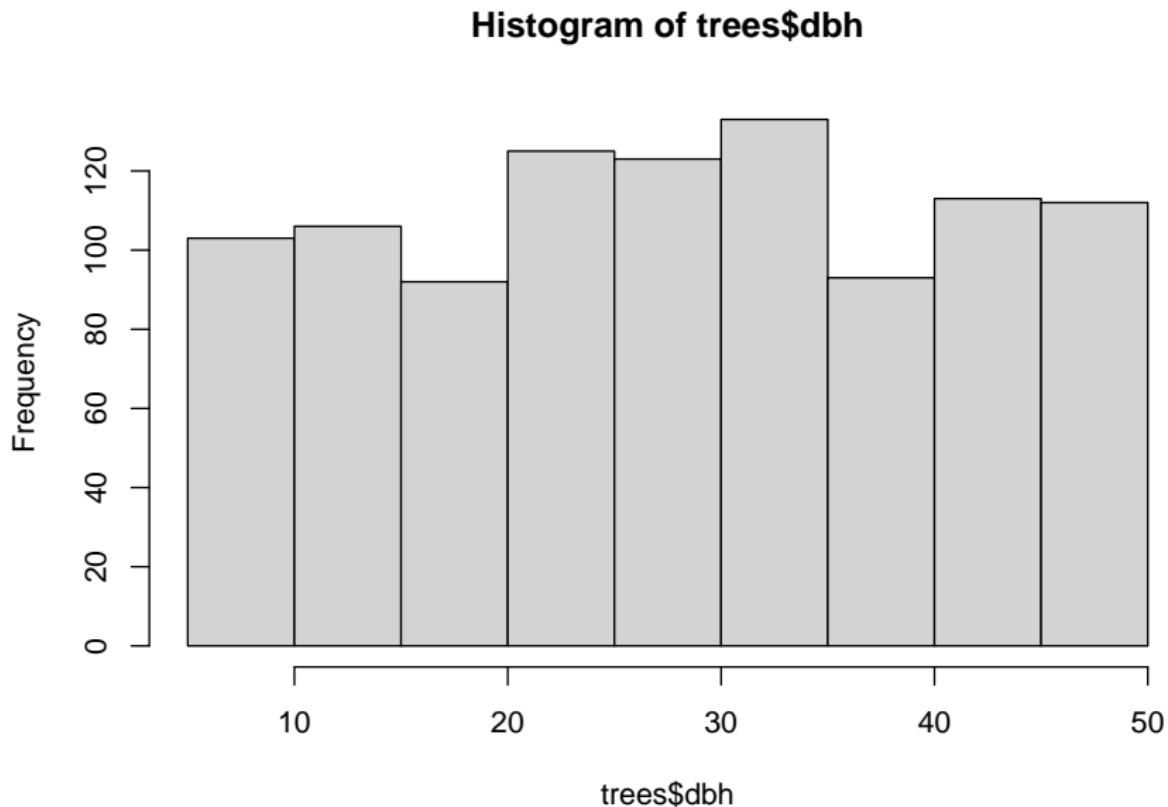
Histogram of response variable

```
hist(trees$height)
```



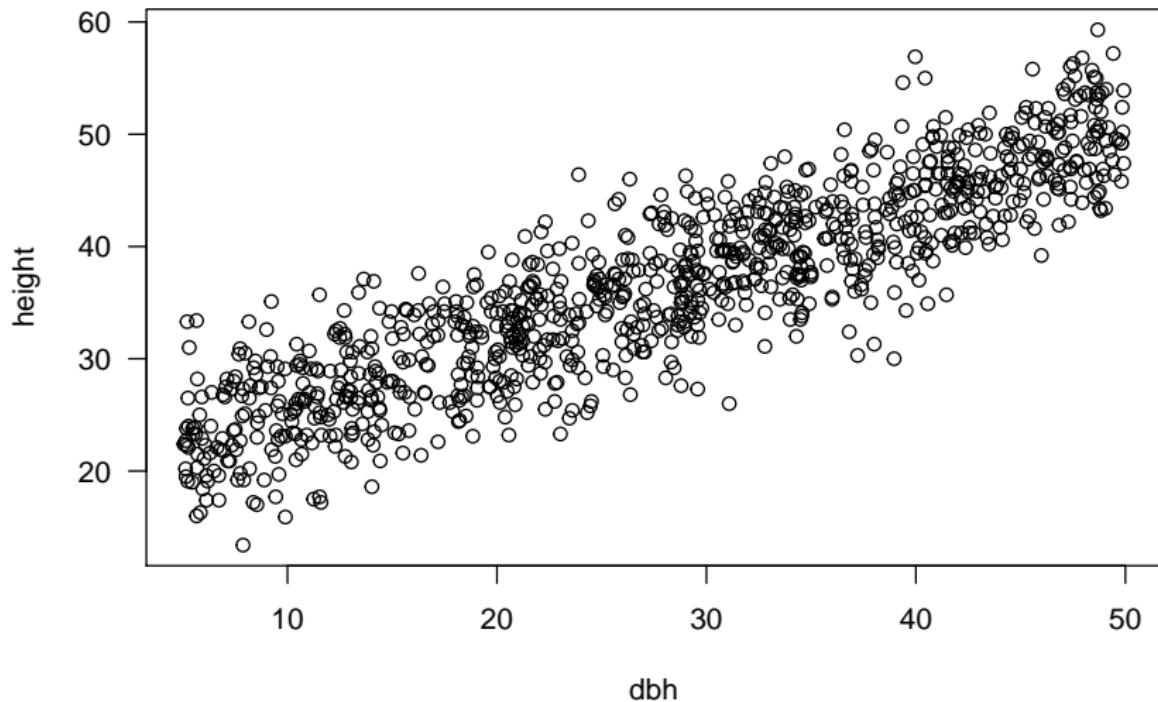
Histogram of predictor variable

```
hist(trees$dbh)
```



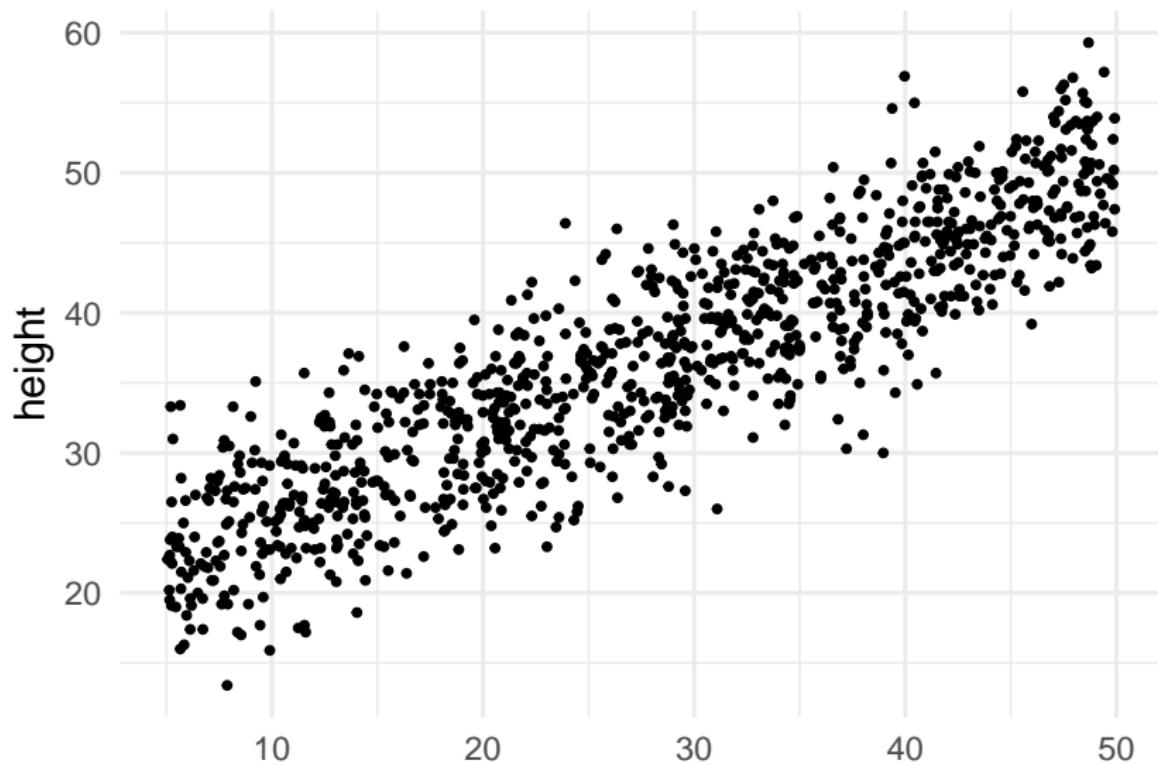
Scatterplot

```
plot(height ~ dbh, data = trees, las = 1)
```



Scatterplot

```
ggplot(trees) +  
  geom_point(aes(dbh, height))
```



Model fitting

Now fit model

Hint: 1m

Now fit model

Hint: `lm`

```
m1 <- lm(height ~ dbh, data = trees)
```

which corresponds to

$$\begin{aligned} Height_i &= a + b \cdot DBH_i + \varepsilon_i \\ \varepsilon_i &\sim N(0, \sigma^2) \end{aligned}$$

Model interpretation

What does this mean?

Call:

```
lm(formula = height ~ dbh, data = trees)
```

Residuals:

Min	1Q	Median	3Q	Max
-13.3270	-2.8978	0.1057	2.7924	12.9511

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	19.33920	0.31064	62.26	<2e-16 ***
dbh	0.61570	0.01013	60.79	<2e-16 ***

Signif. codes:	0 ***	0.001 **	0.01 *	0.05 .
	0.1	'	'	1

Residual standard error: 4.093 on 998 degrees of freedom

Multiple R-squared: 0.7874, Adjusted R-squared: 0.7871

F-statistic: 3695 on 1 and 998 DF, p-value: < 2.2e-16

Quiz

<https://pollev.com/franciscorod726>

Communicating results

Avoid dichotomania of statistical significance



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It's time to talk about ditching statistical significance

- ▶ 'Never conclude there is 'no difference' or 'no association' just because $p > 0.05$ or CI includes zero'

Avoid dichotomania of statistical significance



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It's time to talk about ditching statistical significance

- ▶ 'Never conclude there is 'no difference' or 'no association' just because $p > 0.05$ or CI includes zero'
- ▶ Estimate and communicate effect sizes and their uncertainty

Avoid dichotomania of statistical significance



EDITORIAL • 20 MARCH 2019

It's time to talk about ditching statistical significance

- ▶ 'Never conclude there is 'no difference' or 'no association' just because $p > 0.05$ or CI includes zero'
- ▶ Estimate and communicate effect sizes and their uncertainty
- ▶ <https://doi.org/10.1038/d41586-019-00857-9>

Communicating results

We found a significant positive relationship between DBH and Height ($p < 0.05$) ($b = 0.61$, $SE = 0.01$).

Presenting model results

```
kable(xtable::xtable(m1), digits = 2)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	19.34	0.31	62.26	0
dbh	0.62	0.01	60.79	0

Presenting model results

```
texreg::texreg(m1, single.row = TRUE)
```

Model 1	
(Intercept)	19.34 (0.31)***
dbh	0.62 (0.01)***
R ²	0.79
Adj. R ²	0.79
Num. obs.	1000

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$

Table 2: Statistical models

Retrieving model coefficients

```
coef(m1)
```

	dbh
(Intercept)	19.3391968
	0.6157036

Tidy up model coefficients with broom

```
library(broom)
tidy(m1)

# A tibble: 2 x 5
  term      estimate std.error statistic p.value
  <chr>      <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept) 19.3      0.311     62.3      0
2 dbh          0.616     0.0101    60.8      0

glance(m1)

# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic p.value    df logLik     AIC     BIC
  <dbl>        <dbl>     <dbl>     <dbl>     <dbl> <dbl> <dbl> <dbl> <dbl>
1 0.787        0.787    4.09     3695.      0      1 -2827. 5660. 5675.
# ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

Confidence intervals

```
confint(m1)

              2.5 %    97.5 %
(Intercept) 18.7296053 19.948788
dbh          0.5958282  0.635579
```

Using effects package

```
library(effects)
summary(allEffects(m1))
```

model: height ~ dbh

dbh effect

dbh	5	20	30	40	50
dbh	22.41771	31.65327	37.81030	43.96734	50.12438

Lower 95 Percent Confidence Limits

dbh	5	20	30	40	50
dbh	21.89682	31.35487	37.55287	43.61733	49.61669

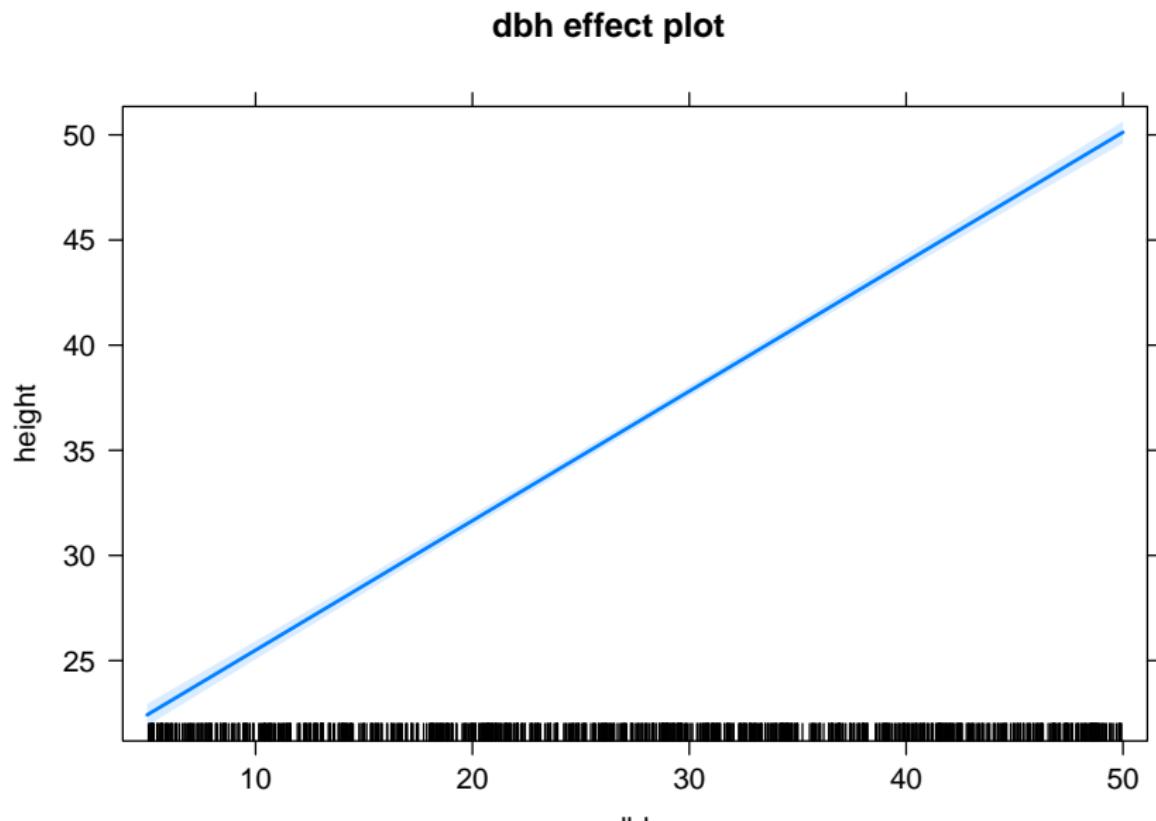
Upper 95 Percent Confidence Limits

dbh	5	20	30	40	50
dbh	22.93861	31.95167	38.06774	44.31735	50.63207

Visualising fitted model

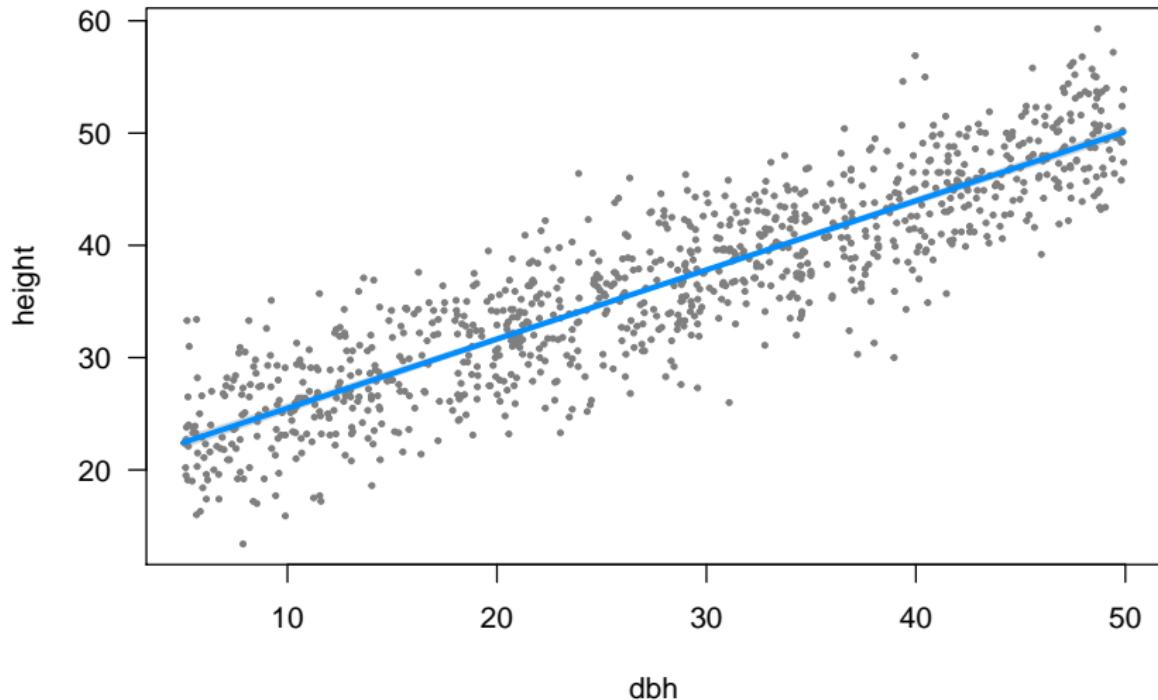
Plot effects

```
plot(allEffects(m1))
```

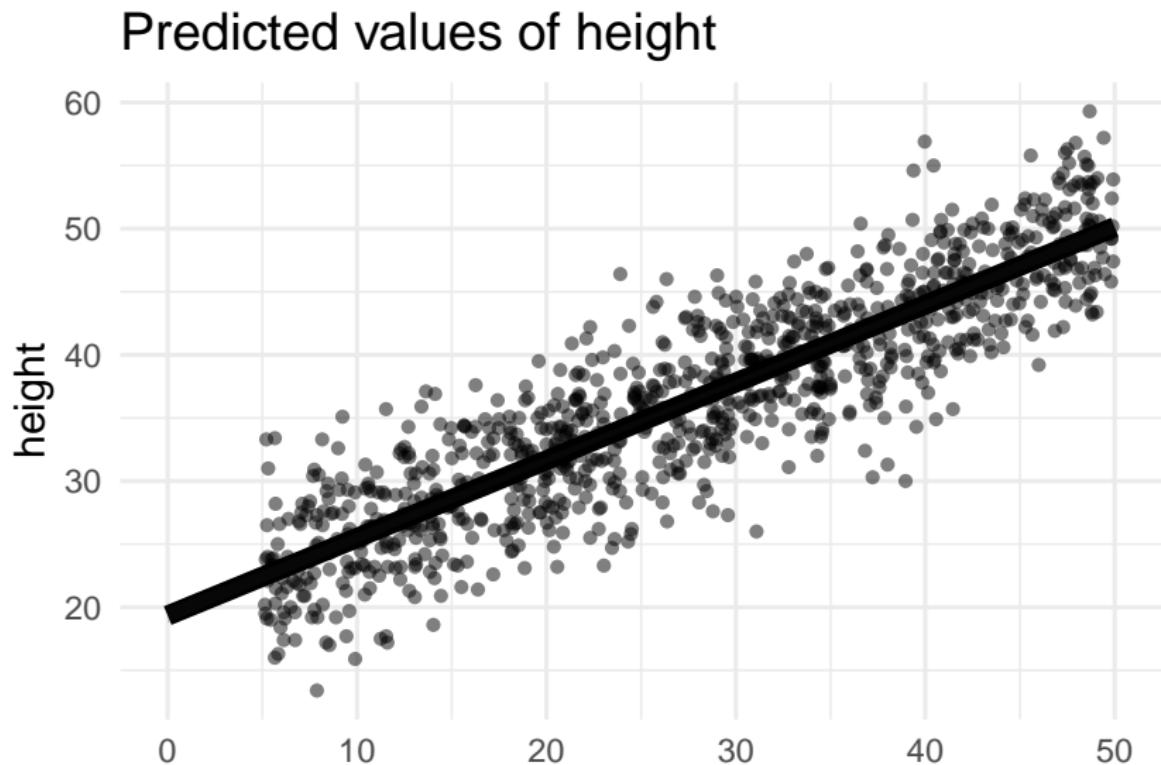


Plot model (visreg)

```
library(visreg)
visreg(m1)
```



Plot model (sjPlot - ggplot2)



Model checking

Linear model assumptions

- ▶ Linearity (transformations, GAM...)

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- ▶ Residuals:

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 - ▶ Independent

Linear model assumptions

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- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance

Linear model assumptions

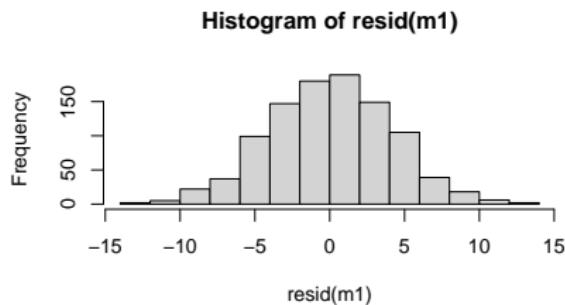
- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance
 - ▶ Normal

Linear model assumptions

- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance
 - ▶ Normal
- ▶ No measurement error in predictors

Are residuals normal?

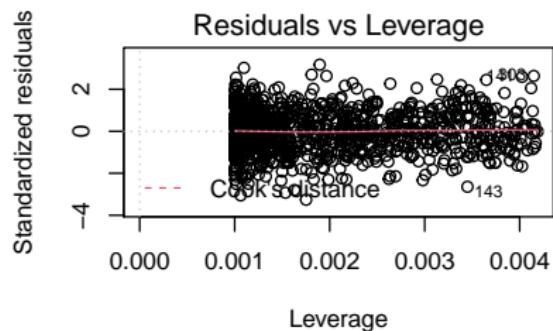
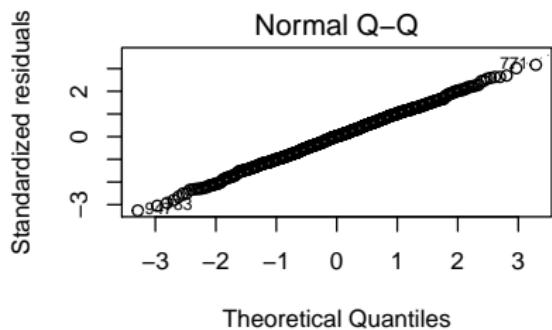
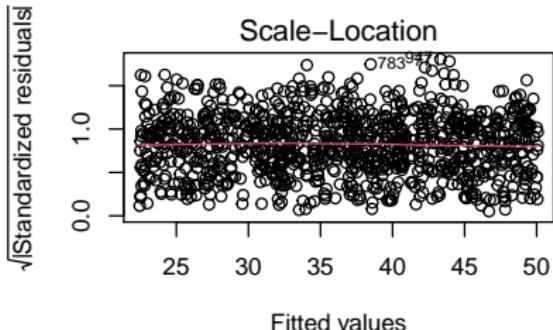
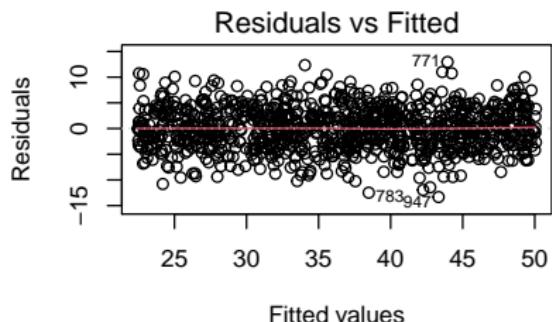
```
hist(resid(m1))
```



SD of residuals = 4.09 coincides with estimate of sigma.

```
lm(formula = height ~ dbh, data = trees)
  coef.est coef.se
  (Intercept) 19.34      0.31
  dbh          0.62      0.01
  ---
  n = 1000, k = 2
  residual sd = 4.09, R-Squared = 0.79
```

Model checking: residuals

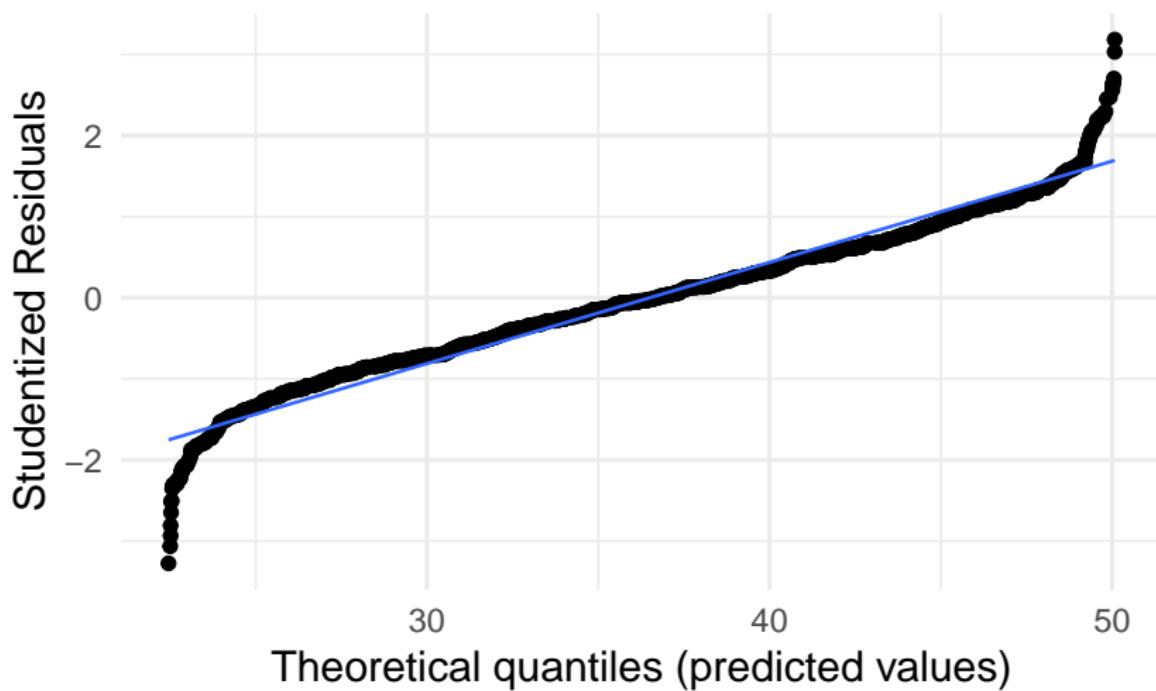


Model checking (sjPlot)

```
plot_model(m1, type = "diag")[[1]]
```

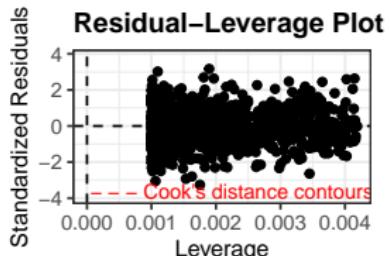
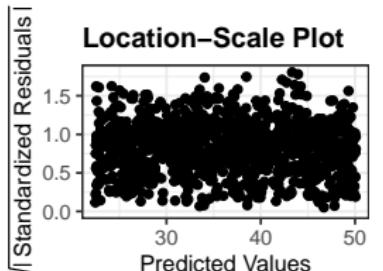
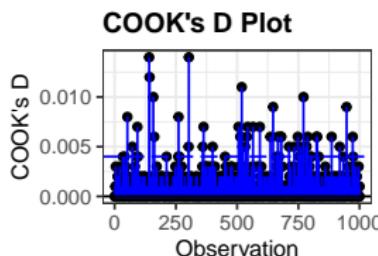
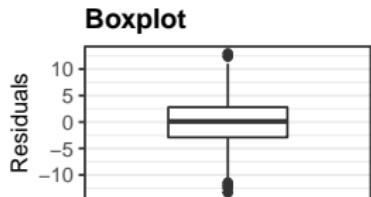
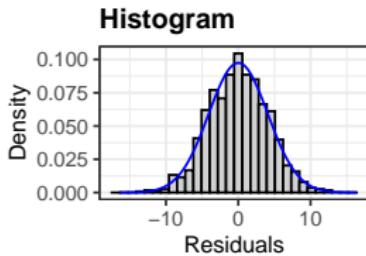
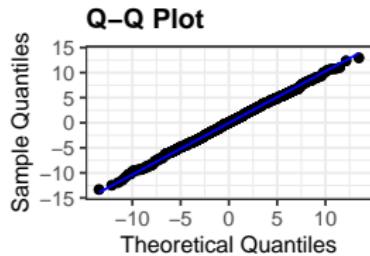
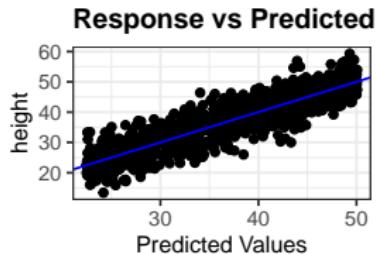
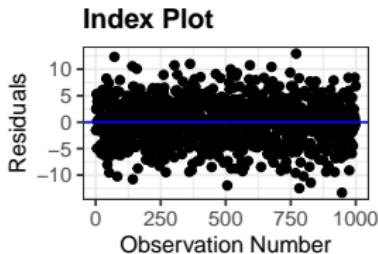
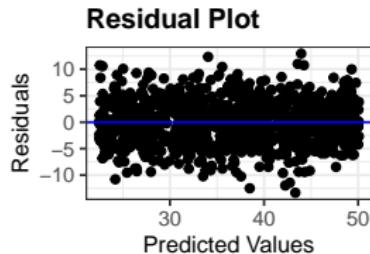
Non-normality of residuals and outliers

Dots should be plotted along the line



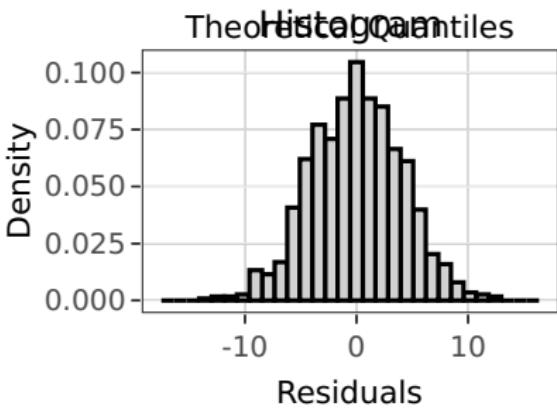
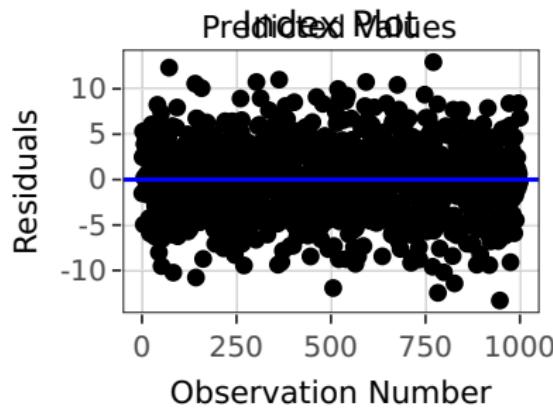
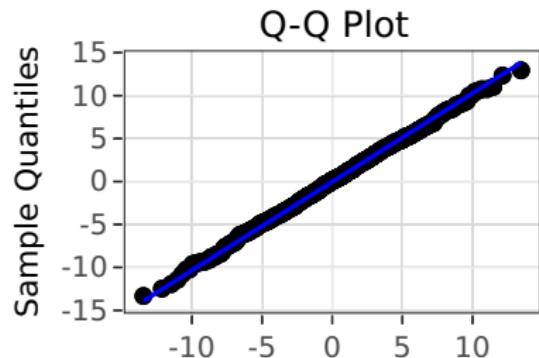
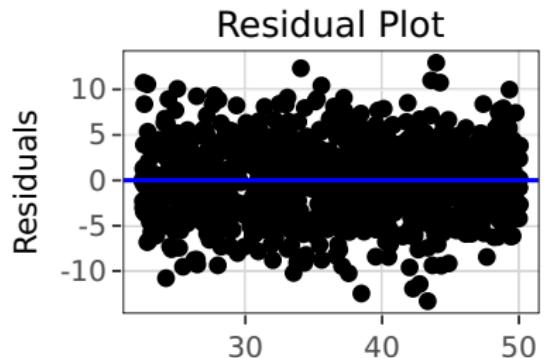
Model checking (ggResidpanel)

```
ggResidpanel:::resid_panel(m1, plots = "all")
```



Interactive model checking (ggResidpanel)

```
ggResidpanel:::resid_interact(m1)
```



Using model for prediction

How good is the model in predicting tree height?

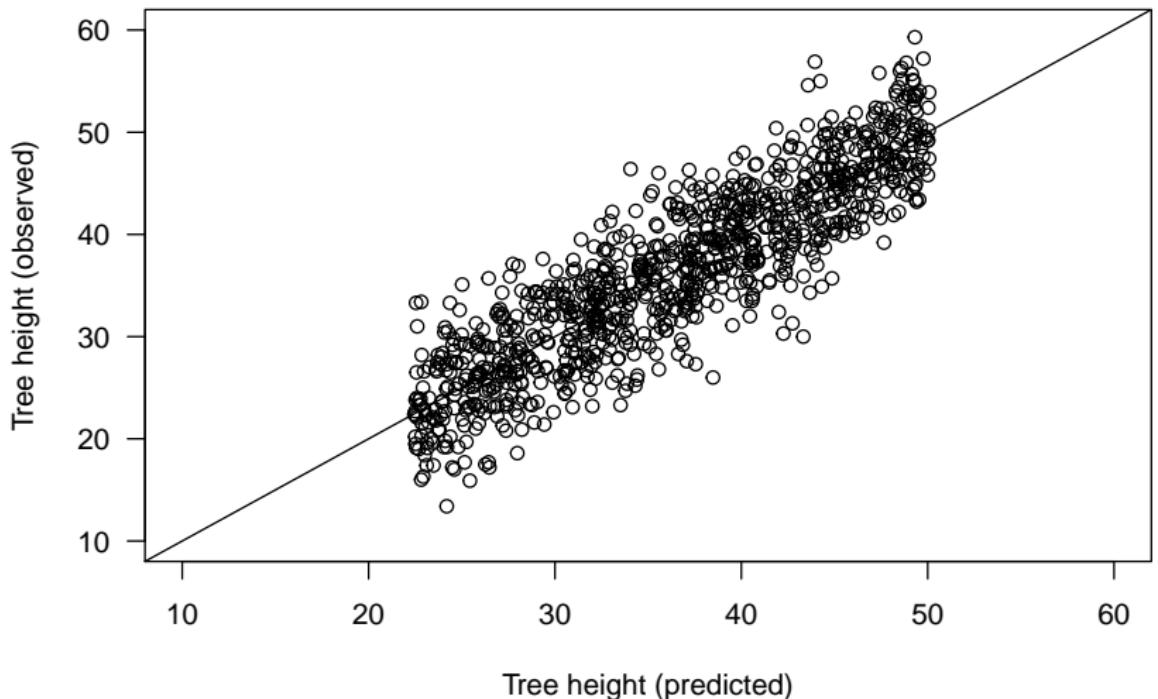
`fitted` gives predictions for each observation

```
trees$height.pred <- fitted(m1)  
head(trees)
```

	site	dbh	height	sex	dead	height.pred
1	4	29.68	36.1	male	0	37.61328
2	5	33.29	42.3	male	0	39.83597
3	2	28.03	41.9	female	0	36.59737
4	5	39.86	46.5	female	0	43.88114
5	1	47.94	43.9	female	0	48.85603
6	1	10.82	26.2	male	0	26.00111

Calibration plot: Observed vs Predicted values

```
plot(trees$height.pred, trees$height,  
      xlab = "Tree height (predicted)", ylab = "Tree height (obse
```



Using fitted model for prediction

Q: Expected tree height if DBH = 39 cm?

```
new.dbh <- data.frame(dbh = c(39))
predict(m1, new.dbh, se.fit = TRUE)
```

```
$fit
```

```
1
```

```
43.35164
```

```
$se.fit
```

```
[1] 0.1715514
```

```
$df
```

```
[1] 998
```

```
$residual.scale
```

```
[1] 4.092629
```

Using fitted model for prediction

Q: Expected tree height if DBH = 39 cm?

```
predict(m1, new.dbh, interval = "confidence")
```

	fit	lwr	upr
1	43.35164	43.01499	43.68828

```
predict(m1, new.dbh, interval = "prediction")
```

	fit	lwr	upr
1	43.35164	35.31344	51.38983

Workflow

- ▶ **Visualise data**

Workflow

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- ▶ **Understand fitted model** (`summary`, `allEffects...`)

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- ▶ **Visualise model** (`plot(allEffects)`, `visreg`, `plot_model...`)

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- ▶ **Check model** (`plot`, `resid_panel`, `calibration plot...`)

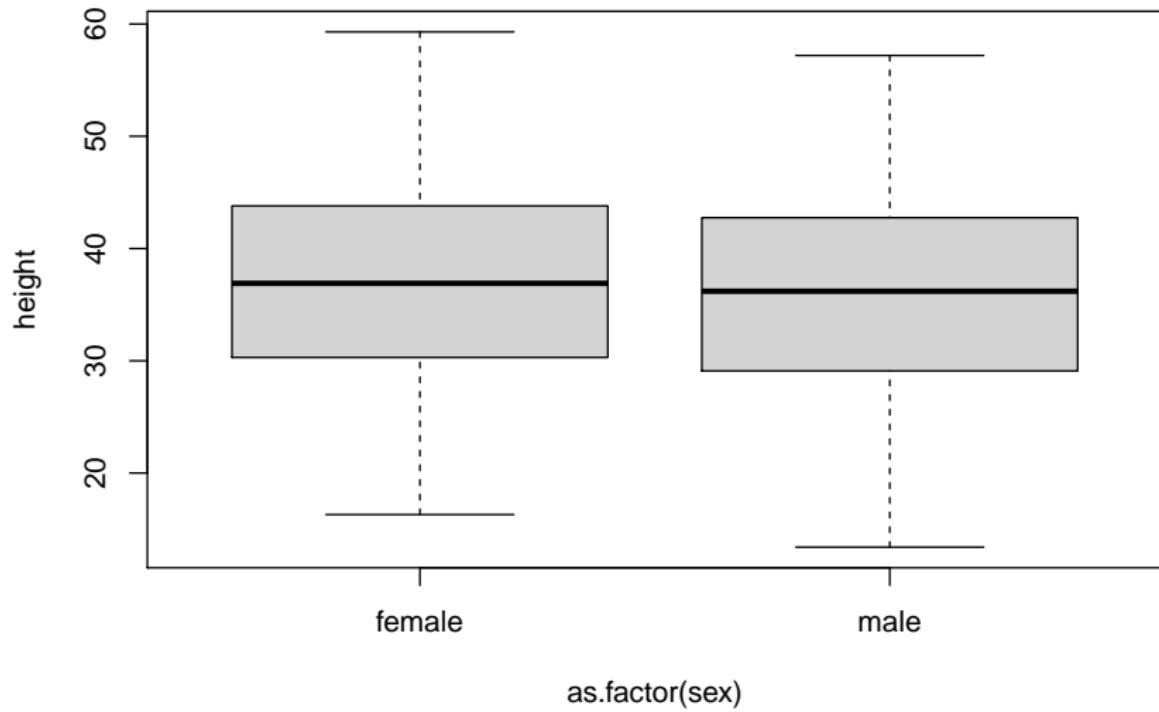
Workflow

- ▶ **Visualise data**
- ▶ **Understand fitted model** (`summary`, `allEffects...`)
- ▶ **Visualise model** (`plot(allEffects)`, `visreg`, `plot_model...`)
- ▶ **Check model** (`plot`, `resid_panel`, `calibration plot...`)
- ▶ **Predict** (`fitted`, `predict`)

Categorical predictors (factors)

Q: Does tree height vary with sex?

```
plot(height ~ as.factor(sex), data = trees)
```



Model height ~ sex

```
m2 <- lm(height ~ sex, data = trees)
```

Call:

```
lm(formula = height ~ sex, data = trees)
```

Residuals:

Min	1Q	Median	3Q	Max
-22.6881	-6.7881	-0.0097	6.7261	22.3687

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)		
(Intercept)	36.9312	0.3981	92.778	<2e-16 ***		
sexmale	-0.8432	0.5607	-1.504	0.133		

Signif. codes:	0 '***'	0.001 '**'	0.01 '*'	0.05 '.'	0.1 ' '	1

Residual standard error: 8.865 on 998 degrees of freedom

Multiple R-squared: 0.002261, Adjusted R-squared: 0.001261

F-statistic: 2.261 on 1 and 998 DF, p-value: 0.133

Linear model with categorical predictors

```
m2 <- lm(height ~ sex, data = trees)
```

corresponds to

$$\begin{aligned} Height_i &= a + b_{male} + \varepsilon_i \\ \varepsilon_i &\sim N(0, \sigma^2) \end{aligned}$$

Model height ~ sex

```
m2 <- lm(height ~ sex, data = trees)
```

Call:

```
lm(formula = height ~ sex, data = trees)
```

Residuals:

Min	1Q	Median	3Q	Max
-22.6881	-6.7881	-0.0097	6.7261	22.3687

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Signif. codes:	0 ***	0.001 **	0.01 *	0.05 .
	1	1	1	1

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Quiz

<https://pollev.com/franciscorod726>

Presenting model results

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	36.93	0.40	92.78	0.00
sexmale	-0.84	0.56	-1.50	0.13

Effects: Height ~ sex

Compare CIs

```
summary(allEffects(m2))
```

model: height ~ sex

sex effect

sex

female	male
36.93125	36.08810

Lower 95 Percent Confidence Limits

sex

female	male
36.15012	35.31319

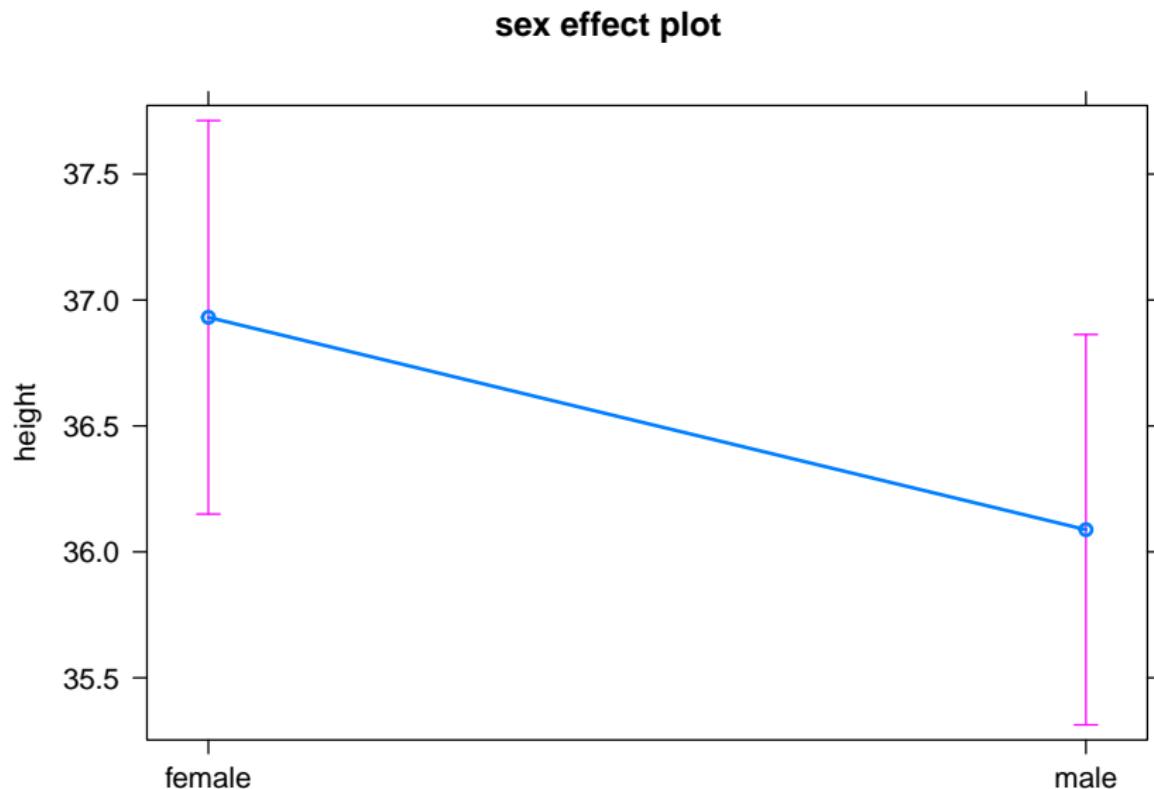
Upper 95 Percent Confidence Limits

sex

female	male
37.71238	36.86300

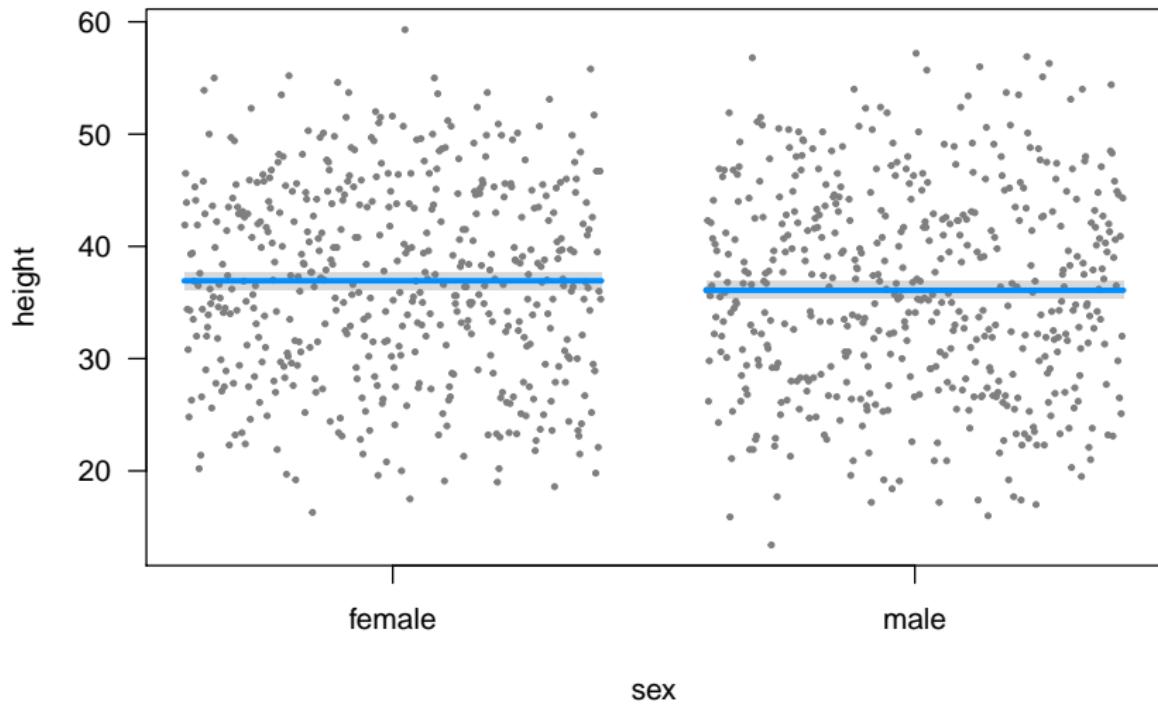
Plot

```
plot(allEffects(m2))
```



Plot (visreg)

```
visreg(m2)
```



Plot model (sjPlot)

```
plot_model(m2, type = "eff")
```

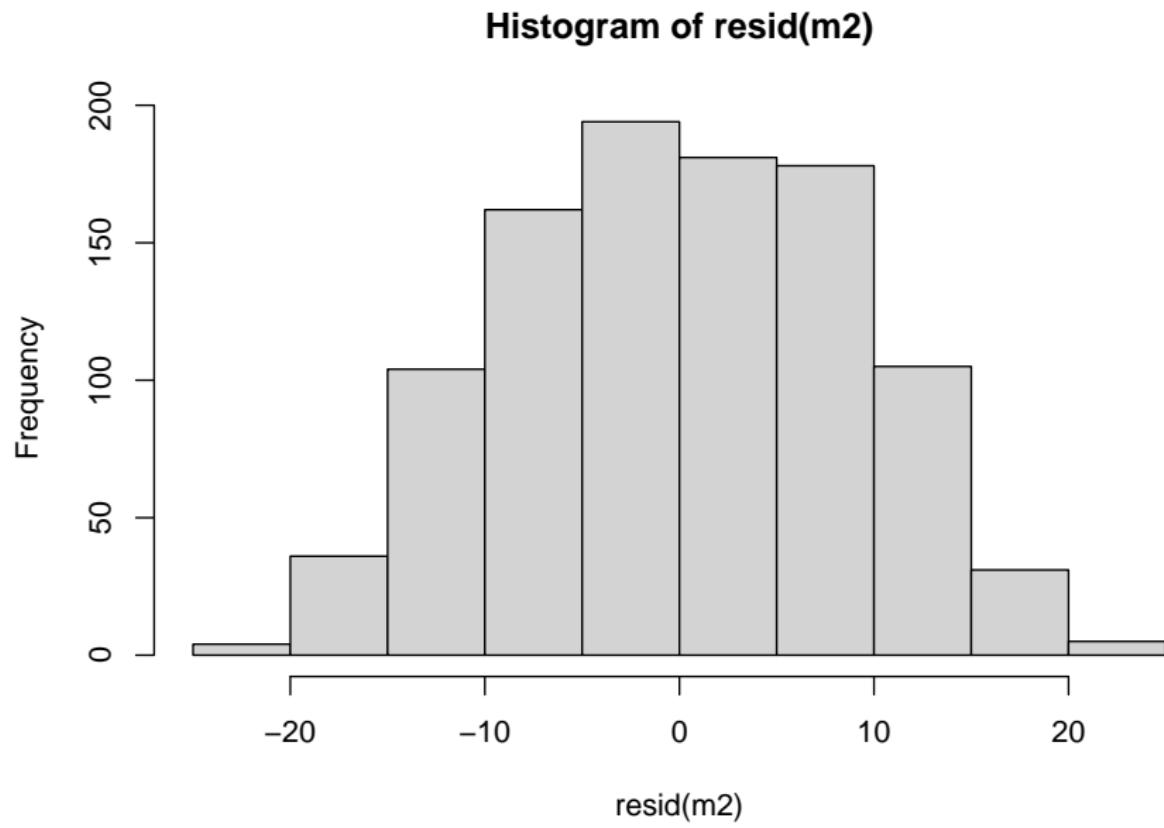
\$sex

Predicted values of height

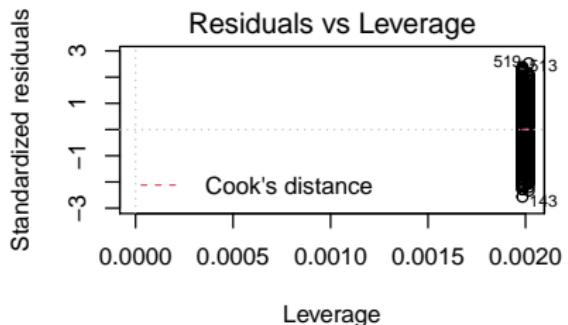
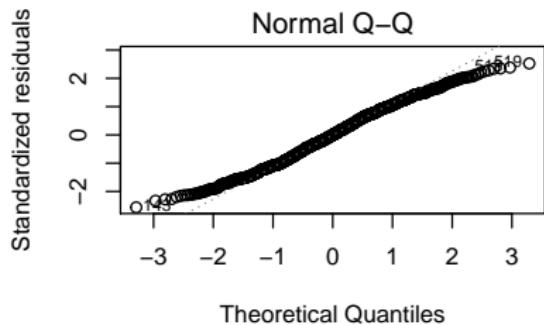
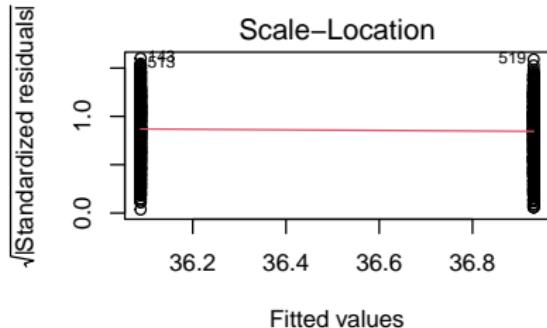
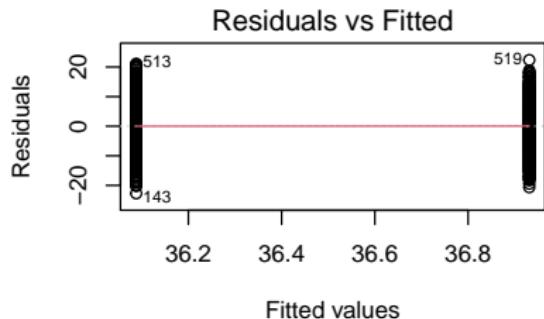


Model checking: residuals

```
hist(resid(m2))
```

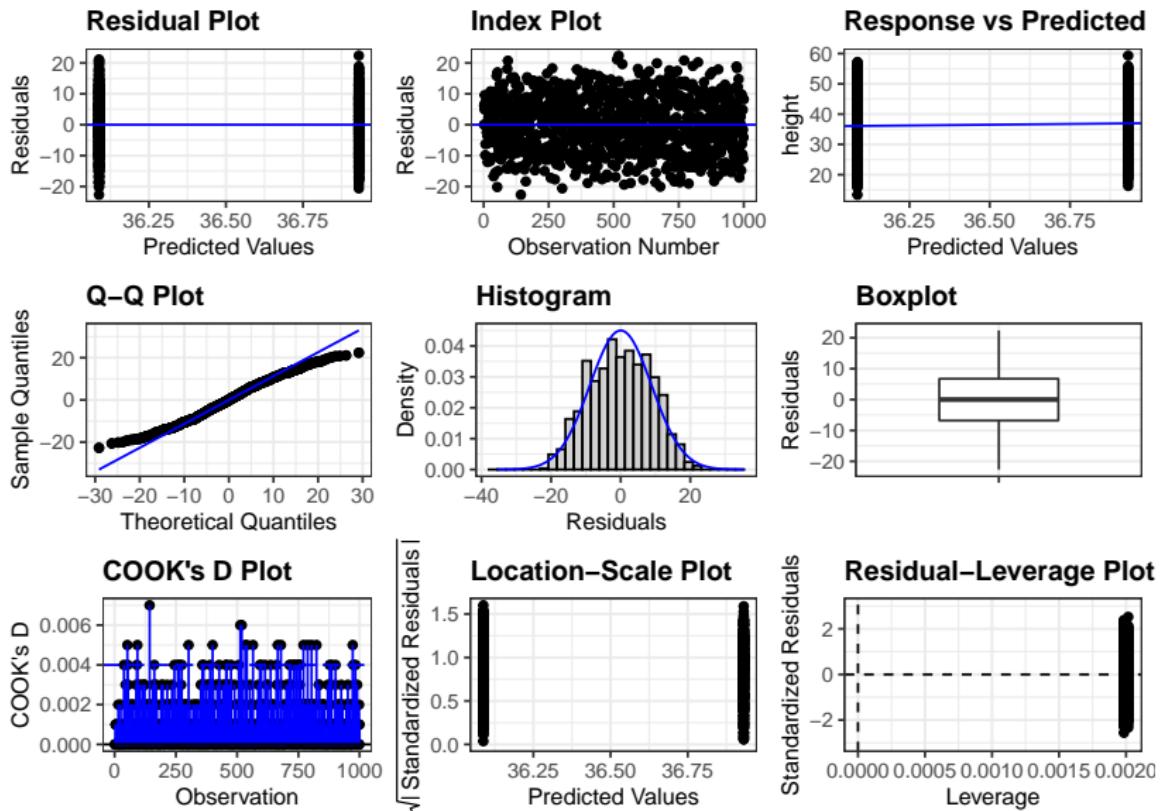


Model checking: residuals



Model checking (ggResidpanel)

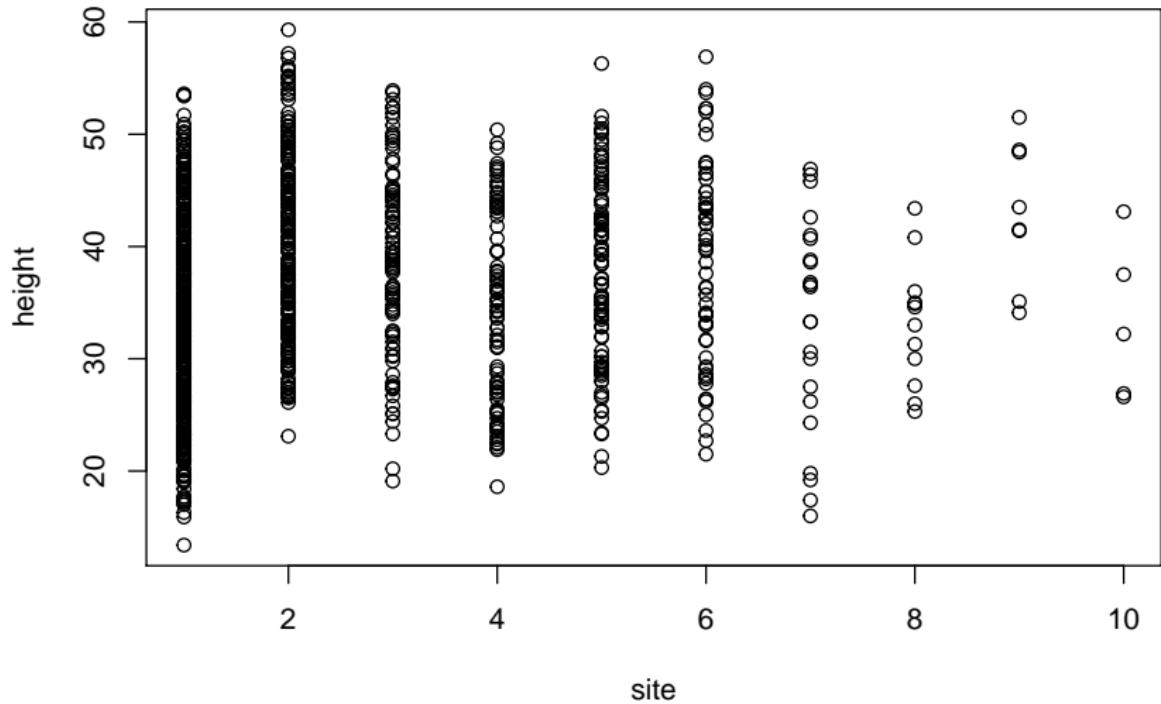
```
ggResidpanel:::resid_panel(m2, plots = "all")
```



Q: Does height differ among field sites?

Plot data first

```
plot(height ~ site, data = trees)
```



Linear model with categorical predictors

```
m3 <- lm(height ~ site, data = trees)
```

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + \dots + \varepsilon_i$$
$$\varepsilon_i \sim N(0, \sigma^2)$$

Model Height ~ site

All right here?

```
m3 <- lm(height ~ site, data = trees)
```

Call:

```
lm(formula = height ~ site, data = trees)
```

Residuals:

Min	1Q	Median	3Q	Max
-22.4498	-6.7049	0.0709	6.7537	23.0640

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	35.4636	0.4730	74.975	< 2e-16 ***
site	0.3862	0.1413	2.733	0.00639 **

Signif. codes:	0 ***	0.001 **	0.01 *	0.05 .
	0.1	'	'	1

Residual standard error: 8.842 on 998 degrees of freedom

Multiple R-squared: 0.007429, Adjusted R-squared: 0.006435

F-statistic: 7.47 on 1 and 998 DF, p-value: 0.006385

site is a factor!

```
trees$site <- as.factor(trees$site)
```

Model Height ~ site

```
Call:
lm(formula = height ~ site, data = trees)

Residuals:
    Min      1Q  Median      3Q     Max
-20.4416 -6.9004  0.0379  6.3051 19.7584

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 33.8416    0.4266  79.329 < 2e-16 ***
site2        6.3411    0.7126   8.899 < 2e-16 ***
site3        4.9991    0.9828   5.086 4.36e-07 ***
site4        0.5329    0.9872   0.540  0.58949    
site5        4.3723    0.9425   4.639 3.97e-06 ***
site6        4.7601    1.1709   4.065 5.18e-05 ***
site7       -0.7416    1.8506  -0.401  0.68871    
site8       -0.6832    2.4753  -0.276  0.78258    
site9        9.1709    3.0165   3.040  0.00243 **  
site10      -0.5816    3.8013  -0.153  0.87843    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 8.446 on 990 degrees of freedom
Multiple R-squared: 0.1016, Adjusted R-squared: 0.09344
F-statistic: 12.44 on 9 and 990 DF, p-value: < 2.2e-16

Presenting model results

```
kable(xtable::xtable(m3), digits = 2)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	33.84	0.43	79.33	0.00
site2	6.34	0.71	8.90	0.00
site3	5.00	0.98	5.09	0.00
site4	0.53	0.99	0.54	0.59
site5	4.37	0.94	4.64	0.00
site6	4.76	1.17	4.07	0.00
site7	-0.74	1.85	-0.40	0.69
site8	-0.68	2.48	-0.28	0.78
site9	9.17	3.02	3.04	0.00
site10	-0.58	3.80	-0.15	0.88

Estimated tree heights for each site

```
summary(allEffects(m3))

model: height ~ site

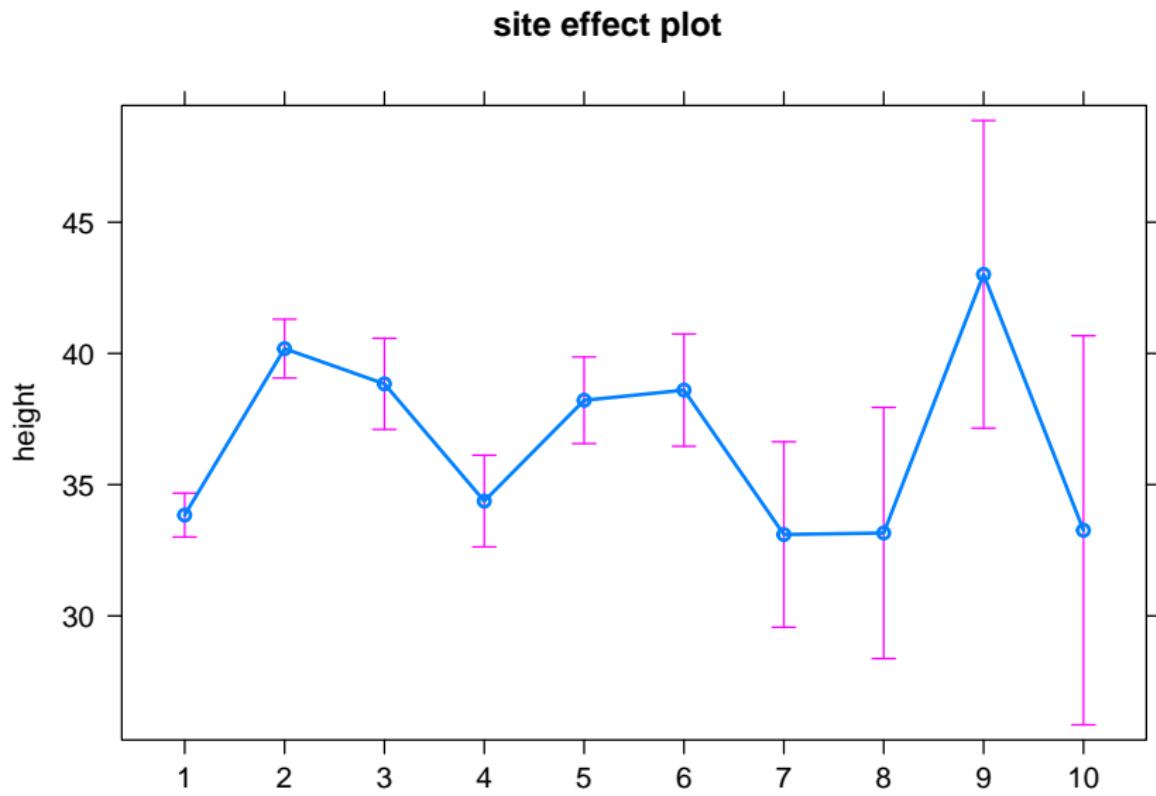
site effect
site
    1      2      3      4      5      6      7      8
33.84158 40.18265 38.84066 34.37444 38.21386 38.60167 33.10000 33.15833
    9      10
43.01250 33.26000

Lower 95 Percent Confidence Limits
site
    1      2      3      4      5      6      7      8
33.00444 39.06264 37.10317 32.62733 36.56463 36.46190 29.56629 28.37367
    9      10
37.15251 25.84764

Upper 95 Percent Confidence Limits
site
    1      2      3      4      5      6      7      8
34.67872 41.30265 40.57814 36.12156 39.86309 40.74143 36.63371 37.94299
    9      10
48.87249 40.67236
```

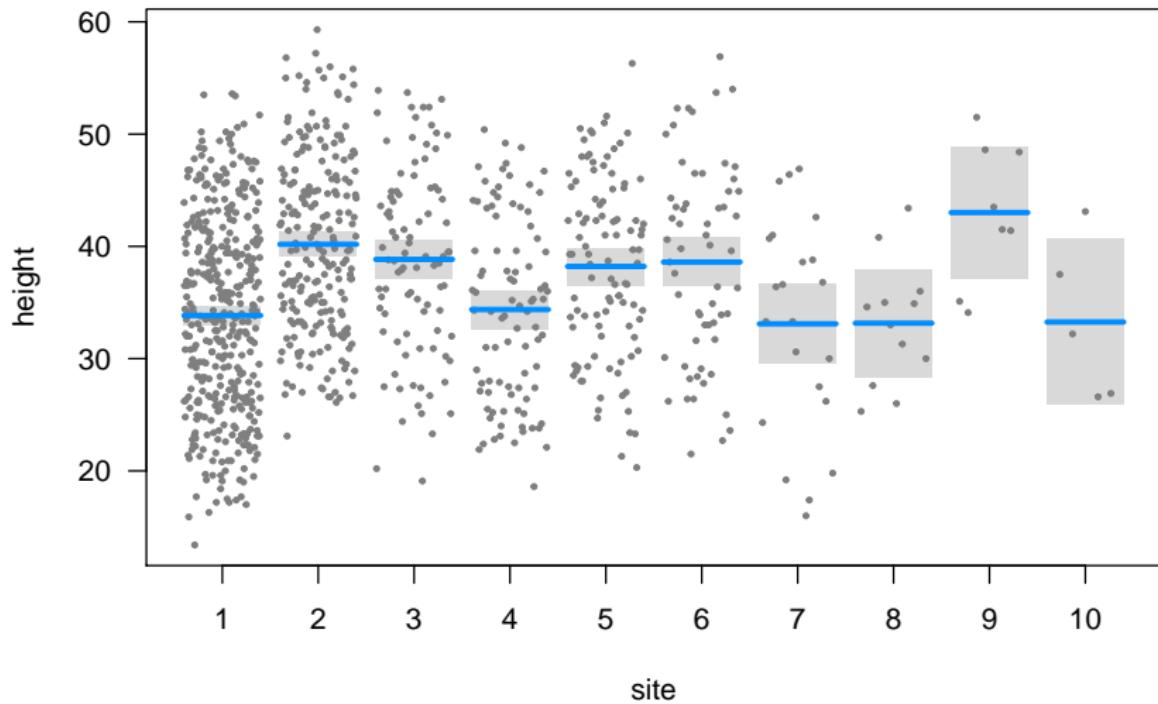
Plot

```
plot(allEffects(m3))
```



Plot (visreg)

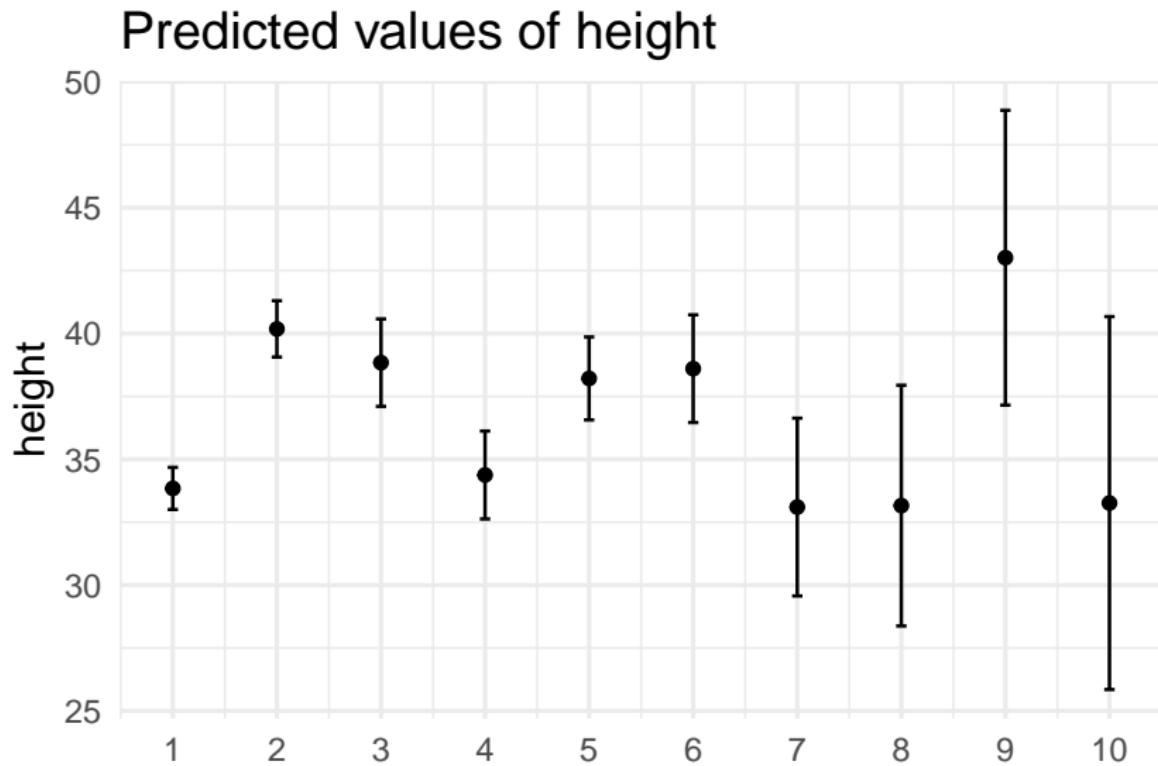
```
visreg(m3)
```



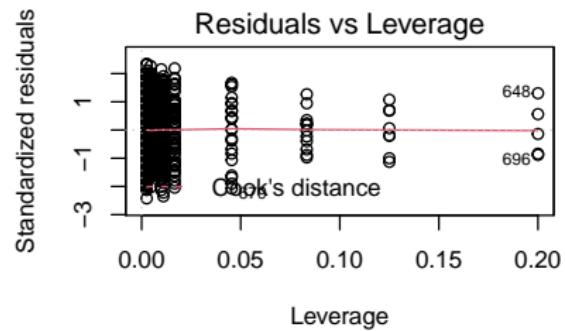
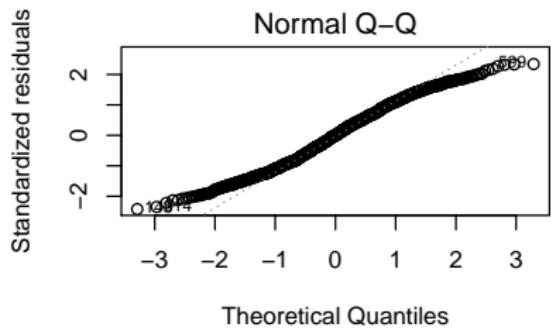
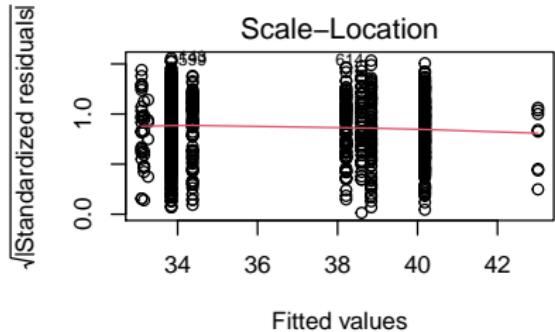
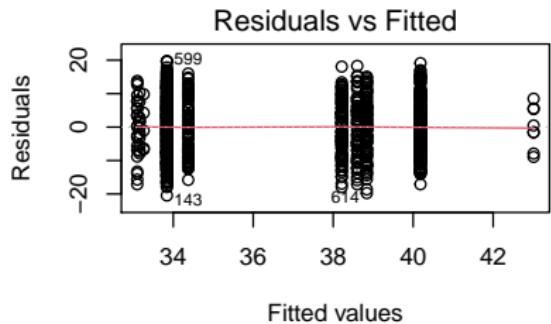
Plot model (sjPlot)

```
plot_model(m3, type = "eff")
```

\$site



Model checking: residuals



Combining continuous and categorical predictors

Predicting tree height based on dbh and site

```
lm(height ~ site + dbh, data = trees)
```

corresponds to

$$y_i = a + b_{site2} + c_{site3} + d_{site4} + e_{site5} + \dots + k \cdot DBH_i + \varepsilon_i$$
$$\varepsilon_i \sim N(0, \sigma^2)$$

Predicting tree height based on dbh and site

Call:

```
lm(formula = height ~ site + dbh, data = trees)
```

Residuals:

Min	1Q	Median	3Q	Max
-10.1130	-1.9885	0.0582	2.0314	11.3320

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	16.699037	0.260565	64.088	< 2e-16 ***
site2	6.504303	0.256730	25.335	< 2e-16 ***
site3	4.357457	0.354181	12.303	< 2e-16 ***
site4	1.934650	0.356102	5.433	6.98e-08 ***
site5	3.637432	0.339688	10.708	< 2e-16 ***
site6	4.204511	0.421906	9.966	< 2e-16 ***
site7	-0.176193	0.666772	-0.264	0.7916
site8	-5.312648	0.893603	-5.945	3.82e-09 ***
site9	5.437049	1.087766	4.998	6.84e-07 ***
site10	2.263338	1.369986	1.652	0.0988 .
dbh	0.617075	0.007574	81.473	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.043 on 989 degrees of freedom

Multiple R-squared: 0.8835, Adjusted R-squared: 0.8823

F-statistic: 750 on 10 and 989 DF, p-value: < 2.2e-16

Presenting model results

```
kable(xtable::xtable(m4), digits = 2)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	16.70	0.26	64.09	0.00
site2	6.50	0.26	25.34	0.00
site3	4.36	0.35	12.30	0.00
site4	1.93	0.36	5.43	0.00
site5	3.64	0.34	10.71	0.00
site6	4.20	0.42	9.97	0.00
site7	-0.18	0.67	-0.26	0.79
site8	-5.31	0.89	-5.95	0.00
site9	5.44	1.09	5.00	0.00
site10	2.26	1.37	1.65	0.10
dbh	0.62	0.01	81.47	0.00

Estimated tree heights for each site

```
summary(allEffects(m4))

model: height ~ site + dbh

site effect
site
  1      2      3      4      5      6      7      8
33.90437 40.40868 38.26183 35.83902 37.54181 38.10889 33.72818 28.59173
  9      10
39.34142 36.16771

Lower 95 Percent Confidence Limits
site
  1      2      3      4      5      6      7      8
33.60276 40.00512 37.63569 35.20858 36.94739 37.33787 32.45495 26.86438
  9      10
37.22831 33.49623

Upper 95 Percent Confidence Limits
site
  1      2      3      4      5      6      7      8
34.20599 40.81223 38.88798 36.46947 38.13622 38.87990 35.00141 30.31907
  9      10
41.45454 38.83919

dbh effect
dbh
  5      20      30      40      50
22.38634 31.64246 37.81321 43.98396 50.15471

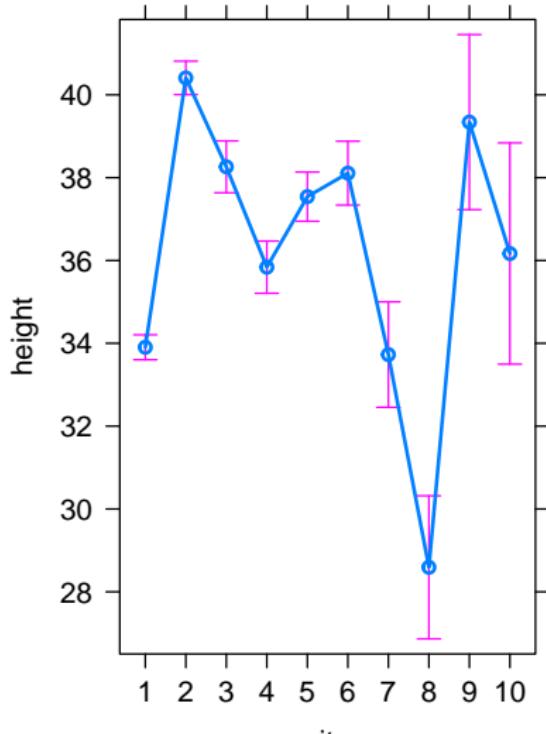
Lower 95 Percent Confidence Limits

```

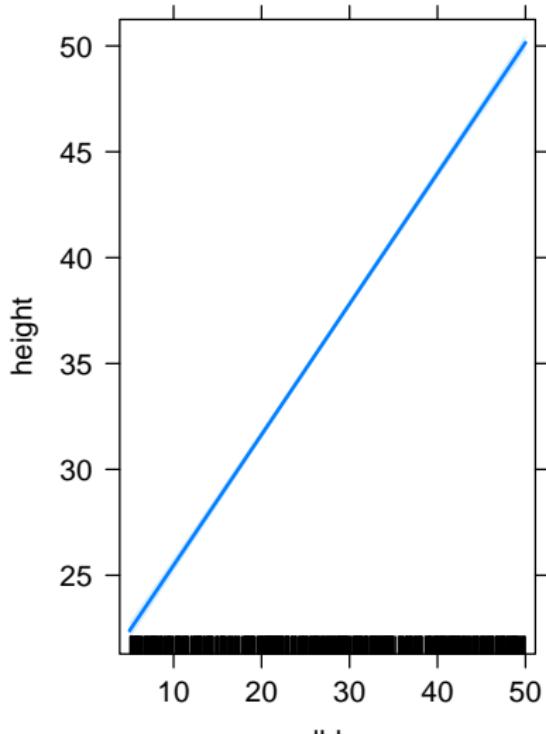
Plot

```
plot(allEffects(m4))
```

site effect plot

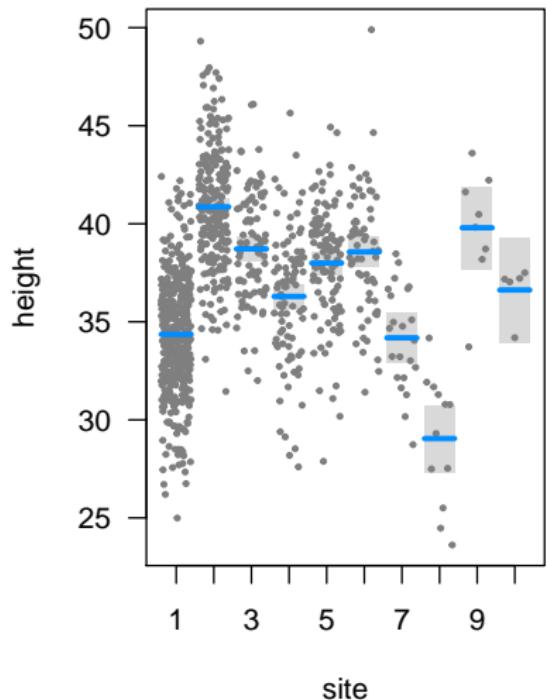


dbh effect plot



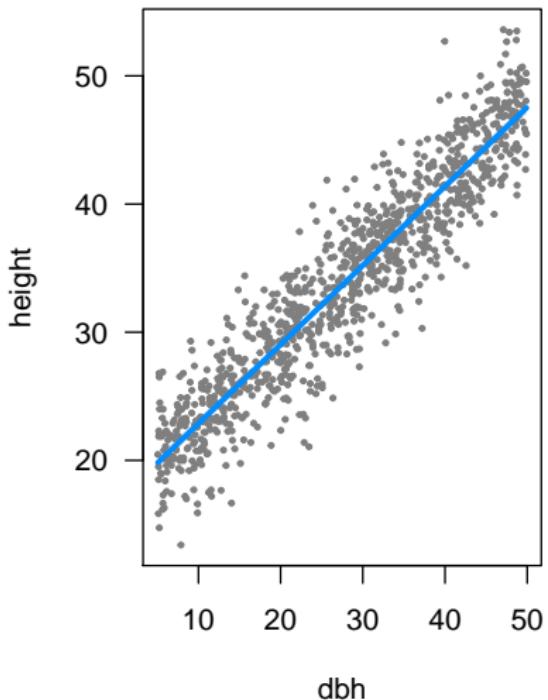
Plot (visreg)

```
visreg(m4)
```



null device

1

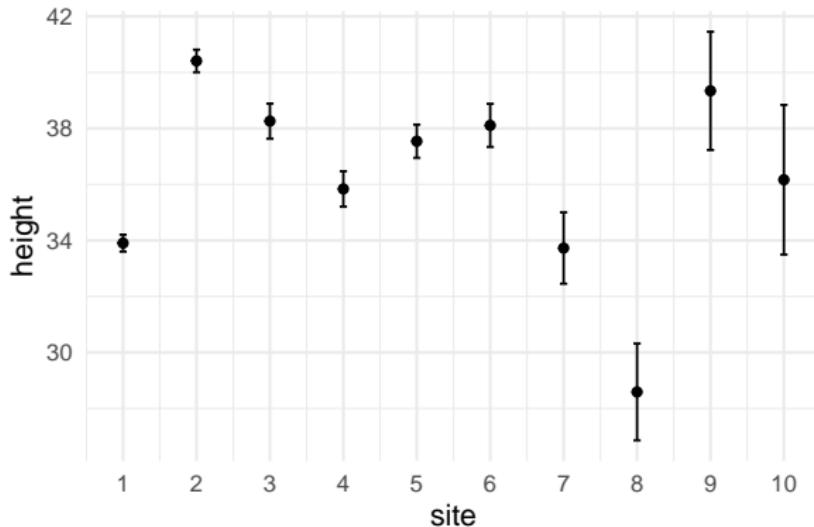


Plot model (sjPlot)

```
plot_model(m4, type = "eff")
```

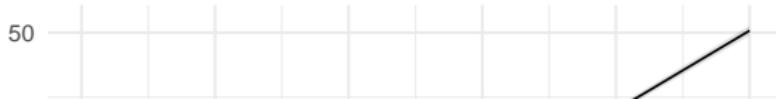
\$site

Predicted values of height



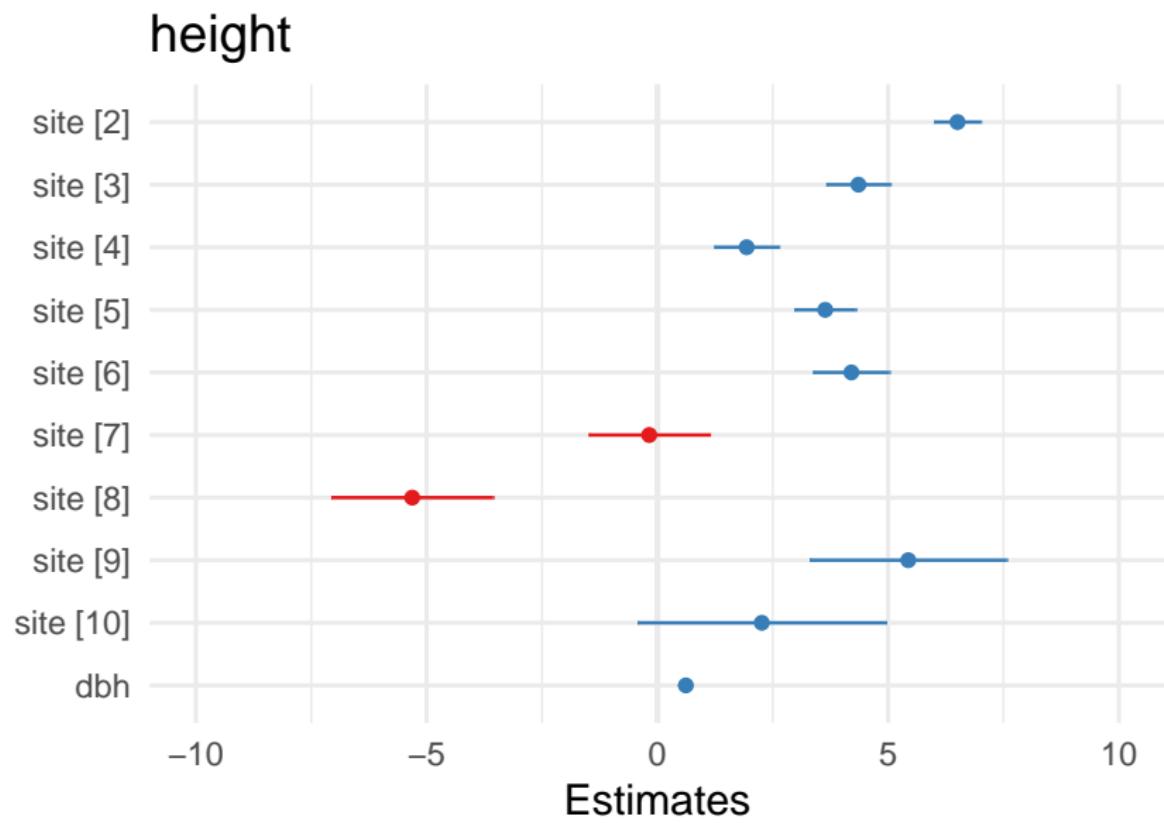
\$dbh

Predicted values of height

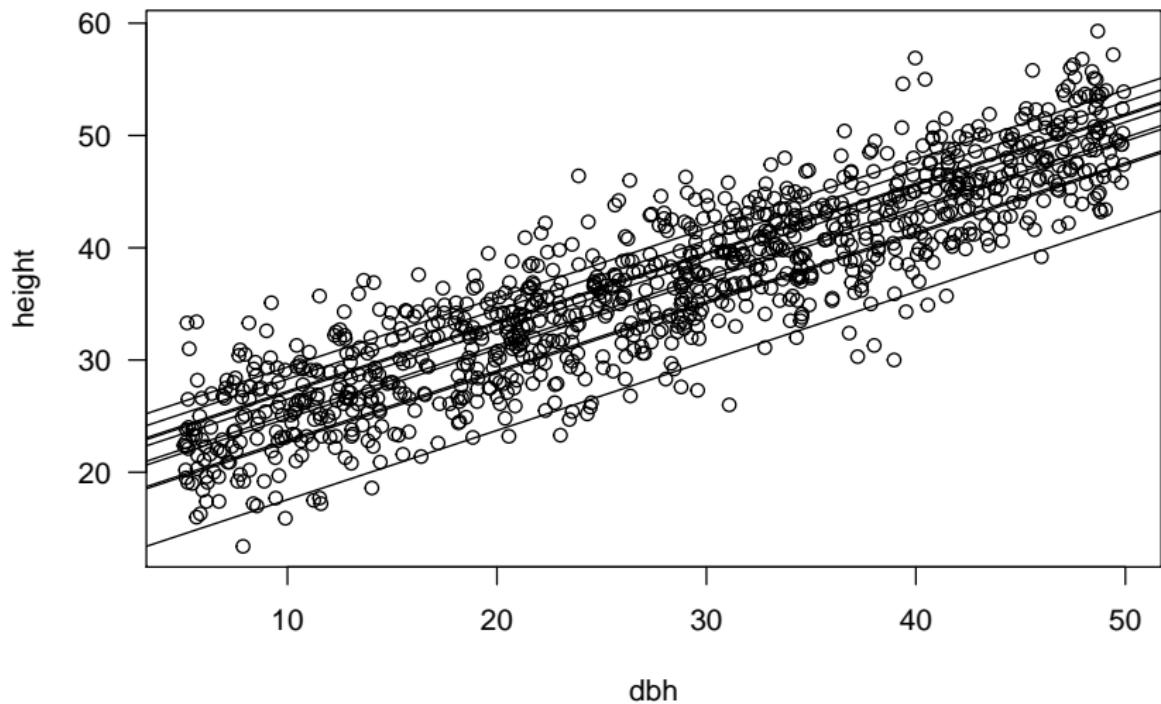


Plot model (sjPlot)

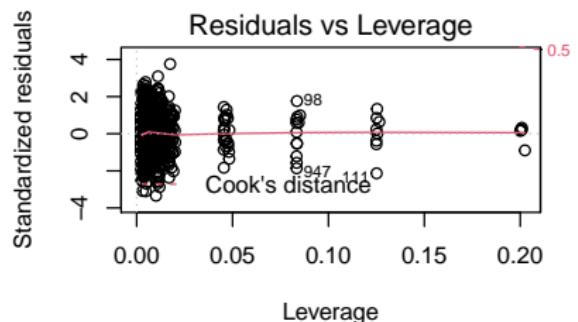
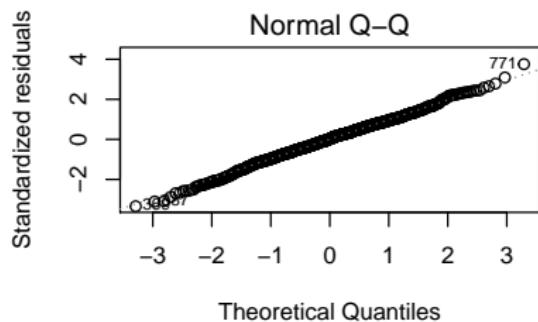
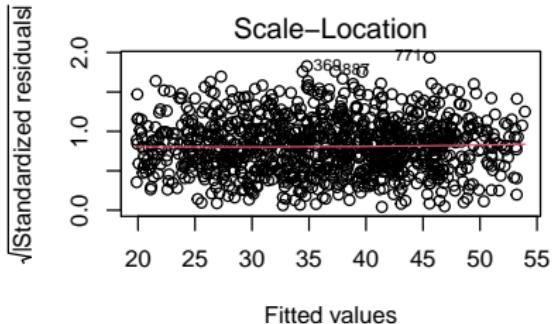
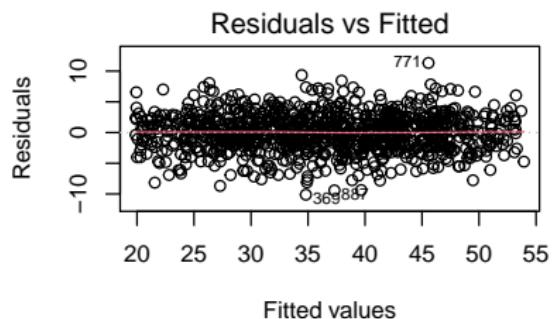
```
plot_model(m4, type = "est")
```



We have fitted model w/ many intercepts and single slope

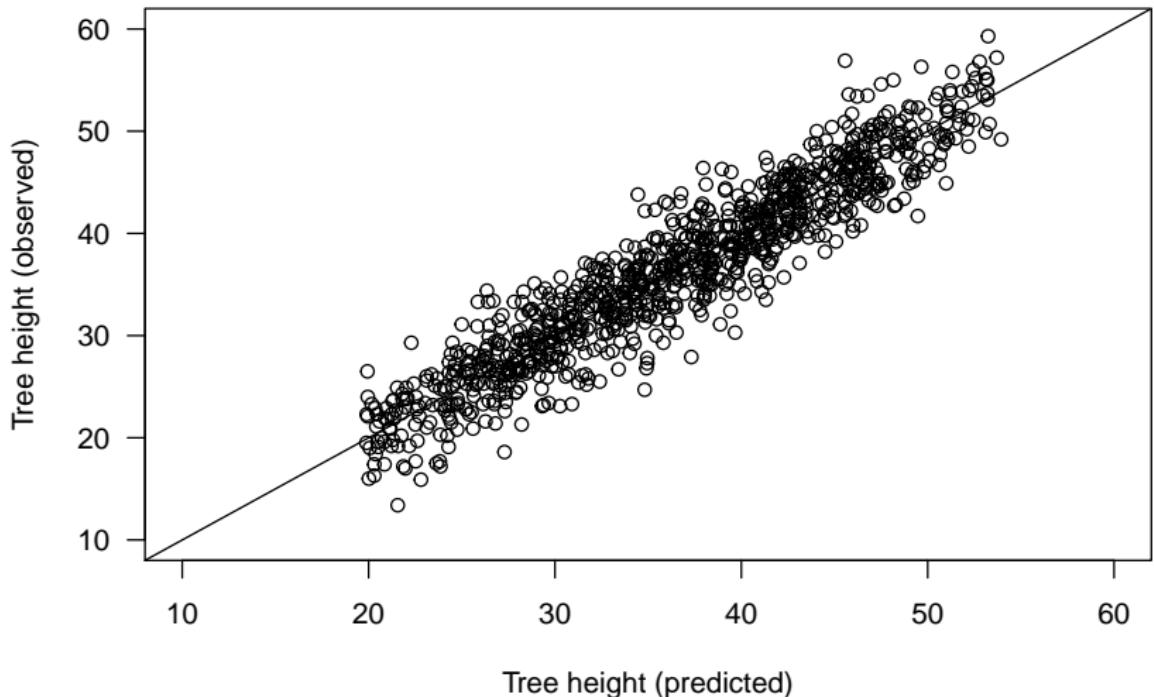


Model checking: residuals



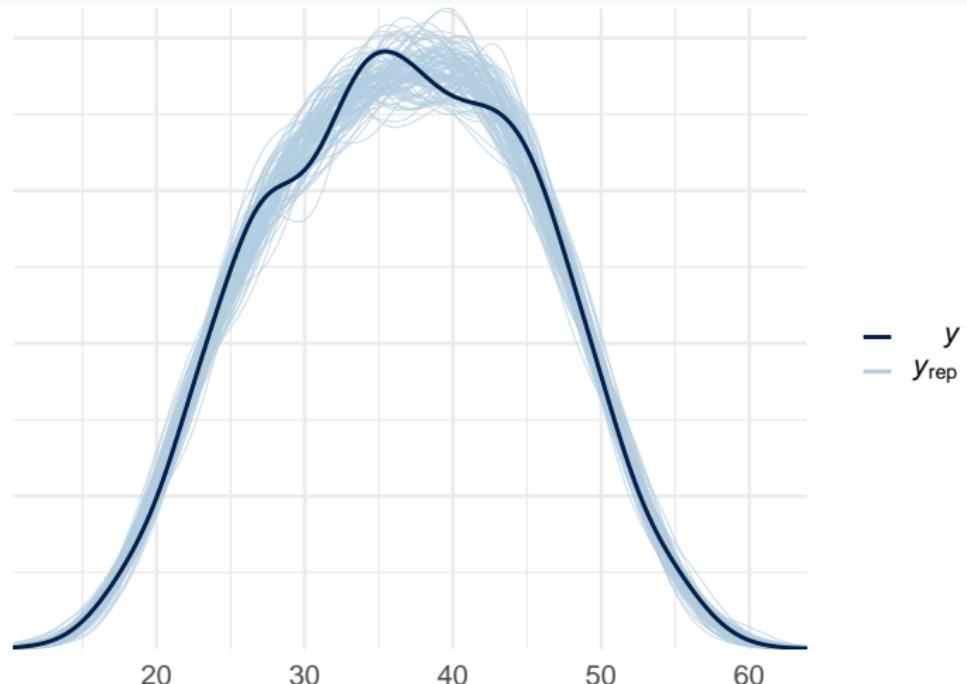
How good is this model? Calibration plot

```
trees$height.pred <- fitted(m4)
plot(trees$height.pred, trees$height, xlab = "Tree height (predicted)", ylab = "Tree height (observed)", main = "Calibration plot")
abline(a = 0, b = 1)
```



Model checking with simulated data

```
library(bayesplot)
sims <- simulate(m4, nsim = 100)
ppc_dens_overlay(trees$height, yrep = t(as.matrix(sims)))
```



Q: Does allometric relationship between DBH
and Height vary among sites?

Model with interactions

```
Call:
lm(formula = height ~ site * dbh, data = trees)

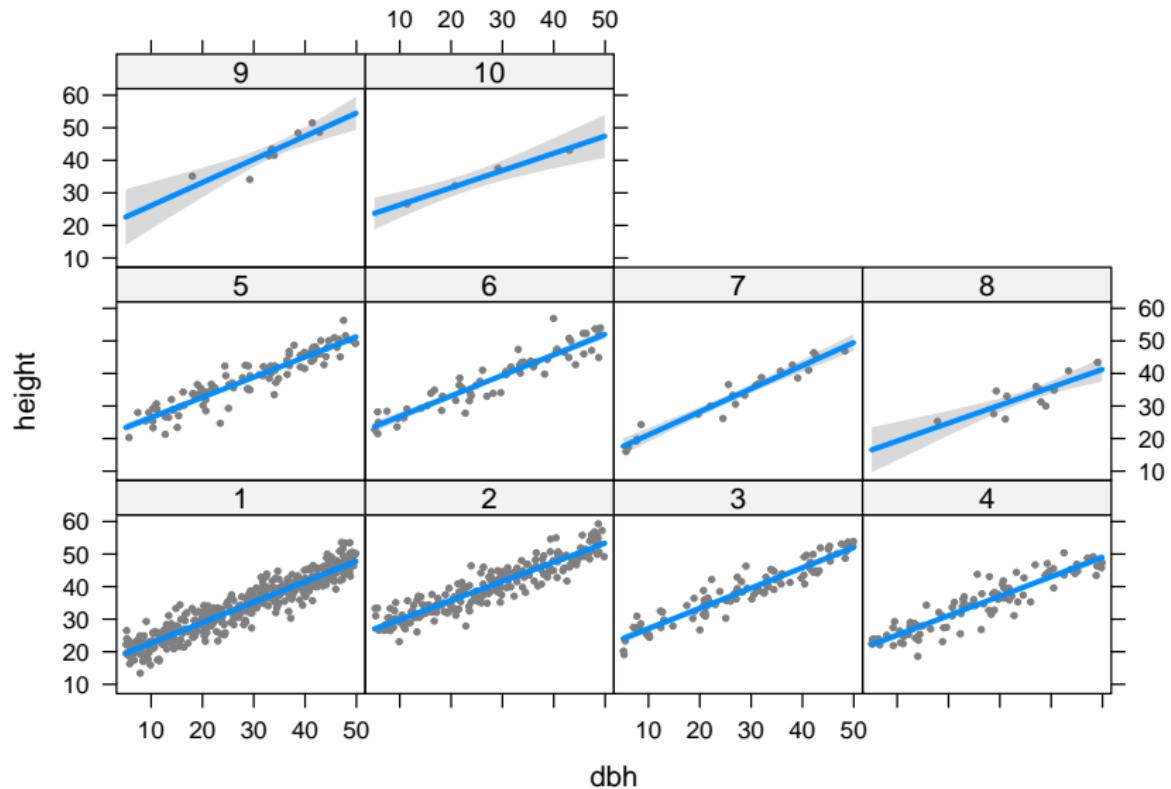
Residuals:
    Min      1Q  Median      3Q     Max 
-10.1017 -1.9839  0.0645  2.0486 11.1789 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 16.359437  0.360054 45.436 < 2e-16 ***
site2        7.684781  0.609657 12.605 < 2e-16 ***
site3        4.518568  0.867008  5.212 2.28e-07 ***
site4        2.769336  0.813259  3.405 0.000688 ***
site5        3.917607  0.870983  4.498 7.68e-06 ***
site6        4.155161  1.009379  4.117 4.17e-05 ***
site7        -2.306799  1.551303 -1.487 0.137334    
site8        -2.616095  4.090671 -0.640 0.522630    
site9        2.621560  5.073794  0.517 0.605492    
site10       4.662340  2.991072  1.559 0.119378    
dbh          0.629299  0.011722 53.685 < 2e-16 ***
site2:dbh   -0.042784  0.020033 -2.136 0.032950 *  
site3:dbh   -0.006031  0.027640 -0.218 0.827312    
site4:dbh   -0.031633  0.028225 -1.121 0.262677    
site5:dbh   -0.010173  0.027887 -0.365 0.715334    
site6:dbh   0.001337  0.032109  0.042 0.966797    
site7:dbh   0.079728  0.052056  1.532 0.125951    
site8:dbh   -0.079027  0.113386 -0.697 0.485984    
site9:dbh   0.081035  0.146649  0.553 0.580679    
site10:dbh  -0.101107  0.114520 -0.883 0.377522    
...
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.041 on 980 degrees of freedom
Multiple R-squared:  0.8847,    Adjusted R-squared:  0.8825 
F-statistic: 395.7 on 19 and 980 DF,  p-value: < 2.2e-16
```

Does slope vary among forests?

```
visreg(m5, xvar = "dbh", by = "site")
```



Extra exercises

- ▶ [paperplanes](#): How does flight distance differ with age, gender or paper type?

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- ▶ [mammal sleep](#): Are sleep patterns related to diet?

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- ▶ [racing pigeons](#): is speed related to sex?