Linear models

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

Example dataset: forest trees

- Download this dataset (or the entire zip file)

```r
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
```

Example dataset: forest trees

- Download this dataset (or the entire zip file)
- Import:

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

```
  site   dbh height    sex dead
1    4 29.68   36.1   male    0
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6    1 10.82   26.2   male    0
```

Questions

- What is the relationship between DBH and height?

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- Do taller trees have bigger trunks?

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- Do taller trees have bigger trunks?

- Can we predict height from DBH? How well?

Always plot your data first!

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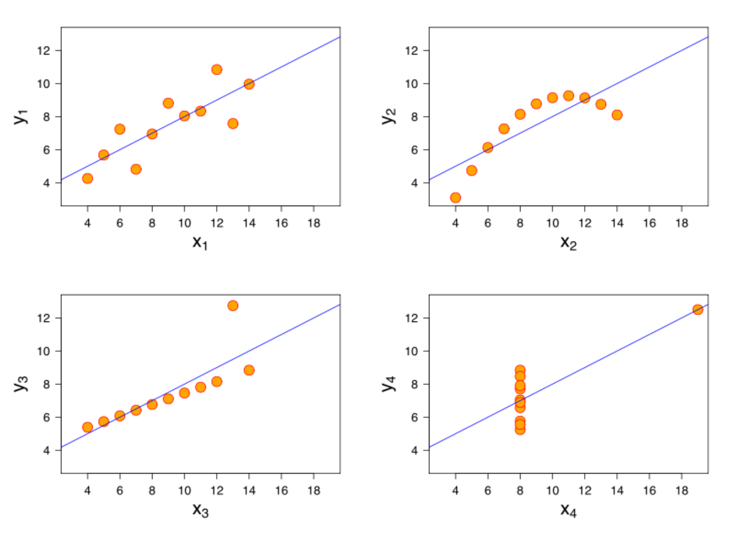
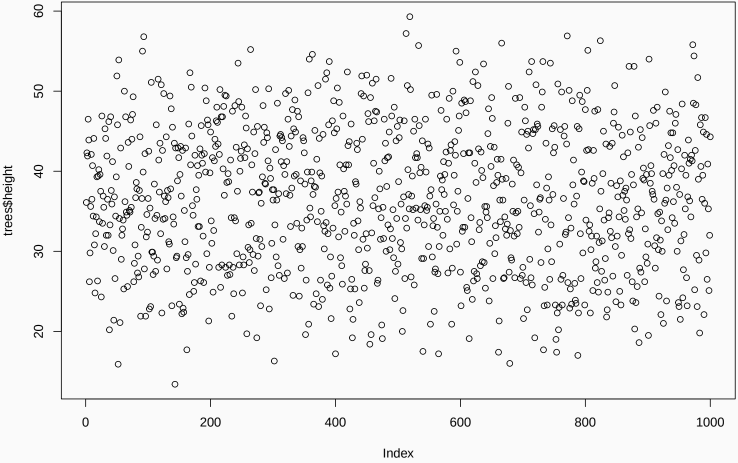


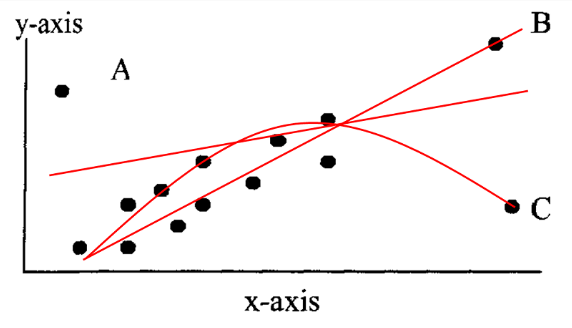
Exploratory Data Analysis (EDA)

Outliers

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



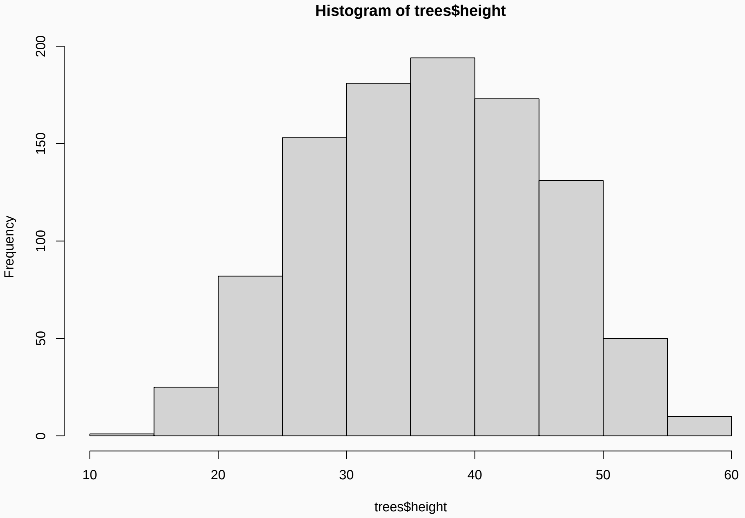
Outliers impact on regression



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

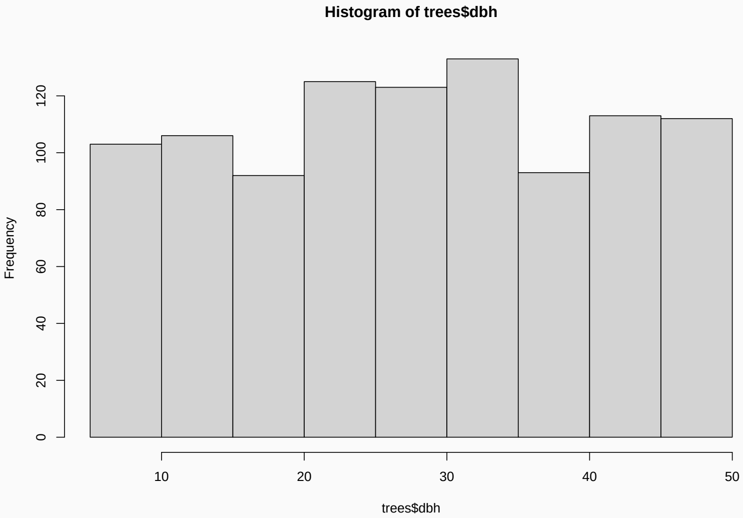
Histogram of response variable

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



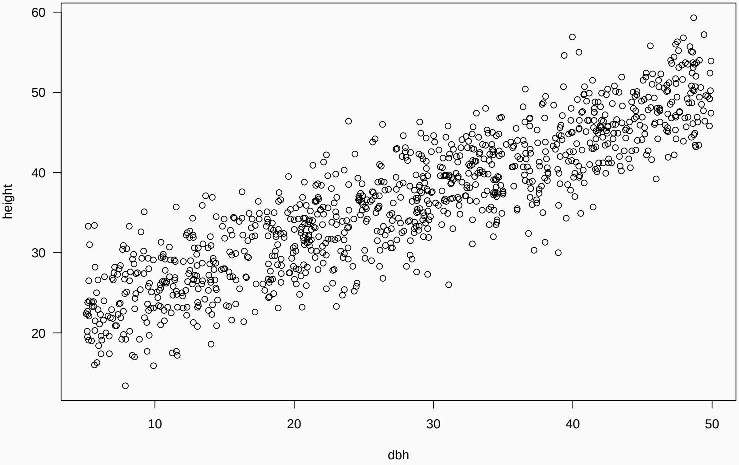
Histogram of predictor variable

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



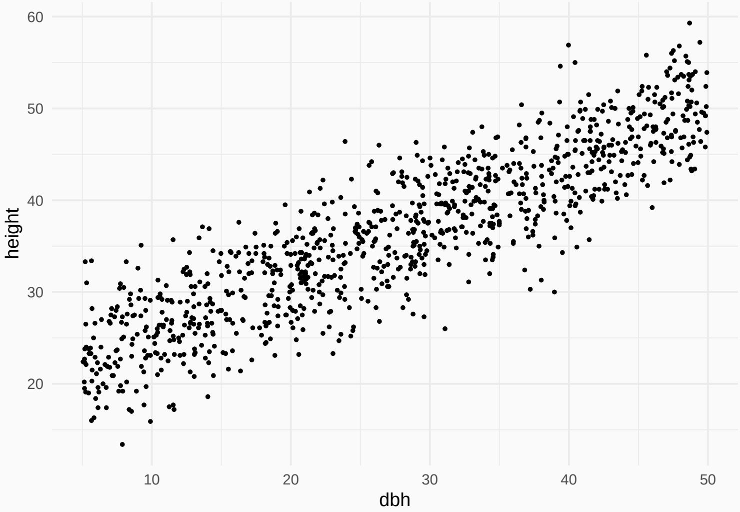
Scatterplot

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



Scatterplot

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



Model fitting

Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

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

which corresponds to

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

Package `equatiomatic` returns model structure

```r
library(”equatiomatic”)
m1 <- lm(height ~ dbh, data = trees)
equatiomatic::extract_eq(m1)
```

$$\operatorname{height} = \alpha + \beta_{1}(\operatorname{dbh}) + \epsilon \tag{1}$$

```r
equatiomatic::extract_eq(m1, use_coefs = TRUE)
```

$$\widehat{\operatorname{height}} = 19.34 + 0.62(\operatorname{dbh}) \tag{2}$$

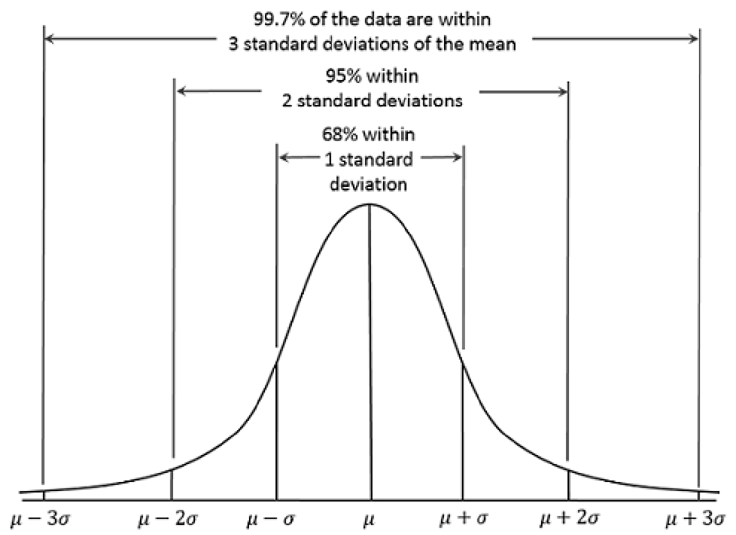
Model interpretation

What does this mean?

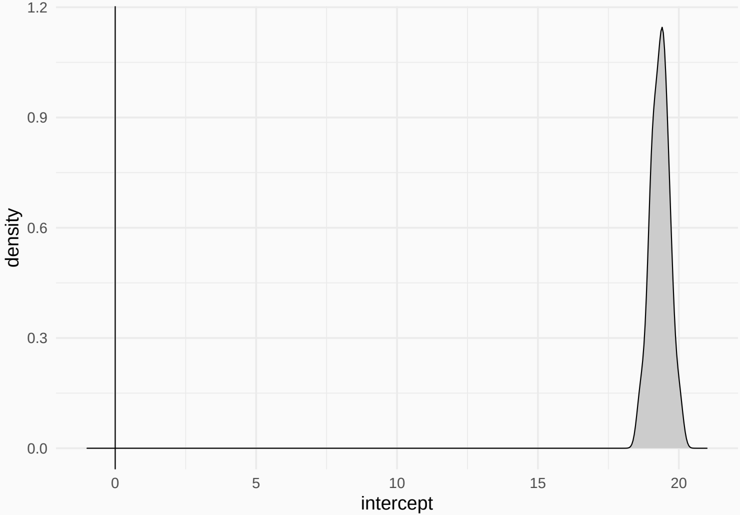
```r
summary(m1)
```

```
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
```

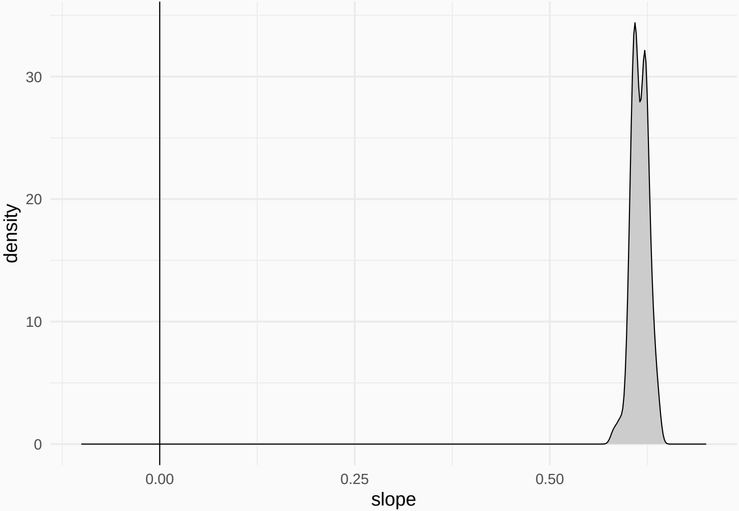
Remember that in a Normal distribution



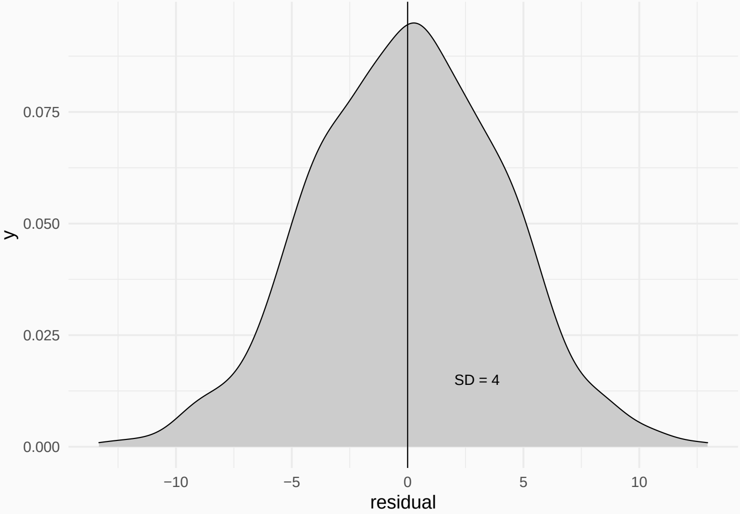
Estimated distribution of the intercept parameter



Estimated distribution of the slope parameter



Distribution of residuals



Degrees of freedom

DF = n - p

n = sample size

p = number of estimated parameters

R-squared

Proportion of ‘explained’ variance

$$R^2 = 1 - \frac{ResidualVariation}{TotalVariation}$$

Adjusted R-squared

Accounts for model complexity (number of parameters)

$R^2_{adj} = 1 - \left(1 - R^2\right)\frac{n-1}{n-p-1}$

Quiz

https://pollev.com/franciscorod726

Retrieving model coefficients

```r
coef(m1)
```

```
(Intercept)         dbh 
 19.3391968   0.6157036 
```

Confidence intervals for parameters

```
confint(m1)
```

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

Tidy up model coefficients with broom

```r
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
```

```r
glance(m1)
```

```
# A tibble: 1 x 12
  r.squ~1 adj.r~2 sigma stati~3 p.value    df logLik   AIC   BIC devia~4 df.re~5
    <dbl>   <dbl> <dbl>   <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>   <dbl>   <int>
1   0.787   0.787  4.09   3695.       0     1 -2827. 5660. 5675.  16716.     998
# ... with 1 more variable: nobs <int>, and abbreviated variable names
#   1: r.squared, 2: adj.r.squared, 3: statistic, 4: deviance, 5: df.residual
```

https://broom.tidymodels.org/

Retrieving model parameters with `parameters` package

```r
library("parameters")
parameters(m1)
```

```
Parameter   | Coefficient |   SE |         95% CI | t(998) |      p
-------------------------------------------------------------------
(Intercept) |       19.34 | 0.31 | [18.73, 19.95] |  62.26 | < .001
dbh         |        0.62 | 0.01 | [ 0.60,  0.64] |  60.79 | < .001
```

https://easystats.github.io/parameters/

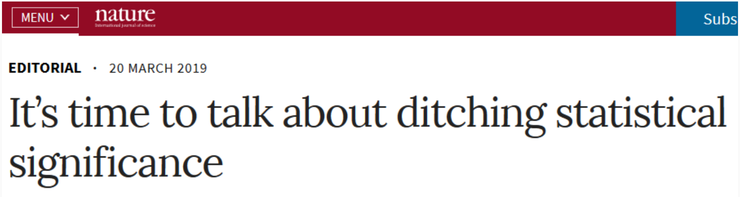
Understanding the fitted effects with `effects` package

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

```
 model: height ~ dbh

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

 Lower 95 Percent Confidence Limits
dbh
       5       20       30       40       50 
21.89682 31.35487 37.55287 43.61733 49.61669 

 Upper 95 Percent Confidence Limits
dbh
       5       20       30       40       50 
22.93861 31.95167 38.06774 44.31735 50.63207 
```

Communicating results

Avoid dichotomania of statistical significance

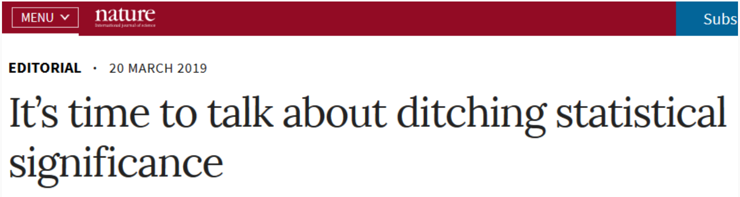


EDITORIAL · 20 MARCH 2019

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**”

Avoid dichotomania of statistical significance



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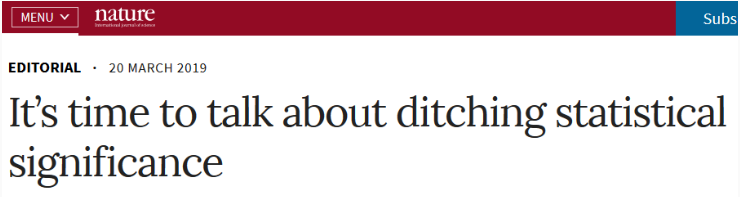
It's time to talk about ditching statistical significance

- "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 relationship** between DBH and Height **($p<0.05$)**.

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

Models that describe themselves

```
library(”report”)
report(m1)
```

We fitted a linear model (estimated using OLS) to predict height with dbh (formula: height ~ dbh). The model explains a statistically significant and substantial proportion of variance (R2 = 0.79, F(1, 998) = 3695.40, p < .001, adj. R2 = 0.79). The model's intercept, corresponding to dbh = 0, is at 19.34 (95% CI [18.73, 19.95], t(998) = 62.26, p < .001). Within this model:

- The effect of dbh is statistically significant and positive (beta = 0.62, 95% CI [0.60, 0.64], t(998) = 60.79, p < .001; Std. beta = 0.89, 95% CI [0.86, 0.92])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

https://easystats.github.io/report/

Generating table with model results: `xtable`

```r
library(”xtable”)
xtable(m1, digits = 2)
```

% latex table generated in R 4.2.1 by xtable 1.8-4 package % Sat Sep 17 21:12:52 2022

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	19.34	0.31	62.26	0.00
dbh	0.62	0.01	60.79	0.00

Generating table with model results: `texreg`

```
library("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 1: Statistical models

Generating table with model results: modelsummary

```r
library(”modelsummary”)
modelsummary(m1, output = ”markdown”)
```

	Model 1
(Intercept)	19.339
	(0.311)
dbh	0.616
	(0.010)
Num.Obs.	1000
R2	0.787
R2 Adj.	0.787
AIC	5660.3
BIC	5675.0
Log.Lik.	-2827.125
F	3695.395
RMSE	4.09

Generating table with model results: gtsummary

```
library(”gtsummary”)
tbl_regression(m1, intercept = TRUE)
```

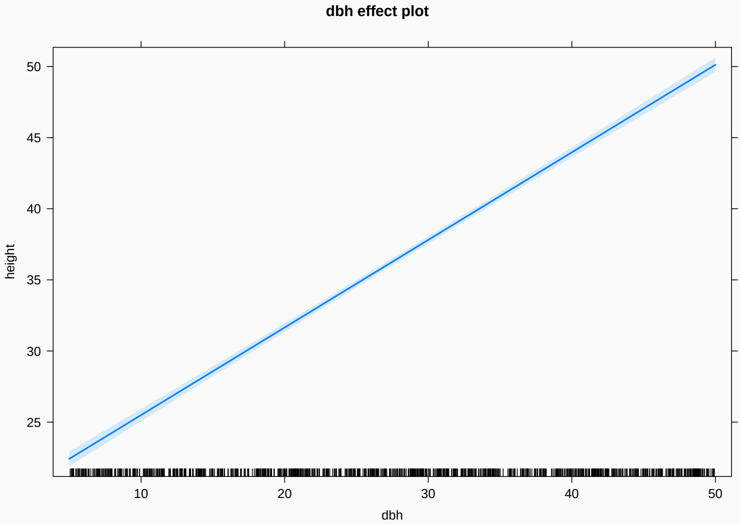
Characteristic	**Beta**	**95% CI**	**p-value**
(Intercept)	19	19, 20	<0.001
dbh	0.62	0.60, 0.64	<0.001

https://www.danieldsjoberg.com/gtsummary

Visualising fitted model

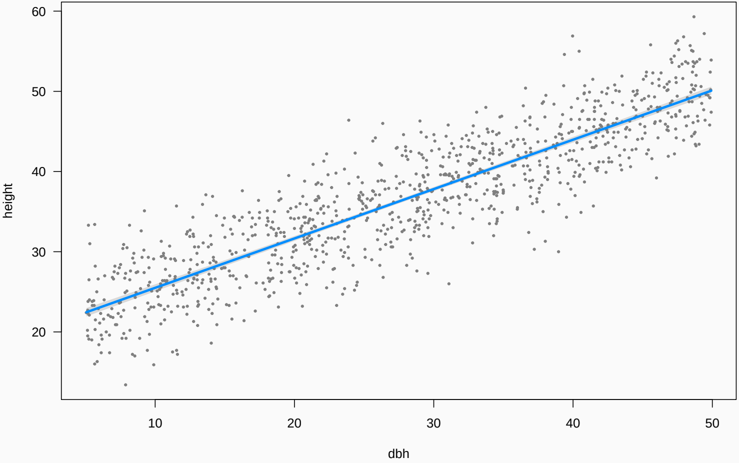
Plot model: `effects` package

```
library("effects")
plot(allEffects(m1))
```



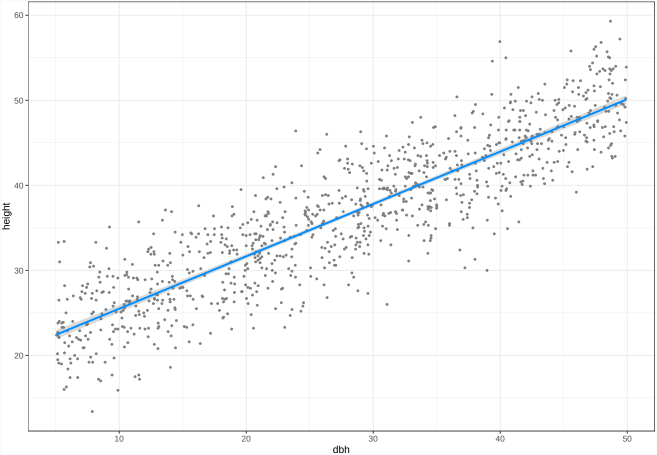
Plot model: visreg

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



visreg can use ggplot2 too

```r
visreg(m1, gg = TRUE) + theme_bw()
```

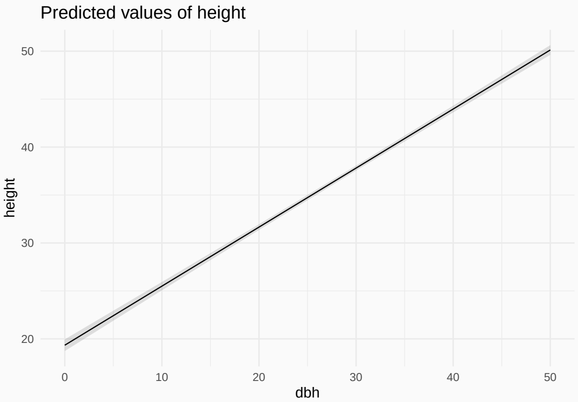


https://pbreheny.github.io/visreg

Plot model: sjPlot

```r
library("sjPlot")
plot_model(m1, type = "eff")
```

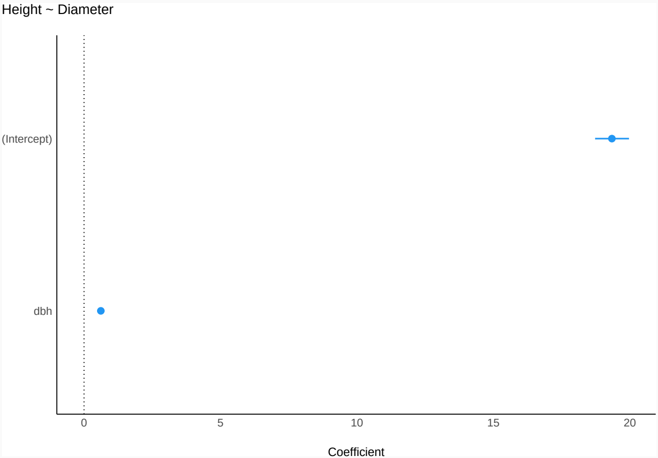
```
$dbh
```



https://strengejacke.github.io/sjPlot

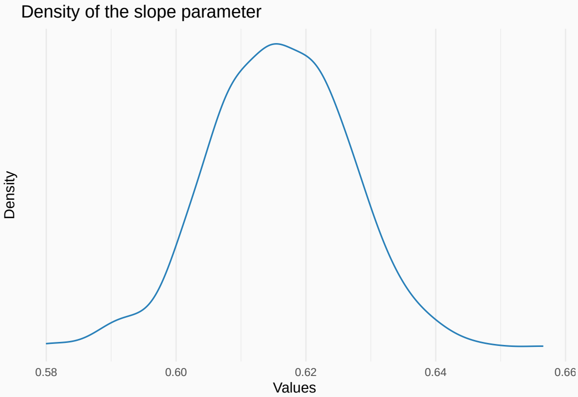
Plot model: see

```
library("see")
plot(parameters(m1), show_intercept = TRUE) +
  labs(title = "Height ~ Diameter")   # ggplot2
```



Plot parameters’ estimated distribution: see

```
plot(simulate_parameters(m1)) +
  labs(title = ”Density of the slope parameter”)
```



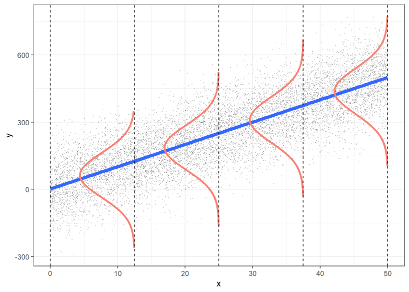
Model checking

Linear model assumptions

- **Linearity** (transformations, GAM…)

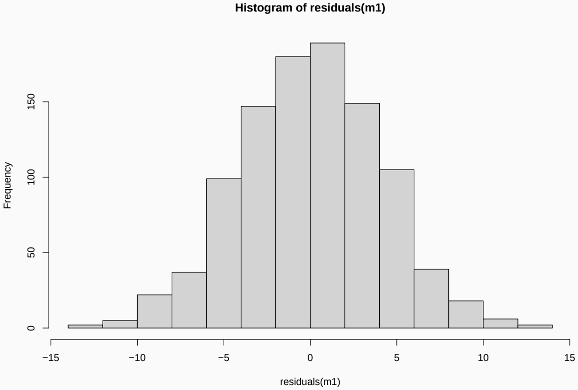
- **Residuals**:
  - Independent
  - Equal variance
  - Normal

- Negligible **measurement error** in predictors



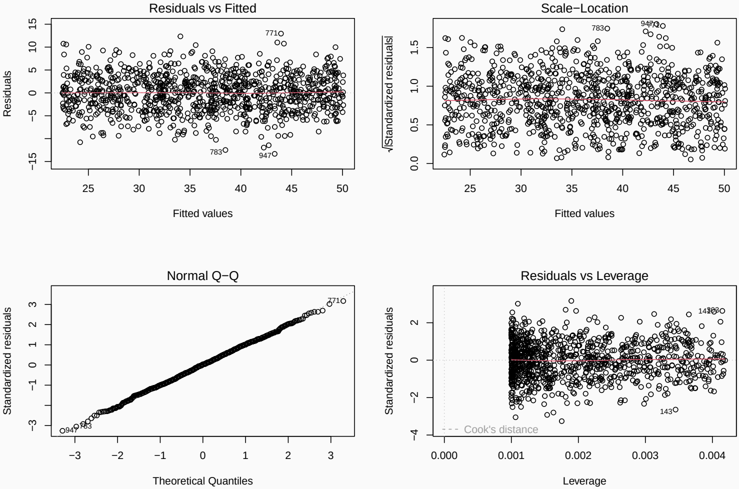
Are residuals normal?

```
hist(residuals(m1))
```



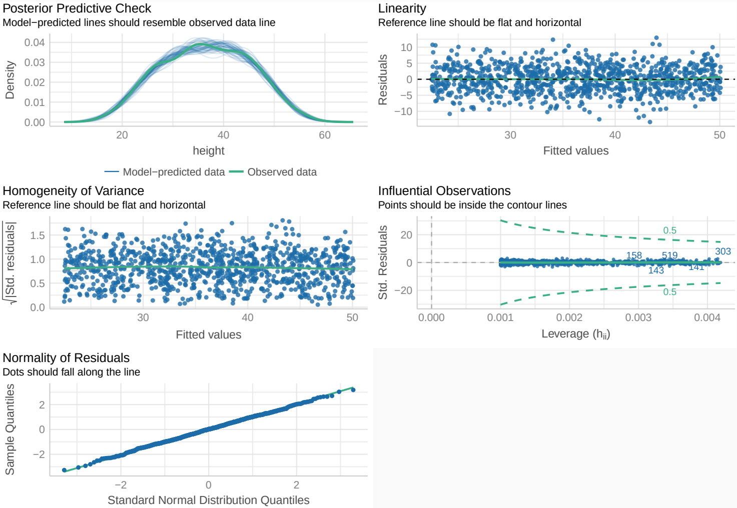
SD = 4.09

Model checking: `plot(model)`



Model checking with `performance` package

```
library("performance")
check_model(m1)
```



A dashboard to explore the full model

```
library(”easystats”)
model_dashboard(m1)
```

Using model for prediction

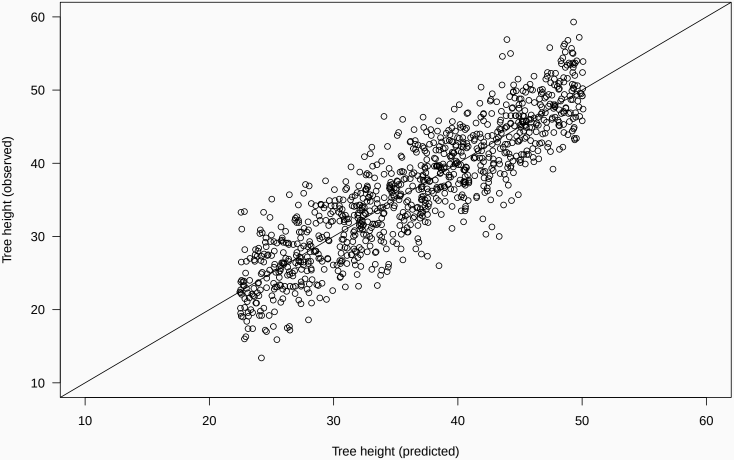
How good is the model in predicting tree height?

`fitted` gives expected value for each observation

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

```
  site   dbh height    sex dead height.pred      resid
1    4 29.68   36.1   male    0    37.61328 -1.5132797
2    5 33.29   42.3   male    0    39.83597  2.4640303
3    2 28.03   41.9 female    0    36.59737  5.3026313
4    5 39.86   46.5 female    0    43.88114  2.6188577
5    1 47.94   43.9 female    0    48.85603 -4.9560274
6    1 10.82   26.2   male    0    26.00111  0.1988903
```

Calibration plot: Observed vs Predicted values



Making predictions for new data

Q: Expected tree height if DBH = 39 cm?

```r
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
```

Confidence vs Prediction Intervals

Q: Expected tree height if DBH = 39 cm?

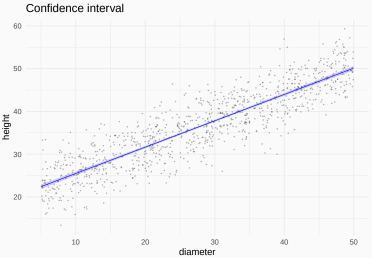
```
predict(m1, new.dbh, interval = ”confidence”)
```

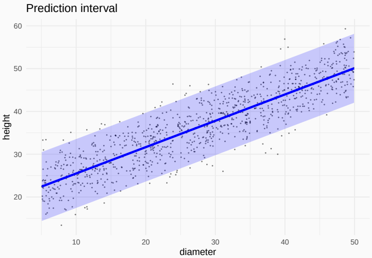
```
       fit      lwr      upr
1 43.35164 43.01499 43.68828
```

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

```
       fit      lwr      upr
1 43.35164 35.31344 51.38983
```

Confidence vs Prediction Intervals





Workflow

- Visualise data

Workflow

- Visualise data
- Understand fitted model (`summary`, `allEffects`...)

Workflow

- Visualise data

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

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

Workflow

- Visualise data
- Understand fitted model (`summary`, `allEffects`...)
- Visualise model (`plot(allEffects)`, `visreg`, `see`, `plot_model`...)
- Check model (`plot`, `check_model`, calibration plot...)

Workflow

- Visualise data

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

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

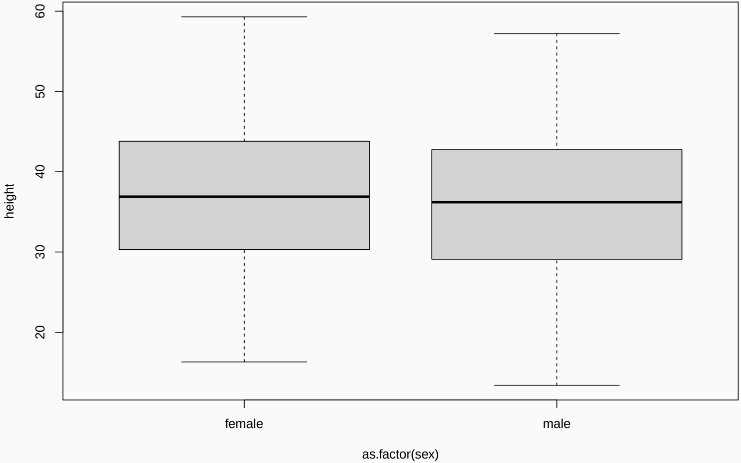
- Check model (`plot`, `check_model`, calibration plot...)

- Predict (`fitted`, `predict`)

Categorical predictors (factors)

Q: Does tree height vary with sex?

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



Model height ~ sex

```r
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

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

corresponds to

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

Model height ~ sex

```r
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
```

Quiz

https://pollev.com/franciscorod726

Let’s read the model report…

```r
report(m2)
```

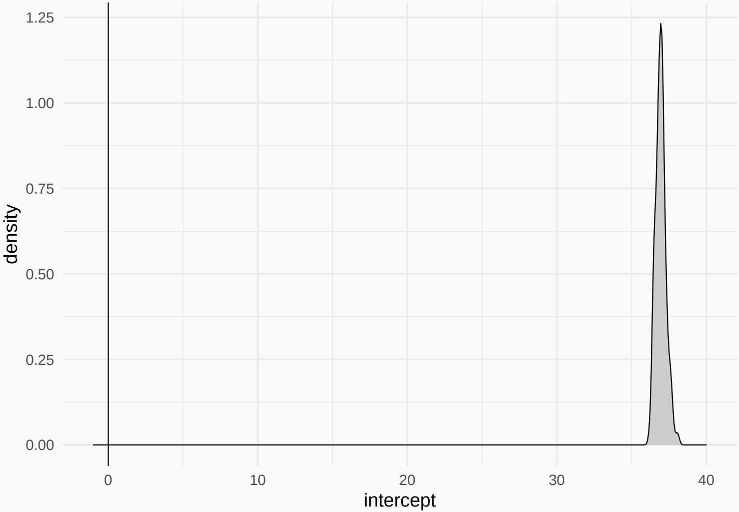
We fitted a linear model (estimated using OLS) to predict height with sex (formula: height ~ sex). The model explains a statistically not significant and very weak proportion of variance (R2 = 2.26e-03, F(1, 998) = 2.26, p = 0.133, adj. R2 = 1.26e-03). The model’s intercept, corresponding to sex = female, is at 36.93 (95% CI [36.15, 37.71], t(998) = 92.78, p < .001). Within this model:

- The effect of sex [male] is statistically non-significant and negative (beta = -0.84, 95% CI [-1.94, 0.26], t(998) = -1.50, p = 0.133; Std. beta = -0.10, 95% CI [-0.22, 0.03])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

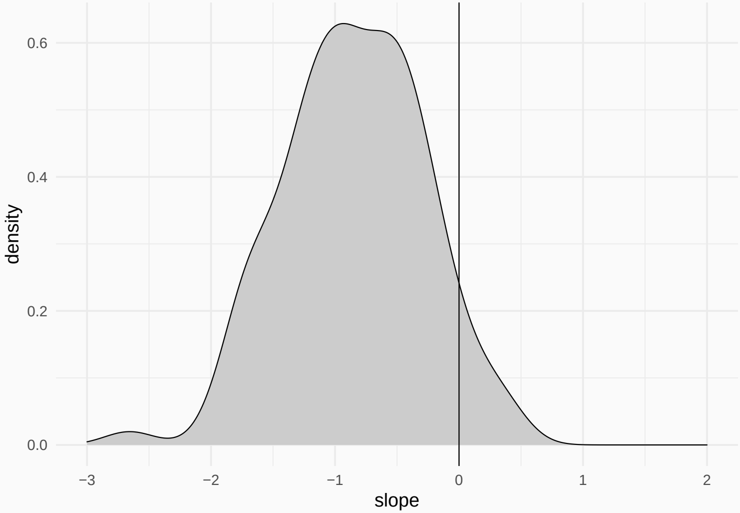
Estimated distribution of the intercept parameter

Intercept = Height of females



Estimated distribution of the *beta* parameter

beta = height difference of males vs females



Analysing differences among factor levels

```r
library("modelbased")
estimate_means(m2)
```

```
Estimated Marginal Means

sex    |  Mean |   SE |          95% CI
----------------------------------------
male   | 36.09 | 0.39 | [35.31, 36.86]
female | 36.93 | 0.40 | [36.15, 37.71]

Marginal means estimated at sex
```

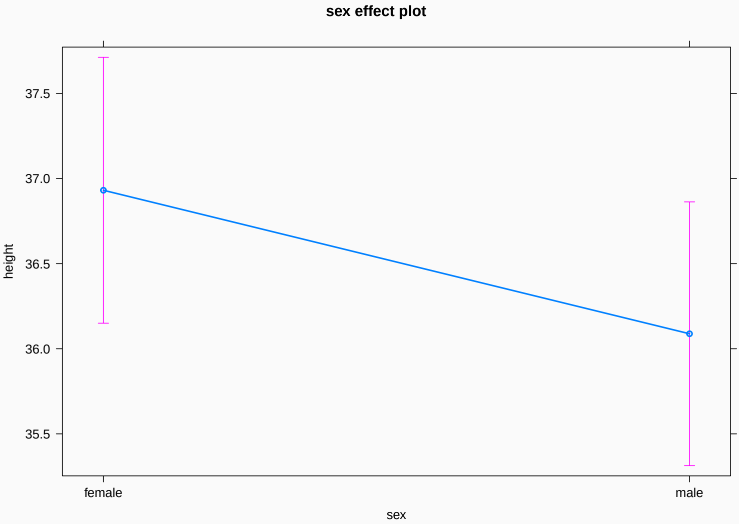
Analysing differences among factor levels

```
estimate_contrasts(m2)
```

```
Marginal Contrasts Analysis

Level1 | Level2 | Difference |         95% CI |   SE | t(998) |     p
--------------------------------------------------------------------
male   | female |      -0.84 | [-1.94, 0.26] | 0.56 |  -1.50 | 0.133

Marginal contrasts estimated at sex
p-value adjustment method: Holm (1979)
```

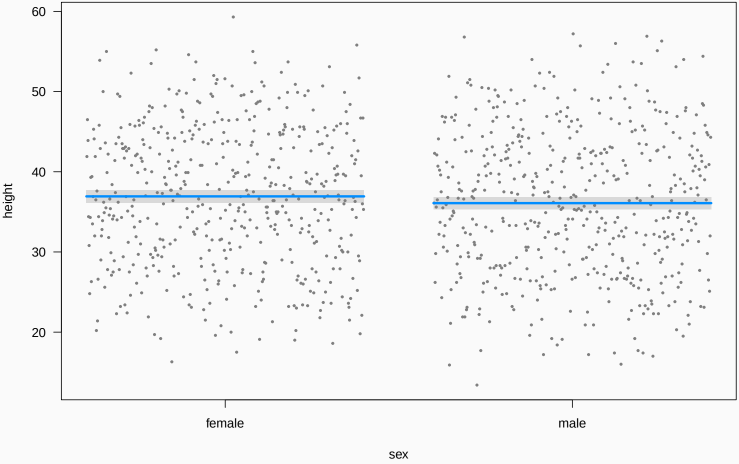
Plot

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



Plot (visreg)

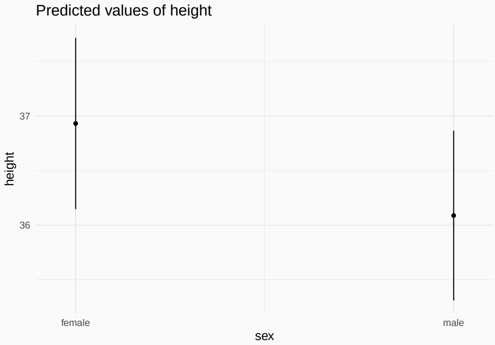
```r
visreg(m2)
```



Plot model (sjPlot)

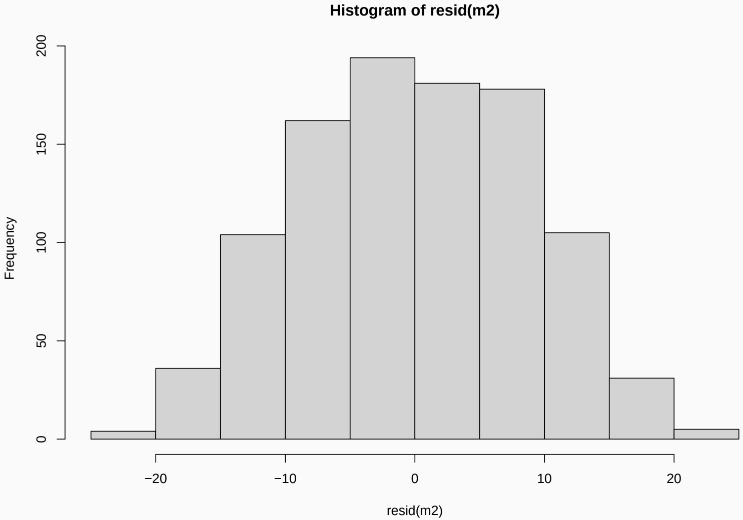
```
plot_model(m2, type = "eff")
```

```
$sex
```

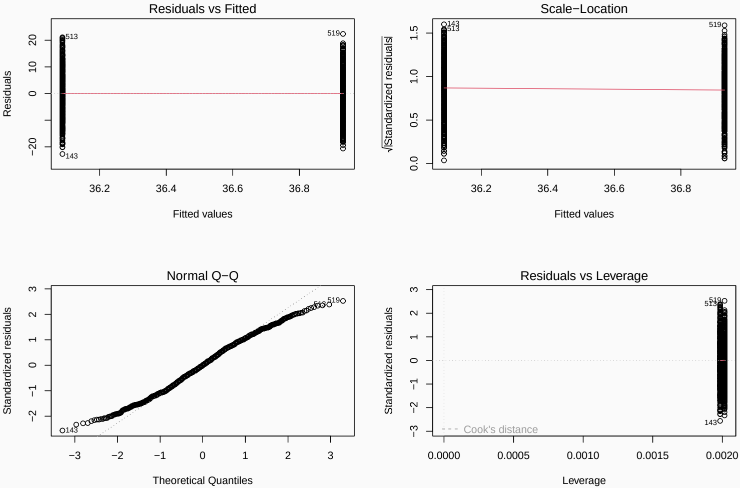


Model checking: residuals

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

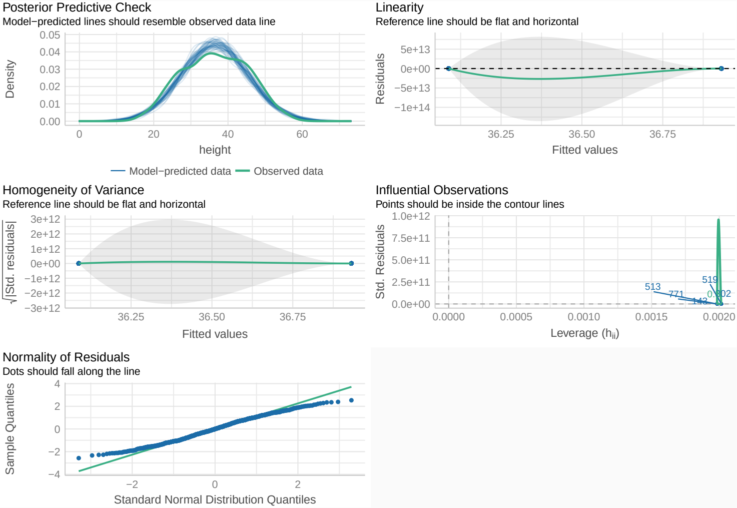


Model checking: residuals



Model checking

```
library("performance")
check_model(m2)
```



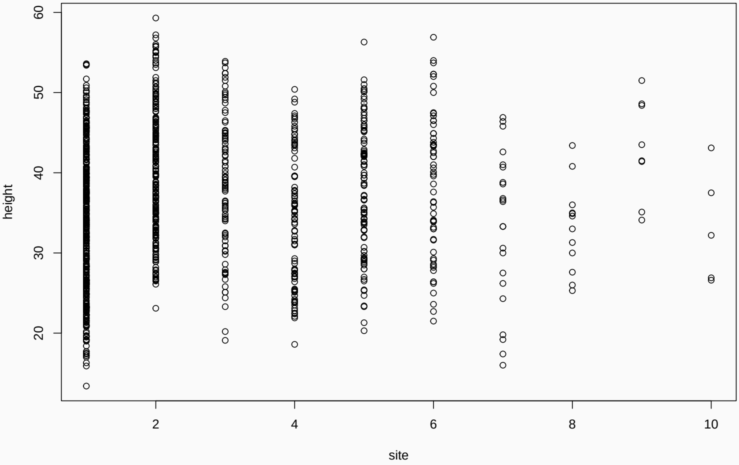
Model dashboard

```
model_dashboard(m2)
```

Q: Does height differ among field sites?

Plot data first

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



Linear model with categorical predictors

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

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

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
```

Let's check model structure with `equatiomatic`

```
extract_eq(m3)
```

$$\text{height} = \alpha + \beta_{1}(\text{site}) + \epsilon \tag{3}$$

site is a factor!

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

Let’s check model structure with `equatiomatic`

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

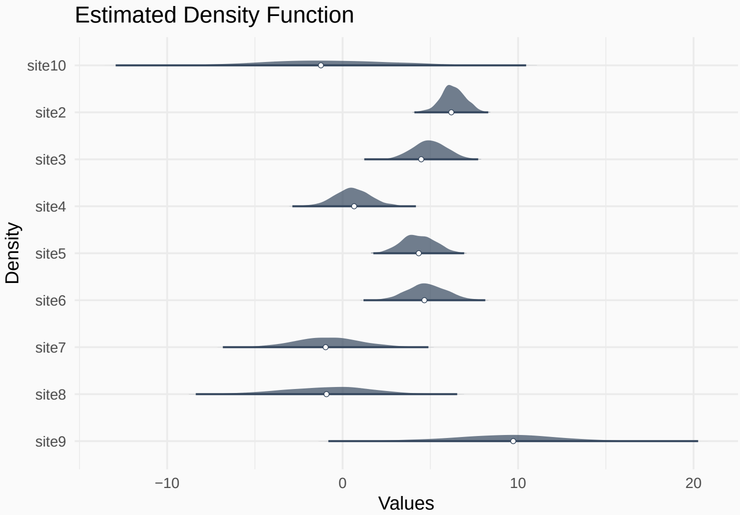
$$\text{height} = \alpha + \beta_{1}(\text{site}_{2}) + \beta_{2}(\text{site}_{3}) + \beta_{3}(\text{site}_{4}) + \beta_{4}(\text{site}_{5}) + \beta_{5}(\text{site}_{6}) + \beta_{6}(\text{site}_{7}) + \beta_{7}(\text{s} \tag{4}$$

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
```

Estimated parameter distributions

```
plot(simulate_parameters(m3), stack = FALSE)
```



Analysing differences among factor levels

```
library("modelbased")
estimate_means(m3)
```

```
Estimated Marginal Means

site |  Mean |   SE |         95% CI
------------------------------------
1    | 33.84 | 0.43 | [33.00, 34.68]
2    | 40.18 | 0.57 | [39.06, 41.30]
3    | 38.84 | 0.89 | [37.10, 40.58]
4    | 34.37 | 0.89 | [32.63, 36.12]
5    | 38.21 | 0.84 | [36.56, 39.86]
6    | 38.60 | 1.09 | [36.46, 40.74]
7    | 33.10 | 1.80 | [29.57, 36.63]
8    | 33.16 | 2.44 | [28.37, 37.94]
9    | 43.01 | 2.99 | [37.15, 48.87]
10   | 33.26 | 3.78 | [25.85, 40.67]
```

Analysing differences among factor levels

For finer control see `emmeans` package

```
estimate_contrasts(m3)
```

```
Marginal Contrasts Analysis

Level1 | Level2 | Difference |          95% CI |   SE | t(990) |      p
-----------------------------------------------------------------------
site1  | site10 |       0.58 | [-11.85, 13.01] | 3.80 |   0.15 | > .999
site1  |  site2 |      -6.34 | [ -8.67, -4.01] | 0.71 |  -8.90 | < .001
site1  |  site3 |      -5.00 | [ -8.21, -1.78] | 0.98 |  -5.09 | < .001
site1  |  site4 |      -0.53 | [ -3.76,  2.70] | 0.99 |  -0.54 | > .999
site1  |  site5 |      -4.37 | [ -7.45, -1.29] | 0.94 |  -4.64 | < .001
site1  |  site6 |      -4.76 | [ -8.59, -0.93] | 1.17 |  -4.07 | 0.002
site1  |  site7 |       0.74 | [ -5.31,  6.79] | 1.85 |   0.40 | > .999
site1  |  site8 |       0.68 | [ -7.41,  8.78] | 2.48 |   0.28 | > .999
site1  |  site9 |      -9.17 | [-19.04,  0.69] | 3.02 |  -3.04 | 0.073
site2  | site10 |       6.92 | [ -5.57, 19.42] | 3.82 |   1.81 | 0.728
site2  |  site3 |       1.34 | [ -2.10,  4.79] | 1.05 |   1.27 | 0.959
site2  |  site4 |       5.81 | [  2.35,  9.27] | 1.06 |   5.49 | < .001
site2  |  site5 |       1.97 | [ -1.35,  5.29] | 1.02 |   1.94 | 0.643
site2  |  site6 |       1.58 | [ -2.44,  5.61] | 1.23 |   1.28 | 0.957
site2  |  site7 |       7.08 | [  0.90, 13.26] | 1.89 |   3.75 | 0.007
site2  |  site8 |       7.02 | [ -1.17, 15.21] | 2.50 |   2.81 | 0.136
site2  |  site9 |      -2.83 | [-12.77,  7.11] | 3.04 |  -0.93 | 0.995
site3  | site10 |       5.58 | [ -7.11, 18.27] | 3.88 |   1.44 | 0.915
site3  |  site4 |       4.47 | [  0.36,  8.57] | 1.26 |   3.56 | 0.014
site3  |  site5 |       0.63 | [ -3.37,  4.62] | 1.22 |   0.51 | > .999
site3  |  site6 |       0.24 | [ -4.35,  4.83] | 1.40 |   0.17 | > .999
site3  |  site7 |       5.74 | [ -0.82, 12.30] | 2.01 |   2.86 | 0.118
site3  |  site8 |       5.68 | [ -2.80, 14.17] | 2.59 |   2.19 | 0.464
site3  |  site9 |      -4.17 | [-14.36,  6.01] | 3.11 |  -1.34 | 0.944
site4  | site10 |       1.11 | [-11.58, 13.81] | 3.88 |   0.29 | > .999
site4  |  site5 |      -3.84 | [ -7.84,  0.16] | 1.22 |  -3.14 | 0.055
site4  |  site6 |      -4.23 | [ -8.83,  0.38] | 1.41 |  -3.00 | 0.081
```

Presenting model results

```r
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

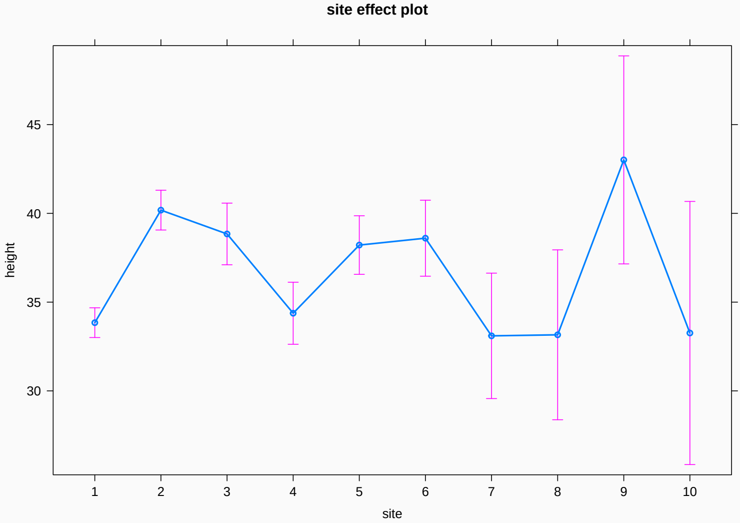
Estimated tree heights for each site

```
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 
```

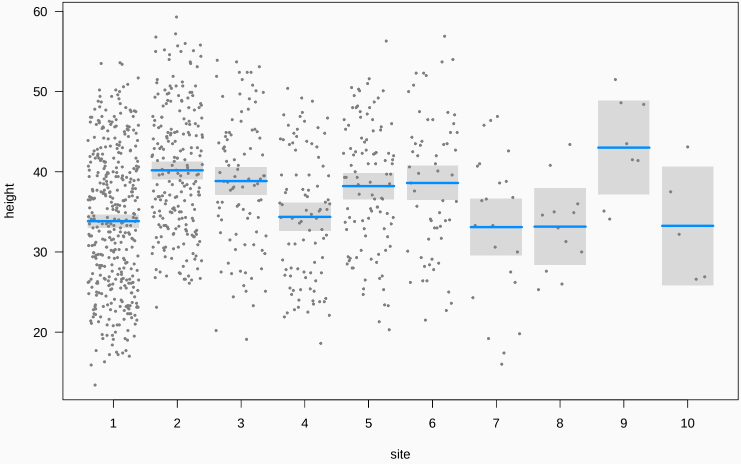
Plot

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



Plot (visreg)

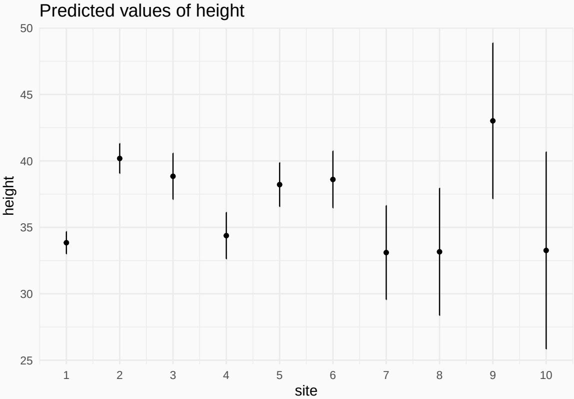
```
visreg(m3)
```



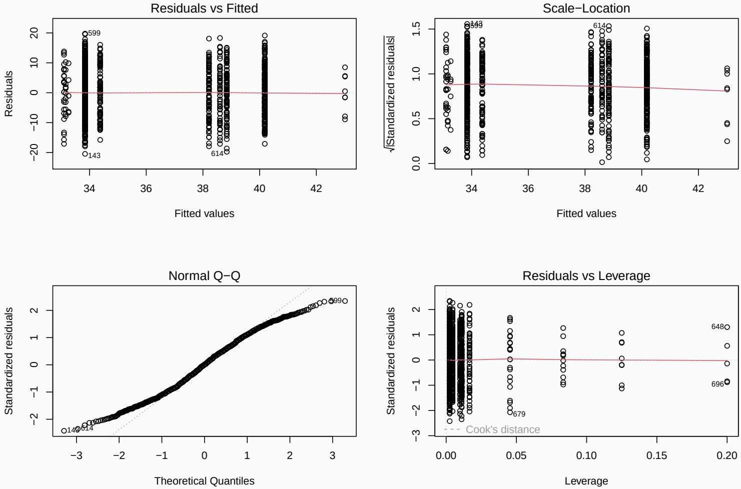
Plot model (sjPlot)

```
plot_model(m3, type = ”eff”)
```

```
$site
```

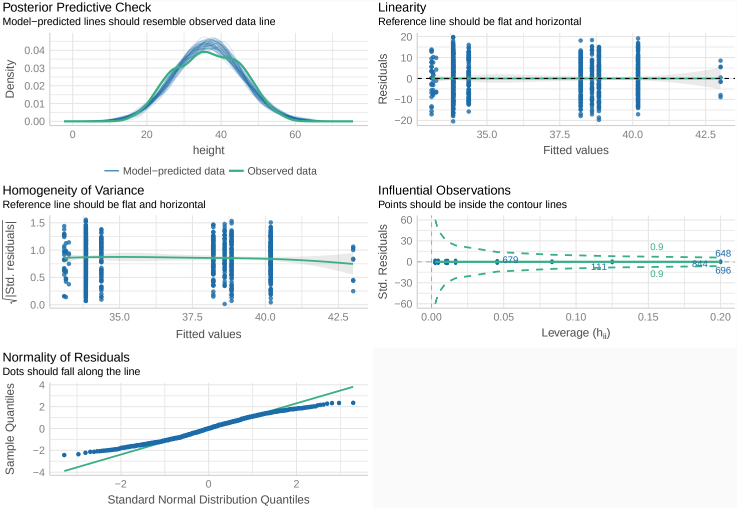


Model checking: residuals



Model checking: residuals

```
check_model(m3)
```



Combining continuous and categorical predictors

Predicting tree height based on dbh and site

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

corresponds to

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

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
```

Presenting model results

```r
parameters(m4)
```

```
Parameter   | Coefficient |       SE |         95% CI | t(989) |      p
-----------------------------------------------------------------------
(Intercept) |       16.70 |     0.26 | [16.19, 17.21] |  64.09 | < .001
site [2]    |        6.50 |     0.26 | [ 6.00,  7.01] |  25.34 | < .001
site [3]    |        4.36 |     0.35 | [ 3.66,  5.05] |  12.30 | < .001
site [4]    |        1.93 |     0.36 | [ 1.24,  2.63] |   5.43 | < .001
site [5]    |        3.64 |     0.34 | [ 2.97,  4.30] |  10.71 | < .001
site [6]    |        4.20 |     0.42 | [ 3.38,  5.03] |   9.97 | < .001
site [7]    |       -0.18 |     0.67 | [-1.48,  1.13] |  -0.26 | 0.792 
site [8]    |       -5.31 |     0.89 | [-7.07, -3.56] |  -5.95 | < .001
site [9]    |        5.44 |     1.09 | [ 3.30,  7.57] |   5.00 | < .001
site [10]   |        2.26 |     1.37 | [-0.43,  4.95] |   1.65 | 0.099 
dbh         |        0.62 | 7.57e-03 | [ 0.60,  0.63] |  81.47 | < .001
```

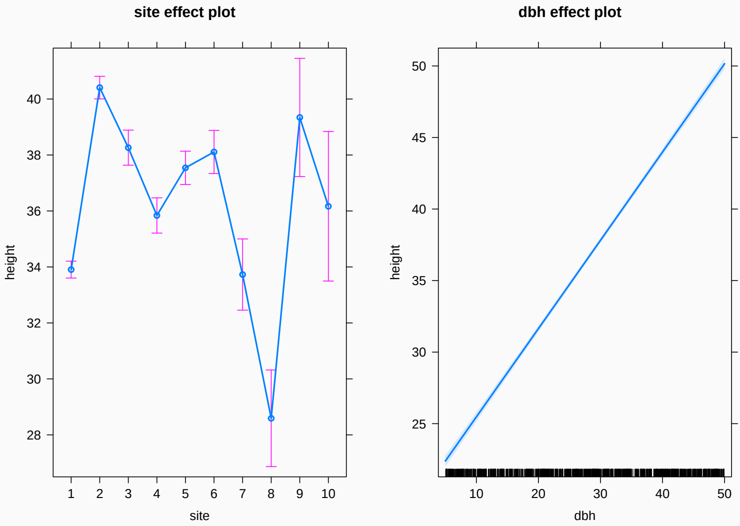
Estimated tree heights for each site

```
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
```

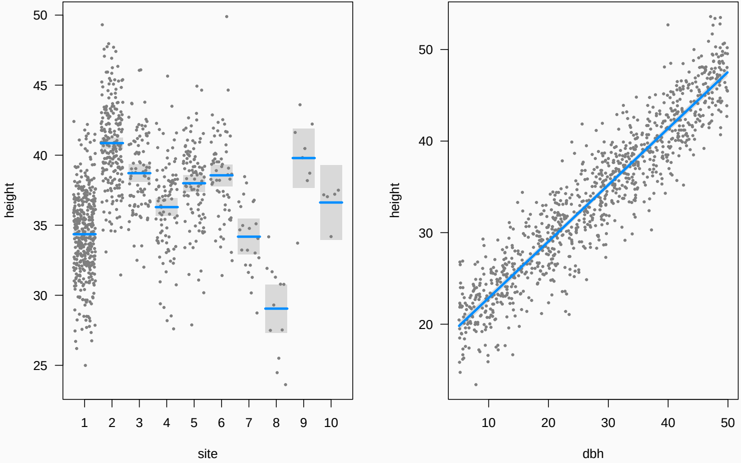
Plot

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



Plot (visreg)

```
visreg(m4)
```

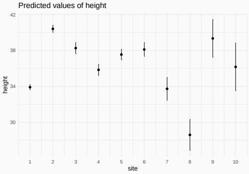


```
null device
          1
```

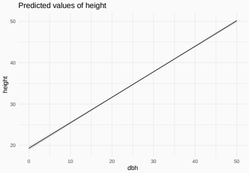
Plot model (sjPlot)

```
plot_model(m4, type = ”eff”)
```

```
$site
```

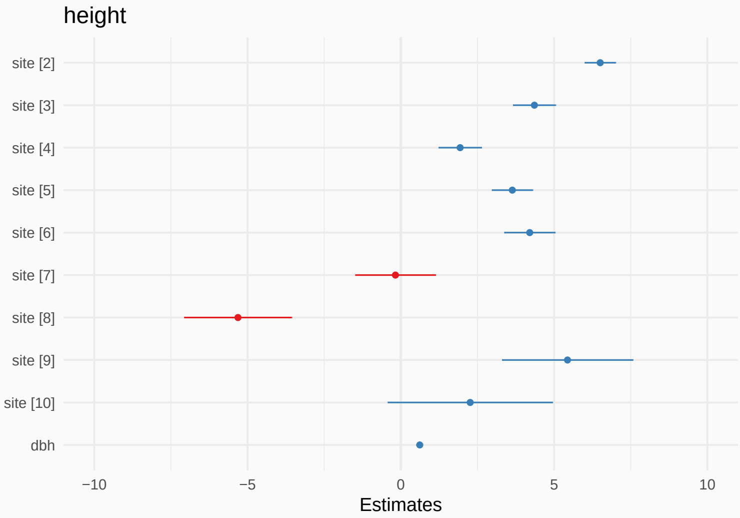


```
$dbh
```



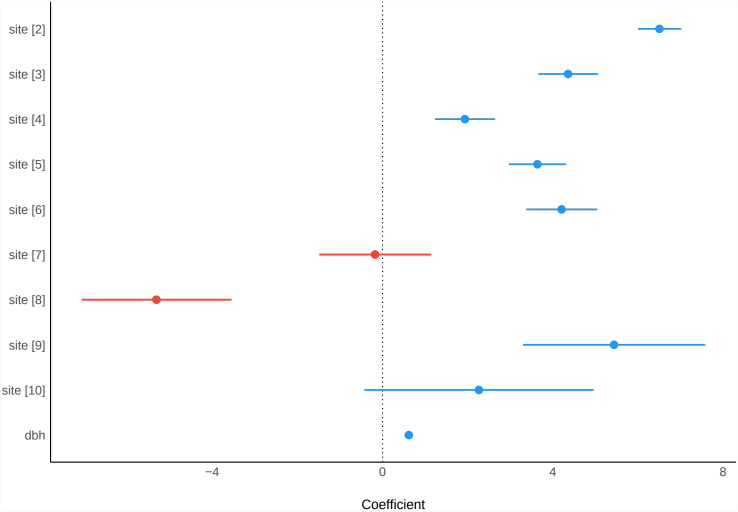
Plot model (sjPlot)

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

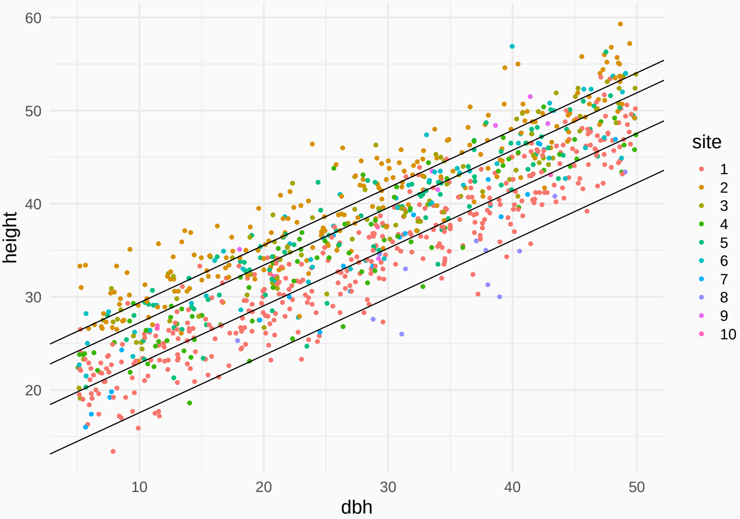


Plot model (see)

```
plot(parameters(m4))
```



We have fitted model w/ many intercepts and single slope

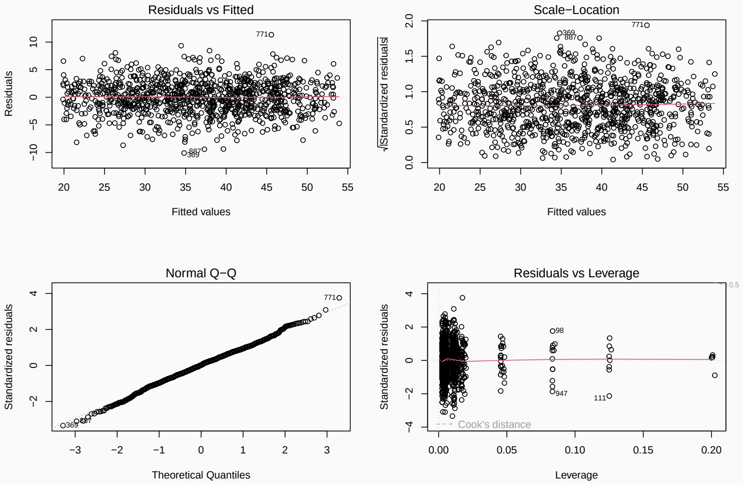


Slope is the same for all sites

```r
estimate_slopes(m4)
```

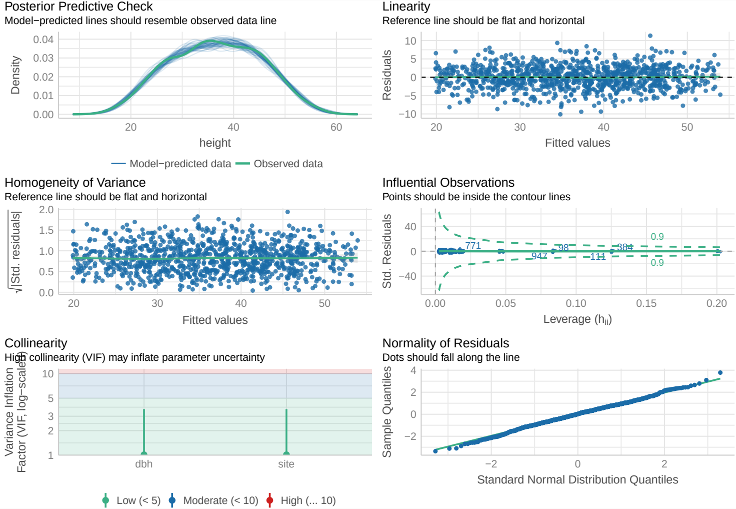
```
Estimated Marginal Effects

Coefficient |       SE |       95% CI | t(989) |      p
-------------------------------------------------------
0.62        | 7.57e-03 | [0.60, 0.63] |  81.47 | < .001
Marginal effects estimated for dbh
```

Model checking: residuals



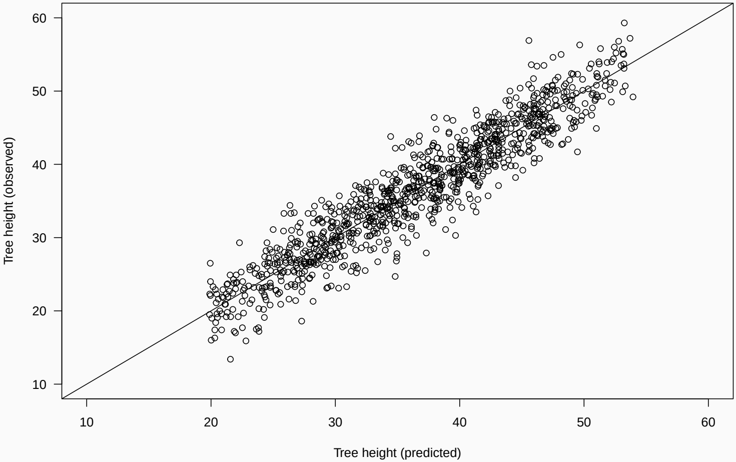
Model checking: residuals

```
check_model(m4)
```



How good is this model? Calibration plot

```
trees$height.pred <- fitted(m4)
plot(trees$height.pred, trees$height, xlab = ”Tree height (predicte
abline(a = 0, b = 1)
```

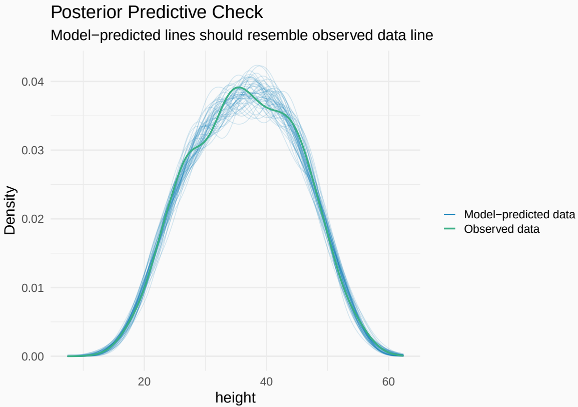


Posterior predictive checking

Simulating response data from fitted model (`yrep`)

and comparing with observed response (`y`)

```
performance::check_predictions(m4)
```



Using model for prediction

Expected height of 10-cm diameter tree in each site?

```
trees.10cm <- data.frame(site = as.factor(1:10),
                         dbh = 10)
trees.10cm
```

```
   site dbh
1     1  10
2     2  10
3     3  10
4     4  10
5     5  10
6     6  10
7     7  10
8     8  10
9     9  10
10   10  10
```

Using model for prediction

Confidence interval

```
predict(m4, newdata = trees.10cm, interval = ”confidence”)
```

```
        fit      lwr      upr
1  22.86979 22.46878 23.27079
2  29.37409 28.89388 29.85430
3  27.22724 26.54160 27.91289
4  24.80444 24.13410 25.47477
5  26.50722 25.84952 27.16492
6  27.07430 26.25490 27.89370
7  22.69359 21.39601 23.99117
8  17.55714 15.79282 19.32146
9  28.30683 26.16606 30.44761
10 25.13312 22.45540 27.81085
```

Using model for prediction

Prediction interval (accounting for residual variance)

```
predict(m4, newdata = trees.10cm, interval = ”prediction”)
```

```
        fit      lwr      upr
1  22.86979 16.88478 28.85480
2  29.37409 23.38325 35.36493
3  27.22724 21.21645 33.23804
4  24.80444 18.79537 30.81350
5  26.50722 20.49955 32.51489
6  27.07430 21.04678 33.10181
7  22.69359 16.58268 28.80451
8  17.55714 11.33039 23.78388
9  28.30683 21.96314 34.65053
10 25.13312 18.58868 31.67757
```

Using model for prediction

Prediction interval (99%)

```
predict(m4, newdata = trees.10cm, interval = ”prediction”,
        level = 0.99)
```

```
        fit       lwr      upr
1  22.86979 14.998587 30.74098
2  29.37409 21.495225 37.25295
3  27.22724 19.322133 35.13235
4  24.80444 16.901598 32.70727
5  26.50722 18.606216 34.40822
6  27.07430 19.147195 35.00140
7  22.69359 14.656813 30.73037
8  17.55714  9.368019 25.74626
9  28.30683 19.963913 36.64976
10 25.13312 16.526183 33.74007
```

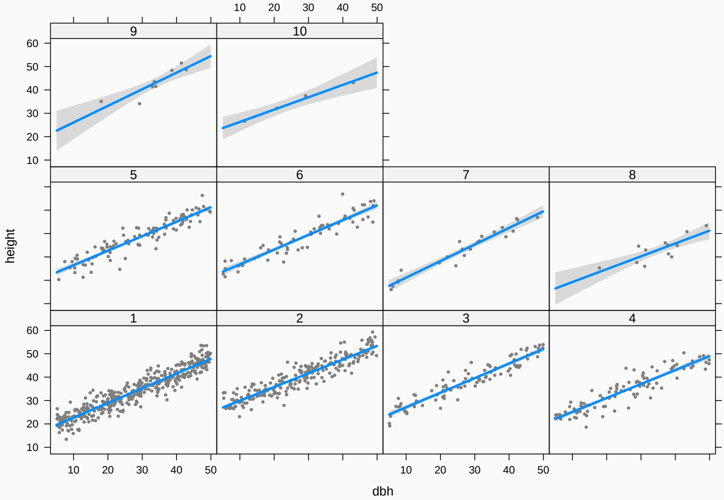
Q: Does allometric relationship between Height and Diameter vary among sites?

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
```

Does slope vary among sites?

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



Examining fitted model with {modelStudio}

```r
library(”modelStudio”)
m5.explain <- DALEX::explain(m5, data = trees, y = trees$height)
modelStudio(m5.explain)
```

Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?

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- Penguins data: Body mass ~ Flipper length, Bill length ~ Bill depth, differences across sites…
- racing pigeons: is speed related to sex?