Linear models

Example dataset: forest trees

- Go to https://tinyurl.com/treesdata

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

```
  plot   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

- Go to https://tinyurl.com/treesdata
- Download zip file and uncompress (within your project folder!)

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

```
  plot   dbh height    sex dead
1    4 29.68   36.1   male    0
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```

Questions

- What is the relationship between DBH and height?

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- Do taller trees have bigger trunks?

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- 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!

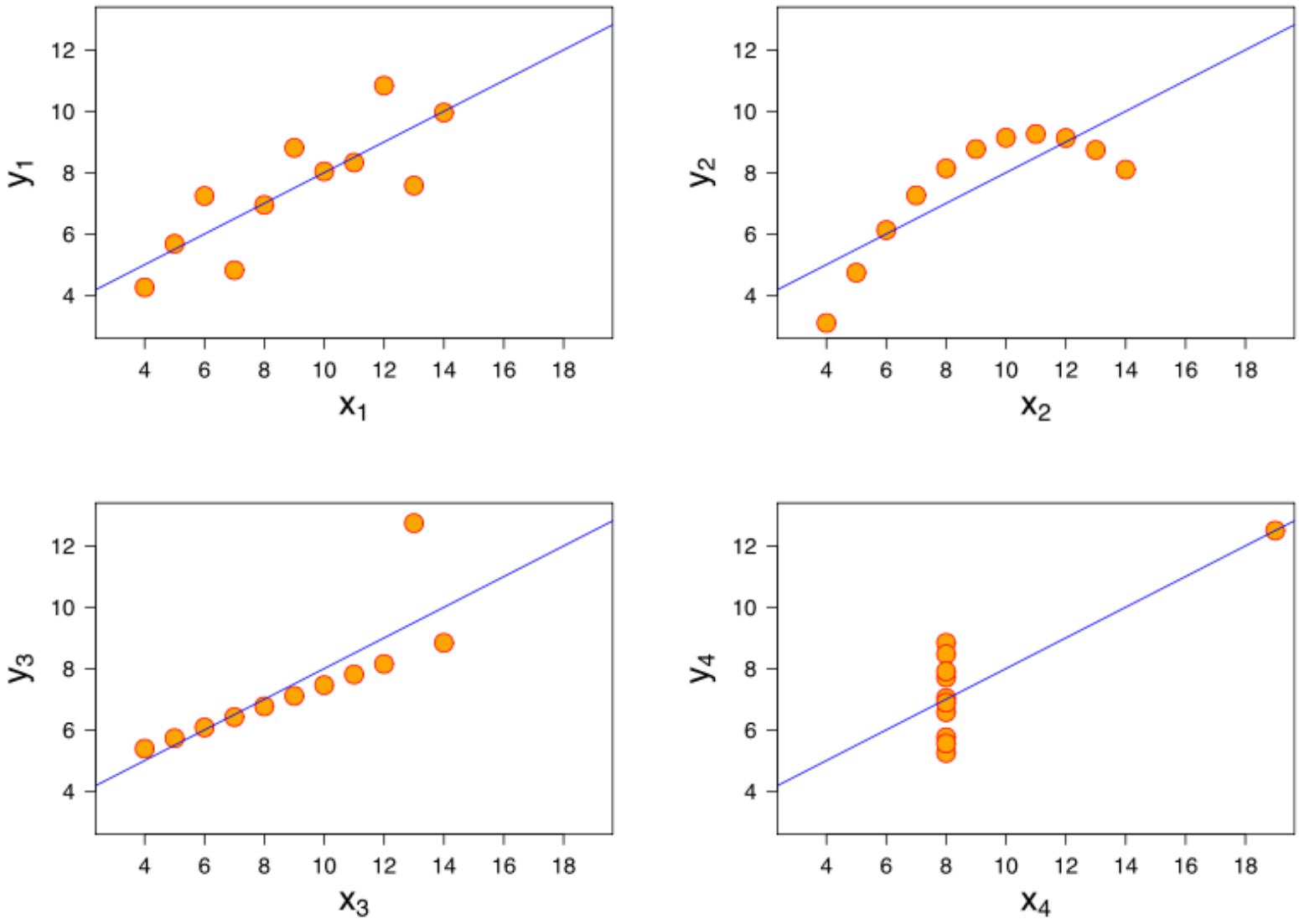
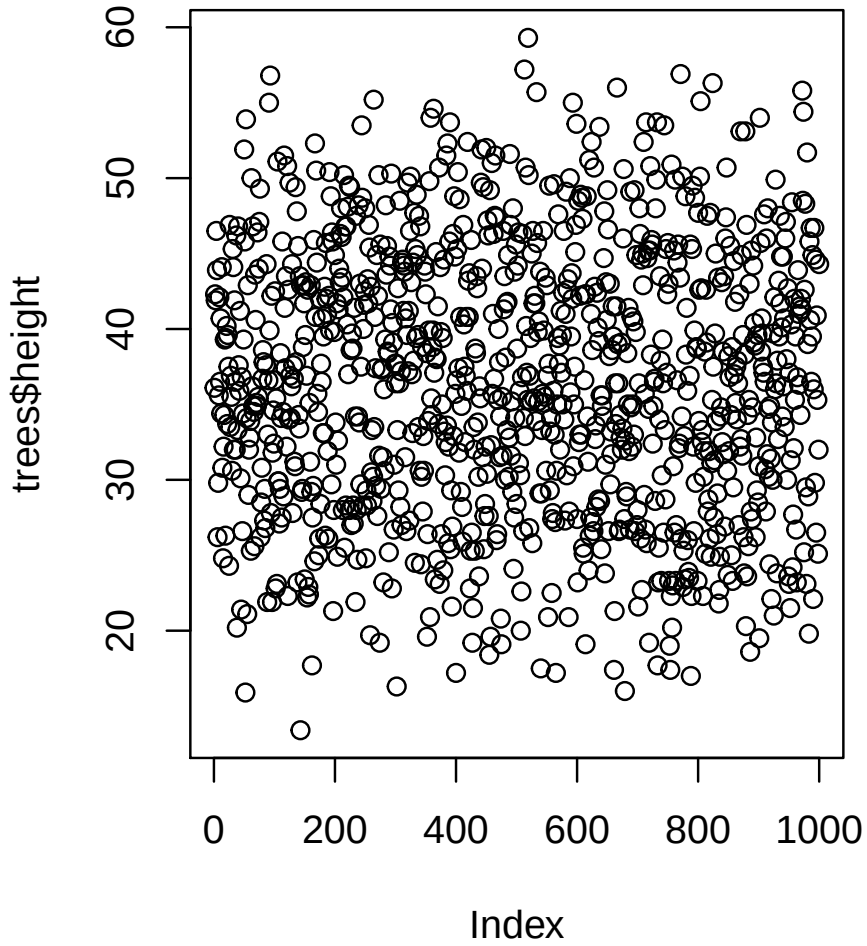


Figure 1:

Exploratory Data Analysis (EDA)

Outliers

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



Outliers impact on regression

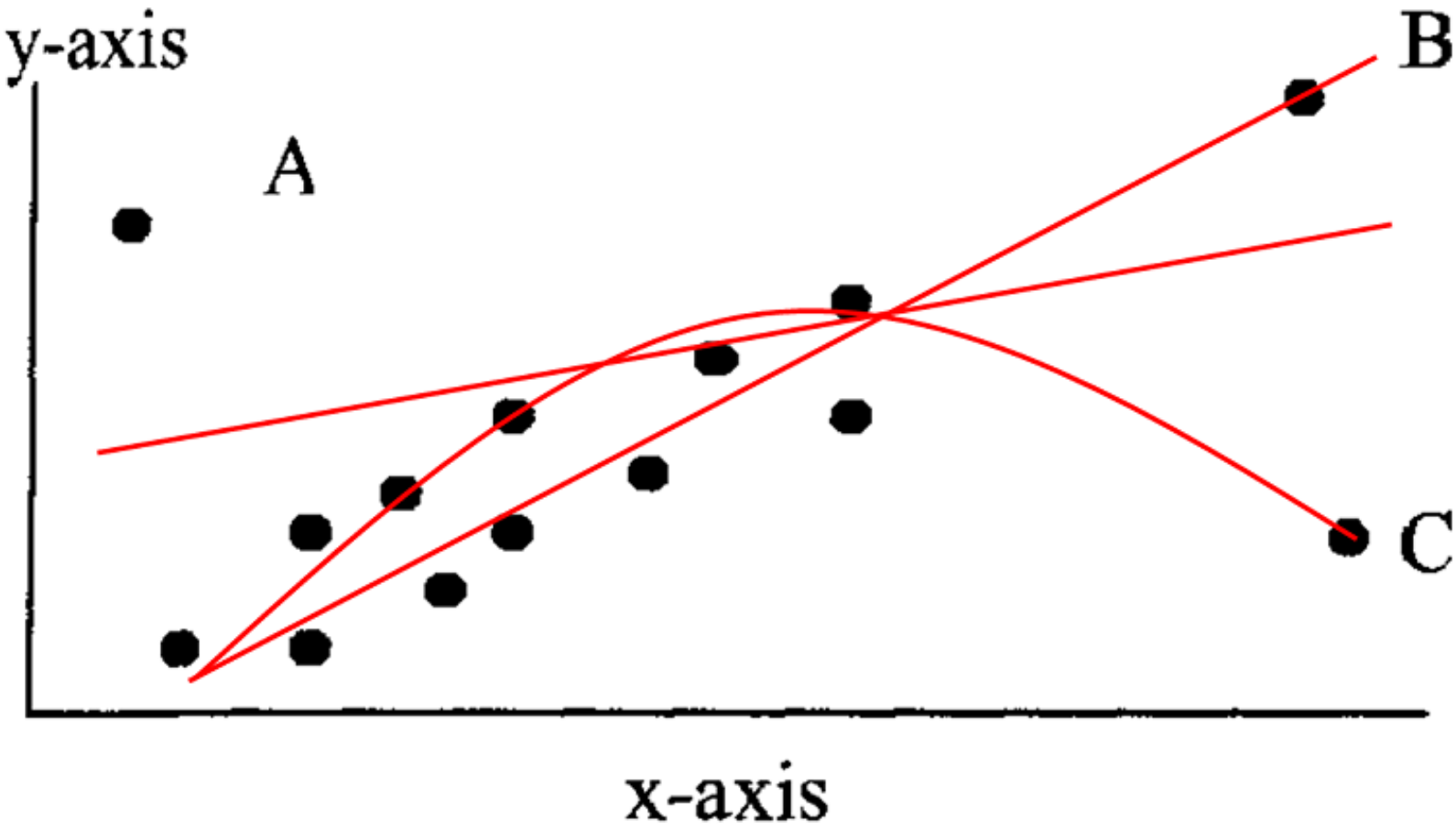
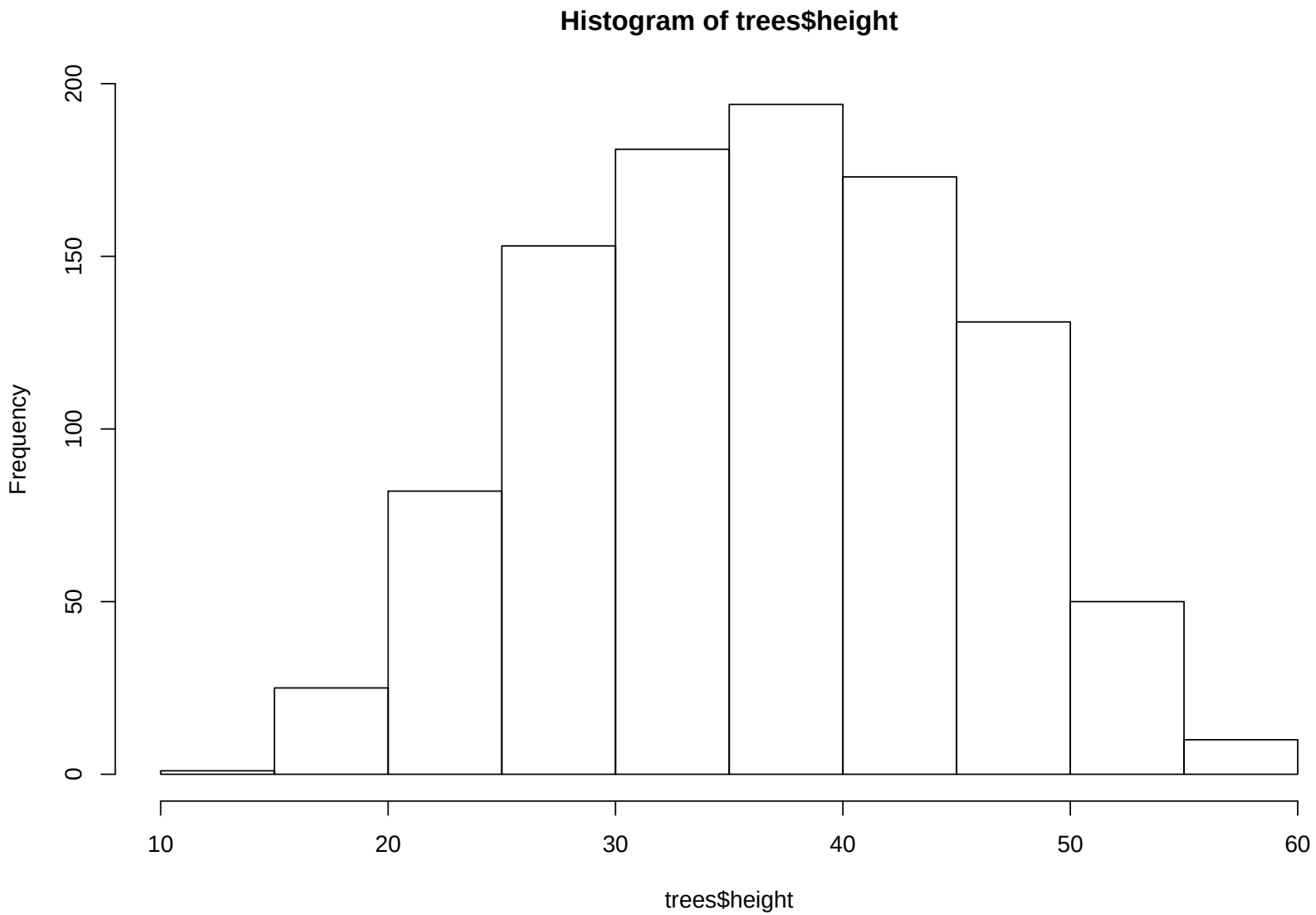


Figure 2:

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

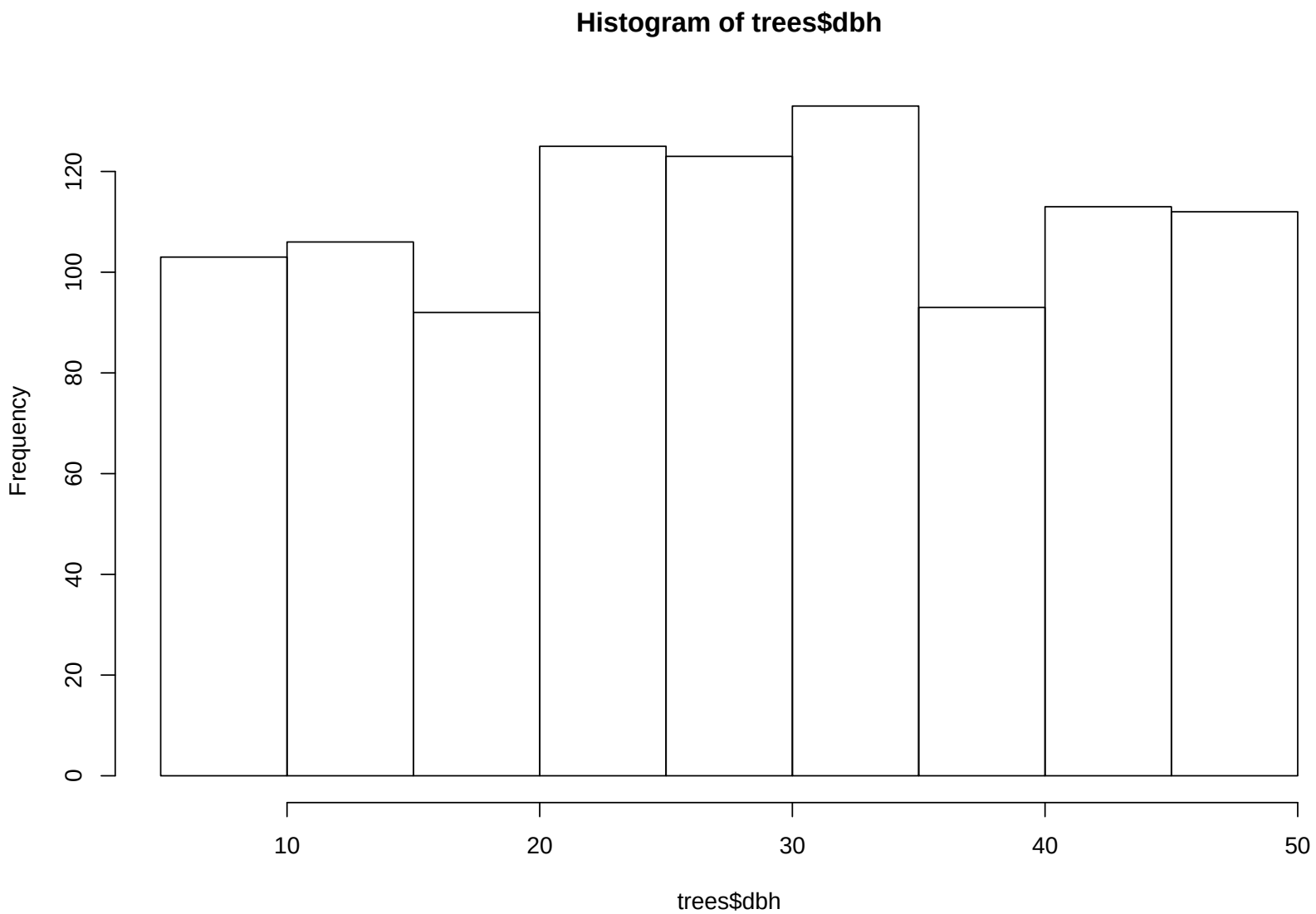
Histogram of response variable

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



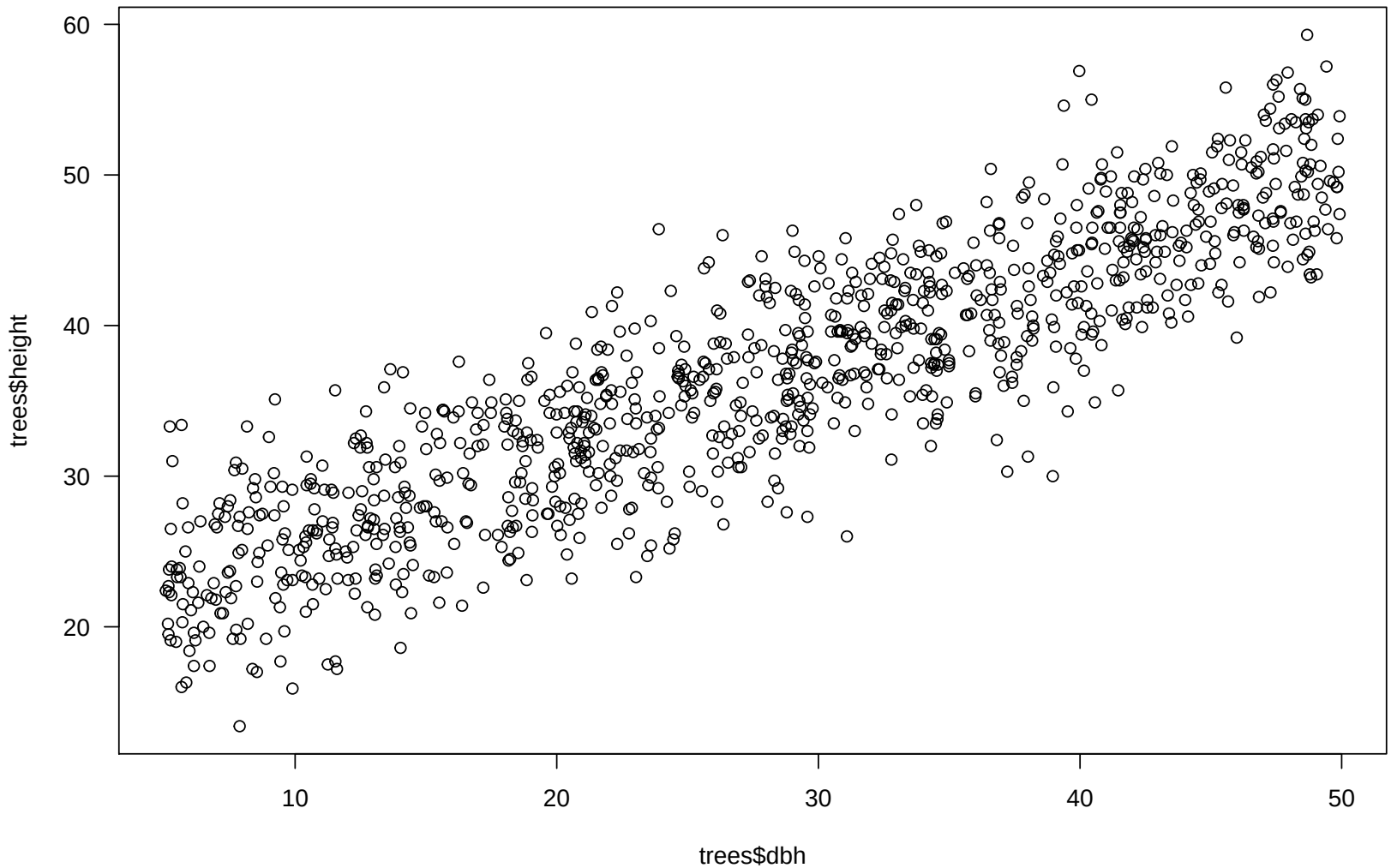
Histogram of predictor variable

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



Scatterplot

```
plot(trees$dbh, trees$height, las = 1)
```



Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

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

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
```

Retrieving model coefficients

```
coef(m1)
```

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

Tidy up model coefficients with broom

```
library(broom)
tidy(m1)
```

```
         term   estimate  std.error statistic p.value
1 (Intercept) 19.3391968 0.31064458  62.25506       0
2         dbh  0.6157036 0.01012841  60.78976       0
```

```
glance(m1)
```

```
  r.squared adj.r.squared    sigma statistic p.value df    logLi
1 0.7873608     0.7871477 4.092629  3695.395       0  2 -2827.12
       BIC deviance df.residual
1 5674.973 16716.11         998
```

Confidence intervals

```
confint(m1)
```

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

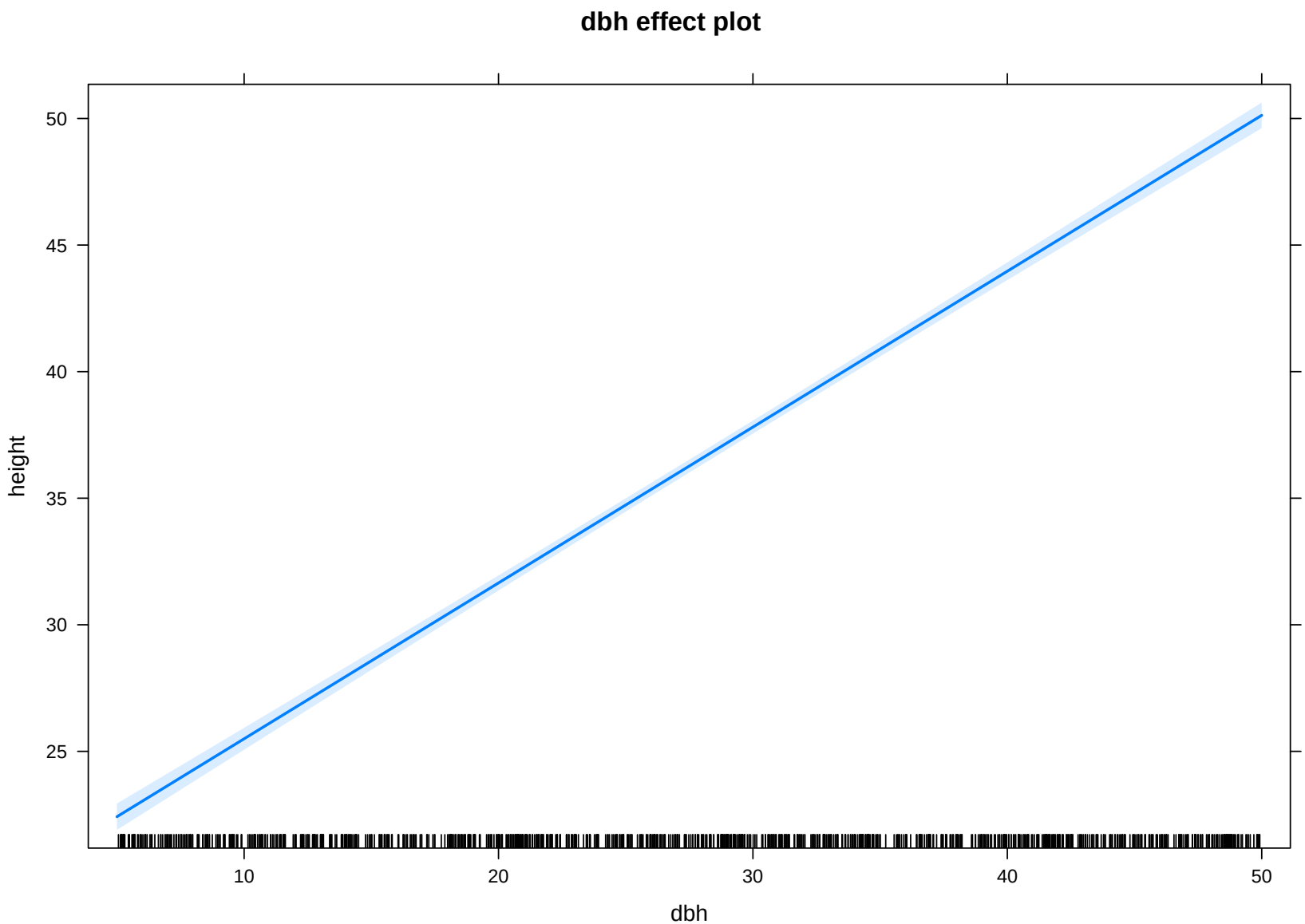
Using effects package

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

```
 model: height ~ dbh

 dbh effect
dbh
       5        20        30        40        50
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
```

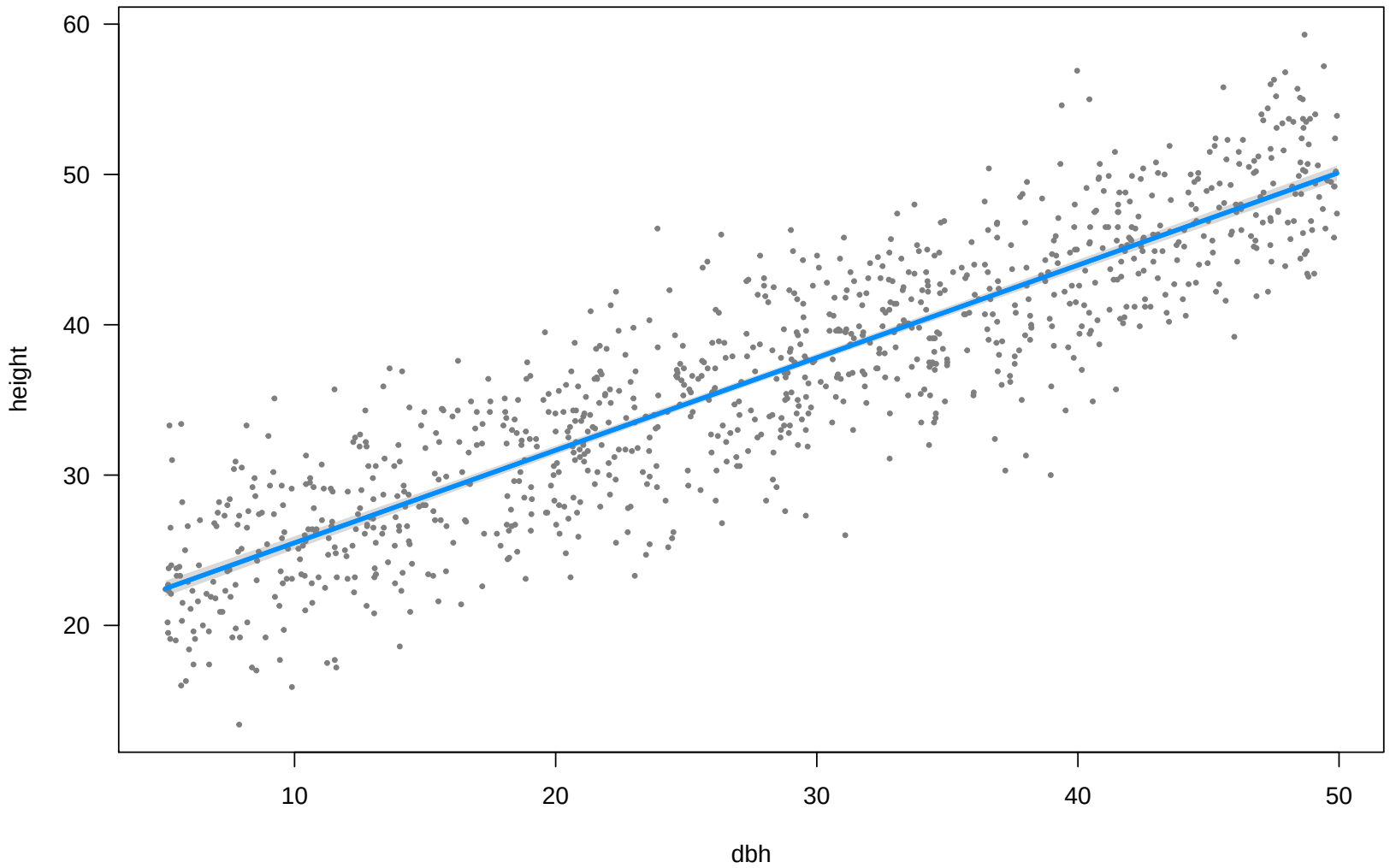
Plot effects

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



Plot model (visreg)

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



Linear model assumptions

- Linearity (transformations, GAM. . .)

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- Residuals:

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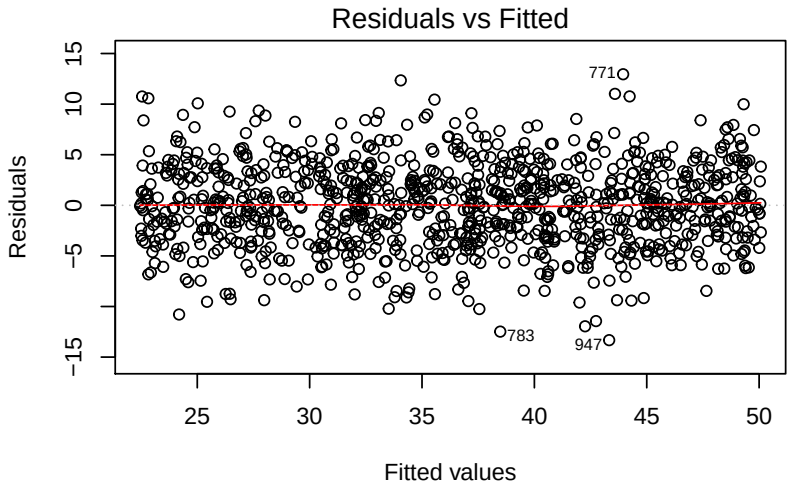
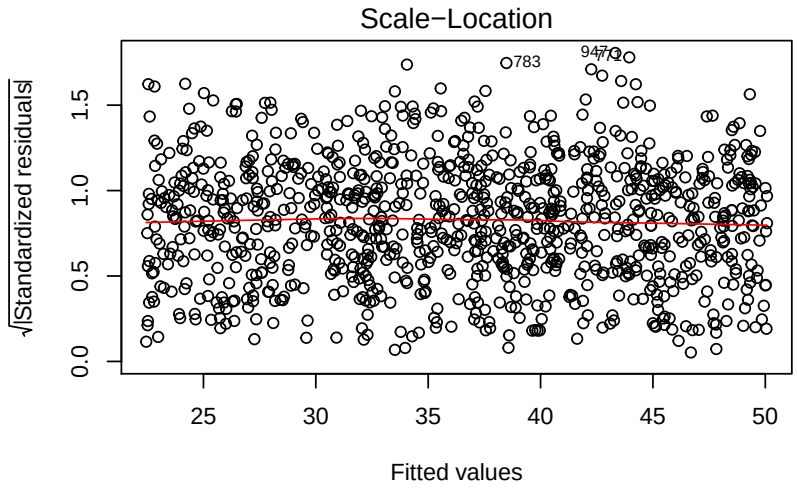
- Residuals:
  - Independent
  - Equal variance
  - Normal

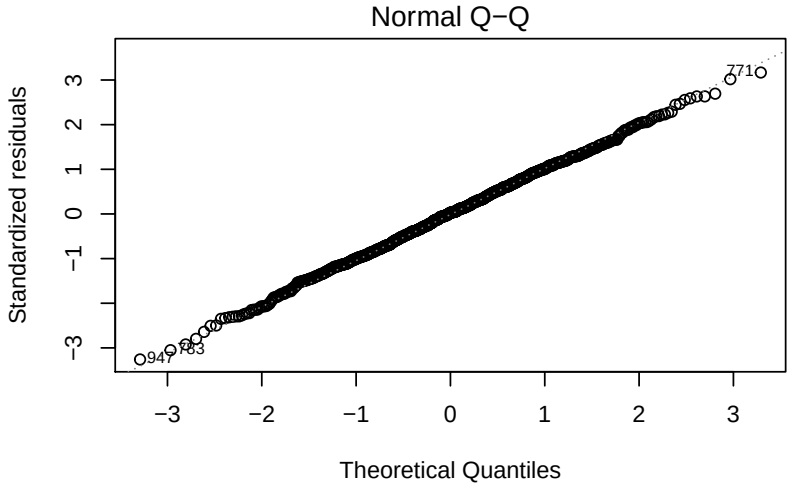
Linear model assumptions

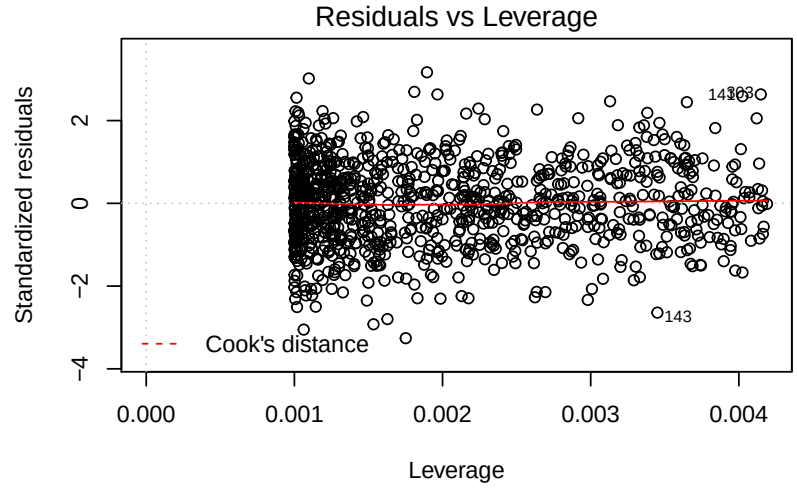
- Linearity (transformations, GAM...)
- Residuals:
  - Independent
  - Equal variance
  - Normal
- No measurement error in predictors

Model checking: residuals



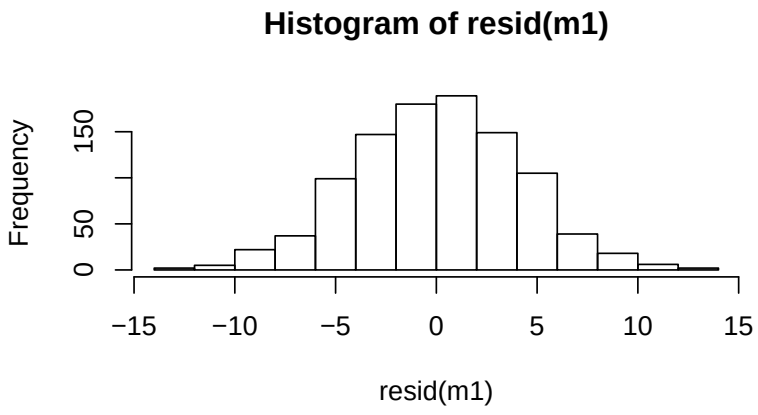






Are residuals normal?

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




```
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
```

SD of residuals = 4.09 coincides with estimate of `sigma`.

How good is the model in predicting tree height?

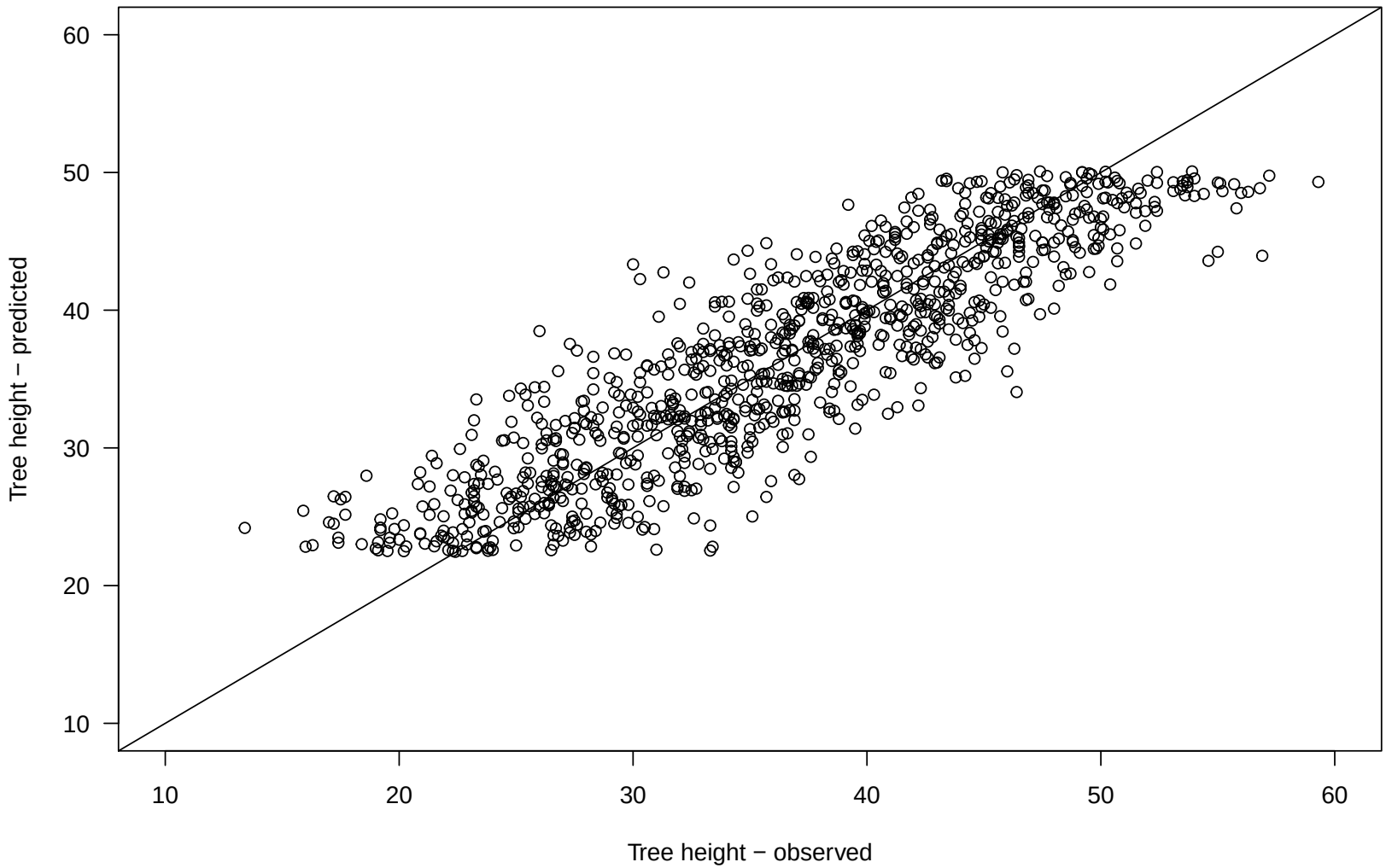
`fitted` gives predictions for each observation

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

```
  plot   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$height, trees$height.pred, xlab = "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
```

Important functions

- `plot`

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- `plot`
- `summary`

Important functions

- `plot`
- `summary`
- `coef`

Important functions

- `plot`
- `summary`
- `coef`
- `confint`

Important functions

- `plot`
- `summary`
- `coef`
- `confint`
- `fitted`

Important functions

- `plot`
- `summary`
- `coef`
- `confint`
- `fitted`
- `resid`

Important functions

- `plot`
- `summary`
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- `confint`
- `fitted`
- `resid`
- `allEffects`

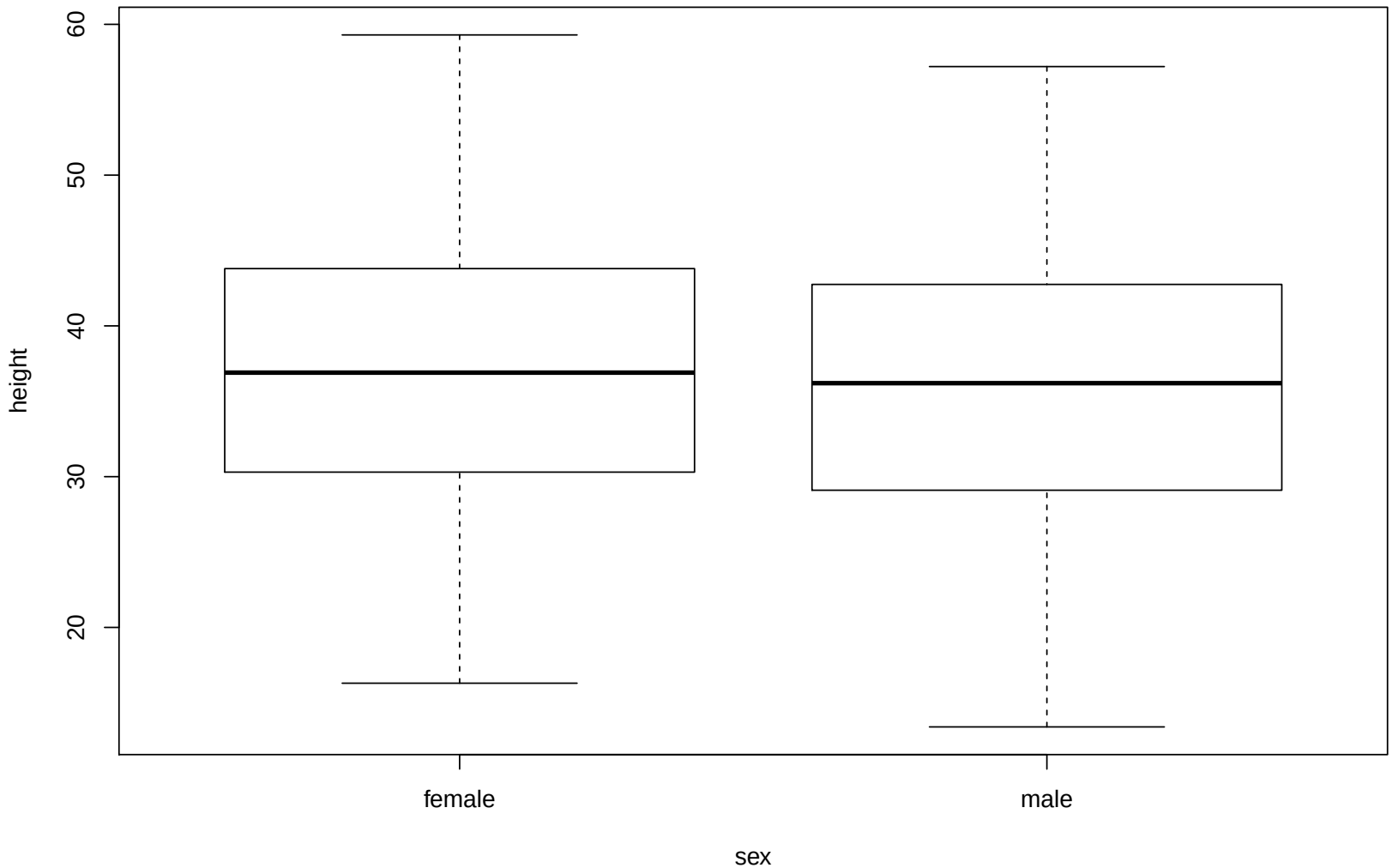
Important functions

- `plot`
- `summary`
- `coef`
- `confint`
- `fitted`
- `resid`
- `allEffects`
- `predict`

Categorical predictors (factors)

Q: Does tree height vary with sex?

```
plot(height ~ 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

$$y_i = a + bx_i + \varepsilon_i$$

$$y_i = a + b_{male} + \varepsilon_i$$

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:
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(Intercept)  36.9312     0.3981  92.778   <2e-16 ***
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Multiple R-squared:  0.002261,  Adjusted R-squared:  0.001261
F-statistic: 2.261 on 1 and 998 DF,  p-value: 0.133
```

Effects: Height ~ sex

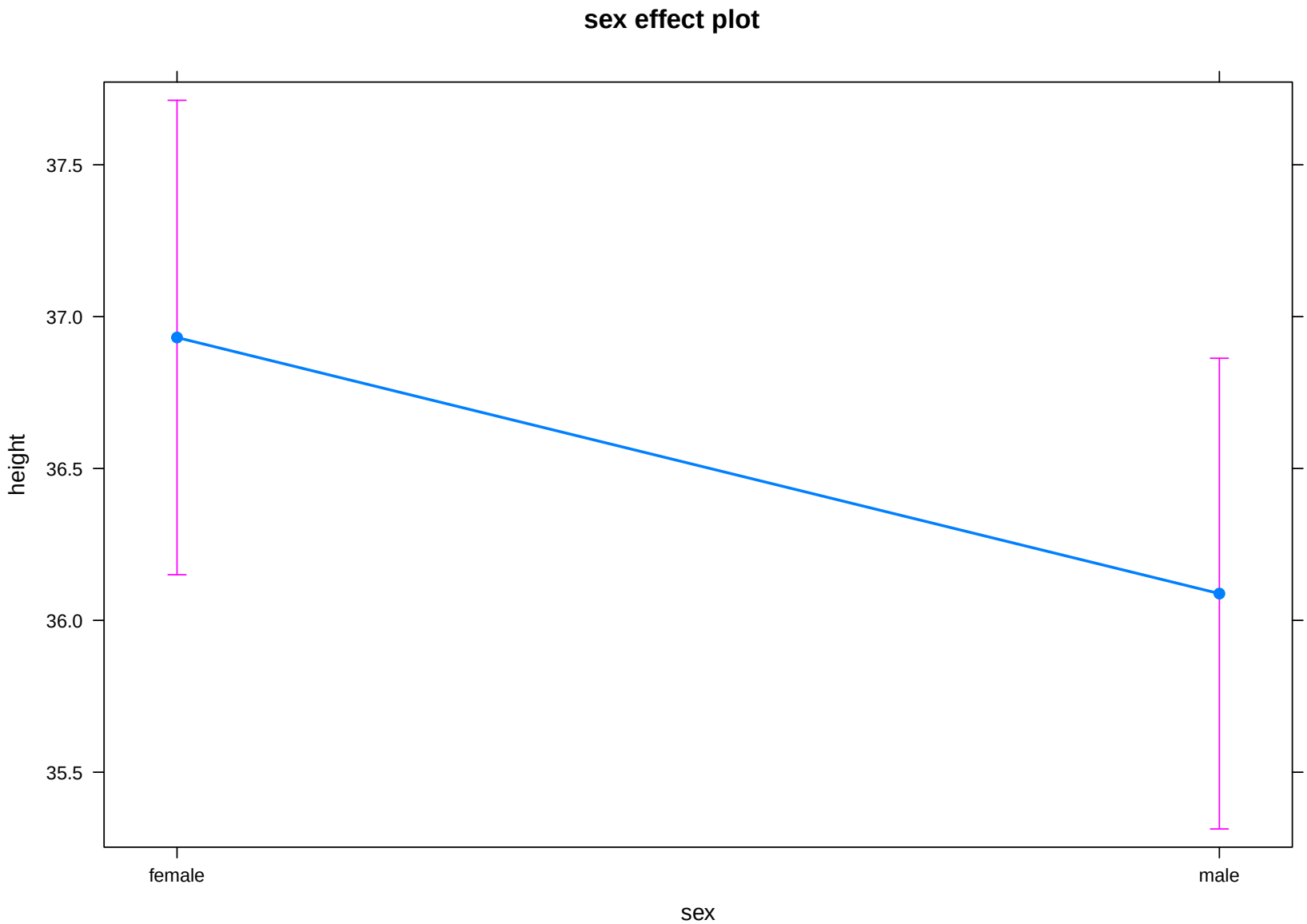
Compare CIs

```
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
```

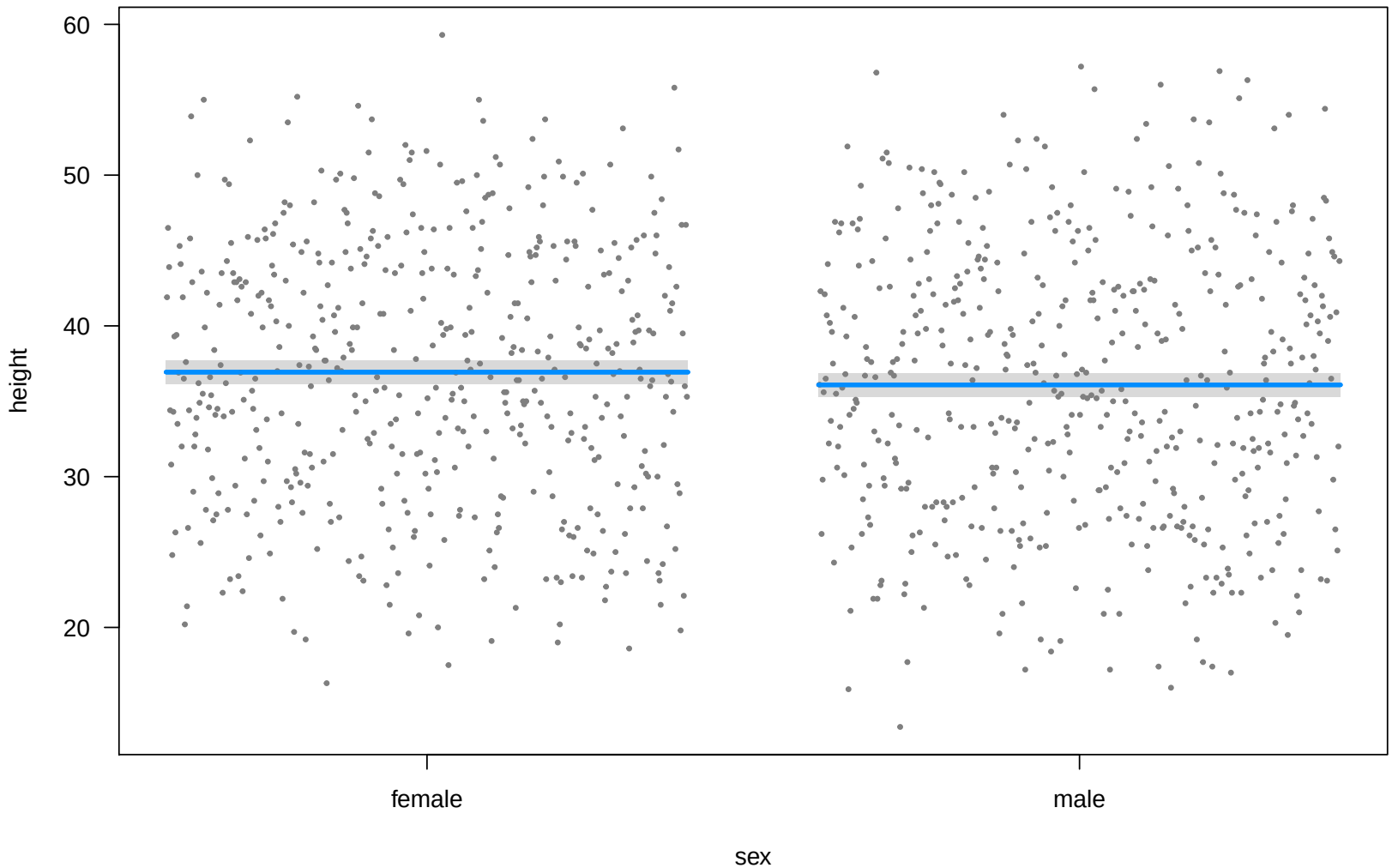
Plot

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

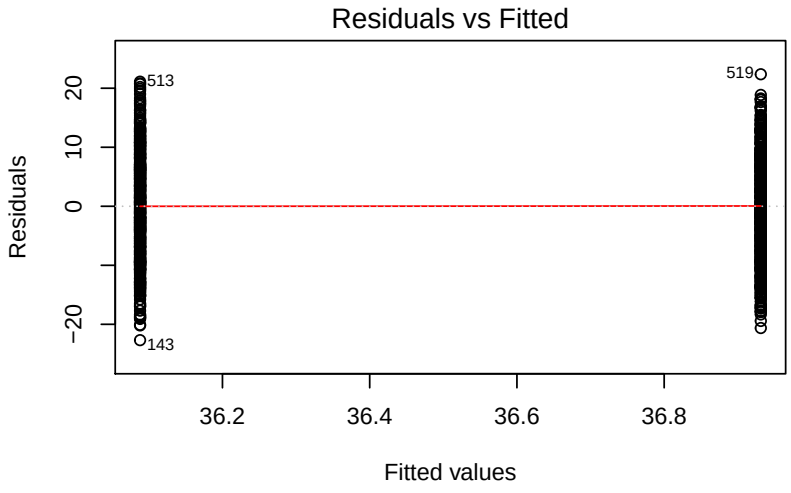


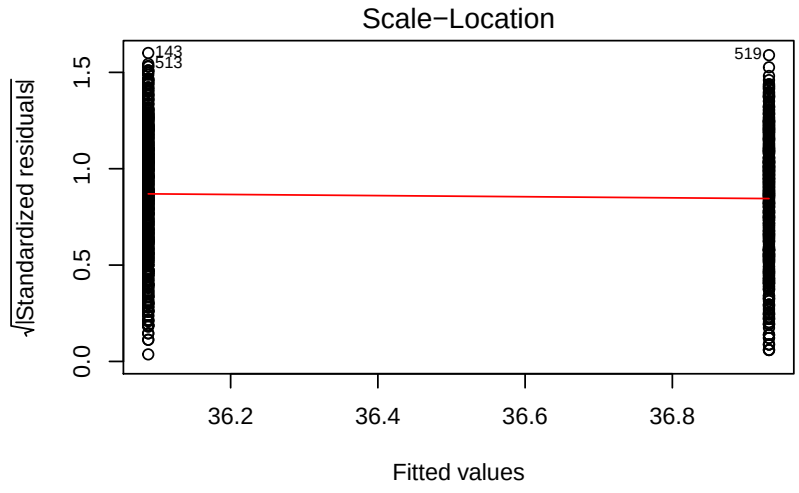
Plot (visreg)

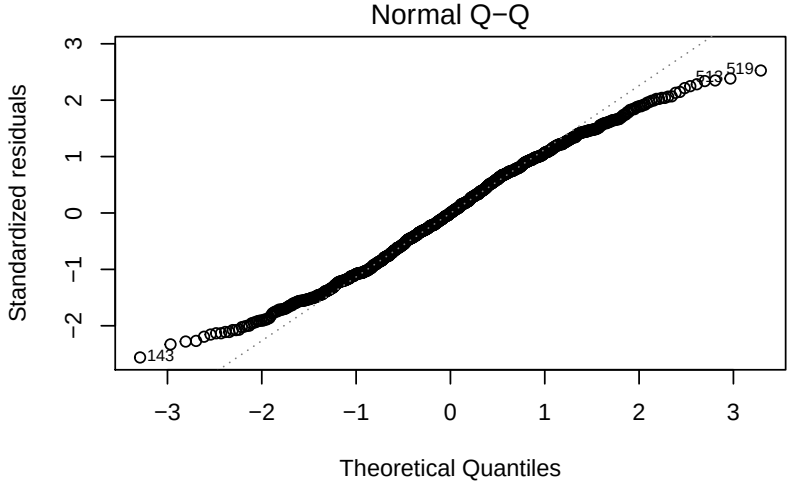
```
visreg(m2)
```

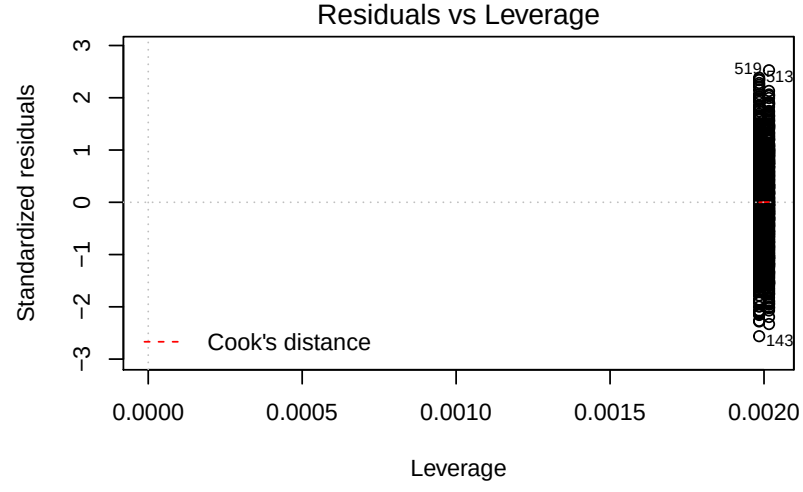


Model checking: residuals



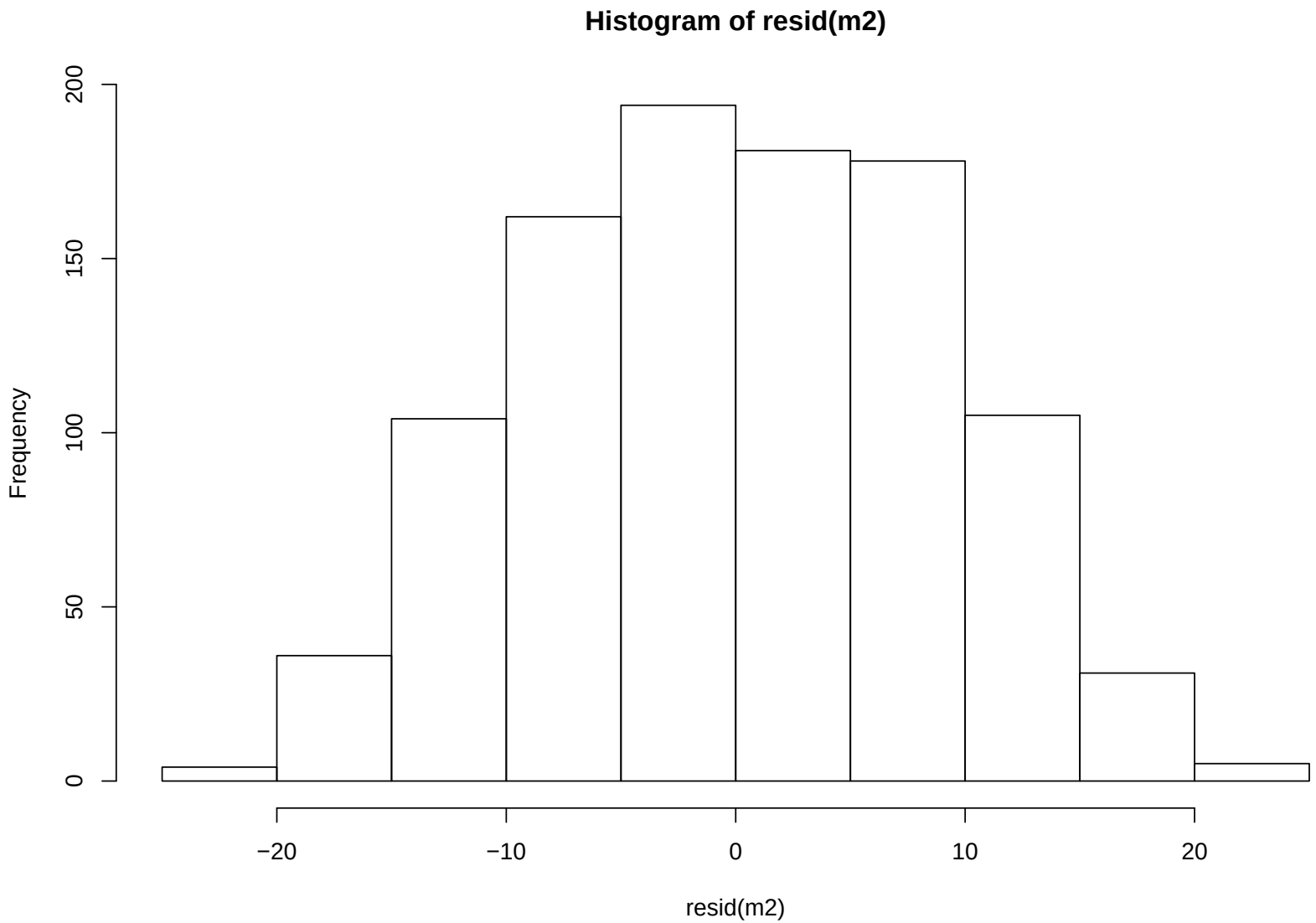






Model checking: residuals

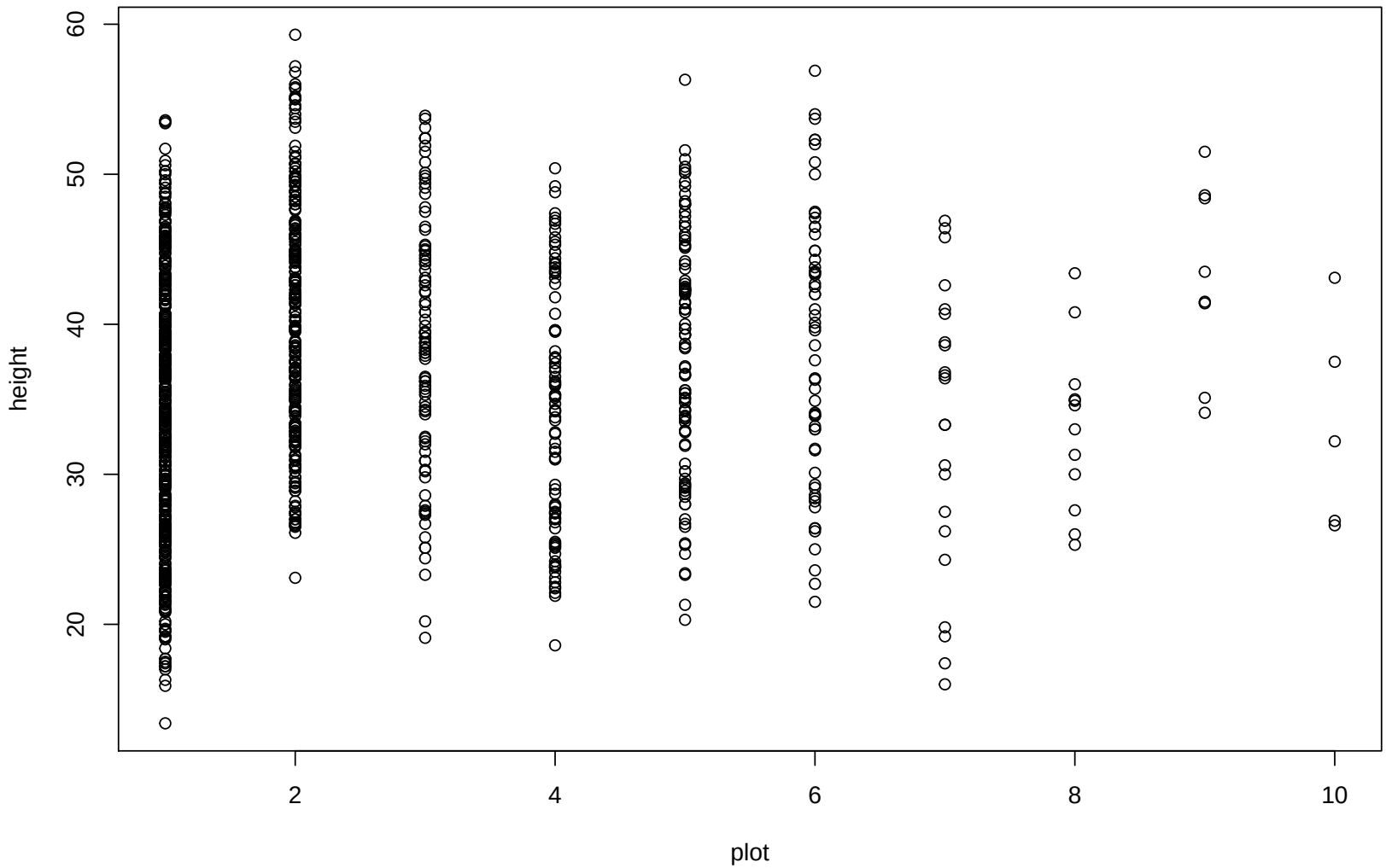
```
hist(resid(m2))
```



Q: Does height differ among field plots?

Plot data first

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



Linear model with categorical predictors

$$y_i = a + bx_i + \varepsilon_i$$

$$y_i = a + b_{plot2} + c_{plot3} + d_{plot4} + e_{plot5} + ... + \varepsilon_i$$

Model Height ~ Plot

All right here?

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

```
Call:
lm(formula = height ~ plot, 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 ***
plot          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
```

Plot is a factor!

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

Model Height ~ Plot

```
Call:
lm(formula = height ~ plot, 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 ***
plot2         6.3411     0.7126   8.899  < 2e-16 ***
plot3         4.9991     0.9828   5.086 4.36e-07 ***
plot4         0.5329     0.9872   0.540  0.58949
plot5         4.3723     0.9425   4.639 3.97e-06 ***
plot6         4.7601     1.1709   4.065 5.18e-05 ***
plot7        -0.7416     1.8506  -0.401  0.68871
plot8        -0.6832     2.4753  -0.276  0.78258
plot9         9.1709     3.0165   3.040  0.00243 **
plot10       -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
```

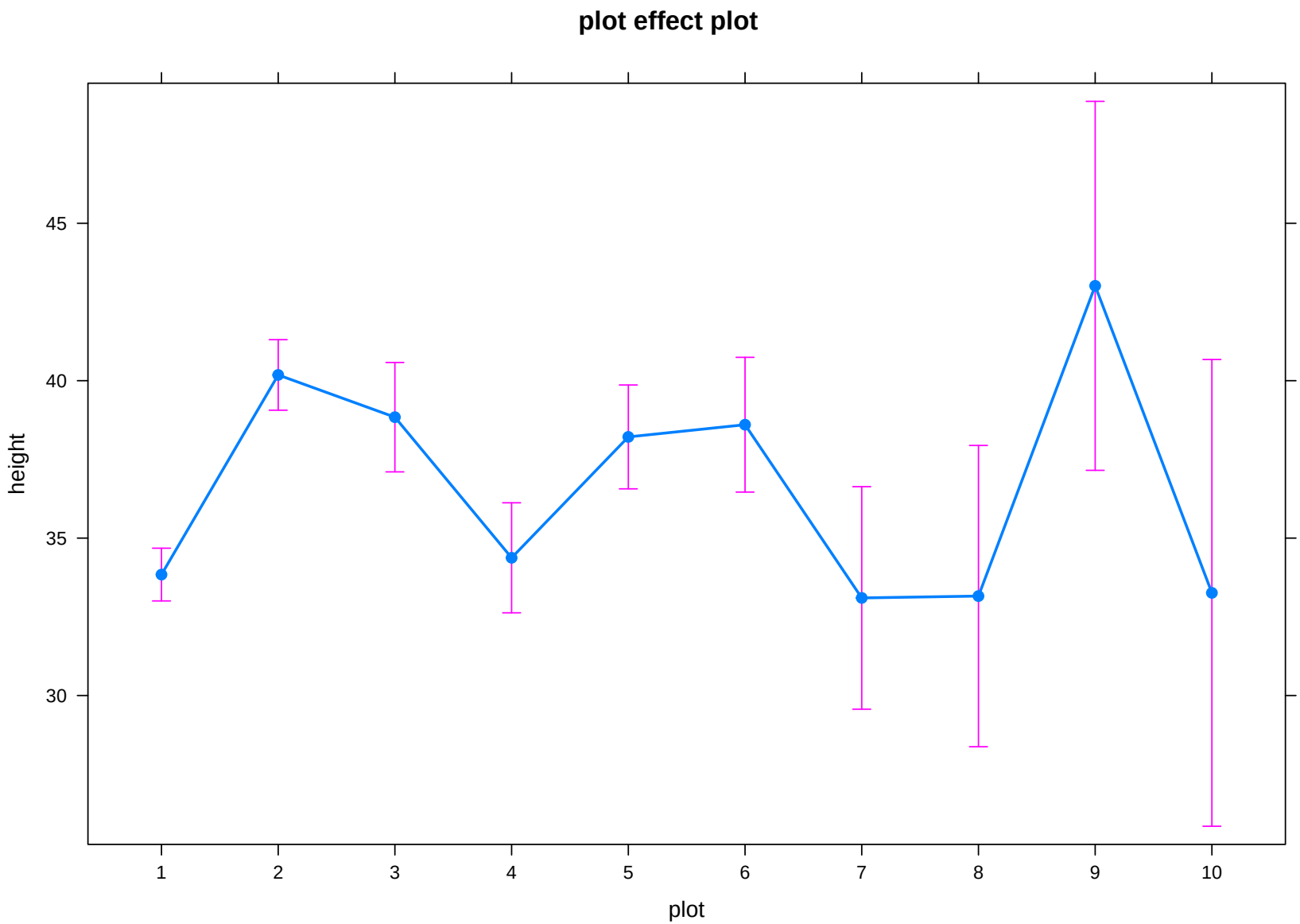
Estimated tree heights for each site

```
summary(allEffects(m3))
```

```
 model: height ~ plot

 plot effect
plot
       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
plot
       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
plot
       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
```

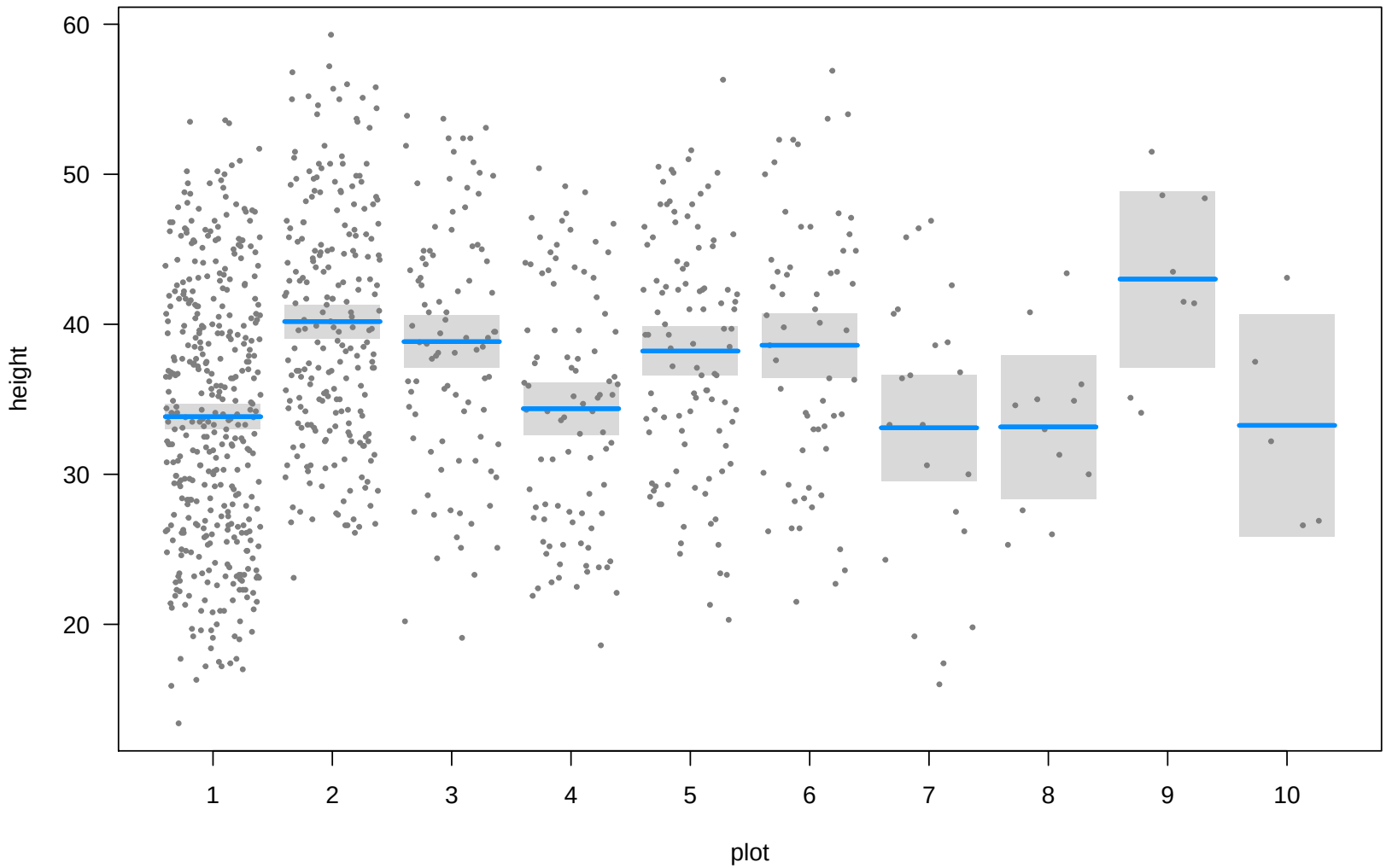
Plot

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

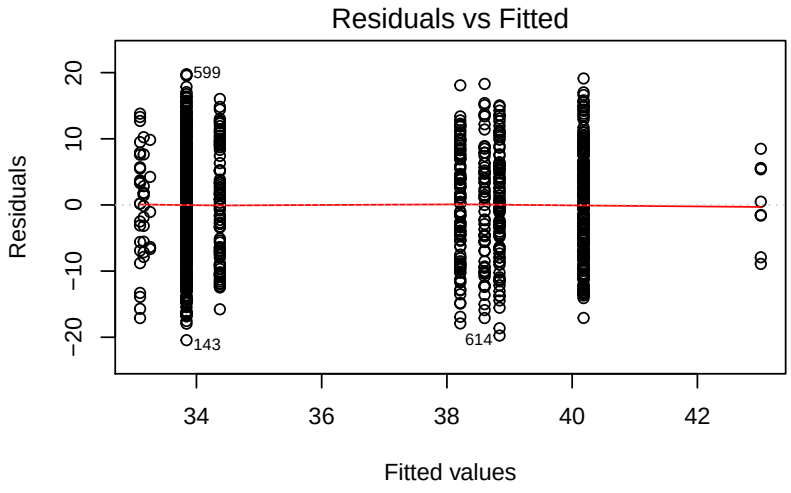


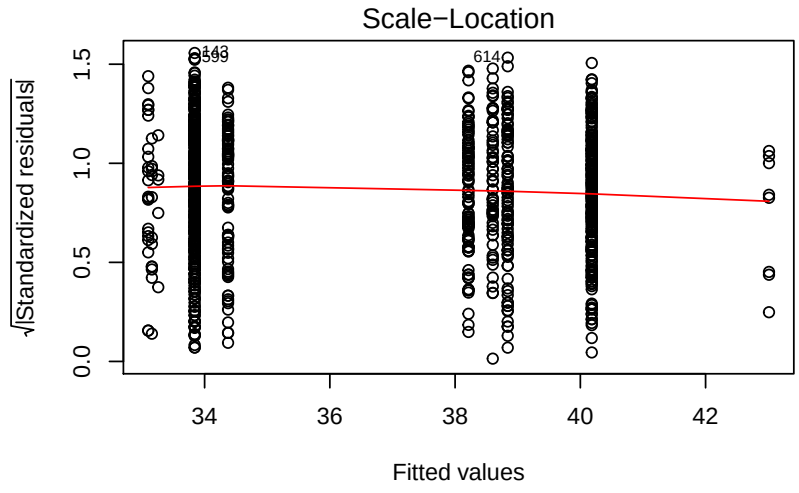
Plot (visreg)

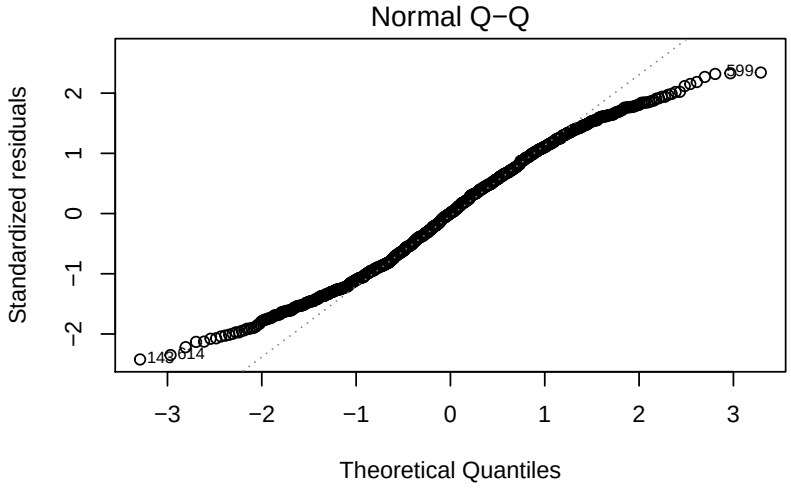
```
visreg(m3)
```

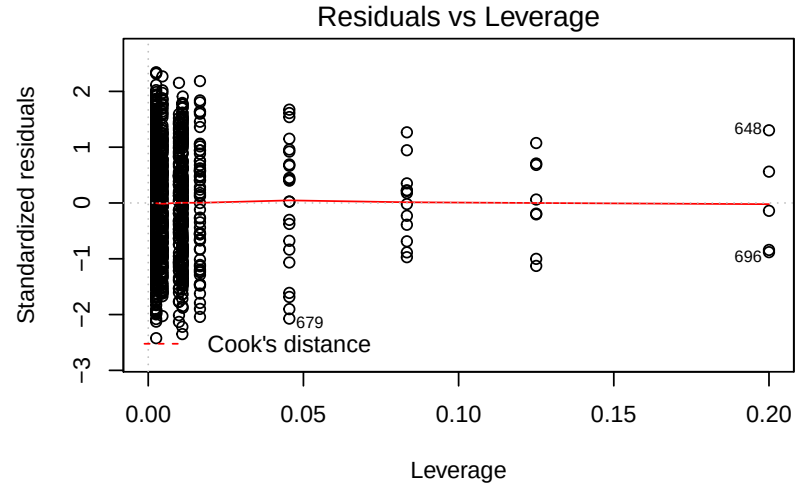


Model checking: residuals









Combining continuous and categorical predictors

Predicting tree height based on dbh and site

$$y_i = a + bx_i + \varepsilon_i$$

$$y_i = a + b_{plot2} + c_{plot3} + d_{plot4} + e_{plot5} + \ldots + k \cdot DBH_i + \varepsilon_i$$

Predicting tree height based on dbh and site

```
Call:
lm(formula = height ~ plot + 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 ***
plot2        6.504303   0.256730  25.335  < 2e-16 ***
plot3        4.357457   0.354181  12.303  < 2e-16 ***
plot4        1.934650   0.356102   5.433 6.98e-08 ***
plot5        3.637432   0.339688  10.708  < 2e-16 ***
plot6        4.204511   0.421906   9.966  < 2e-16 ***
plot7       -0.176193   0.666772  -0.264   0.7916
plot8       -5.312648   0.893603  -5.945 3.82e-09 ***
plot9        5.437049   1.087766   4.998 6.84e-07 ***
plot10       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
```

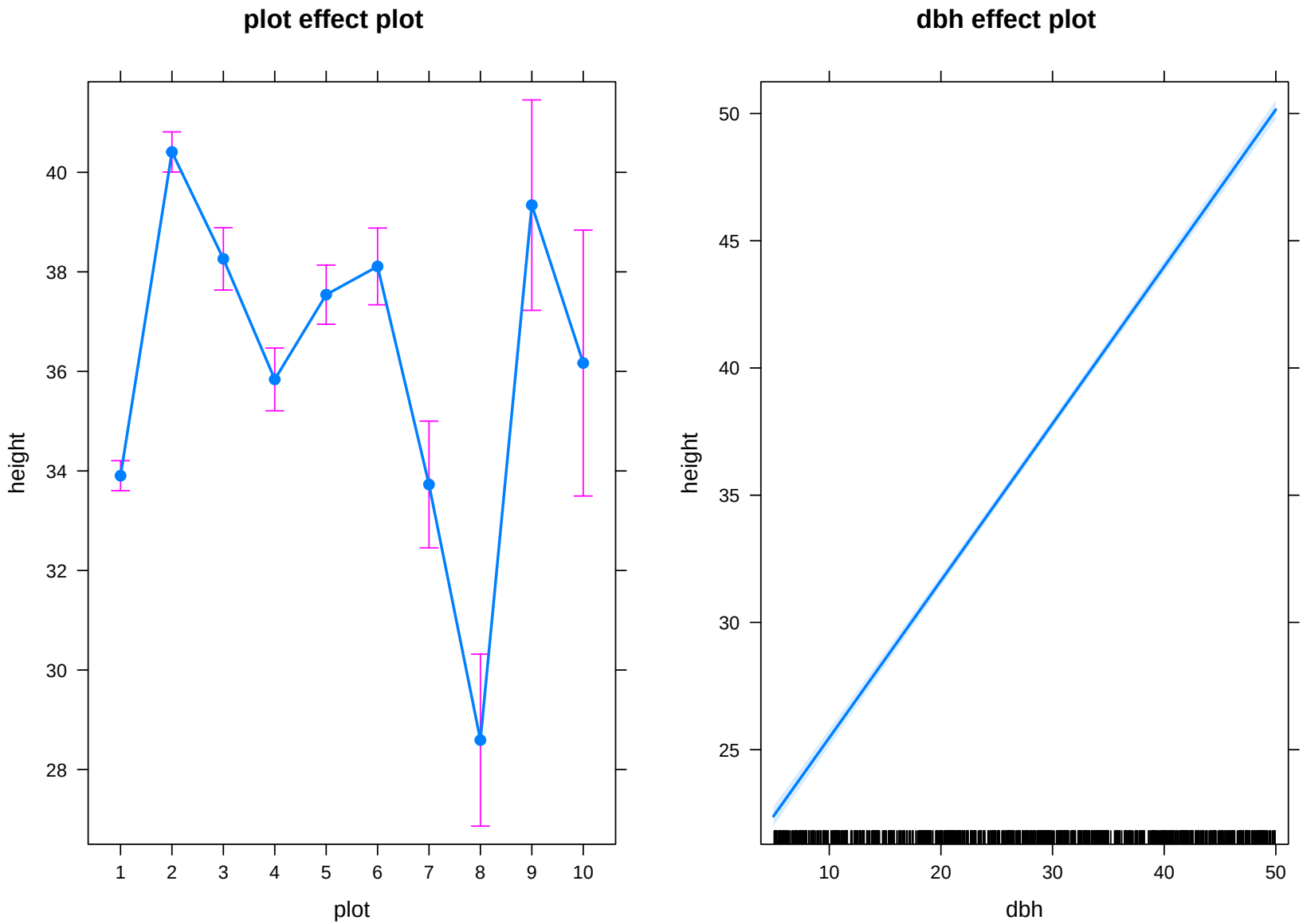
Estimated tree heights for each site

```
summary(allEffects(multreg))
```

```
 model: height ~ plot + dbh

 plot effect
plot
       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
plot
       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
plot
       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
```

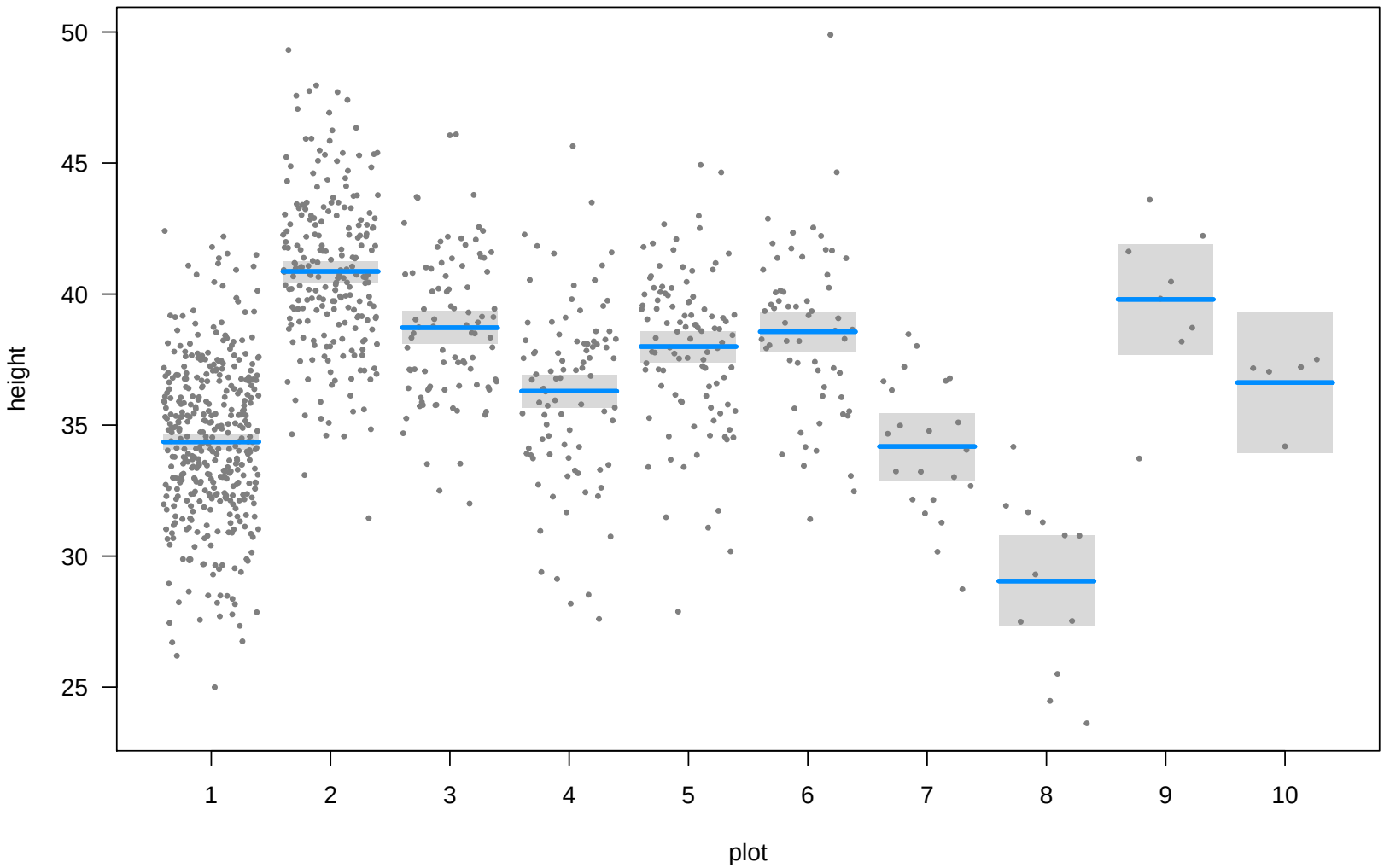
Plot

```
plot(allEffects(multreg))
```

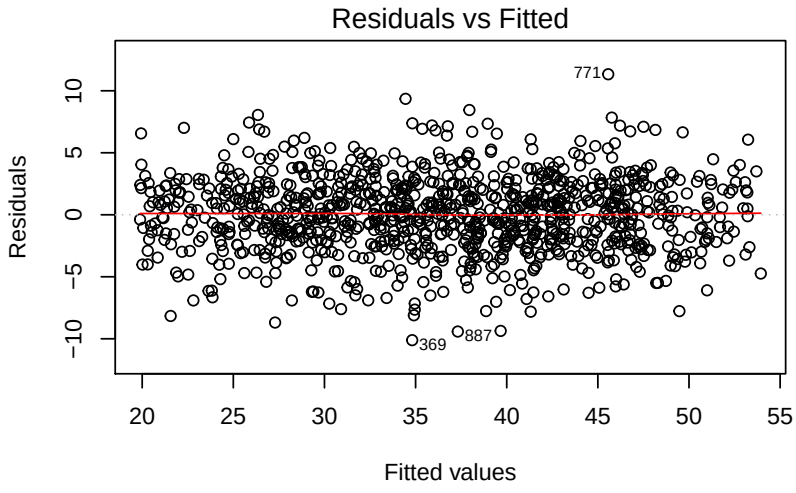


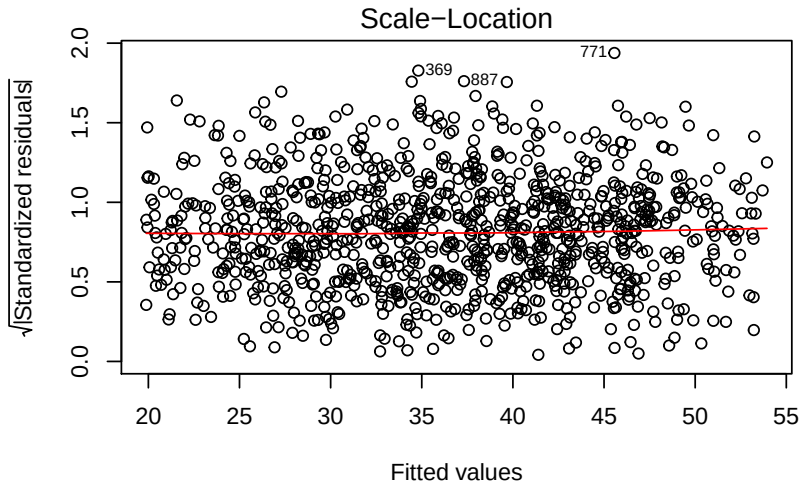
Plot (visreg)

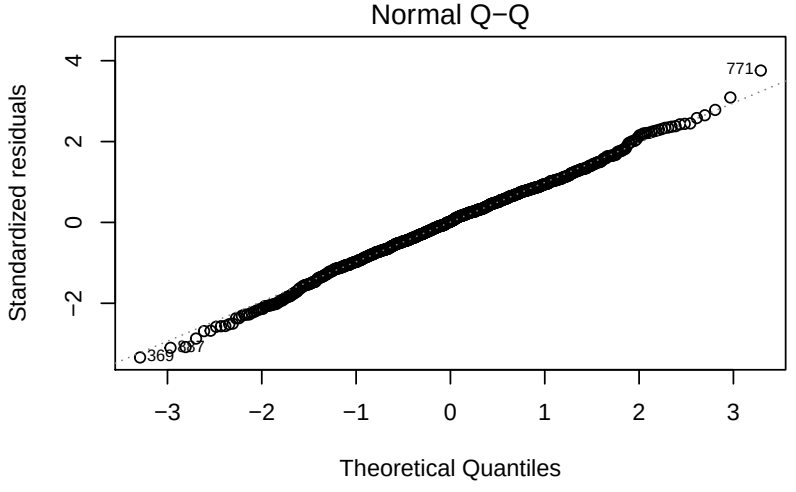
```
visreg(multreg)
```

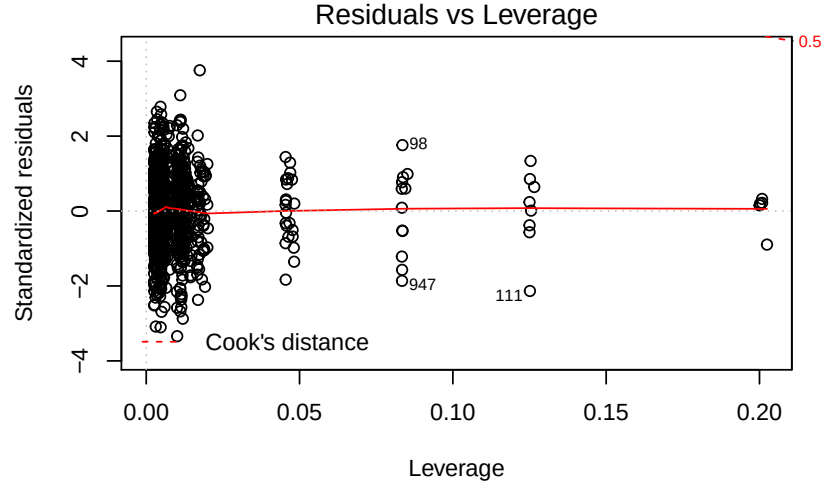


Model checking: residuals



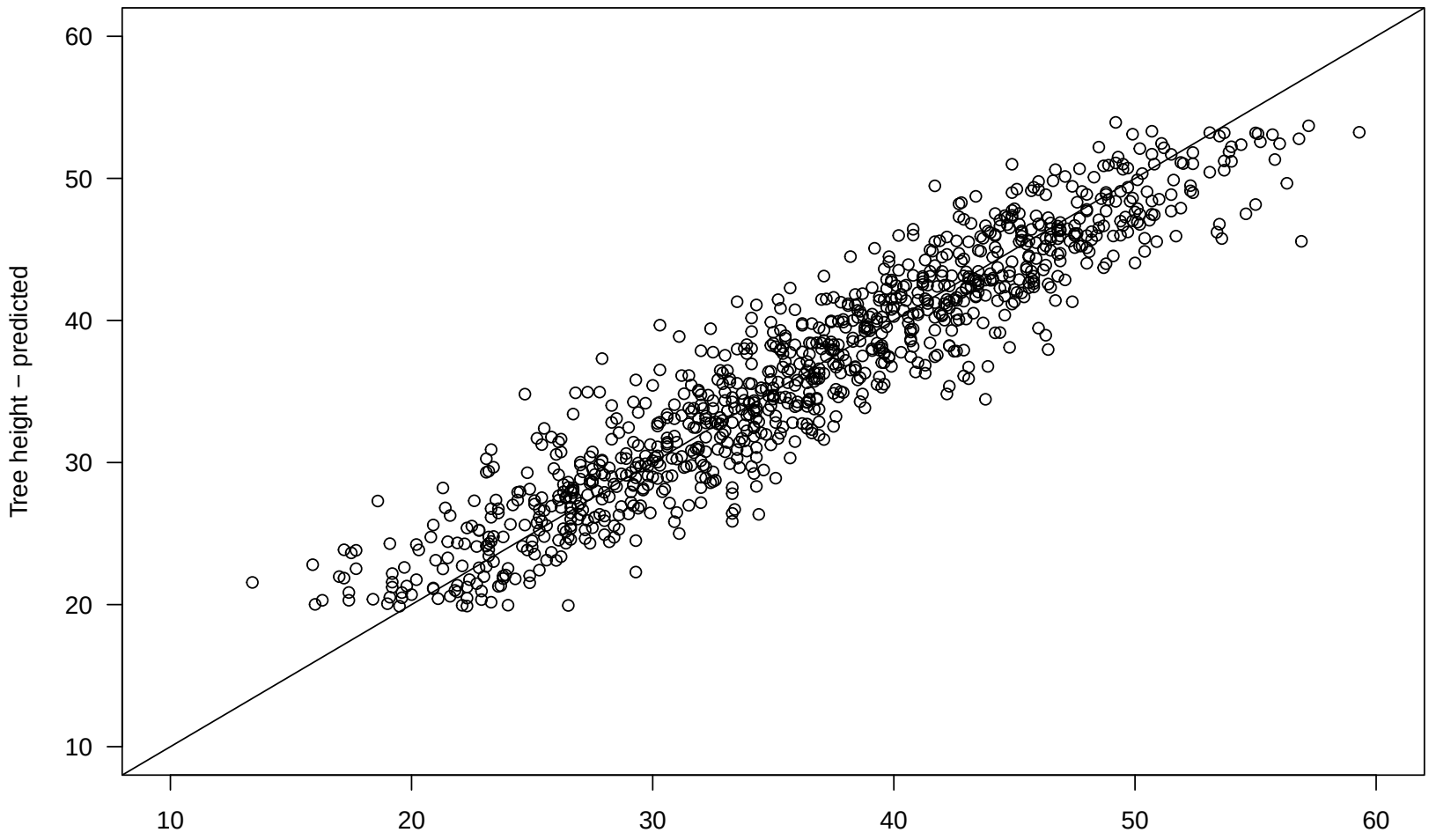






How good is this model? Calibration plot

```
trees$height.pred <- fitted(multreg)
plot(trees$height, trees$height.pred, xlab = "Tree height - obse
abline(a = 0, b = 1)
```



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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- paperplanes: How does flight distance differ with age, gender or paper type?
- mammal sleep: Are sleep patterns related to diet?
- iris: Predict petal length $\sim$ petal width and species