

## R02 - Regression diagnostics

STAT 5870 (Engineering)  
Iowa State University

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# All models are wrong!

George Box (Empirical Model-Building and Response Surfaces, 1987):

*All models are wrong, but some are useful.*

<http://stats.stackexchange.com/questions/57407/what-is-the-meaning-of-all-models-are-wrong-but-some-are-useful>

*"All models are wrong" that is, every model is wrong because it is a simplification of reality. Some models, especially in the "hard" sciences, are only a little wrong. They ignore things like friction or the gravitational effect of tiny bodies. Other models are a lot wrong - they ignore bigger things.*

*"But some are useful" - simplifications of reality can be quite useful. They can help us explain, predict and understand the universe and all its various components.*

*This isn't just true in statistics! Maps are a type of model; they are wrong. But good maps are very useful.*

# Simple Linear Regression

The simple linear regression model is

$$Y_i \stackrel{iid}{\sim} N(\beta_0 + \beta_1 X_i, \sigma^2)$$

this can be rewritten as

$$Y_i = \beta_0 + \beta_1 X_i + \epsilon_i \quad \epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2).$$

Key assumptions are:

- The errors are
  - normally distributed,
  - have constant variance, and
  - are independent of each other.
- There is a linear relationship between the expected response and the explanatory variables.

# Multiple Regression

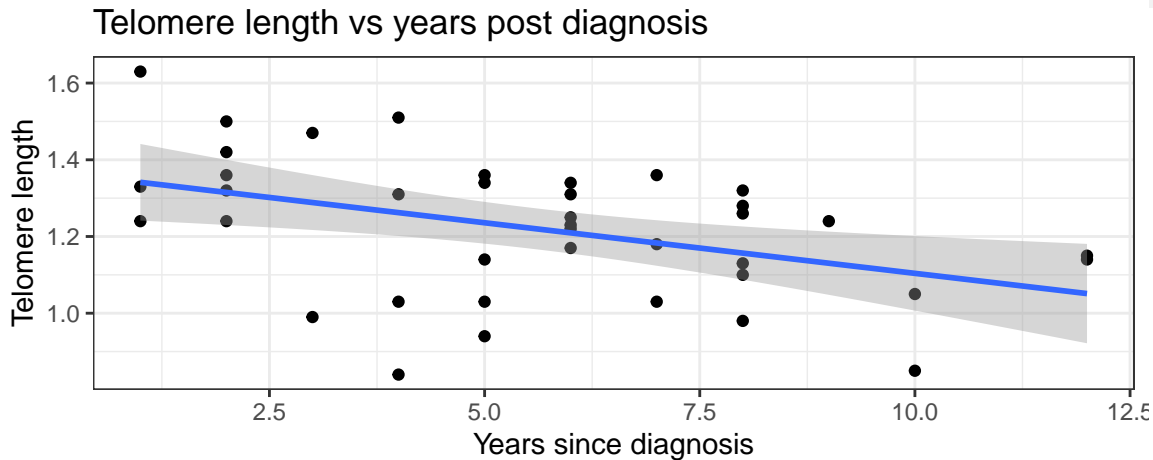
The **multiple regression** model is

$$Y_i = \beta_0 + \beta_1 X_{i,1} + \cdots + \beta_p X_{i,p} + \epsilon_i \quad \epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2).$$

Key assumptions are:

- The errors are
  - normally distributed,
  - have constant variance, and
  - are independent of each other.
- There is a specific relationship between the expected response and the explanatory variables.

## Telomere data

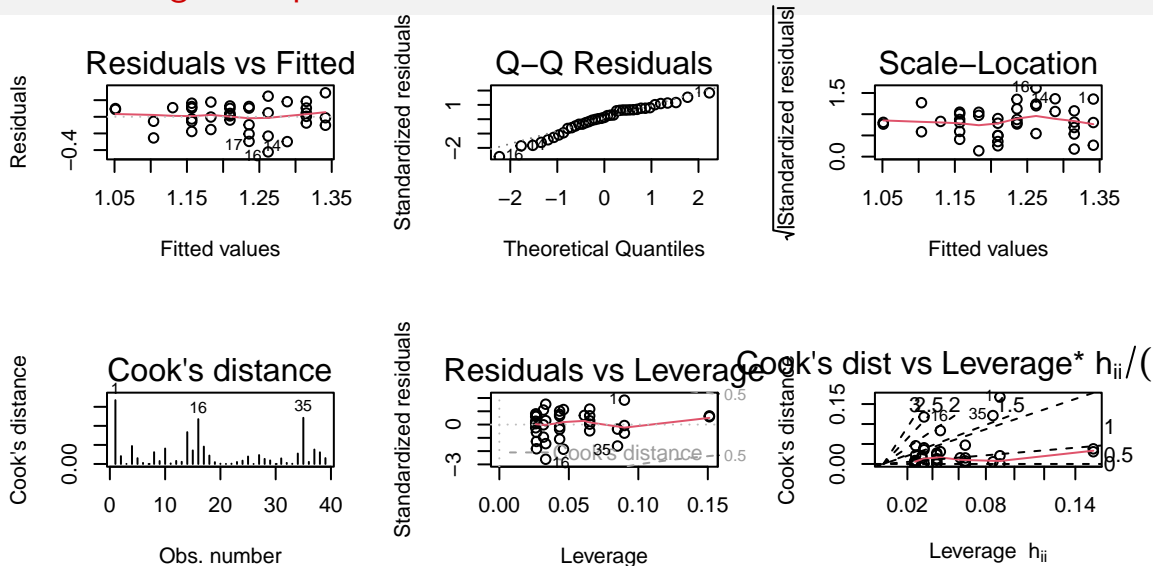


# Case statistics

To evaluate these assumptions, we will calculate a variety of **case statistics**:

- Leverage
- Fitted values
- Residuals
  - Standardized residuals
  - Studentized residuals
- Cook's distance

# Default diagnostic plots in R



# Leverage

The **leverage** ( $0 \leq h_i \leq 1$ ) of an observation  $i$  is a measure of how far away that observation's explanatory variable value is from the other observations. Larger leverage indicates a larger **potential** influence of a single observation on the regression model.

In simple linear regression,

$$h_i = \frac{1}{n} + \frac{(\bar{x} - x_i)^2}{(n-1)s_X^2}$$

which is involved in the standard error for the line for a location  $x_i$ .

The variability in the residuals is a function of the leverage, i.e.

$$Var[r_i] = \sigma^2(1 - h_i)$$



# Telomere data

```
m <- lm(telomere.length~years, Telomeres)

cbind(Telomeres, leverage = hatvalues(m)) %>%
  select(years, leverage) %>%
  unique() %>%
  arrange(-years)
```

	years	leverage
37	12	0.15113547
35	10	0.08504307
39	9	0.06115897
27	8	0.04338293
25	7	0.03171496
20	6	0.02615505
12	5	0.02670321
10	4	0.03335944
8	3	0.04612373
4	2	0.06499608
1	1	0.08997651
2	1	0.08997651

# Residuals and Fitted values

A regression model can be expressed as

$$Y_i = \mu_i + \epsilon_i = \beta_0 + \beta_1 X_i + \epsilon_i, \quad \epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2)$$

A **fitted value**  $\hat{Y}_i$  for an observation  $i$  is

$$\hat{Y}_i = \hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 X_i$$

and the **residual** is

$$r_i = Y_i - \hat{Y}_i = \hat{\epsilon}_i$$

# Standardized residuals

Often we will **standardize** residuals, i.e.

$$\frac{r_i}{\sqrt{\widehat{Var}[r_i]}} = \frac{r_i}{\hat{\sigma}\sqrt{1-h_i}}$$

If  $|r_i|$  is large, it will have a large impact on  $\hat{\sigma}^2 = \sum_{i=1}^n r_i^2 / (n-2)$ . Thus, we can calculate an **externally studentized residual**

$$\frac{r_i}{\hat{\sigma}_{(i)}\sqrt{1-h_i}}$$

where  $\hat{\sigma}_{(i)}^2 = \sum_{j \neq i} r_j^2 / (n-3)$ .

Both of these residuals can be compared to a standard normal distribution.

# Telomere data: residuals

	years	telomere.length	leverage	residual	standardized	studentized
1	1	1.63	0.08997651	0.288692247	1.84050794	1.90475158
2	1	1.24	0.08997651	-0.101307753	-0.64587021	-0.64070443
3	1	1.33	0.08997651	-0.011307753	-0.07209064	-0.07111476
4	2	1.50	0.06499608	0.185066562	1.16399233	1.16977226
5	2	1.42	0.06499608	0.105066562	0.66082533	0.65571510
6	2	1.36	0.06499608	0.045066562	0.28345009	0.27989750
7	2	1.32	0.06499608	0.005066562	0.03186659	0.03143344
8	3	1.47	0.04612373	0.181440877	1.12984272	1.13420749
9	2	1.24	0.06499608	-0.074933438	-0.47130041	-0.46628962
10	4	1.51	0.03335944	0.247815192	1.53293696	1.56251168
11	4	1.31	0.03335944	0.047815192	0.29577555	0.29209673
12	5	1.36	0.02670321	0.124189507	0.76558098	0.76121769
13	5	1.34	0.02670321	0.104189507	0.64228860	0.63711129
14	3	0.99	0.04612373	-0.298559123	-1.85914473	-1.92601533
15	4	1.03	0.03335944	-0.232184808	-1.43625042	-1.45793267
16	4	0.84	0.03335944	-0.422184808	-2.61155376	-2.85227987
17	5	0.94	0.02670321	-0.295810493	-1.82355895	-1.88546999
18	5	1.03	0.02670321	-0.205810493	-1.26874325	-1.27962563
19	5	1.14	0.02670321	-0.095810493	-0.59063518	-0.58536500
20	6	1.17	0.02615505	-0.039436179	-0.24304058	-0.23992534
21	6	1.23	0.02615505	0.020563821	0.12673244	0.12503525
22	6	1.25	0.02615505	0.040563821	0.24999011	0.24679724
23	6	1.31	0.02615505	0.100563821	0.61976313	0.61452870
24	6	1.34	0.02615505	0.130563821	0.80464964	0.80073848
25	7	1.36	0.03171496	0.176938136	1.09357535	1.09656310
26	6	1.22	0.02615505	0.010563821	0.06510360	0.06422148
27	8	1.32	0.04338293	0.163312451	1.01549809	1.01593894
28	8	1.28	0.04338293	0.123312451	0.76677288	0.76242192
29	8	1.26	0.04338293	0.103312451	0.64241028	0.63723335

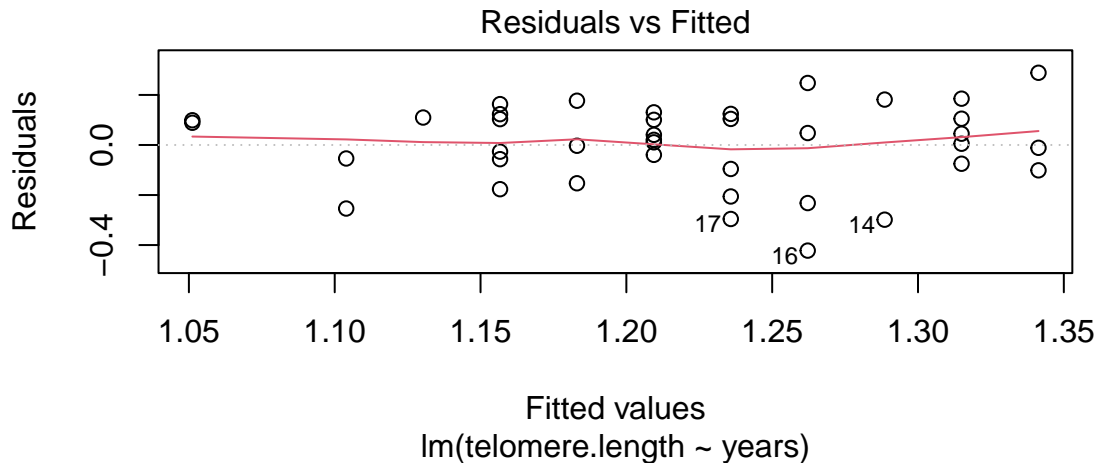
# Cook's distance

The **Cook's distance** for an observation  $i$  ( $d_i > 0$ ) is a measure of how much the regression parameter estimates change when that observation is included versus when it is excluded.

Operationally, we might be concerned when  $d_i$  is

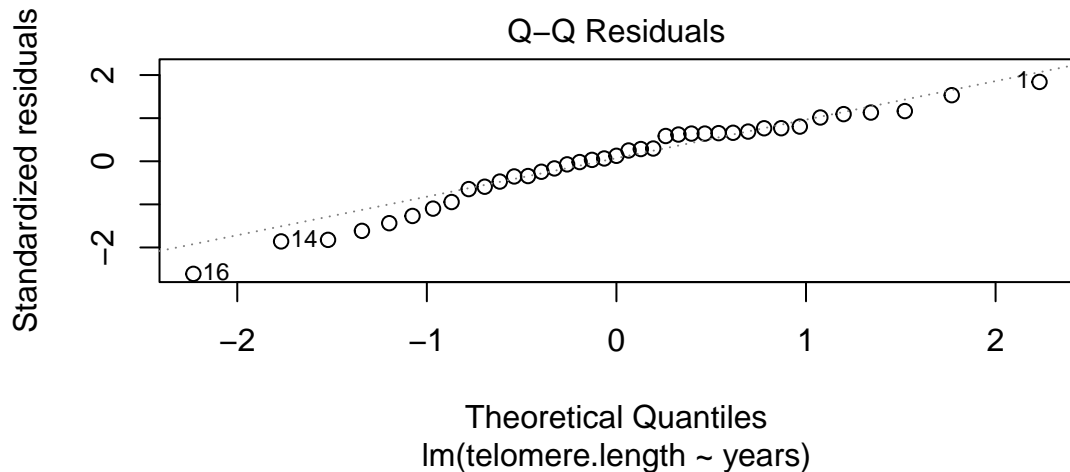
- larger than 1 or
- larger than  $4/n$ .

# Residuals vs fitted values



Assumption	Violation
Linearity	Curvature
Constant variance	Funnel shape

# QQ-plot



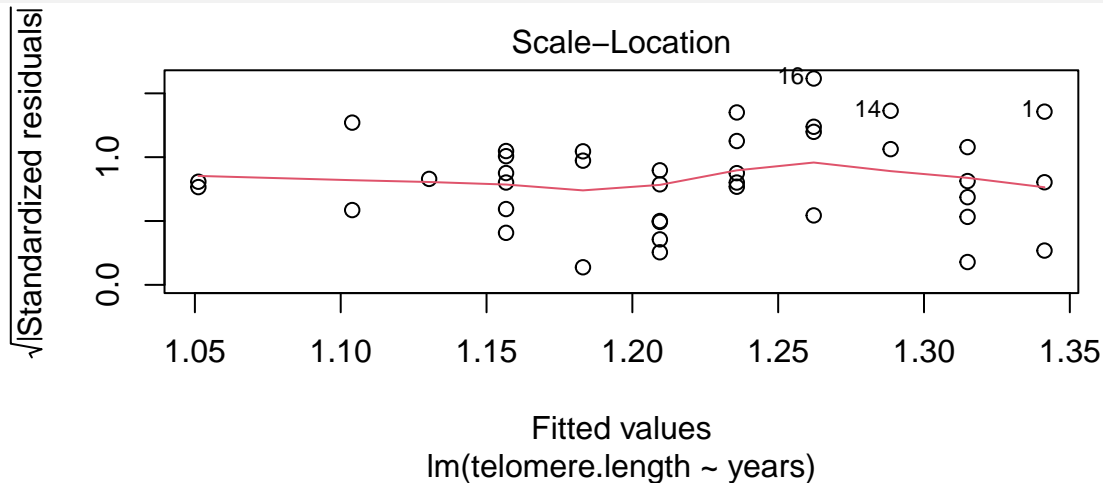
Assumption

Violation

Normality

Points don't generally fall along the line

# Absolute standardized residuals vs fitted values



Assumption

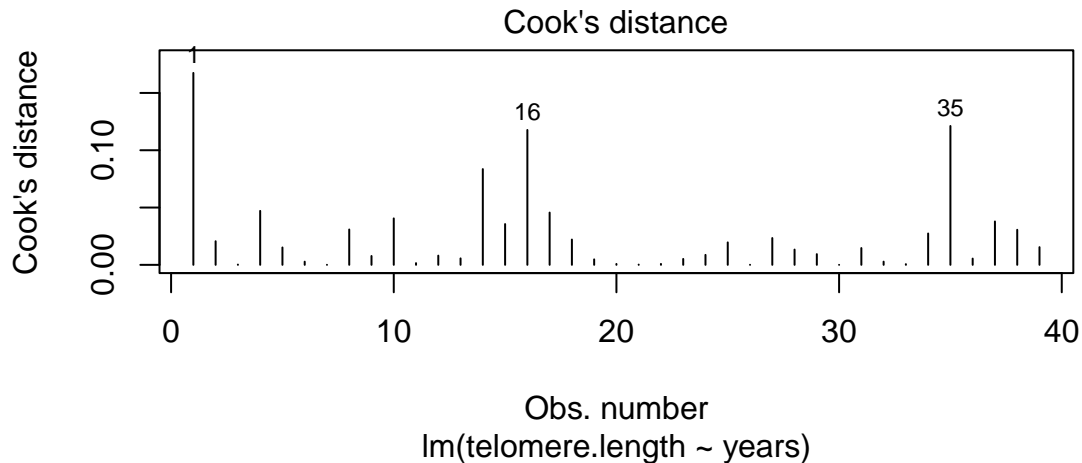
Violation

Constant variance

Increasing (or decreasing) trend



# Cook's distance



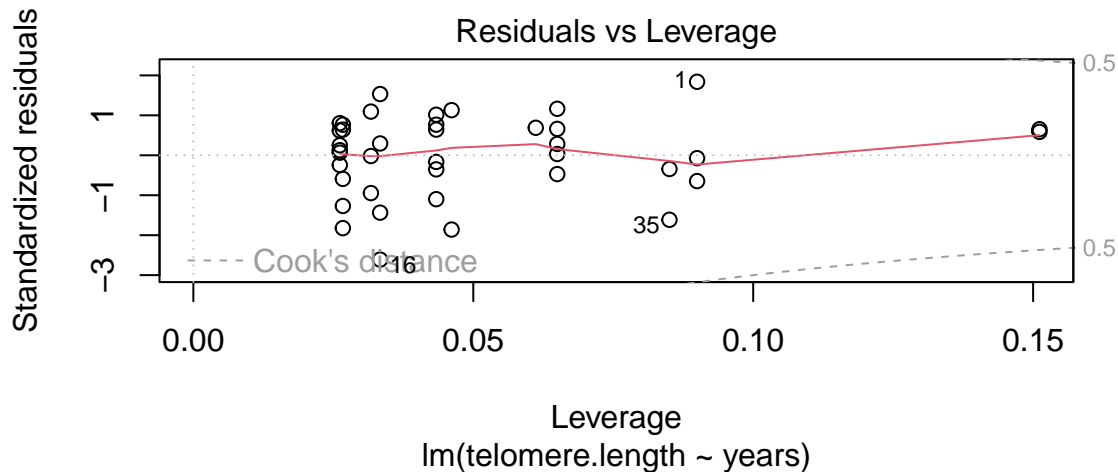
Outlier

Violation

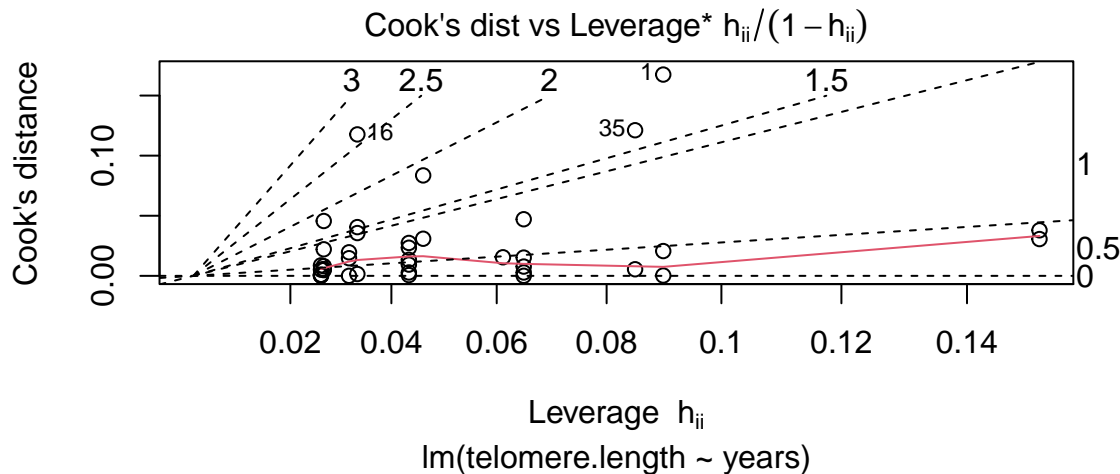
Influential observation

Cook's distance larger than  $(1 \text{ or } 4/n)$

# Residuals vs leverage



# Cooks' distance vs leverage



This plot is pretty confusing.

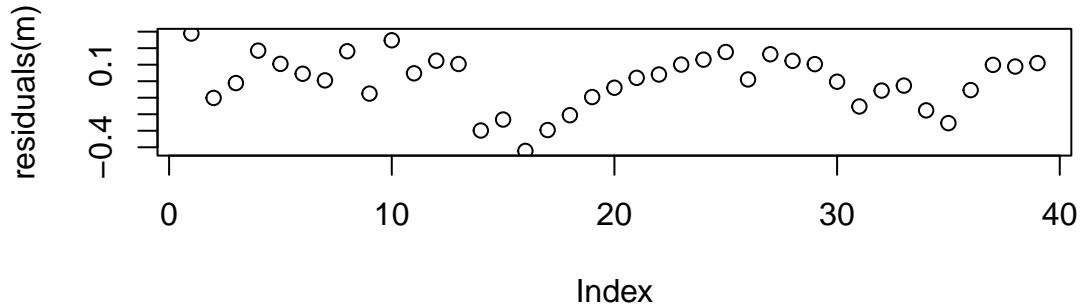
## Additional plots

Default plots do not assess all model assumptions.

Two additional suggested plots:

- Residuals vs row number
- Residuals vs (each) explanatory variable

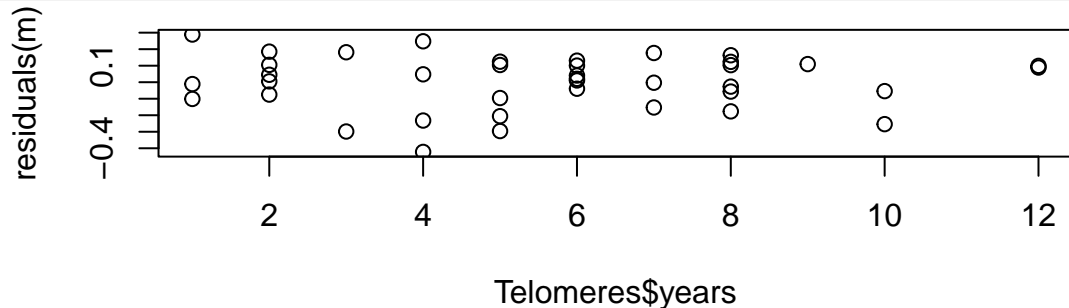
## Plot residuals vs row number (index)



```
plot(residuals(m))
```

Assumption	Violation
Independence	A pattern suggests temporal correlation (or an artefact)

# Residual vs explanatory variable

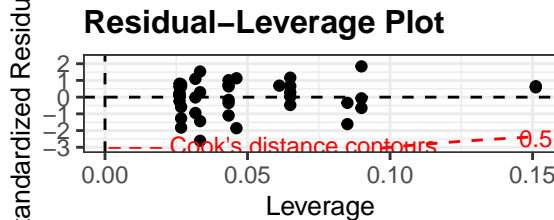
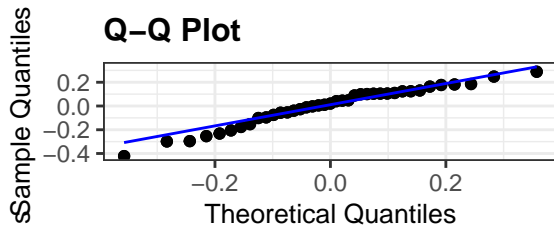
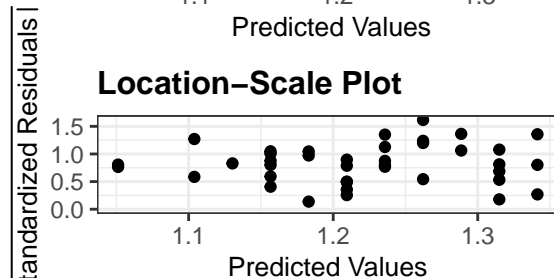
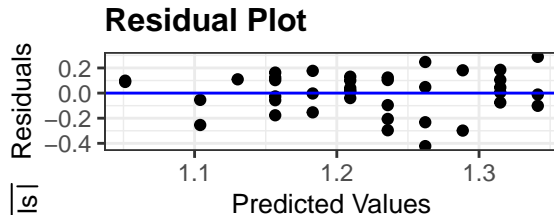


```
plot(Telomeres$years, residuals(m))
```

Assumption	Violation
Linearity	A pattern suggests non-linearity

# ggResidpanel: R default

```
resid_panel(m, plots = "R")
```

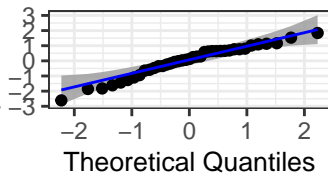


# ggResidpanel: R all plots

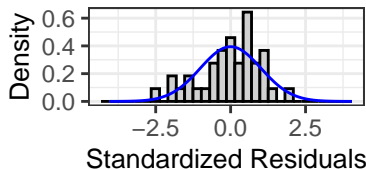
```
resid_panel(m, plots = c("qq", "hist", "resid", "index", "yvp", "cookd"),
  bins = 30, smoother = TRUE, qqbands = TRUE,
  type = "standardized") # what I was calling studentized
```

Standardized Residuals Sample Quantiles

## Q-Q Plot

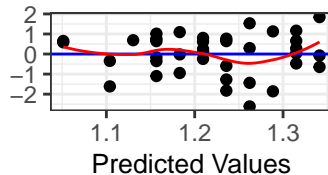


## Histogram

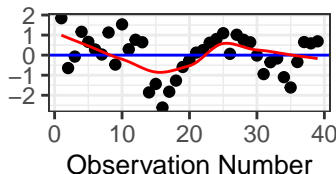


Standardized Residuals

## Residual Plot

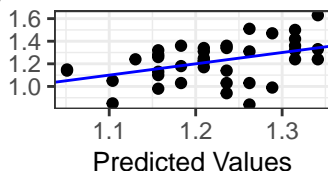


## Index Plot



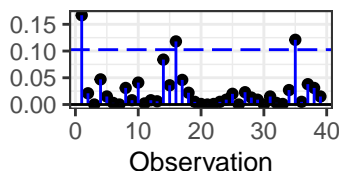
telomere.length

## Response vs Predicted



COOK's D

## COOK's D Plot

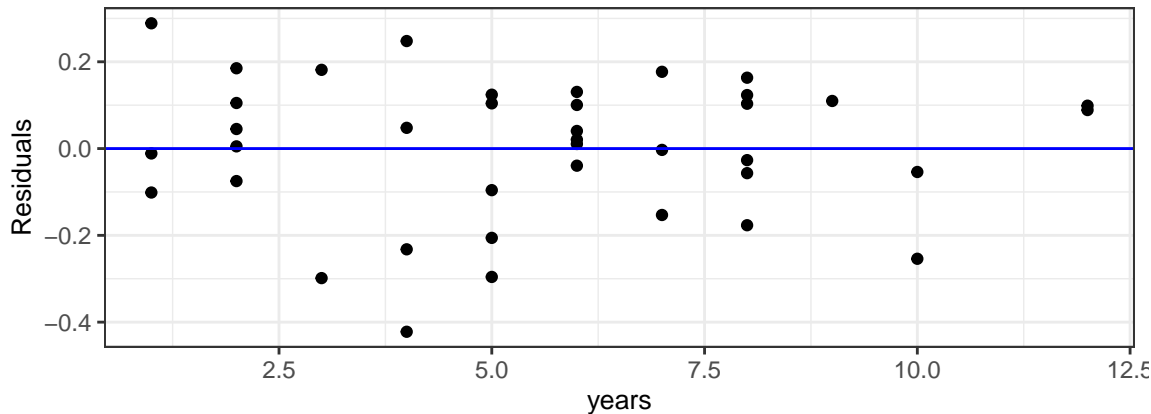




# ggResidpanel: R explanatory

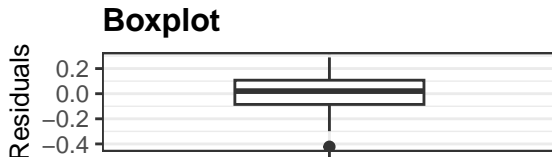
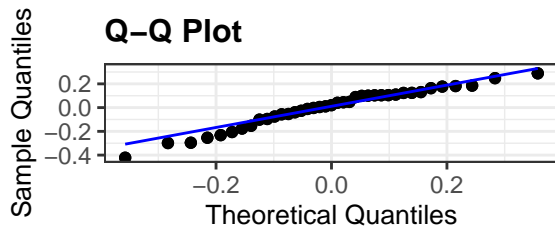
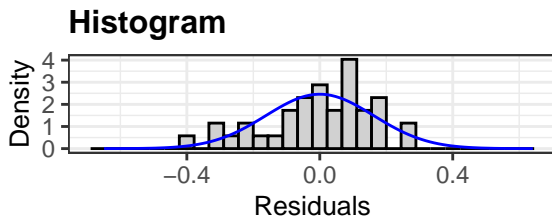
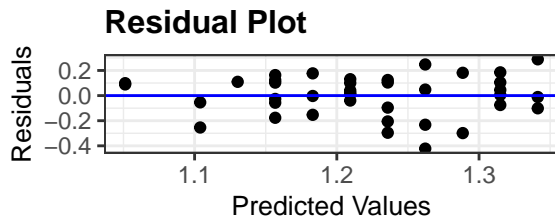
```
resid_xpanel(m)
```

## Plots of Residuals vs Predictor Variables



# ggResidpanel: SAS

```
resid_panel(m, plots = "SAS")
```



# Summary

## Case statistics:

- Fitted values
- Leverage
- Residuals
  - Standardized residuals
  - Studentized residuals
- Cook's distance

## Model assumptions:

- Normality
- Constant variance
- Independence
- Linearity