1.4 Bootstrap CIs

We will look at five different ways to create confidence intervals using the boostrap and discuss which to use when.

1. Percentile Bootstrap CI
2. Basic Bootstrap CI
3. Standard Normal Bootstrap CI
4. Bootstrap t (studentized)
5. Accelerated Bias-Corrected (BCa)
   = adjusted for skewness

+ which to use when!

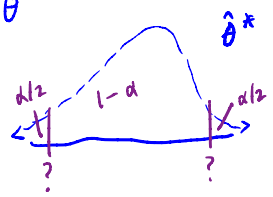
Key ideas:

(1) When you say "we used bootstrapping to estimate CI" you need to say which one.

(2) Whatever you are bootstrapping needs to be independent

(3) Bootstrapping is an attempt to simulate replication (think about interpretation of a CI).

estimate sampling dsn of $\hat{\theta}$ via bootstrap.



1.4.1 Percentile Bootstrap CI

Let $\hat{\theta}^{(1)}, \ldots, \hat{\theta}^{(B)}$ be bootstrap replicates and let $\hat{\theta}_{\alpha/2}$ be the $\alpha/2$ quantile of $\hat{\theta}^{(1)}, \ldots, \hat{\theta}^{(B)}$.

estimate of sampling dsn "bootstrap dsn"

Then, the $100(1-\alpha)\%$ Percentile Bootstrap CI for θ is

$$\left(\hat{\theta}_{\alpha/2}, \hat{\theta}_{1-\alpha/2} \right)$$

In R, if `bootstrap.reps = c(`$\hat{\theta}^{(1)}, \ldots, \hat{\theta}^{(B)}$`)`, the percentile CI is

vector of bootstrap replicates.

```
quantile(bootstrap.reps, c(alpha/2, 1 - alpha/2))
```

Assumptions/usage

(1) widely used because simple to implement & explain

(2) Use when little bias and skewness in bootstrap dsn.

(3) Drawback: CI's usually too narrow! (coverage too low).

(4) BCa intervals usually perform better (nominal coverage).

1.4.2 Basic Bootstrap CI (corrects for bias).

The $100(1-\alpha)\%$ Basic Bootstrap CI for θ is

$$\left(\hat{\theta} - \left[\hat{\theta}_{1-\alpha/2} - \hat{\theta}\right],\ \hat{\theta} - \left[\hat{\theta}_{\alpha/2} - \hat{\theta}\right]\right)$$

$\hat{\theta}_{1-\alpha/2}$: $1-\alpha/2$ quantile of bootstrap dsn for $\hat{\theta}$

$\hat{\theta}$: estimate of θ from original sample.

recentering the interval based on estimated bias.

simplified.

$$\Rightarrow \left(2\hat{\theta} - \hat{\theta}_{1-\alpha/2},\ 2\hat{\theta} - \hat{\theta}_{\alpha/2}\right).$$

Assumptions/usage

(1) Better than percentile bootstrap b/c corrects for bias.
(does nothing for skewness!).

(2) Harder to explain.

1.4.3 Standard Normal Bootstrap CI

From the CLT,

$$Z = \frac{\hat{\theta} - E(\hat{\theta})}{se(\hat{\theta})} \dot{\sim} N(0,1).$$

under some assumptions...

So, the $100(1-\alpha)\%$ Standard Normal Bootstrap CI for θ is

$$\hat{\theta} \pm z_{1-\alpha/2} \widehat{se}(\hat{\theta}).$$

comes from bootstrap replicates.

$sd(\hat{\theta}^{(1)}, \ldots, \hat{\theta}^{(B)})$.

Assumptions/usage

(1) $\hat{\theta} \dot{\sim} N(E(\hat{\theta}), se(\hat{\theta})^2)$ ← BIG assumption if $\hat{\theta}$ is not a sample mean.

(2) If $\hat{\theta}$ is unbiased $\Rightarrow E(\hat{\theta}) = \theta$ ✓

(If not unbiased, bias corrected version w/ this method too) → see later code.

(3) typically requires large n.

this is a misleading name.

1.4.4 Bootstrap t CI (Studentized Bootstrap)

Even if the distribution of $\hat{\theta}$ is Normal and $\hat{\theta}$ is unbiased for θ, the Normal distribution is not exactly correct for z. (because we estimate $se(\hat{\theta})$).

$$t^* = \frac{\hat{\theta} - E(\hat{\theta})}{\hat{se}(\hat{\theta})} \sim t_{n-1} \; ? \; \times$$

$\hat{se}(\hat{\theta})$ ← is not $s/\sqrt{n}$!

Additionally, the distribution of $\hat{se}(\hat{\theta})$ is unknown.

So we cannot claim $t^* \sim t_{n-1}$

$\Rightarrow$ The bootstrap t interval does not use a Student t distribution as the reference distribuion, instead we estimate the distribution of a "t type" statistic by resampling.

studentized. bootstrap

The $100(1-\alpha)\%$ Bootstrap t CI is quantile of the bootstrap "t-type" statistic.

$$\left(\hat{\theta} - t^*_{1-\alpha/2} \cdot \hat{se}(\hat{\theta}) \;,\; \hat{\theta} + t^*_{\alpha/2} \cdot \hat{se}(\hat{\theta}) \right)$$

$\hat{\theta}$: estimate of θ from original sample

$\hat{se}(\hat{\theta})$ = se based on $(\hat{\theta}^{(1)}, \ldots, \hat{\theta}^{(B)})$.

Overview

need se of this ↓ ↓ bootstrap standard for θ

t-type statistic $t^{(1)} = \dfrac{\hat{\theta}^{(1)} - \hat{\theta}}{\hat{se}(\hat{\theta}^{(1)})}, \ldots, t^{(B)} = \dfrac{\hat{\theta}^{(B)} - \hat{\theta}}{\hat{se}(\hat{\theta}^{(B)})}$.

$\hat{se}(\hat{\theta}^{(1)})$ = bootstrap estimate of se of $\hat{\theta}$ based on the first bootstrap sample

DOUBLE BOOTSTRAP!

WOAH!

To estimate the "t style distribution" for $\hat{\theta}$,

1. Compute $\hat{\theta}$ [based on sample $x_1, \ldots, x_n$].
2. for each replicate $b = 1, \ldots, B$
   a) sample w/ replacement from $\underline{x}$
      $\underline{x}^{(b)} = (x_1^{(b)}, \ldots, x_n^{(b)})$.
   b) Compute $\hat{\theta}^{(b)}$.
   c) for each replicate $r = 1, \ldots, R$
      i) sample w/ replacement from $\underline{x}^{(b)}$
         $\underline{x}^{(b)(r)} = (x_1^{(b)(r)}, \ldots, x_n^{(b)(r)})$
      ii) Compute $\hat{\theta}^{(b)(r)}$.
   d) Compute $\hat{se}(\hat{\theta}^{(b)}) = sd(\hat{\theta}^{(b)(1)}, \ldots, \hat{\theta}^{(b)(R)})$
   e) Compute "t style" statistics $t^{(b)} = \dfrac{\hat{\theta}^{(b)} - \hat{\theta}}{\hat{se}(\hat{\theta}^{(b)})}$.
3. get quantiles $t^*_{1-\alpha/2}, t^*_{\alpha/2}$
4. Compute CI.

Assumptions/usage

(1) Require small bias and skewness in bootstrap dsn.

(2) Computationally intensive.

(3) Need $\hat{\theta}$ independent of $\hat{se}(\hat{\theta})$.

"accelerated Bias corrected."

1.4.5 BCa CIs

Modified version of percentile intervals that adjusts for bias of estimator and skewness of the sampling distribution.

This method automatically selects a transformation so that the normality assumption holds.

Idea:

Assume there exists a monotonically increasing function g and constants a, b s.t.

$$U = \frac{g(\hat{\theta}) - g(\theta)}{1 + a\, g(\theta)} + b \sim N(0, 1).$$

where $1 + a\, g(\theta) > 0$.

The BCa method uses bootstrapping to estimate the bias and skewness then modifies which percentiles are chosen to get the appropriate confidence limits for a given data set.

In summary,

BCa is like percentile bootstrap, but instead of $(\hat{\theta}_{\alpha/2}, \hat{\theta}_{1-\alpha/2})$.

BCa chooses better quantiles (not $\alpha/2$, $1-\alpha/2$) to account for both bias and skewness.

Assumptions / usage

(1) Better theoretical & practical performance than percentile method (better coverage)

(2) harder to explain.

Your Turn

We will consider a telephone repair example from Hesterberg (2014). `Verizon` has repair times, with two groups, CLEC and ILEC, customers of the "Competitive" and "Incumbent" local exchange carrier.

↑ other carriers ↑ verizon customers

Verizon required by law to serve both at same speed.

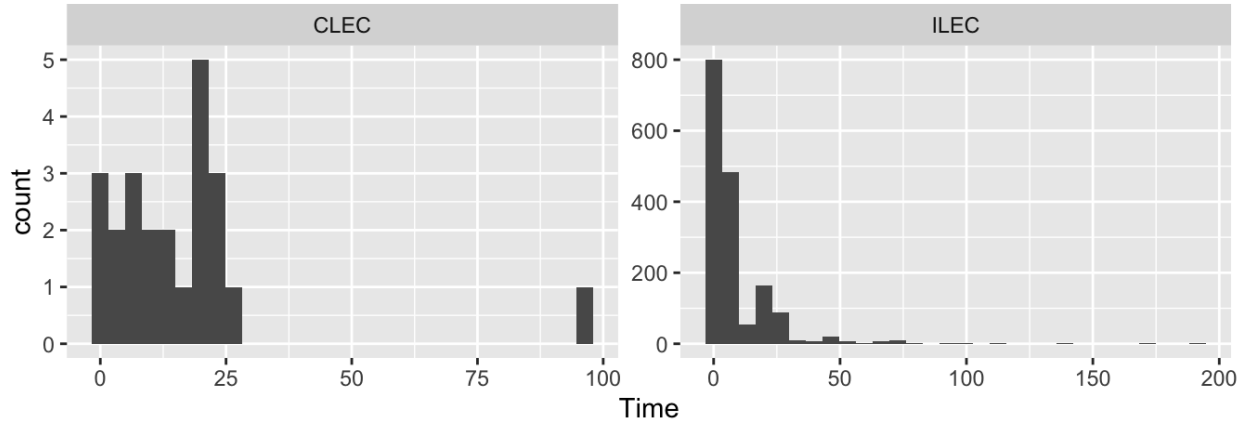
```
library(resample) # package containing the data

data(Verizon)
head(Verizon)
```

```
##    Time Group
## 1 17.50  ILEC
## 2  2.40  ILEC
## 3  0.00  ILEC
## 4  0.65  ILEC
## 5 22.23  ILEC
## 6  1.20  ILEC
```

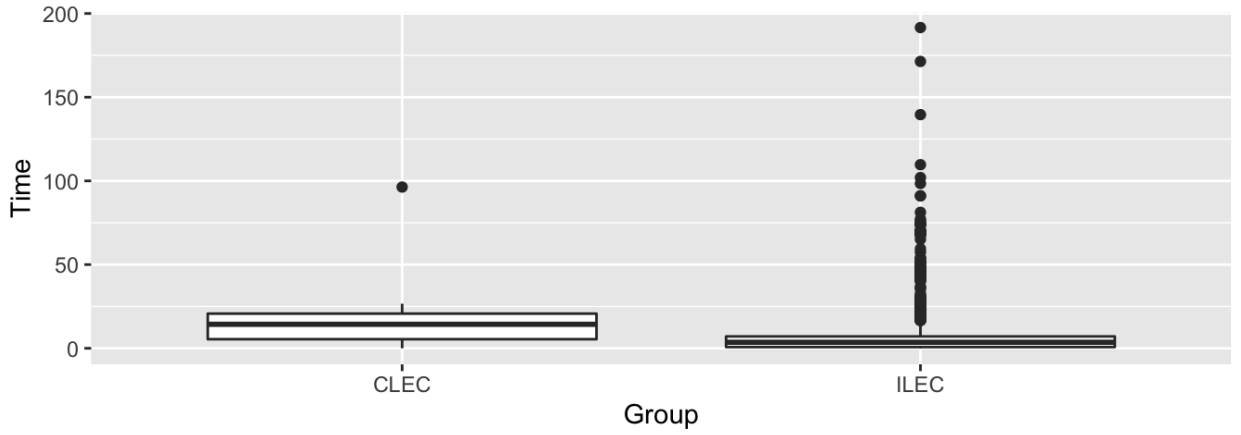
```
Verizon %>%
  group_by(Group) %>%
  summarize(mean = mean(Time), sd = sd(Time), min = min(Time), max =
  max(Time)) %>%
  kable()
```

Group	mean	sd	min	max	n
CLEC	16.509130	19.50358	0	96.32	23
ILEC	8.411611	14.69004	0	191.60	1664

```
ggplot(Verizon) +
  geom_histogram(aes(Time)) +
  facet_wrap(.~Group, scales = "free")
```




```
ggplot(Verizon) +
  geom_boxplot(aes(Group, Time))
```

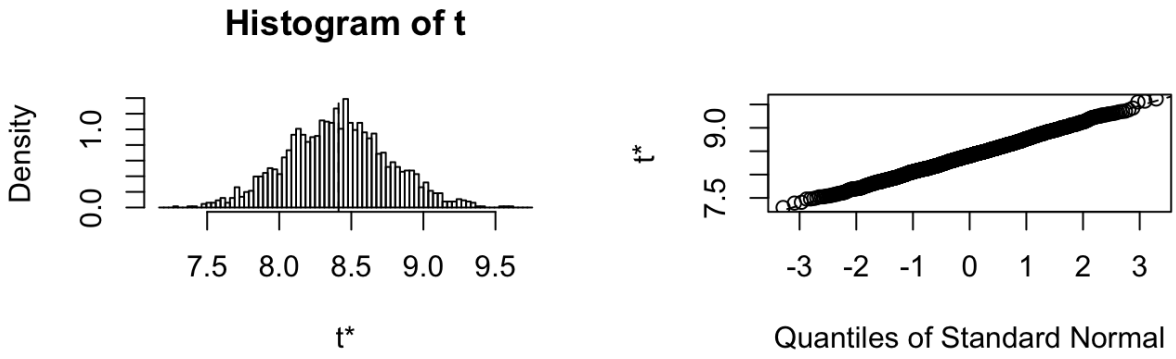


1.5 Bootstrapping CIs

There are many bootstrapping packages in `R`, we will use the `boot` package. The function `boot` generates R resamples of the data and computes the desired statistic(s) for each sample. This function requires 3 arguments:

1. data = the data from the original sample (data.frame or matrix).
2. statistic = a function to compute the statistic from the data where the first argument is the data and the second argument is the indices of the obervations in the boostrap sample.
3. R = the number of bootstrap replicates.

```
library(boot) # package containing the bootstrap function

mean_func <- function(x, idx) {
  mean(x[idx])
}

ilec_times <- Verizon[Verizon$Group == "ILEC",]$Time
boot.ilec <- boot(ilec_times, mean_func, 2000)

plot(boot.ilec)
```



If we want to get Bootstrap CIs, we can use the `boot.ci` function to generate the 5 different nonparamteric bootstrap confidence intervals.

```
boot.ci(boot.ilec, conf = .95, type = c("perc", "basic", "norm",
  "bca"))
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot.ilec, conf = 0.95, type = c("perc", "basic",
```

```
##     "norm", "bca"))
##
## Intervals :
## Level      Normal              Basic
## 95%   ( 7.719,  9.114 )   ( 7.709,  9.119 )
##
## Level     Percentile            BCa
## 95%   ( 7.704,  9.114 )   ( 7.752,  9.164 )
## Calculations and Intervals on Original Scale
```

```
## we can do some of these on our own
## normal
mean(boot.ilec$t) + c(-1, 1)*qnorm(.975)*sd(boot.ilec$t)
```

```
## [1] 7.709670 9.104182
```

```
## normal is bias corrected
2*mean(ilec_times) - (mean(boot.ilec$t) - c(-1,
  1)*qnorm(.975)*sd(boot.ilec$t))
```

```
## [1] 7.719039 9.113551
```

```
## percentile
quantile(boot.ilec$t, c(.025, .975))
```

```
##     2.5%    97.5%
## 7.707656 9.111150
```

```
## basic
2*mean(ilec_times) - quantile(boot.ilec$t, c(.975, .025))
```

```
##    97.5%     2.5%
## 7.712071 9.115565
```

To get the studentized bootstrap CI, we need our statistic function to also return the variance of $\hat{\theta}$.

```
mean_var_func <- function(x, idx) {
  c(mean(x[idx]), var(x[idx])/length(idx))
}

boot.ilec_2 <- boot(ilec_times, mean_var_func, 2000)
boot.ci(boot.ilec_2, conf = .95, type = "stud")
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot.ilec_2, conf = 0.95, type = "stud")
##
## Intervals :
## Level    Studentized
## 95%   ( 7.733,  9.231 )
## Calculations and Intervals on Original Scale
```

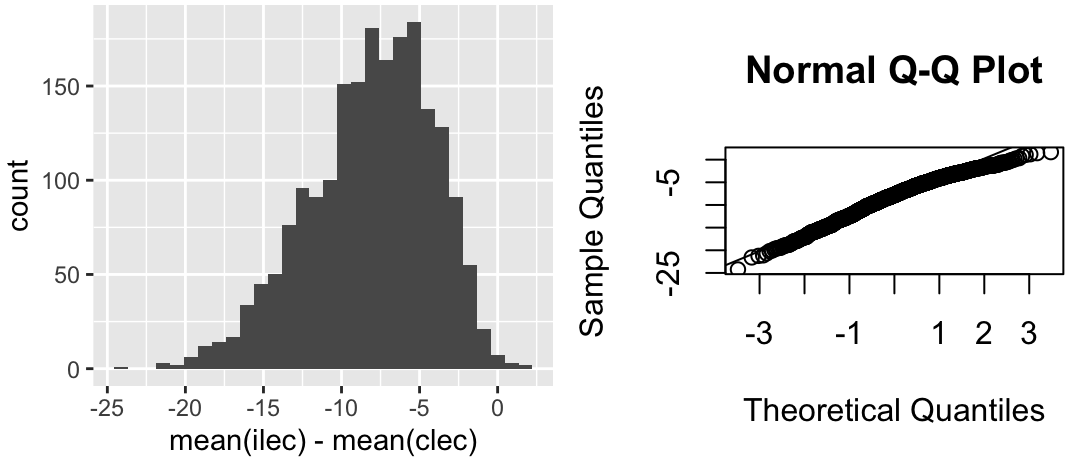
Which CI should we use?

1.6 Bootstrapping for the difference of two means

Given iid draws of size n and m from two populations, to compare the means of the two groups using the bootstrap,

The function `two.boot` in the `simpleboot` package is used to bootstrap the difference between univariate statistics. Use the bootstrap to compute the shape, bias, and bootstrap sample error for the samples from the `Verizon` data set of CLEC and ILEC customers.

```
library(simpleboot)

clec_times <- Verizon[Verizon$Group == "CLEC",]$Time

diff_means.boot <- two.boot(ilec_times, clec_times, "mean", R = 2000)

ggplot() +
  geom_histogram(aes(diff_means.boot$t)) +
  xlab("mean(ilec) - mean(clec)")

qqnorm(diff_means.boot$t)
qqline(diff_means.boot$t)
```




```
# Your turn: estimate the bias and se of the sampling distribution
```

Which confidence intervals should we use?

```
# Your turn: get the chosen CI using boot.ci
```

Is there evidence that

$$H_0 : \mu_1 - \mu_2 = 0$$
$$H_a : \mu_1 - \mu_2 < 0$$

is rejected?

2 Parametric Bootstrap

In a **nonparametric bootstrap**, we

In a **parametric bootstrap**,

For both methods,

2.1 Bootstrapping for linear regression

Consider the regression model $Y_i = \boldsymbol{x}_i^T \boldsymbol{\beta} + \epsilon_i, i = 1, \ldots, n$ with $\epsilon_i \overset{iid}{\sim} N(0, \sigma^2)$.

Two approaches for bootstrapping linear regression models –

1.

2.

2.1.1 Bootstrapping the residuals

1. Fit the regression model using the original data
2. Compute the residuals from the regression model,

$$\hat{\epsilon}_i = y_i - \hat{y}_i = y_i - \boldsymbol{x}_i^T \hat{\boldsymbol{\beta}}, \quad i = 1, \ldots, n$$

3. Sample $\hat{\epsilon}_1^*, \ldots, \hat{\epsilon}_n^*$ with replacement from $\hat{\epsilon}_1, \ldots, \hat{\epsilon}_n$.
4. Create the bootstrap sample

$$y_i^* = \boldsymbol{x}_i^T \hat{\boldsymbol{\beta}} + \epsilon_i^*, \quad i = 1, \ldots, n$$

5. Estimate $\hat{\boldsymbol{\beta}}^*$
6. Repeat steps 2-4 B times to create B bootstrap estimates of $\hat{\beta}$.

Assumptions:

2.1.2 Paired bootstrapping

Resample $z_i^* = (y_i, \boldsymbol{x}_i)^*$ from the empirical distribution of the pairs $(y_i, \boldsymbol{x}_i)$.

Assumptions:

2.1.3 Which to use?

1. Standard inferences -

2. Bootstrapping the residuals -

3. Paired bootstrapping -

Your Turn

This data set is the Puromycin data in R. The goal is to create a regression model about the rate of an enzymatic reaction as a function of the substrate concentration.

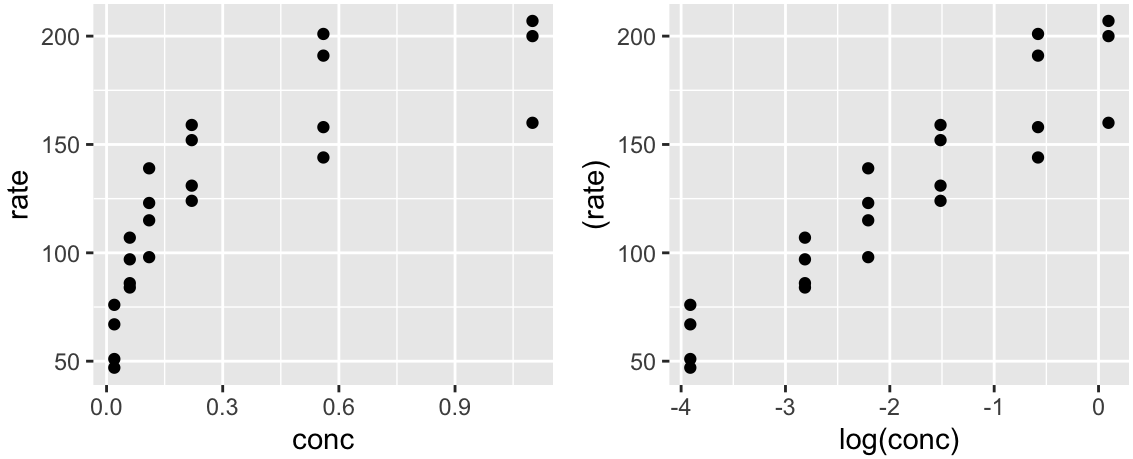
```
head(Puromycin)
```

```
##   conc rate   state
## 1 0.02   76 treated
## 2 0.02   47 treated
## 3 0.06   97 treated
## 4 0.06  107 treated
## 5 0.11  123 treated
## 6 0.11  139 treated
```

```
dim(Puromycin)
```

```
## [1] 23  3
```

```
ggplot(Puromycin) +
  geom_point(aes(conc, rate))

ggplot(Puromycin) +
  geom_point(aes(log(conc), (rate)))
```



2.1.4 Standard regression

```
m0 <- lm(rate ~ conc, data = Puromycin)
plot(m0)
summary(m0)
```

```
##
## Call:
## lm(formula = rate ~ conc, data = Puromycin)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -49.861 -15.247  -2.861  15.686  48.054
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)    93.92       8.00   11.74 1.09e-10 ***
## conc          105.40      16.92    6.23 3.53e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 28.82 on 21 degrees of freedom
## Multiple R-squared:  0.6489, Adjusted R-squared:  0.6322
## F-statistic: 38.81 on 1 and 21 DF,  p-value: 3.526e-06
```

```
confint(m0)
```

```
##                2.5 %   97.5 %
## (Intercept) 77.28643 110.5607
## conc        70.21281 140.5832
```

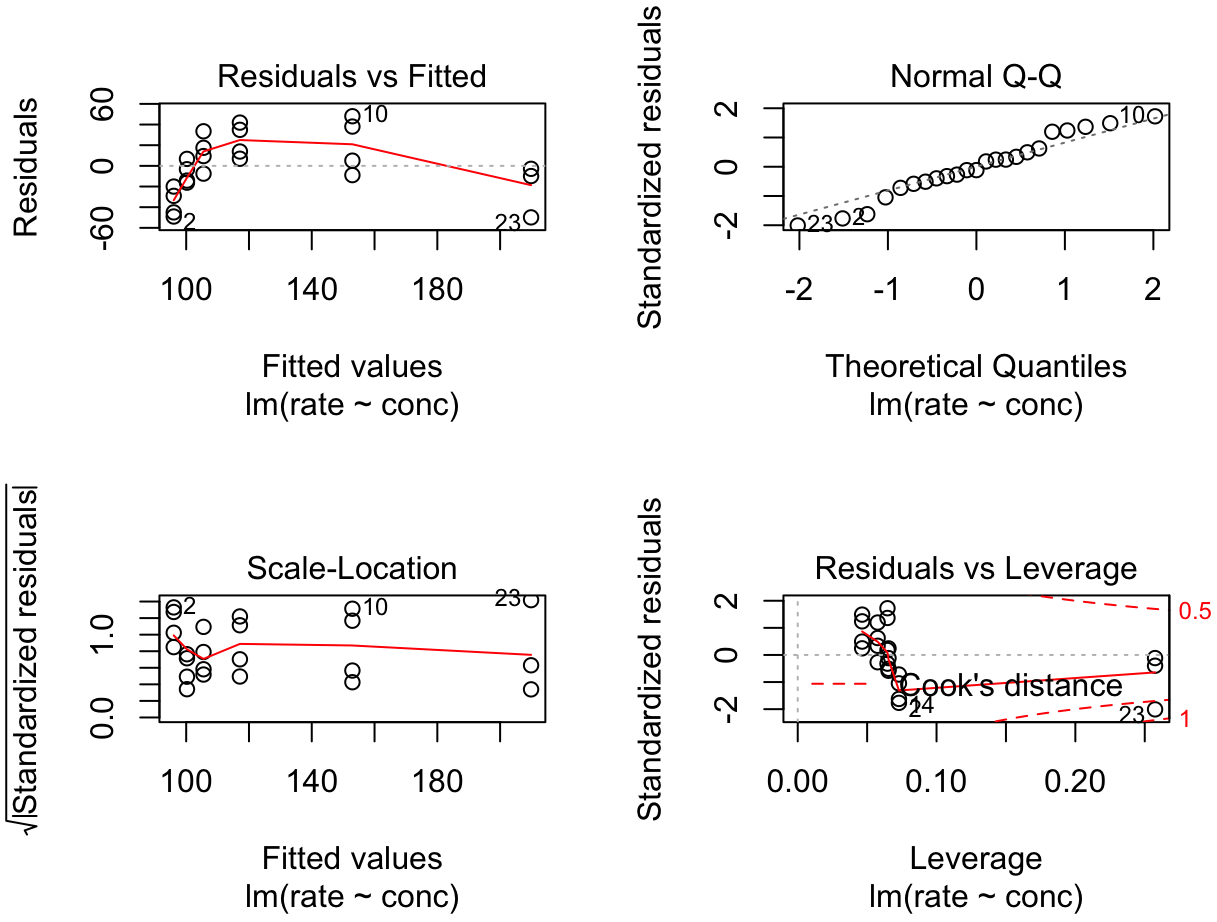
```
m1 <- lm(rate ~ log(conc), data = Puromycin)
plot(m1)
summary(m1)
```

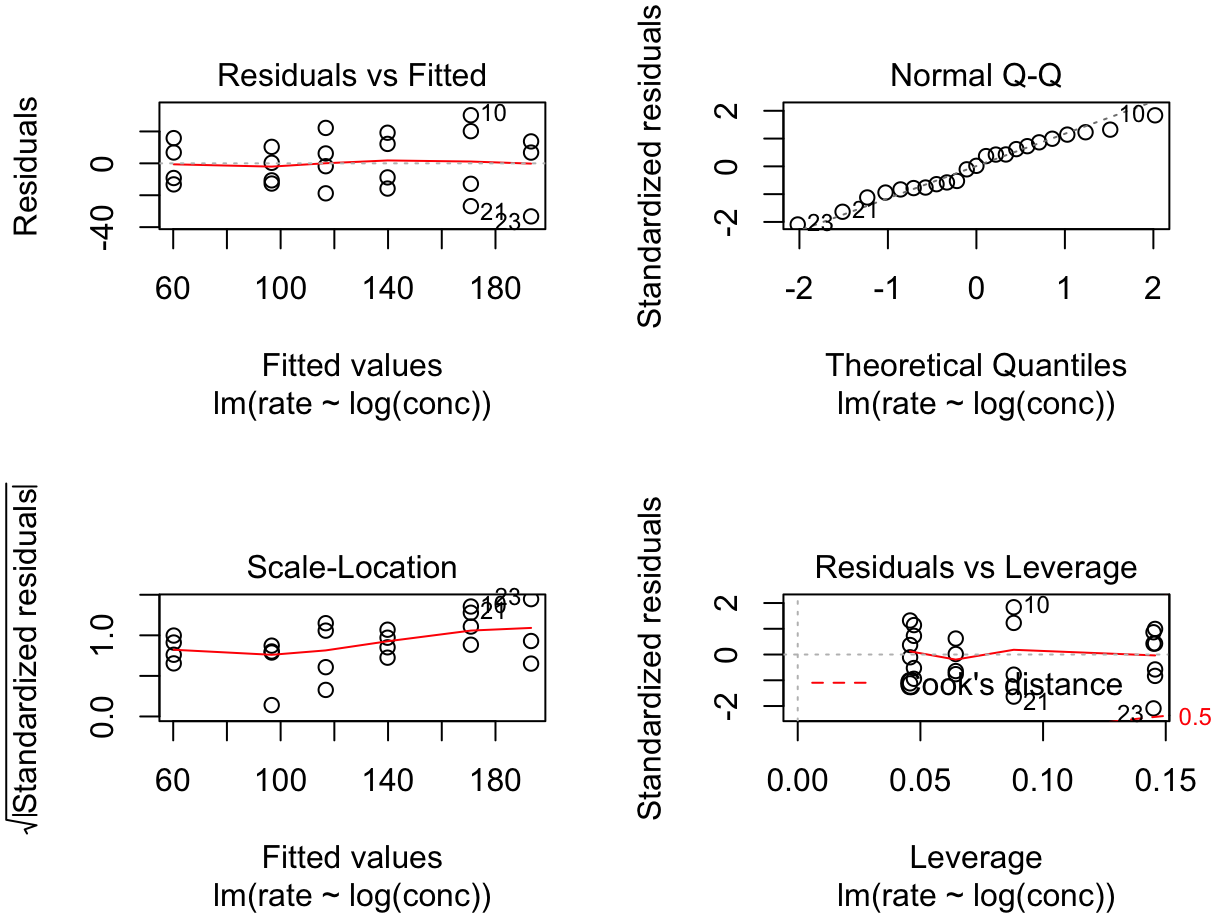
```
##
## Call:
## lm(formula = rate ~ log(conc), data = Puromycin)
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -33.250 -12.753   0.327  12.969  30.166
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  190.085      6.332   30.02  < 2e-16 ***
## log(conc)     33.203      2.739   12.12 6.04e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.2 on 21 degrees of freedom
## Multiple R-squared:  0.875,  Adjusted R-squared:  0.869
## F-statistic: 146.9 on 1 and 21 DF,  p-value: 6.039e-11
```

```
confint(m1)
```

```
##                 2.5 %   97.5 %
## (Intercept) 176.91810 203.2527
## log(conc)    27.50665  38.8987
```


Residuals vs Fitted
Residuals
Fitted values
lm(rate ~ conc)
Normal Q-Q
Standardized residuals
Theoretical Quantiles
lm(rate ~ conc)
Scale-Location
√|Standardized residuals|
Fitted values
lm(rate ~ conc)
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage
lm(rate ~ conc)



2.1.5 Paired bootstrap

```
# Your turn
library(boot)

reg_func <- function(dat, idx) {
  # write a regression function that returns fitted beta
}

# use the boot function to get the bootstrap samples

# examing the bootstrap sampling distribution, make histograms

# get confidence intervals for beta_0 and beta_1 using boot.ci
```

2.1.6 Bootstrapping the residuals

```
# Your turn
library(boot)

reg_func_2 <- function(dat, idx) {
  # write a regression function that returns fitted beta
  # from fitting a y that is created from the residuals

}

# use the boot function to get the bootstrap samples

# examing the bootstrap sampling distribution, make histograms

# get confidence intervals for beta_0 and beta_1 using boot.ci
```