Wednesday, January 22

Parameter Estimation

There are *many* ways to estimate the parameters of a regression model. One useful and common approach is to use the method of *least squares*.

Least Squares Estimation of $\beta_0, \beta_1, \dots, \beta_k$

Consider the linear model

$$E(Y_i) = \beta_0 + \beta_1 x_{i1} + \cdots + \beta_k x_{ik}.$$

The *least squares estimates* of $\beta_0, \beta_1, \dots, \beta_p$ are those values that minimize

$$\sum_{i=1}^{n}(y_i - \mu_i)^2 = (y_1 - \mu_1)^2 + (y_2 - \mu_2)^2 + \cdots + (y_n - \mu_n)^2,$$

where

$$\mu_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}.$$

These estimates are denoted as $\hat{\beta}_0, \hat{\beta}_1, \dots, \hat{\beta}_k$. They are labeled under `Estimate` from the output of the `summary` function.

Estimation of a Linear Function of Parameters

Replacing $\beta_0, \beta_1, \dots, \beta_k$ with $\hat{\beta}_0, \hat{\beta}_1, \dots, \hat{\beta}_k$ in

$$\ell = a_0\beta_0 + a_1\beta_1 + \cdots + a_k\beta_k + b$$

gives the *estimate* of the linear function ℓ,

$$\hat{\ell} = a_0\hat{\beta}_0 + a_1\hat{\beta}_1 + \cdots + a_k\hat{\beta}_k + b.$$

These estimates are labeled as `estimate` when using the `lincon` and `contrast` functions.

Estimation of the Response Variable Variance

The typical linear model also has one additional parameter, the variance of Y_i (denoted as σ^2), which is assumed to be a constant (i.e., the same regardless of the values of the explanatory variables). The usual estimator of σ^2 is

$$\hat{\sigma}^2 = \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n - k - 1}.$$

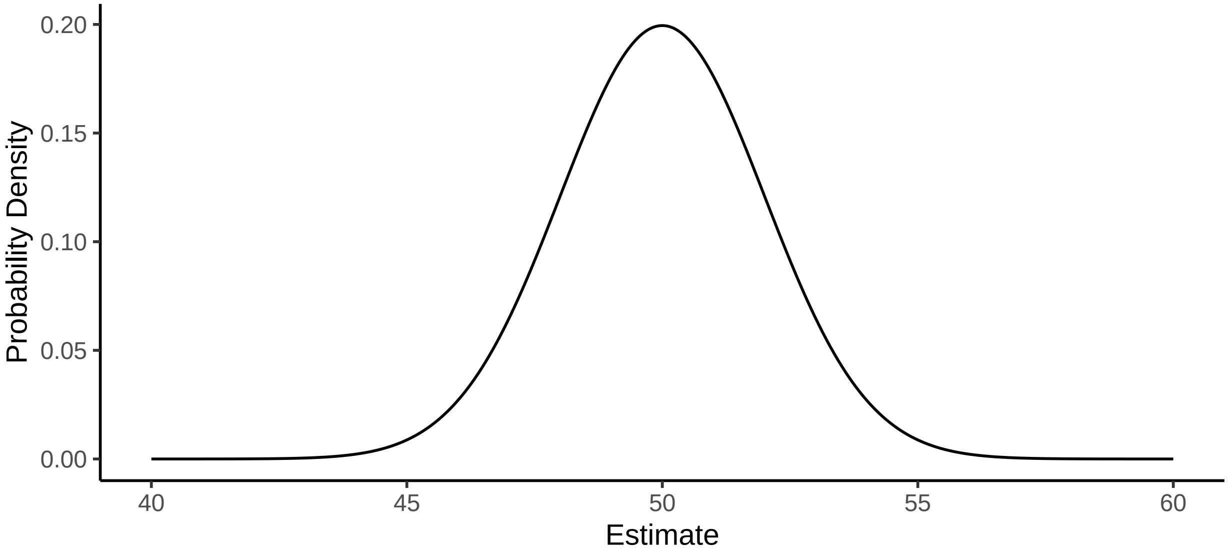
The estimate of σ (not σ^2) is labeled as the "residual standard error" from the output of `summary`, and the "degrees of freedom" " associated with it is $n - k - 1$ (more generally, this degrees of freedom is n minus the number of β parameters in the model so we would define it as $n - p$ where p is the number of parameters other than σ^2).

Note: We sometimes make a distinction between an *estimator* (i.e., the formula/procedure that produces a *estimate*), and the *estimate* (i.e., a specific value produced by an *estimator*).

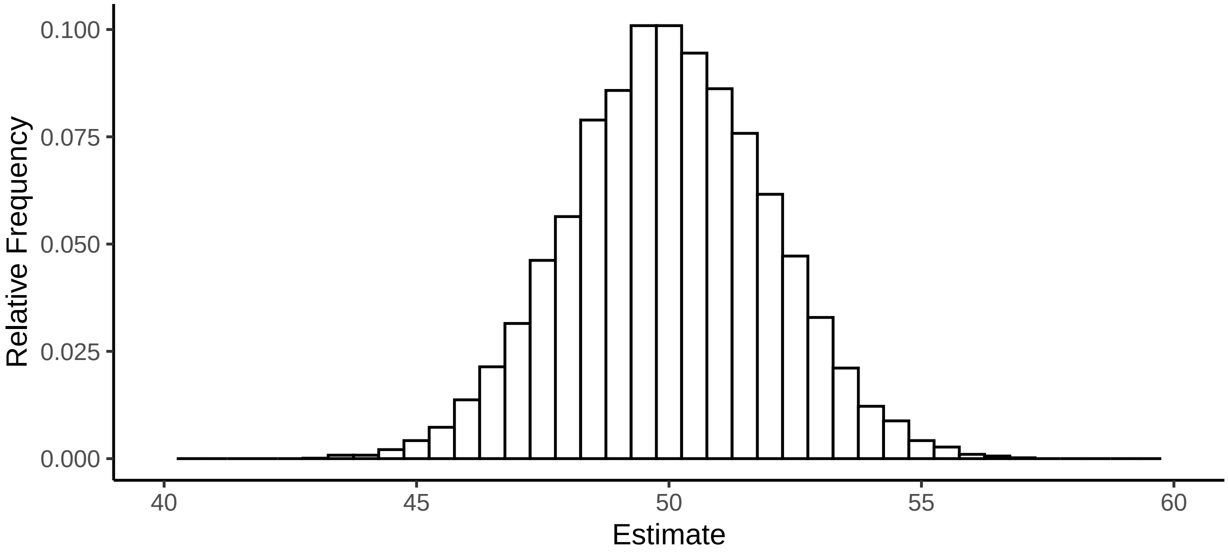
Sampling Distributions

A **sampling distribution** is the probability distribution of an estimator.

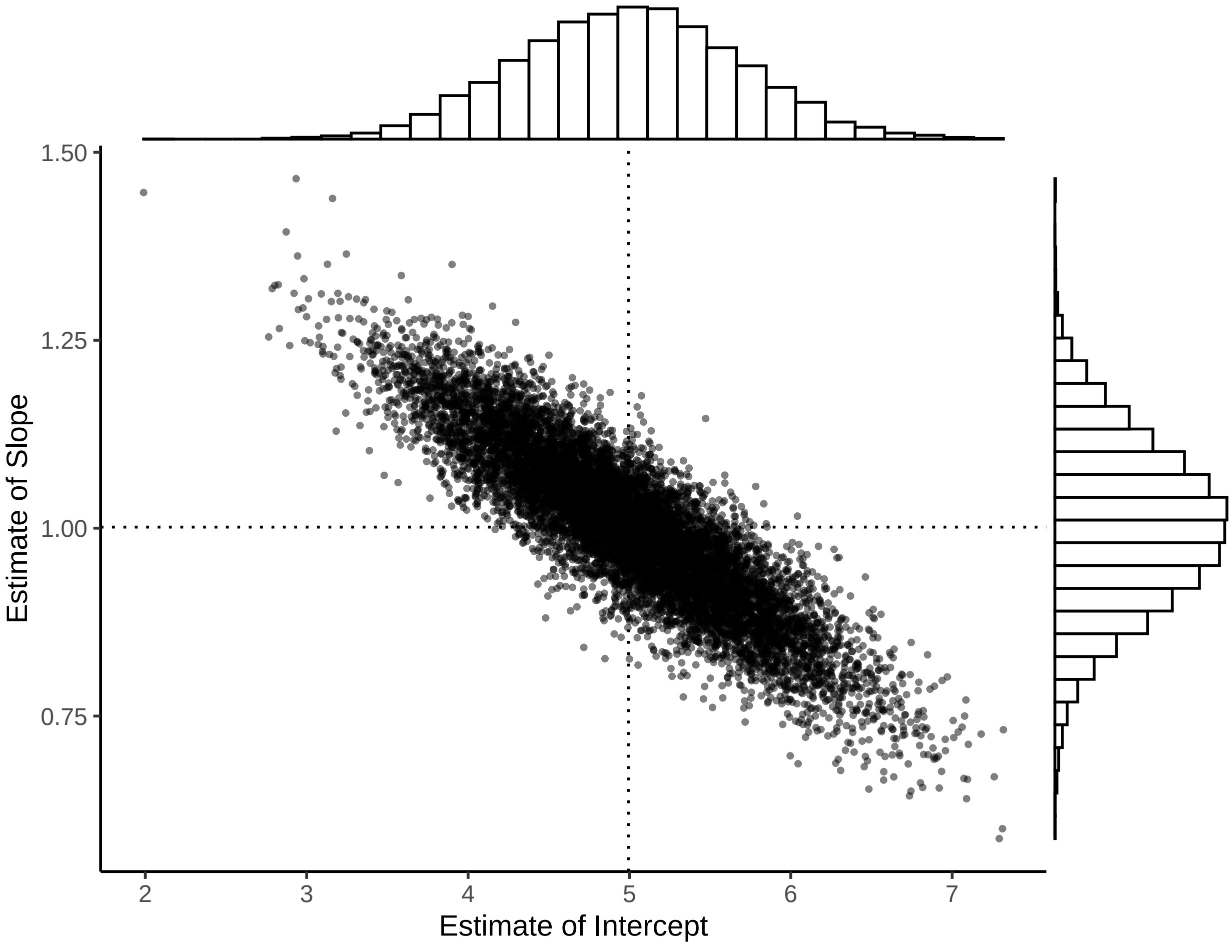
Example: Consider the model $E(Y_i) = \beta_0$, and assume that $\beta_0 = 50$ and also that the standard deviation of Y_i is $\sigma = 10$. The probability distribution below shows the sampling distribution of $\hat{\beta}_0$.



The figure below is a histogram of $\hat{\beta}_0$ from 1000 samples of $n = 25$ observations $Y_1, Y_2, \ldots, Y_{25}$.



Example: Consider the model $E(Y_i) = \beta_0 + \beta_1 x_i$ where $x_1 = 1$, $x_2 = 2$, …, $x_{10} = 10$, $\beta_0 = 5$, $\beta_1 = 1$, and $\sigma = 1$. The figure below shows the distribution of $\hat{\beta}_0$ and $\hat{\beta}_1$ from 10000 samples of observations of $Y_1, Y_2, \ldots, Y_{10}$.



Three properties of a sampling distribution are of interest.

1. The **mean** of a sampling distribution of an estimator (i.e., the *expected value* of the estimator). Ideally this is equal to the parameter we are estimating (in which case we the estimator is *unbiased*), or relatively close.
2. The **standard deviation** of the sampling distribution of an estimator, which is referred to as the **standard error** of the estimator.
3. The **shape** of the sampling distribution. Typically as n increases the shape "approaches" that of a normal distribution.

Standard Errors

We can often *estimate* standard errors of estimators of parameters or linear functions thereof. These are labeled as `Std. Error` in the output of the `summary` function, and as `se` in the output of the `lincon` and `contrast` functions.

Example: Consider the model for the `whiteside` data.

```
library(MASS) # contains the whiteside and anorexia data frames
mgas <- lm(Gas ~ Insul + Temp + Insul:Temp, data = whiteside)
summary(mgas)$coefficients
```

```
                Estimate Std. Error t value  Pr(>|t|)
(Intercept)       6.8538    0.13596  50.409 7.997e-46
```

```
InsulAfter       -2.1300    0.18009 -11.827 2.316e-16
Temp             -0.3932    0.02249 -17.487 1.976e-23
InsulAfter:Temp   0.1153    0.03211   3.591 7.307e-04
```

Recall that the model can be written as

$$E(G_i) = \beta_0 + \beta_1 d_i + \beta_2 t_i + \beta_3 d_i t_i,$$

where d_i is an indicator variable for *after* insulation so that we can also write the model as

$$E(G_i) = \begin{cases} \beta_0 + \beta_2 t_i, & \text{if the } i\text{-th observation is before insulation,} \\ \beta_0 + \beta_1 + (\beta_2 + \beta_3) t_i, & \text{if the } i\text{-th observation is after insulation.} \end{cases}$$

Estimates of the standard errors are reported by `summary`. Standard errors are also shown by `lincon` and `contrast`.

```
library(trtools)
lincon(mgas, a = c(0,0,1,1)) # b2 + b3
```

```
            estimate      se   lower   upper tvalue df    pvalue
(0,0,1,1),0  -0.2779 0.02292 -0.3239 -0.2319 -12.12 52 8.936e-17
```

```
contrast(mgas,
  a = list(Insul = c("Before","After"), Temp = 2),
  b = list(Insul = c("Before","After"), Temp = 1),
  cnames = c("before","after"))
```

```
       estimate      se   lower   upper tvalue df    pvalue
before  -0.3932 0.02249 -0.4384 -0.3481 -17.49 52 1.976e-23
after   -0.2779 0.02292 -0.3239 -0.2319 -12.12 52 8.936e-17
```

We can also obtain standard errors for estimating the expected weight change under each treatment condition for the `anorexia` study/model.

```
anorexia$change <- anorexia$Postwt - anorexia$Prewt
mwght <- lm(change ~ Treat, data = anorexia)
contrast(mwght, a = list(Treat = c("Cont","CBT","FT")),
  cnames = c("Control","Cognitive","Family"))
```

```
          estimate    se  lower  upper  tvalue df    pvalue
Control     -0.450 1.476 -3.395  2.495 -0.3048 69 0.7614470
Cognitive    3.007 1.398  0.218  5.796  2.1509 69 0.0349920
Family       7.265 1.826  3.622 10.907  3.9787 69 0.0001688
```

Because the *shape* of a sampling distribution is usually approximately normal, we can say the following.

1. The *mean distance* between the parameter and the estimator is approximately SE $\times \sqrt{2/\pi} \approx$ SE $\times$ 0.8.
2. The *median distance* between the parameter and the estimator is approximately SE $\times$ 0.67.
3. The *95th percentile* of the distance between the parameter and the estimator is approximately SE$\times 1.96 \approx$ SE $\times$ 2.

Note that all of these quantities are *proportional* to the standard error. Standard errors give us an idea of how (in)accurate a given estimator is for a given parameter in a given model for a given design — the larger the standard error the farther away the estimator will tend to be to the parameter (or function thereof) being estimated.

Also note that in many cases the estimate and the (estimated) standard error are sufficient for computing both confidence intervals and test statistics as shown in the next two sections.

Confidence Intervals

A **confidence interval** is an *interval estimator* (as opposed to a *point estimator* which is a single value) with the property that the estimator has a specified probability of being correct (i.e., the *confidence level* of the interval). Note that this probability is a property of the estimator, not an estimate.

One common kind of confidence interval (sometimes called a *Wald* confidence interval) has the general form

$$\text{estimator} \pm \text{multiplier} \times \text{standard error}.$$

For example,

$$\hat{\beta}_j \pm t \times \text{SE}(\hat{\beta}_j)$$

where $\text{SE}(\hat{\beta}_j)$ is the (estimated) standard error of $\hat{\beta}_j$, and t is a "multiplier" to set the desired confidence level. Similarly a confidence interval for ℓ is

$$\hat{\ell} \pm t \times \text{SE}(\hat{\ell}).$$

In R confidence intervals for model parameters can usually be computed by applying the `confint` function to the model object.

```
confint(mgas) # 95% confidence level is the default
```

```
                   2.5 %  97.5 %
(Intercept)      6.58100  7.1267
InsulAfter      -2.49136 -1.7686
Temp            -0.43836 -0.3481
InsulAfter:Temp  0.05087  0.1797
```

```
confint(mgas, level = 0.99) # 99% confidence level
```

```
                   0.5 %  99.5 %
(Intercept)      6.49030  7.2174
InsulAfter      -2.61150 -1.6485
Temp            -0.45336 -0.3331
InsulAfter:Temp  0.02944  0.2012
```

For some compact output I often use `cbind` to append the confidence intervals to the output from `summary` as follows.

```
cbind(summary(mgas)$coefficients, confint(mgas))
```

```
                Estimate Std. Error t value  Pr(>|t|)    2.5 %  97.5 %
(Intercept)       6.8538    0.13596  50.409 7.997e-46  6.58100  7.1267
InsulAfter       -2.1300    0.18009 -11.827 2.316e-16 -2.49136 -1.7686
Temp             -0.3932    0.02249 -17.487 1.976e-23 -0.43836 -0.3481
InsulAfter:Temp   0.1153    0.03211   3.591 7.307e-04  0.05087  0.1797
```

Note that other functions like `lincon` and `contrast` provide confidence intervals by default.

```
lincon(mgas, a = c(0,0,1,1)) # b2 + b3
```

```
            estimate      se   lower   upper tvalue df    pvalue
(0,0,1,1),0  -0.2779 0.02292 -0.3239 -0.2319 -12.12 52 8.936e-17
```

```
contrast(mgas,
  a = list(Insul = c("Before","After"), Temp = 2),
  b = list(Insul = c("Before","After"), Temp = 1),
  cnames = c("before","after"))
```

```
       estimate      se   lower   upper tvalue df    pvalue
before  -0.3932 0.02249 -0.4384 -0.3481 -17.49 52 1.976e-23
after   -0.2779 0.02292 -0.3239 -0.2319 -12.12 52 8.936e-17
```

They also have a default confidence level of 95%, and will accept a `level` argument to specify other confidence levels.

Significance Tests

We consider four components to a given significance test: *hypotheses*, *test statistics*, *p-values*, and a *decision rule.*

Hypotheses

A significance test for a single parameter concerns a pair of hypotheses such as

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j \neq c,$$

or

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j > c,$$

or

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j < c,$$

where c is some specified value (often but not necessarily zero). Similarly we can have hypotheses concerning ℓ by replacing β_j with ℓ in the above statement such as

$$H_0\colon \ell = c \;\text{ and }\; H_a\colon \ell \neq c.$$

Tests that are reported by default by functions like `summary`, `lincon`, and `contrast` are for the two-sided null hypothesis with $c = 0$ so that the hypotheses are $H_0\colon \beta_j = 0$ versus $H_a\colon \beta_j \neq 0$ (as when using `summary`) or $H_0\colon \ell = 0$ versus $H_a\colon \ell \neq 0$ (as when using `lincon` or `contrast`).

Test Statistics

Assuming H_0 is *true*, the **test statistics**

$$t = \frac{\hat{\beta}_j - \beta_j}{\mathrm{SE}(\hat{\beta}_j)}$$

and

$$t = \frac{\hat{\ell} - \ell}{\mathrm{SE}(\hat{\ell})}$$

have an approximate t distribution with $n - p$ degrees of freedom (usually denoted as `df` in output, where p is the number of β_j parameters). Note that β_j and ℓ are the values of these quantities hypothesized by the *null* hypothesis.

P-Values

The p-value is the probability of a value of the test statistic *as or more extreme than the observed value, assuming H_0 is true.* What is *as or more extreme* is decided by H_a:

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j \neq c \Rightarrow p\text{-value} = P(|t| \geq t_{\text{obs}}|H_0),$$

or

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j > c \Rightarrow p\text{-value} = P(t \geq t_{\text{obs}}|H_0),$$

or

$$H_0\colon \beta_j = c \;\text{ and }\; H_a\colon \beta_j < c \Rightarrow p\text{-value} = P(t \leq t_{\text{obs}}|H_0),$$

where t_{obs} is the observed/computed value of the t test statistic.

Note: Software typically produces the following: (a) a test with a null hypothesis where $\beta_j = 0$ of $\ell = 0$, and (b) p-values only for *two-sided/tailed* tests. This is true of `summary`, `lincon`, and `contrast`. But the p-value for a *one-sided/tailed* test can be obtained as half of the p-value for the two-sided/tailed test (assuming that t_{obs}) is in the direction hypothesized by H_a.

A *composite* null hypothesis such as

$$H_0\colon \beta_j \le c \quad \text{and} \quad H_a\colon \beta_j > c,$$

or

$$H_0\colon \ell \le c \quad \text{and} \quad H_a\colon \ell > c,$$

can be done by assuming the equality under the null (e.g., $\beta_j = c$ or $\ell = c$), and interpreting the computed p-value as the *upper bound* on the p-value.

Decision Rule

The decision rule for a significance test is always

$$p\text{-value} \le \alpha \Rightarrow \text{reject } H_0, \quad p\text{-value} > \alpha \Rightarrow \text{do not reject } H_0,$$

for some specified significance level $0 < \alpha < 1$ (frequently $\alpha = 0.05$).