2.1 Multiple Linear Regression Model

Multiple Linear Regression (MLR) is a natural extension of Simple Linear Regression by adding more predictors. From a practical point of view, this is necessary when the variation left in a SLR model (i.e. RSS) is quite high.

We will start our discussion about MLR with the Birthweight example:

Birthweight Example

The birthweight.csv data set contains data from a study on the birth weight of **42** babies. The variables in the data set are the following:

- ID: Unique Identification number of a baby
- Length: Length of the baby at time of birth in cm (X_1)
- Birthweight: Weight of the baby at time of birth in kg (Y)
- Headcirc : Head circumference of the baby at time of birth in cm (X_2)
- ullet Gestation : Completed weeks of gestation (X_3)
- smoker : Mother is/is not a smoker {0: No, 1: Yes} (X_4)
- mage : Mother's age at time of birth (X_5)
- ullet mnocig : Mother's number of cigarettes smoked per day (X_6)
- mheight : Mother's height in cm (X_7)
- ullet mppwt : Mother's pre-pregnancy weight (X_8)
- fage : Father's age at time of birth (X_9)
- fedyrs : Father's years of education (X_{10})
- ullet fnocig : Father's number of cigarettes smoked per day (X_{11})
- fheight : Father's height (X_{12})
- lowbwt : Low birthweight {0: No, 1:Yes} (X_{13})
- mage35 : Mother's Age \geq 35 or not {0: No, 1: Yes}

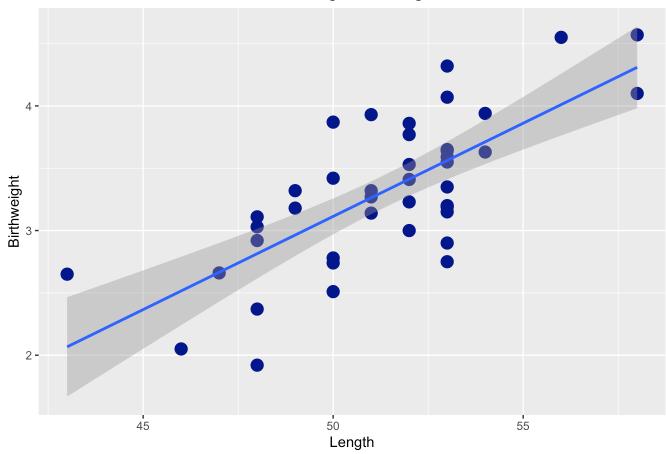
birthweight <- read.csv("data/ch2/Birthweight.csv", header=TRUE)</pre>

Our goal in this example is to estimate the **mean** Birthweight . Based on the literature, we know that the weight of a baby is related to its length. So, let's start by running a SLR between Birthweight (the response) and Length a single predictor.

```
birthweight.slr = lm(Birthweight ~ Length, data=birthweight)
summary(birthweight.slr)
##
## Call:
## lm(formula = Birthweight ~ Length, data = birthweight)
##
## Residuals:
       Min
                      Median
##
                  10
                                    30
                                            Max
## -0.89446 -0.35492 0.01746 0.28674
                                       0.75794
##
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
                           1.14858 -3.798 0.000486 ***
## (Intercept) -4.36244
## Length
               0.14952
                           0.02234 6.693 5.03e-08 ***
## ---
## Signif. codes:
                  0 '*** 0.001 '** 0.01 '* 0.05 '. 0.1 ' 1
##
## Residual standard error: 0.4199 on 40 degrees of freedom
## Multiple R-squared: 0.5283, Adjusted R-squared: 0.5165
## F-statistic: 44.8 on 1 and 40 DF, p-value: 5.029e-08
```

We also plot the data with the fitted regression line on top:

Birthweight vs. Length



Looking both at the regression output and the scatterplot, we observe that there is still a lot of variation in the data that is not explained by Length alone. This means that other factors/variables are (possibly) responsible for the variation that has not been explained by Length .

In many situations, like the example above, a **single** predictor variable in the model provides an inadequate description, since a **number of key variables** affect the response variable in important and distinctive ways. In addition, in situations like this, we frequently find that predictions of the response variable based on a model containing only a single predictor are too imprecise to be useful. A more complex model, containing additional predictor variables, typically is more helpful in providing sufficiently precise predictions of the response.

2.1.1 MLR Formulation

We consider a model with more than one predictor. Suppose x_1 , x_2 , ..., x_p be p predictors of a response y. In this case, the data will be of the form

and the model can be written as:

$$y_i = eta_1 x_{i1} + eta_2 x_{i2} + \dots + eta_p x_{ip} + arepsilon_i, \qquad i = 1, \dots, n$$

where we denote $\mathbf{x_i} = (x_{i1,\ldots,x_ip})^T$, with $x_{i1} = 1$.

Here $(\beta_1, \beta_2, \dots, \beta_p; \sigma^2)$ are unknown true parameters.

- eta_1 is the *intercept*, which means that $x_{i1}=1,$ $i=1,\ldots,n.$
- $\beta_2, \beta_3, \dots, \beta_p$ are partial slopes.
- $\varepsilon_1, \varepsilon_2, \dots, \varepsilon_n$ are the *random errors*. As usual, we assume that they satisfy the same conditions as in the case of simple linear regression:
 - \circ zero mean: $\mathbb{E}(arepsilon_i)=0$; i,
 - \circ uncorrelated: $Cov(arepsilon_i,arepsilon_j)=0,\;i
 eq j$, and
 - \circ homoscedastic: $Var(arepsilon_i) = \sigma^2$ (i.e. does not depend on i).

In the Birthweight example, a snapshot of the data is shown below:

head(birthweight)

##		ID	Length	Birthwe	eight He	adcirc	Gestation	smoker	mage	mnocig	mheight	mppwt
##	1	1360	56		4.55	34	44	0	20	0	162	57
##	2	1016	53		4.32	36	40	0	19	0	171	62
##	3	462	58		4.10	39	41	0	35	0	172	58
##	4	1187	53		4.07	38	44	0	20	0	174	68
##	5	553	54		3.94	37	42	0	24	0	175	66
##	6	1636	51		3.93	38	38	0	29	0	165	61
##		fage	fedvrs	fnocig	fheight	lowbwi	t mage35					
		- 5	,									
##	1	23	10	35	179	(0					
			-		179 183							
##	2	23	10	35		(0					
## ##	2	23 19	10 12	35	183	(0 0					
## ## ##	2 3 4	23 19 31	10 12 16	35 0 25	183 185	(0 0 1 0 0					

Here Column 3 (Birthweight) is the response and all other columns are predictors. Using the notation defined above, we have n=42.

dim(birthweight)

[1] 42 16

We are going to write our Multiple Linear Regression model in matrix formulation. First define the following vectors/matrices:

$$\mathbf{y} = egin{pmatrix} y_1 \ y_2 \ dots \ y_n \end{pmatrix}, \quad arepsilon = egin{pmatrix} arepsilon_1 \ arepsilon_2 \ dots \ arepsilon_p \end{pmatrix}, \quad egin{pmatrix} \mathbf{X} = egin{pmatrix} x_{11} & x_{12} & \cdots & x_{1p} \ x_{21} & x_{22} & \cdots & x_{2p} \ dots & dots & dots & dots \ x_{n1} & x_{n2} & \cdots & x_{np} \end{pmatrix}$$

Using this notation the model equation can be written as:

$$egin{pmatrix} egin{pmatrix} y_1 \ y_2 \ dots \ y_n \end{pmatrix} = egin{pmatrix} x_{11} & x_{12} & \cdots & x_{1p} \ x_{21} & x_{22} & \cdots & x_{2p} \ dots & dots & \ddots & dots \ x_{n1} & x_{n2} & \cdots & x_{np} \end{pmatrix} egin{pmatrix} eta_1 \ eta_2 \ dots \ eta_p \end{pmatrix} & + egin{pmatrix} arepsilon_1 \ arepsilon_2 \ dots \ eta_p \end{pmatrix}$$

or

Matrix Representation of the MLR Model

n: sample size

p: number of predictors or columns of X

${f X}$ is called the **design matrix**

By default the intercept is included in the model in which case the first column of ${\bf X}$ is a vector of 1's.

2.1.2 Least-Squares Estimation in MLR

We want to estimate the **vector** of β coefficients, i.e. obtain:

$$\hat{\beta} = \left(\hat{\beta}_1, \hat{\beta}_2, \dots, \hat{\beta}_p\right)^T$$

The LS estimator of β minimizes the *sum of squared residuals*:

$$RSS = ||y - \mathbf{X}\beta||^2 = (y - \mathbf{X}\beta)^T (y - \mathbf{X}\beta)$$

In order to minimize RSS, we take derivatives with respect to β 's and set to zero (similar to what we did in SLR but in higher dimensions).

$$egin{align} rac{\partial RSS}{\partial eta} &= \mathbf{0}_{p imes 1} \iff \ -2 \ \mathbf{X}_{p imes n}^T (y - \mathbf{X} eta)_{n imes 1} &= \mathbf{0}_{p imes 1} \end{aligned}$$

This leads to the so-called Normal Equations

$$\mathbf{X}^T(y - \mathbf{X}\beta) = \mathbf{0}$$

Solving the Normal Equations

$$(\mathbf{X}^T\mathbf{X}) \ eta = \mathbf{X}^T \ y$$

leads to the

Least Square Estimators in the MLR

$$\hat{\beta} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \ y$$

We <u>assume</u> that **the rank of X is p**, i.e. no columns of **X** are a linear combinations of the other columns of **X**. Since **X** has rank p, the inverse of $(\mathbf{X}^T\mathbf{X})$ <u>exists</u>.

Single Predictor Model in Matrix Format

Just to better understand the formula we derived in the MLR model for the β estimator, we do the calculations "by hand" in the case of a single predictor model

$$y_i = eta_0 + eta_1 x_i + arepsilon_i, \,\, n = 1, \ldots, n$$

If we re-write it in matrix format, we have:

$$\begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix} = \begin{pmatrix} 1 & x_1 \\ 1 & x_2 \\ \vdots & \vdots \\ 1 & x_n \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{pmatrix}$$

Use the formula $\hat{\beta} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T y$ to obtain the estimator from the previous lecture. We compute each term in the expression of $\hat{\beta}$:

$$\mathbf{X}^{T}\mathbf{X} = \begin{pmatrix} 1 & 1 & \dots & 1 \\ x_{1} & x_{2} & \dots & x_{n} \end{pmatrix} \begin{pmatrix} 1 & x_{1} \\ 1 & x_{2} \\ \vdots & \vdots \\ 1 & x_{n} \end{pmatrix} = \begin{pmatrix} n & n\bar{x} \\ n\bar{x} & \sum_{i} x_{i}^{2} \end{pmatrix}$$
$$(\mathbf{X}^{T}\mathbf{X})^{-1} = \frac{1}{n\sum_{i} x_{i}^{2} - (n\bar{x})^{2}} \begin{pmatrix} \sum_{i} x_{i}^{2} & -n\bar{x} \\ -n\bar{x} & n \end{pmatrix}$$
$$\mathbf{X}^{T}y = \begin{pmatrix} 1 & 1 & \dots & 1 \\ x_{1} & x_{2} & \dots & x_{n} \end{pmatrix} \begin{pmatrix} y_{1} \\ y_{2} \\ \vdots \\ y_{n} \end{pmatrix} = \begin{pmatrix} n\bar{y} \\ \sum_{i} x_{i}y_{i} \end{pmatrix}$$

Combining all the above, we obtain that

$$egin{aligned} \hat{eta} &= egin{pmatrix} \hat{eta}_0 \ \hat{eta}_1 \end{pmatrix} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T y \ &= rac{1}{n \sum_i x_i^2 - (n ar{x})^2} egin{pmatrix} \sum_i x_i^2 & -n ar{x} \ -n ar{x} & n \end{pmatrix} egin{pmatrix} n ar{y} \ \sum_i x_i y_i \end{pmatrix} \end{aligned}$$

So, $\hat{\beta}_1$ is given by

$$\hat{eta_1} = rac{-n^2 ar{x} ar{y} + n \sum_i x_i y_i}{n \sum_i x_i^2 - (n ar{x})^2} = rac{\sum_i x_i y_i - n ar{x} ar{y}}{\sum_i x_i^2 - n ar{x}^2}$$

and similarly we can recover the formula for \hat{eta}_0 .

Let's see how we can fit a MLR in R:

Birthweight Example

We start by fitting the full model with all the available variables, that is

$$Y_i = \beta_1 X_1 + \ldots + \beta_{14} X_{14} + \varepsilon_i$$

Here we assume that X_1 is a column of 1's and thus corresponds to the intercept. In R this:

```
# For convenience remove the index column.

# We also remove `mage35` because it is highly correlated with `mage`:

birthweight2 = birthweight[,c(-1, -16)]
```

```
# Run a regression with Birthweight as the
# response and everything else as a predictor:
birthweight.mlr1 = lm(Birthweight~., data=birthweight2)
summary(birthweight.mlr1)
```

```
##
## Call:
## lm(formula = Birthweight ~ ., data = birthweight2)
##
## Residuals:
##
       Min
                 10
                      Median
                                  30
                                          Max
## -0.38656 -0.26722 -0.06068 0.18271
##
## Coefficients:
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.4286417
                         2.1583202 -1.589 0.12339
## Length
               0.0257860 0.0336226 0.767 0.44954
## Headcirc
               0.0850933 0.0297843 2.857 0.00798 **
               0.0916226 0.0322518 2.841 0.00829 **
## Gestation
## smoker
              -0.2198237 0.1728531 -1.272 0.21393
## mage
              -0.0158203 0.0191605
                                   -0.826 0.41597
## mnocia
              0.0002094
                         0.0070011
                                    0.030 0.97635
## mheight
               0.0056438
                         0.0143947
                                   0.392 0.69797
## mppwt
               0.0084338 0.0116016 0.727 0.47329
## fage
               0.0046535
                         0.0167998 0.277 0.78382
## fedyrs
               0.0016448
                         0.0312497 0.053 0.95840
## fnocig
               0.0040531
                          0.0041251
                                   0.983 0.33424
## fheight
              -0.0122665 0.0097854 -1.254 0.22037
## lowbwt
              -0.1751779 0.2346936
                                   -0.746 0.46164
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3367 on 28 degrees of freedom
## Multiple R-squared: 0.7877, Adjusted R-squared: 0.6891
## F-statistic: 7.989 on 13 and 28 DF, p-value: 2.432e-06
```

In the output, we can see the estimated β coefficients. Notice that here we have 13 predictors and 1 intercept which makes $\mathbf{p}=\mathbf{14}$.

2.1.3 Fitted Values & Residuals

We can compute the **fitted values** of y based on the model as follows:

$$egin{aligned} \hat{y}_{n imes 1} &= \mathbf{X}\hat{eta} \ &= \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\ y \ &= \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\ y := \mathbf{H}_{n imes n}y_{n imes 1} \end{aligned}$$

The Hat Matrix

We define

$$\mathbf{H}_{n \times n} = \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T$$

to be the hat matrix, since it returns the "y-hat" values.

We also define the residuals

$$egin{aligned} \mathbf{r}_{n imes 1} &= y - \hat{y} \ &= y - \mathbf{X}\hat{eta} \ &= y - \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\ y \ &= y - \mathbf{H}y \ &= (\mathbf{I} - \mathbf{H})y \end{aligned}$$

The residuals \mathbf{r} are used to estimate the *error variance*:

$$\hat{\sigma}^2 = rac{1}{n-p} \sum_i r_i^2 = rac{RSS}{n-p}$$

Birthweight Example

We can extract all this information using R:

To obtain the fitted values
birthweight.fitted1 = birthweight.mlr1\$fitted.values
head(birthweight.fitted1)

To obtain the residuals
birthweight.resids1 = birthweight.mlr1\$residuals
head(birthweight.resids1)

Properties of the Residuals

The LS estimator is the β vector that satisfies the **normal equations**, that is

$$\mathbf{X}^T(y-\hat{y}) = \mathbf{X}^T(y-\mathbf{X}\hat{eta}) = \mathbf{0}$$

This implies the following properties for the residuals $r_{n\times 1}$:

ullet The cross-products between the residual vector r and each column of ${f X}$ are zero, i.e.

$$\mathbf{X}^{T} r = \mathbf{X}^{T} (y - \mathbf{X}\hat{\beta})$$

$$= \mathbf{X}^{T} y - \mathbf{X}^{T} \mathbf{X} \hat{\beta}$$

$$= \mathbf{X}^{T} y - (\mathbf{X}^{T} \mathbf{X}) (\mathbf{X}^{T} \mathbf{X})^{-1} \mathbf{X}^{T} y = 0$$

• The cross-product between the fitted value \hat{y} and the residual vector r is zero, i.e.

$$\hat{y}^T \ r = \hat{eta}^T X^T \ r = 0$$

This implies that the residual vector r is **orthogonal to each column of** X **and** \hat{y} .

2.1.4 The Hat Matrix Properties

1. Let c be any linear combination of the columns of \mathbf{X} , then

$$\mathbf{H}c = c$$

This is true since

$$\mathbf{H}\mathbf{X} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{X} = \mathbf{X}.$$

2. Symmetric

We can prove this using the definition of ${f H}$. Indeed,

$$\mathbf{H}^T = (\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T)^T = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T = \mathbf{H}.$$

3. *Idempotent*, i.e. $\mathbf{H}\mathbf{H} = \mathbf{H}\mathbf{H}^T = \mathbf{H}^T\mathbf{H} = \mathbf{H}$. Indeed,

$$\mathbf{H}\mathbf{H} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T = \mathbf{H}$$

This also implies that $\mathbf{H}(\mathbf{I} - \mathbf{H}) = \mathbf{0}_{n \times n}$.

4. $trace(\mathbf{H}) = p$, that is the number of LS coefficients we estimated. We can easily prove that as follows:

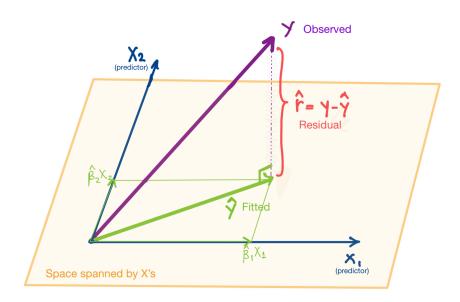
$$trace(\mathbf{H}) = trace(\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T) = trace(\mathbf{X}\mathbf{X}^T(\mathbf{X}^T\mathbf{X})^{-1}) = trace(\mathbf{I}_{p \times p}) = p$$

Here we use the property that trace(AB) = trace(BA).

2.1.5 Geometric Representation of LS

When p=1, the linear regression is represented as a straight line in two dimensions. When p=2, the fitted regression equation corresponds to a plane in three dimensions. When p>2, the fitted regression line is a *hyperplane*, the generalization of a p-dimensional plane in a (p+1)-dimensional space.

Let us focus on the case of 2 predictors x_1, x_2 and consider the representation below:



Observe that the fitted $\hat{\mathbf{y}} = \mathbf{X}\hat{\boldsymbol{\beta}}$ can only range over vectors in the subspace spanned by the columns of \mathbf{X} . This is because $\hat{\mathbf{y}}$ is obtained by minimizing the Euclidean distance between the vectors \mathbf{y} and $\hat{\mathbf{y}}$. In fact, $\hat{\mathbf{y}}$ is the **projection** of \mathbf{y} onto the space spanned by the columns of \mathbf{X} .

We have the following two spaces:

• Estimation Space

- The estimation space is the space spanned by the columns of \mathbf{X} and is a p-dimensional subspace in \mathbb{R}^n . This is a subspace that consists of vectors that can be written as *linear combinations of the columns of* \mathbf{X} .
- \circ The LS squares estimator $\hat{\beta}$ is an element in the estimation space.
- \hat{y} is the *projection* of y onto the estimation space, since it is obtained by minimizing the Euclidean distance between the vectors \mathbf{y} and $\hat{\mathbf{y}}$, i.e. $||y \hat{y}||^2$.

 \circ $\mathbf{H}_{n \times n}$ is *projection/hat matrix* of the estimation space and is symmetric, unique, and idempotent.

• Error Space

- The error space is an (n-p)-dimensional space that is orthogonal to the estimation space. The *projection matrix* of the error space is $(\mathbf{I} \mathbf{H})$.
- \circ The residual ${f r}$ is the *projection* of ${f y}$ onto the error space, and is **orthogonal** to the estimation space. This implies that ${f r}$ is orthogonal to any vector in the estimation space, including each column of ${f X}$.
- When the intercept is included in the model, then

$$\sum_{i=1}^{n} r_i = 0$$

In general, $\sum_{i=1}^n r_i X_{ij} = 0$, $j = 1, \ldots, p$ due to the normal equations.

2.1.6 Rank deficiency

We discussed that the design matrix \mathbf{X} is an $n \times p$ matrix. If this matrix is **not of full rank** (i.e., its columns are not linearly independent), the matrix $\mathbf{X}^T\mathbf{X}$ cannot be inverted (singular matrix). This means that the solution to the Normal Equations is **not** unique. In Statistics, we call this an **identifiability problem**, because we cannot uniquely define estimators for the unknown parameters.

Fortunately, R can cope well with this problem. To solve the LS equations R uses so-called **QR decomposition** method. This method is described below for completeness, but it is beyond the scope of the course.

Birthweight Example

If we want to extract the matrix of a fitted model in R we have:

head(model.matrix(birthweight.mlr1))

##		(Interd	cept) I	Length	Headcirc	Gestation	smoker	mage	mnocig	mheight	mppwt	fage
##	1		1	56	34	44	0	20	0	162	57	23
##	2		1	53	36	40	0	19	0	171	62	19
##	3		1	58	39	41	0	35	0	172	58	31
##	4		1	53	38	44	0	20	0	174	68	26
##	5		1	54	37	42	0	24	0	175	66	30
##	6		1	51	38	38	0	29	0	165	61	31
##		fedyrs	fnoci	g fheig	ht lowbw	t						
##	1	10	3!	5 1	179 (ð						
##	2	12	(0 1	183 (0						
##	3	16	2!	5 1	185 (0						
##	4	14	2!	5 1	189 (0						
##	5	12	(0 1	184	ð						
##	6	16	(0 1	180	0						

We output only the top part of the matrix, since its dimensions are 42×14 .

QR Decomposition: How the LS estimates \hat{eta} are solved in R

Denote the **QR decomposition** (also called **QR** factorization) of ${f X}$ as

$$\mathbf{X}_{n imes p} = \mathbf{Q}_{n imes p} \mathbf{R}_{p imes p}$$

where \mathbf{Q} is an orthogonal matrix (i.e. $\mathbf{Q}^T\mathbf{Q} = \mathbf{I}_{p \times p}$) and \mathbf{R} is an upper triangular matrix, i.e. all the entries in \mathbf{R} below the diagonal are equal to 0. Then,

$$egin{aligned} \hat{eta} &= (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^Ty \ (\mathbf{X}^T\mathbf{X})^{-1} &= (\mathbf{R}^T\mathbf{R})^{-1} &= \mathbf{R}^{-1}(\mathbf{R}^T)^{-1} \ \hat{eta} &= \mathbf{R}^{-1}\mathbf{Q}\mathbf{y} \ \mathbf{R}\hat{eta} &= \mathbf{Q}\mathbf{y} \end{aligned}$$

The last equation is solved easily via backsolving since ${f R}$ is an upper triangular matrix.

Gram-Schmidt Algorithm

One method for computing the QR decomposition is the **Gram-Schmidt algorithm**. It works as follows:\ Take

$$\mathbf{A}_{n imes p} = [a_1 | a_2 | \dots | a_p],$$

where a_j denotes the jth column of ${\bf A}$. Then, define a sequence of e_i 's and ${\bf q}_i's$ recursively:

1.
$$e_1=a_1$$
, ${f q}_1=rac{e_1}{||e_1||}$

2.
$$e_2 = a_2 - (a_2^T \mathbf{q}_1) \mathbf{q}_1$$
, $\mathbf{q}_2 = rac{e_2}{||e_2||}$

3. . . .

4.
$$e_{k+1} = a_{k+1} = \sum_{j=1}^k (a_j^T \mathbf{q}_j) \mathbf{q}_j$$

The resulting QR decomposition is

$$\mathbf{A}_{n imes p} = [a_1|a_2|\dots|a_p] = \mathbf{A}_{n imes p} = [\mathbf{q}_1|\mathbf{q}_2|\dots|\mathbf{q}_p]\mathbf{R} = \mathbf{Q}\mathbf{R}$$

It is easy to check that ${f R}$ is indeed an upper triangular matrix.