

2.1.1(a)

- (i) width (mm) last upper molar
- (ii) numeric continuous
- (iii) *Acropithecus rigidus* specimen
- (iv) n=36

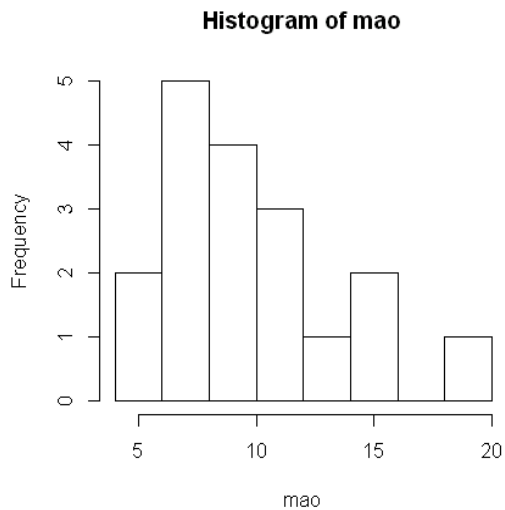
2.1.1(b)

- (i) There are three: birthweight, date-of-birth, mother's race
- (ii) numeric continuous, numeric discrete, categorical nominal
- (iii) baby
- (iv) n=65

2.2.3

R code for histogram:

```
mao=c( 6.8, 8.4, 8.7,11.9,14.2,18.8,9.9, 4.1, 9.7,12.7, 5.2, 7.8,7.8, 7.4, 7.3,10.6,14.5,10.7)  
hist(mao)
```



One example of a tabular frequency distribution is

range frequency

- (4,6] 2
- (6,8] 5
- (8,10] 4
- (10,12] 3
- (12,14] 1
- (14,16] 2
- (16,18] 0
- (18,20] 1

2.3.3

R code:

```
b=c(6.3,5.9,7.0,6.9,5.9)  
mean(b)  
median(b)
```

gives  $\bar{y}=6.4$  nmol/gm (sample mean) and  $\tilde{y}=6.3$  nmol/gm (sample median).

2.3.11

R code:

```
p=c(5,7,7,8,8,8,9,9,9,10,10,10,10,10,10,10,10,10,10,10,11,11,11,11,11,11,11,11,11,11,12,12,12,12,12,13,13,13,14,14)
median(p)
```

This gives  $\tilde{y}=10.5$  piglets

2.4.2

R code:

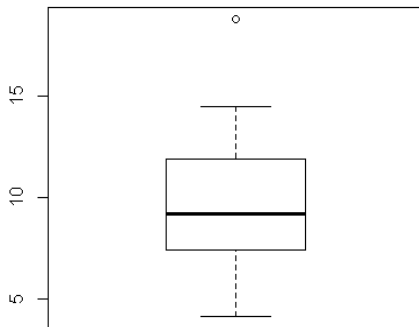
```
mao=c(6.8, 8.4, 8.7,11.9,14.2,18.8,9.9, 4.1, 9.7,12.7, 5.2, 7.8,7.8, 7.4, 7.3,10.6,14.5,10.7)
summary(mao) # gives 5-number summary
IQR(mao) # gives interquartile range
```

(a)  $\tilde{y}=9.2$ ,  $Q1=7.5$ ,  $Q3=11.6$

(b)  $IQR=11.6-7.5=4.1$

(c) upper fence is  $11.6+1.5(4.1)=17.75$

(d) `boxplot(mao)` gives



2.4.7

(a)  $IQR=127.42-113.59=13.83$

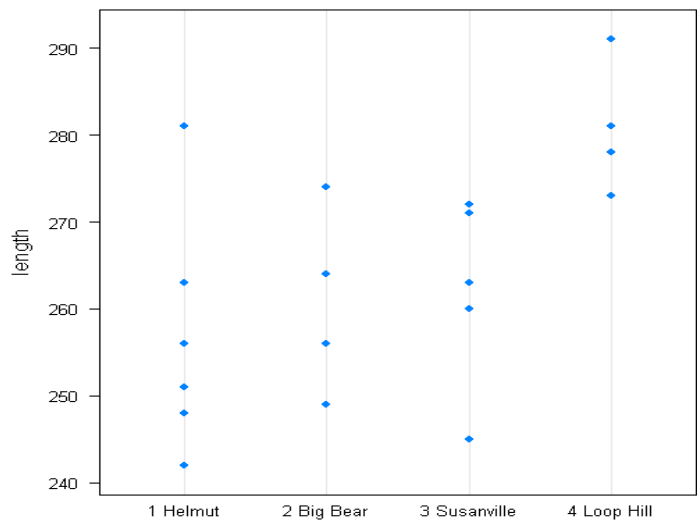
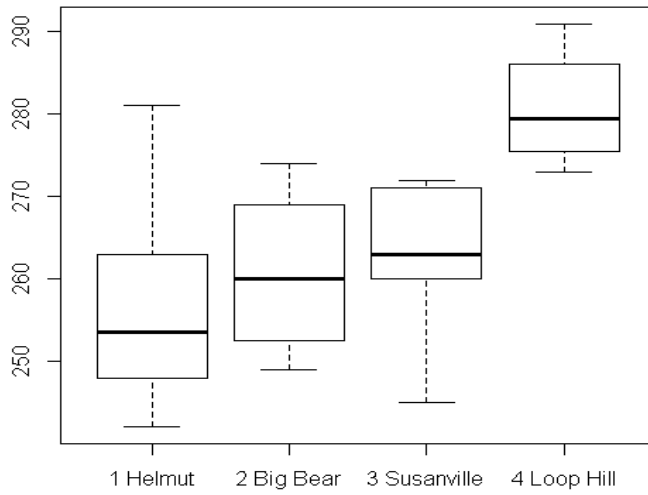
lower fence =  $113.59-1.5(13.83)=92.845$

upper fence =  $127.42+1.5*(13.83)=148.165$

(b) There are no outliers; the smallest value 95.16 is larger than the lower fence, and the largest value 145.11 is smaller than the upper fence

2.5.2

The posted R code gives:

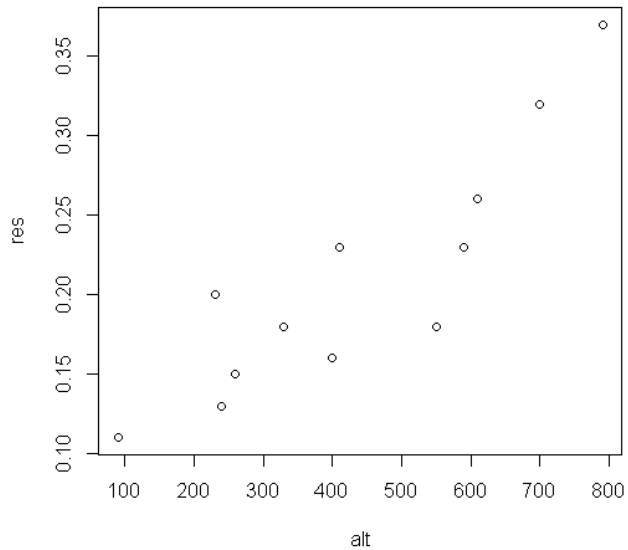


South to North makes more sense, so we can get a feel for what happens to the squirrels' length as we move north.

### 2.5.3

R code:

```
alt=c(90,230,240,260,330,400,410,550,590,610,700,790)
res=c(0.11,0.20,0.13,0.15,0.18,0.16,0.23,0.18,0.23,0.26,0.32,0.37)
plot(alt,res)
```



### 2.6.5

R code:

```
atp=c(1.45,1.19,1.05,1.07)
```

```
mean(atp)
```

```
sd(atp)
```

This gives  $\bar{y}=1.19$  and  $s=0.184$ . You \*can\* do this by hand using the formulas.

$\bar{y}=(1.45+1.19+1.05+1.07)/4=1.19$  and

$s=\sqrt{((1.45-1.19)^2+(1.19-1.19)^2+(1.05-1.19)^2+(1.07-1.19)^2)/3}=0.184$

### 2.6.11

The intervals described are (57.9,138.7), (17.5,179.1), and (-22.9,219.5). The proportions in these intervals are:

26/36=72.2%, 34/36=94.4%, 36/36=100.0%.

### 2.6.12

These are reasonably close to the percentages given by the empirical rule, 68%, 95%, and >99%.

### 2.S.7

R code:

```
> s=c(5,0,9,6,0,0,5,0,6,1,5,0,0,0,0,7,0,0,4,7)
```

```
> mean(s)
```

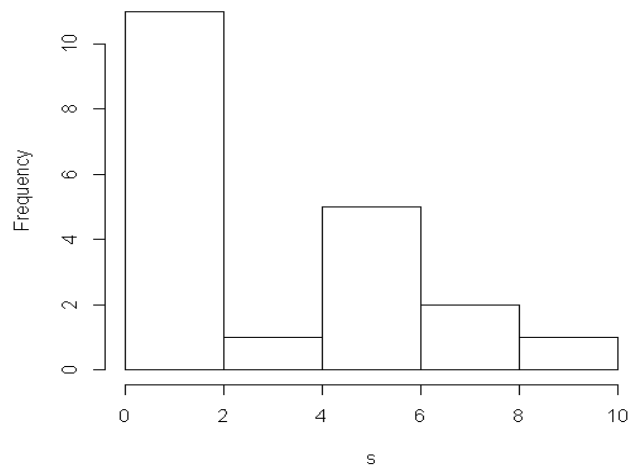
```
[1] 2.75
```

```
> median(s)
```

```
[1] 0.5
```

Gives  $\bar{y}=2.75$  seizures and  $\tilde{y}=0.5$  seizures. Note that mean pulled higher in direction of skew (skewed right).

**Histogram of s**



The most common observation is zero (also called the mode). This is an example of "zero inflated data", which also occurs with variables like medical costs in a month, earthquakes in a year, etc. Often scientists will separate the analysis of such data into the probability of a zero, and the distribution of positive outcomes.

#### 2.S.17

This is a challenging problem!

From looking at the histograms, (a) and (b) will have mean and medians around 40, but (b) will have a larger standard deviation. (c) should have the mean pulled higher than the median. Given all this, (a) is output 2, (b) is output 4, and (c) is output 1.

#### 2.S.19

R code:

```
>
```

```
cal=c(95,110,135,120,88,125,112,100,130,107,86,130,122,122,127,107,107,107,88,126,125,112,78,115,78,102,103,93,88,110,104,122,112,80,121,126,90,96)
```

```
> summary(cal)
```

```
  Min. 1st Qu.  Median   Mean 3rd Qu.   Max.
 78.00  95.25 108.50 107.90 122.00 135.00
```

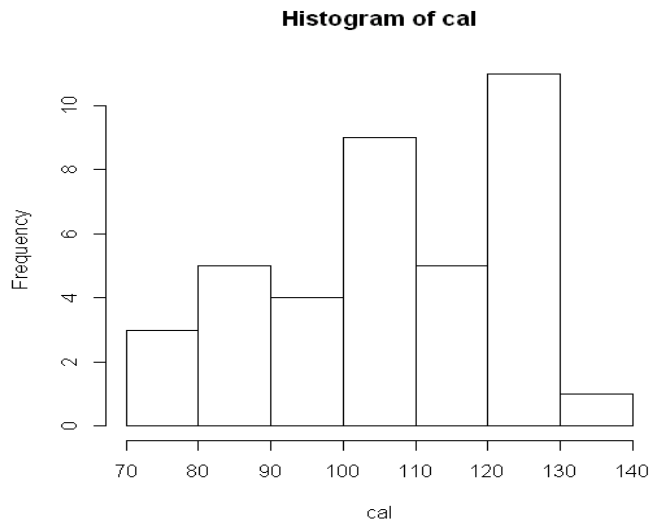
```
> mean(cal)
```

```
[1] 107.8684
```

```
> sd(cal)
```

```
[1] 16.0778
```

```
> hist(cal)
```



The mean and median are both about 108 nM, so this is a typical value. The interval containing the middle 50% of the data has length 27 nM; an observation typically deviates from the mean by 16 nM. The data are very slightly skewed to the left.

**2.S.20**

The key here is the length of the box. The boxplot shows the middle 50% of the data are between, roughly, 21 and 37. The histogram that best match this is (a).