PH525.1x: Week1

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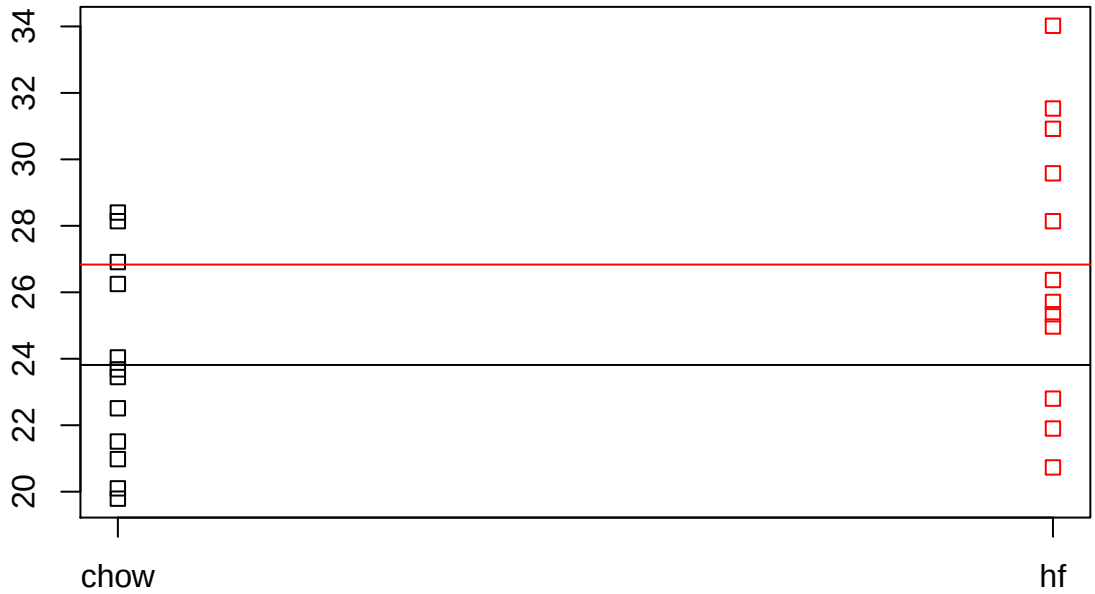
Introduction to Random Varialbe I

```
## Load the data
dat = read.csv("femaleMiceWeights.csv")
## The observed difference between high fat diet and control was
mean(dat[13:24,2]) - mean(dat[1:12,2])
```

```
## [1] 3.020833
```

```
## A strip chart of the weights of these two groups
s = split(dat[,2], dat[,1])
stripchart(s, vertical=TRUE, col=1:2)
## Add the means to the plot
abline(h=sapply(s, mean), col=1:2)
```



```
## Question 1.1 How many of the high fat mice weigh less than the mean of the control mice (chow)?
sum(s$hf < mean(s$chow))
```

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

```
## Question 1.2 How many of the control mice weigh more than the mean of the high fat mice?
sum(s$chow > mean(s$hf))
```

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

```
## Question 1.3  What is the proportion of high fat diet mice over 30?
sum(s$hf > 30)/length(s$hf)
```

```
## [1] 0.25
```

Introduction to Random Variables II

```
## Course example
dat[1:12, 2]
```

```
##  [1] 21.51 28.14 24.04 23.45 23.68 19.79 28.40 20.98 22.51 20.10 26.91
## [12] 26.25
```

```
mean(dat[13:24, 2] - mean(dat[1:12, 2]))
```

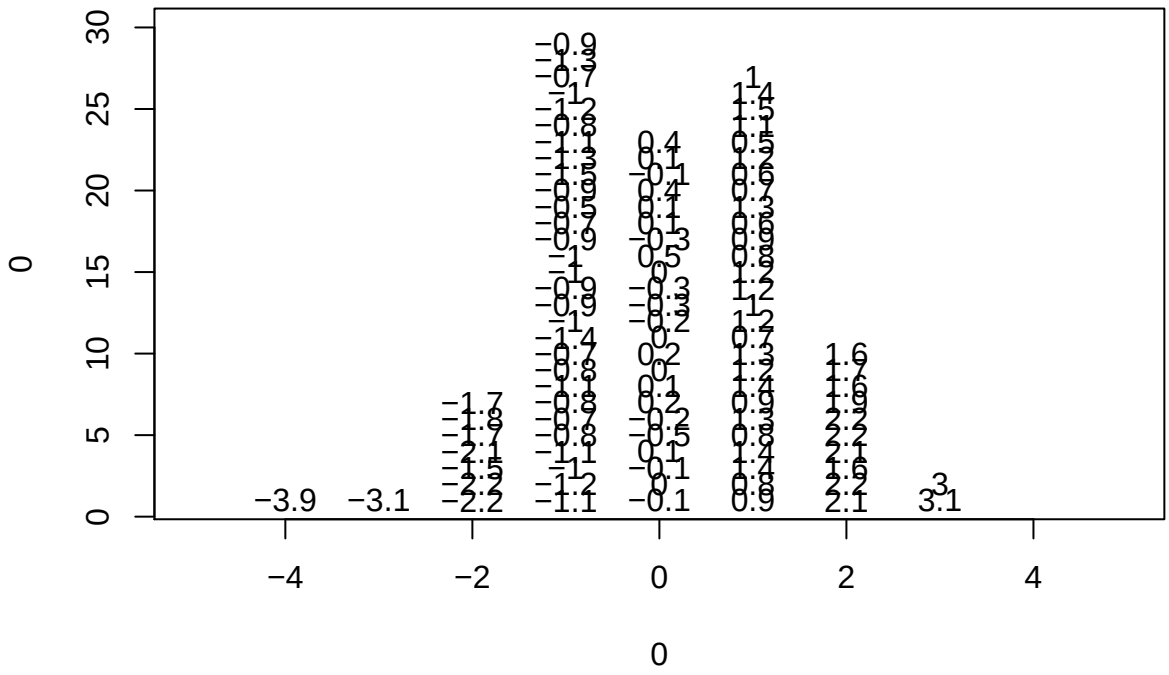
```
## [1] 3.020833
```

```
population <- read.csv("femaleControlsPopulation.csv")

n <- 10000
null <- vector("numeric", n)
for (i in 1:n){
  control <- sample(population[, 1], 12)
  treatment <- sample(population[, 1], 12)
  null[i] <- mean(treatment) -mean(control)
}

diff <- mean(dat[13:24, 2]) - mean(dat[1:12, 2])
#what percent are bigger than `diff`?
mean(null > diff)
```

```
## [1] 0.0141
```

##Illustration of the null distribution Repeat the loop above but this time add a point to the figure every time re-run the experiment

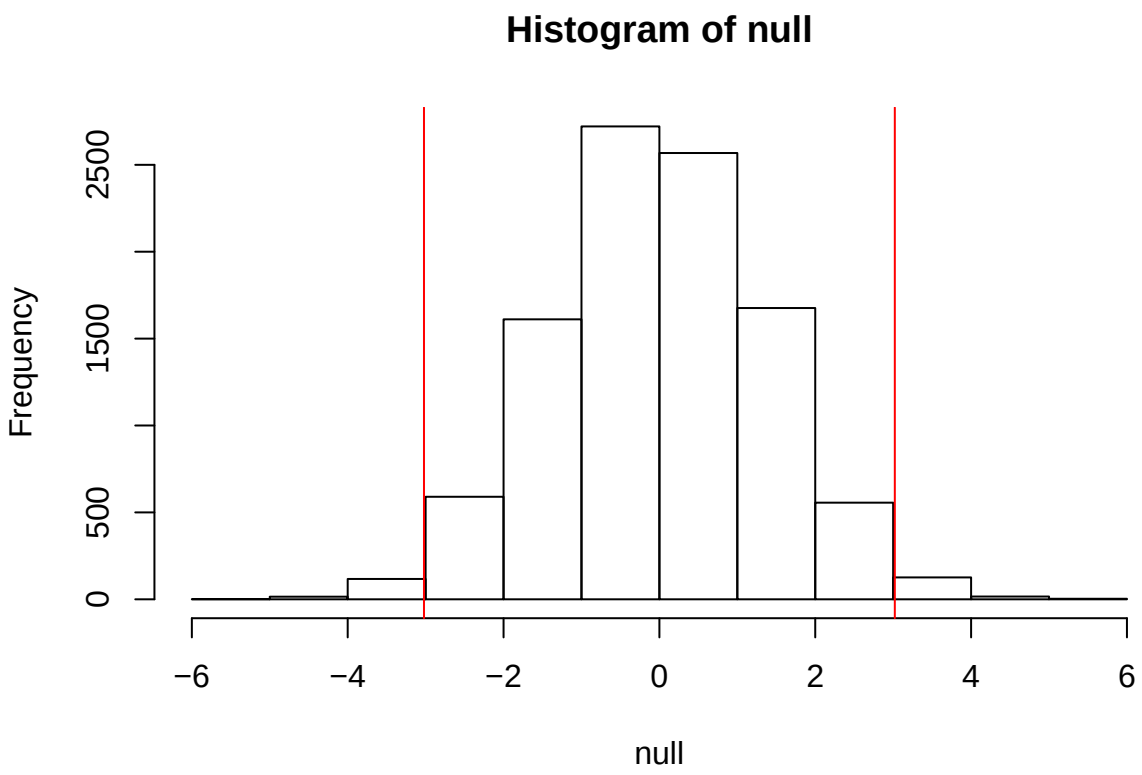
```
# Read the population
n <- 100
plot(0, 0, xlim = c(-5, 5), ylim = c(1, 30), type = "n")
totals <- vector("numeric", 11)
for (i in 1:n){
    control <- sample(population[, 1], 12)
    treatment <- sample(population[, 1], 12)
    nulldiff <- mean(treatment) - mean(control)
    j <- pmax(pmin(round(nulldiff) + 6, 11), 1)
    totals[j] <- totals[j] + 1
    text(j - 6, totals[j], pch = 15, round(nulldiff, 1))
    ##if(i < 15) scan() ## add this line to interactively see values appear
}
```



Rcreate the vector of differences between means of random samples from the control population.

```
null <- replicate(10000, mean(sample(population[, 1], 12)) -
                         mean(sample(population[, 1], 12)))
# Make a histogram
hist(null)

# The original difference observed between the mice fed high fat diets and control mice:
diff = mean(dat[13:24,2]) - mean(dat[1:12,2])
# Add this difference to the histogram:
abline(v=diff, col="red")
# Also add the negative of the difference:
```

```r
abline(v=-diff, col="red")
```



If we look for the number of null distribution values to the right of the (right) red line, we would say "we calculated the probability of observing a larger difference from the null distribution". This is sometimes called a "one-tailed" probability, because we only look at one "tail" of the histogram (the left and right sides where the bars become short).

By looking at the tails on both sides of the histogram, we can say "we calculated the probability of observing as extreme a difference from the null distribution". This is sometimes called a "two-tailed" probability. This probability is commonly referred to as a p-value.

Question 3.1: What is the one-tailed probability of seeing as big a difference as we observed, calculated from your null distribution? (0.0141)

Question 3.2: What is the two-tailed probability of seeing as big a difference as we observed, calculated from your null distribution? (0.0266)

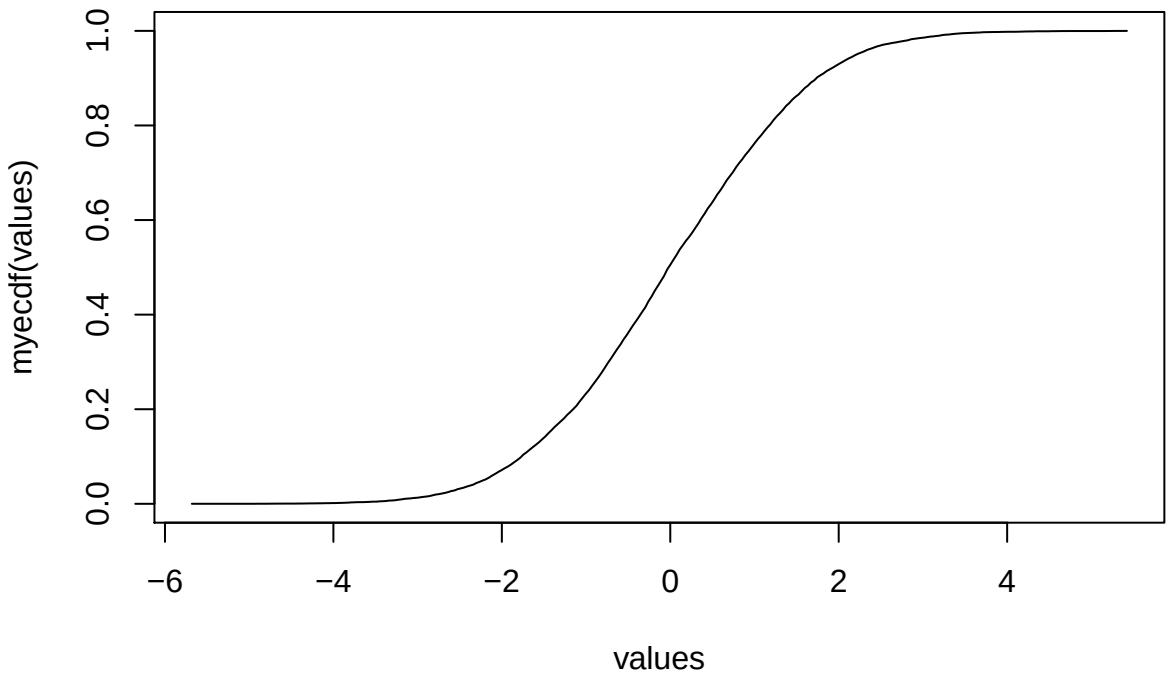
Distributions

A *distribution* is as a compact description of many numbers. For example, in the previous section we defined an object 'null' with 10,000 average differences created under the null. To define a distribution we compute, for all possible values of a the proportion of numbers in our list that are below a. We use the following notation

$$F(a) \equiv \Pr(x \leq a)$$

This is called the empirical cumulative distribution function. We can plot $F(a)$ versus a like this

```
values <- seq(min(null), max(null), len = 300)
myecdf <- ecdf(null)
plot(values, myecdf(values), type = "l")
```



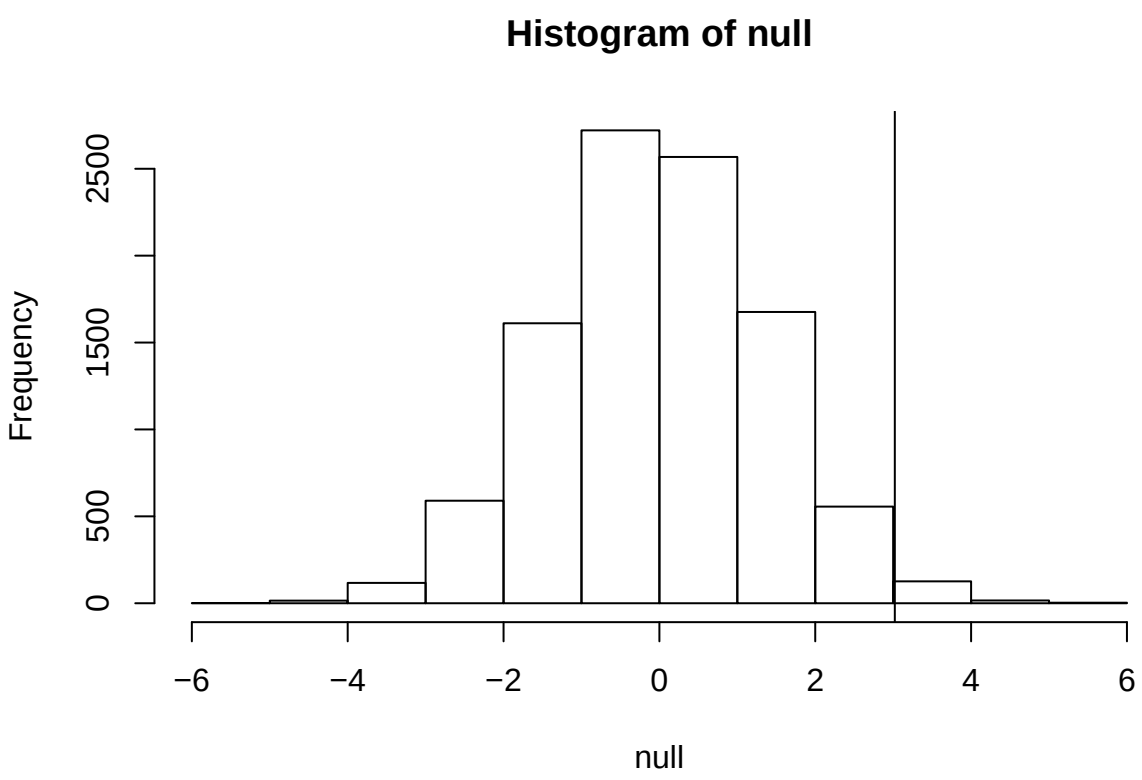
Histograms give us the same information but show us the proportion of values in intervals:

$$\Pr(a \leq x \leq b) = F(b) - F(a)$$

This is a more useful plot because we are usually more interested in intervals. It is also easier to distinguish different types (families) of distributions by looking at histograms.

Note that from the histogram we can see that values as large as `diff` are relatively rare

```
hist(null)
abline(v = diff)
```



Normal distribution

When the histogram of a list of numbers approximates the normal distribution we can use a convenient mathematical formula to approximate the proportion of individuals in any given interval

$$\Pr(a < x < b) = \int_a^b \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(\frac{-(x-\mu)^2}{2\sigma^2}\right) dx$$

Here μ and σ are refereed to as the mean and standard deviation.If this approximation holds for our list then the population mean and variance of our list can be used in the formula above. To see this with an example remember that above we noted that only 1.5% of values on the null distribution were above `diff`. We can compute the proportion of values below a value `x` with `pnorm(x,mu,sigma)` without knowing all the values. The normal approximation works very well here:

```
1-pnorm(diff,mean(null),sd(null))
```

```
## [1] 0.01349906
```

A very useful characteristic of this approximation is that one only needs to know μ and σ to describe the entire distribution. From this we can compute the proportion of values in any interval.

Summary

Note that to make this calculation we did the equivalent of buying all the mice available from Jackson laboratories and performed our experiment over and over again to define the null distribution. This is not something we can do in practice. Statistical Inference is the mathematical theory that permits you to approximate this with only the data from your sample, i.e. the original 24 mice.