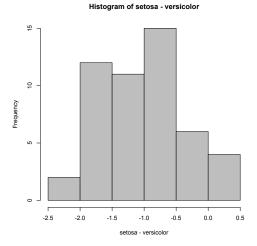
```
#Prototype to run a paired t-test
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#This a test is to compare related (paired) samples
Hypotheses:
H_0 - mean(X_1) = mean(X_2)
H_1 - mean(X_1) \neq mean(X_2)
#Read in the data
iris <- read.table("iris.txt")</pre>
#I want to compare Sepal.Length between "setosa" and "versicolor"
#Subset into two equal-length vectors
setosa <- iris$Sepal.Length[iris$Species == "setosa"]</pre>
versicolor <- iris$Sepal.Length[iris$Species == "versicolor"]</pre>
#A paired t-test is a parametric test. Must check the assumptions:
#Data vectors are the same length
length(setosa)
[1] 50
length(versicolor)
[1] 50
#Differences between pairs are normally distributed
hist(setosa - versicolor, col="grey")
```



#Run t-test manually

```
#Get the data together
```

x1 <- setosa

x2 <- versicolor

#sample size

n <- length(setosa)

#means and standard deviations

x1bar <- mean(setosa)

x2bar <- mean(versicolor)

s1 <- sd(setosa)

s2 <- sd(versicolor)

#Need dbar for paired test

d <- x1-x2

dbar <- mean(d)

s_d <- sqrt(var(d))</pre>

#Calculate test statistic

t <- dbar/(s_d/sqrt(n))

t

[1] -10.1459

#Probability value (two sided case)

degf <- n-1

P <- 2 * pt(t, degf)

```
[1] 1.241915e-13
#Confidence intervals
alpha <- 0.05
#T distribution
c1 <- qt(alpha/2,degf)
c1 <- -c1
#Confidence Intervals
ci_l <- dbar-c1*(s_d/sqrt(n))
ci_u <- dbar+c1*(s_d/sqrt(n))</pre>
CI <- c(ci_l, ci_u)
CI
[1] -1.114203 -0.745797
#Run the test using the built in function
t.test(setosa,versicolor,paired=TRUE, conf.level=0.95)
Paired t-test
data: setosa and versicolor
t = -10.146, df = 49, p-value = 1.242e-13
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-1.114203 -0.745797
sample estimates:
mean of the differences
          -0.93
```

P < 0.05, reject H_0