

## Inference

### Synopsis

something about toothgrowth

### Data Summary

Note the R code used to obtain these results is included in the appendix.

There are 60 observations in the dataset. The length of guinea pig teeth (ondotoblasts) were measured after they had received some dose (either 0.5, 1.0, or 2.0 mg) of vitamen C, which was supplied either as orange juice (OJ) or an aqueous solution of ascorbic acid. (VC). Measurements were taken from 60 guinea pigs, such that each of the six dose/supplement combinations considered was administered to 10 animals. The mean and variance of the measured tooth length is listed below for each group.

supp	dose	meanlen	varlen
OJ	0.5	13.23	19.8890
OJ	1.0	22.70	15.2956
OJ	2.0	26.06	7.0493
VC	0.5	7.98	7.5440
VC	1.0	16.77	6.3268
VC	2.0	26.14	23.0182

Initially, it seems that OJ has a larger effect on tooth length, with higher doses correlating with longer tooth lengths. The analysis below will consider these hypotheses and verify whether or not they are statistically significant.

### Analysis

Will consider lengths from OJ vs lengths from VC, (neglecting dose). Histograms for these groups are plotted in the appendix

Will use a two group independent (unpaired) t-test, assuming unequal variance (or rather, not assuming equal variance) among groups. Note that the t-test assumes that the observations are normally distributed (although apparently it is 'robust' to this assumption).

In this case, the null hypothesis,  $H_0$ , is that the mean tooth length for each group is equal. Our alternate hypothesis,  $H_a$  is that the means are *not* equal, and thus we will use a two sided t-test. We will require a 95% probability for statistical significance, that is, we will reject the null hypothesis if there is less than a 5% probability of it producing the observed data.

hypothesis tests: OJ is better than VC higher dose is better growth per dose?

growth per dose, (or oj >< VC, two sided) dosage - test 0.5 vs 2.0, 0.5 vs 1.0, 1.0 vs 2.0 Dosage regardless of method method regardless of dose method - growth per unit dose

t distribution assumes data iid normal “but it is robust” to this unequal variance (the variances above are not equal) [https://github.com/bcaffo/courses/blob/master/06\\_StatisticalInference/08\\_t^slide 21](https://github.com/bcaffo/courses/blob/master/06_StatisticalInference/08_t^slide%2021)

Can't use paired test, because we can't compute the differences (we have 60 separate hamsters, not 10 that were fed vitamin c multiple times via different methods). independent group t intervals (unequal variance), with alternative that the difference is not equal to zero ( $\mu_{2.0} - \mu_{0.5}$ )

Go over math in first section/method

analysis section, make a bunch of tests

## Appendix

```
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(ggplot2)
head(ToothGrowth)

##   len supp dose
## 1  4.2   VC  0.5
## 2 11.5   VC  0.5
## 3  7.3   VC  0.5
```

```
## 4  5.8  VC  0.5
## 5  6.4  VC  0.5
## 6 10.0  VC  0.5
```

```
ToothGrowth %>% group_by(supp,dose) %>% summarise(meanlen=mean(len),varlen=var(len))
```

```
## Source: local data frame [6 x 4]
## Groups: supp [?]
##
##      supp  dose meanlen    varlen
##    <fctr> <dbl>   <dbl>     <dbl>
## 1      OJ   0.5    13.23  19.889000
## 2      OJ   1.0    22.70  15.295556
## 3      OJ   2.0    26.06   7.049333
## 4      VC   0.5     7.98   7.544000
## 5      VC   1.0    16.77   6.326778
## 6      VC   2.0    26.14  23.018222
```

```
vc <-ToothGrowth %>% filter(supp=='VC')
oj <-ToothGrowth %>% filter(supp=='OJ')
moose<-t.test(x=oj$len,y=vc$len,paired=F)
moose
```

```
##
##  Welch Two Sample t-test
##
## data:  oj$len and vc$len
## t = 1.9153, df = 55.309, p-value = 0.06063
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1710156  7.5710156
## sample estimates:
## mean of x mean of y
## 20.66333 16.96333
```

```
ggplot(data=ToothGrowth,aes(x=len)) + geom_histogram(aes(fill=..count..),binwidth=2) + facet
```

Check some of this stuff. We're running tests on lots of different subgroups, using the same data more than once. Should we be correcting/accounting for multiple testing?

```
doses<-c(0.5,1.0,2.0)
```

```
for (i in 1:2)
```

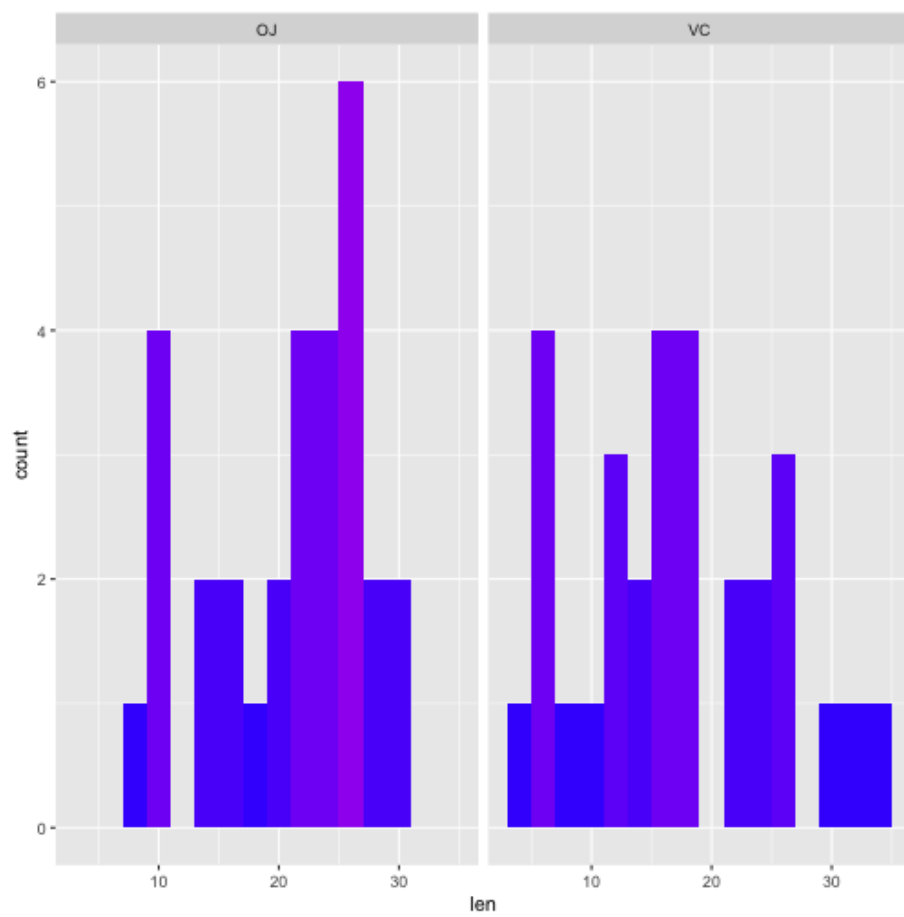


Figure 1: plot of chunk plotdose2

```

{
  for (j in (i+1):3)
  {
    print(paste(doses[i], ' vs ', doses[j]))
    groupa<- ToothGrowth %>% filter(dose ==doses[i])
    groupb<- ToothGrowth %>% filter(dose ==doses[j])
    test<-t.test(x=groupa$len,y=groupb$len,paired=F)
    print(test)
  }
}

## [1] "0.5  vs  1"
##
## Welch Two Sample t-test
##
## data:  groupa$len and groupb$len
## t = -6.4766, df = 37.986, p-value = 1.268e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -11.983781 -6.276219
## sample estimates:
## mean of x mean of y
## 10.605 19.735
##
## [1] "0.5  vs  2"
##
## Welch Two Sample t-test
##
## data:  groupa$len and groupb$len
## t = -11.799, df = 36.883, p-value = 4.398e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -18.15617 -12.83383
## sample estimates:
## mean of x mean of y
## 10.605 26.100
##
## [1] "1  vs  2"
##
## Welch Two Sample t-test
##
## data:  groupa$len and groupb$len
## t = -4.9005, df = 37.101, p-value = 1.906e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:

```

```
## -8.996481 -3.733519
## sample estimates:
## mean of x mean of y
## 19.735 26.100
```

```
ggplot(data=ToothGrowth,aes(x=len)) + geom_histogram(aes(fill=..count..),binwidth=2) + facet
```

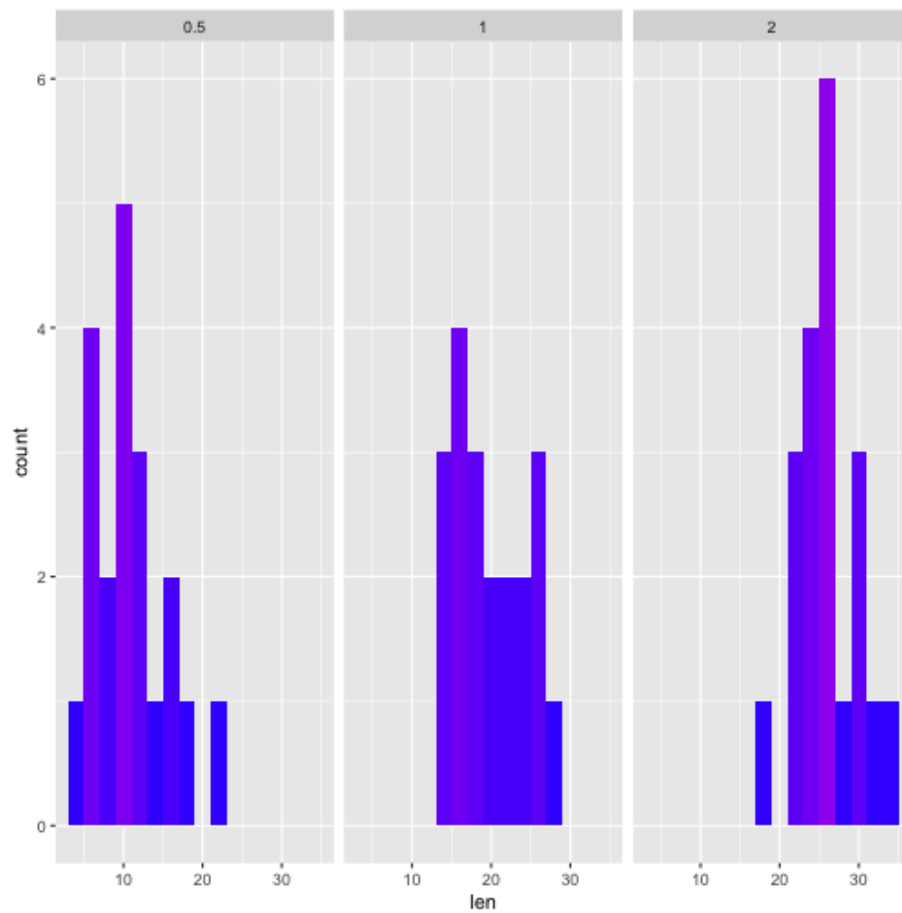


Figure 2: plot of chunk plotdose

```
for (i in 1:3)
{
  ojdose<-ToothGrowth %>% filter(dose == doses[i] ) %>% filter(supp == 'OJ')
  vcdose<-ToothGrowth %>% filter(dose == doses[i] ) %>% filter(supp == 'VC')
  test<-t.test(x=ojdose$len,y=vcdose$len,paired=F)
```

```

    print(test)
}

##
## Welch Two Sample t-test
##
## data:  ojdose$len and vcdose$len
## t = 3.1697, df = 14.969, p-value = 0.006359
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.719057 8.780943
## sample estimates:
## mean of x mean of y
##    13.23    7.98
##
##
## Welch Two Sample t-test
##
## data:  ojdose$len and vcdose$len
## t = 4.0328, df = 15.358, p-value = 0.001038
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  2.802148 9.057852
## sample estimates:
## mean of x mean of y
##    22.70    16.77
##
##
## Welch Two Sample t-test
##
## data:  ojdose$len and vcdose$len
## t = -0.0461, df = 14.04, p-value = 0.9639
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.79807 3.63807
## sample estimates:
## mean of x mean of y
##    26.06    26.14

ggplot(data=ToothGrowth,aes(x=len)) + geom_histogram(aes(fill=..count..),binwidth=2) + facet

```

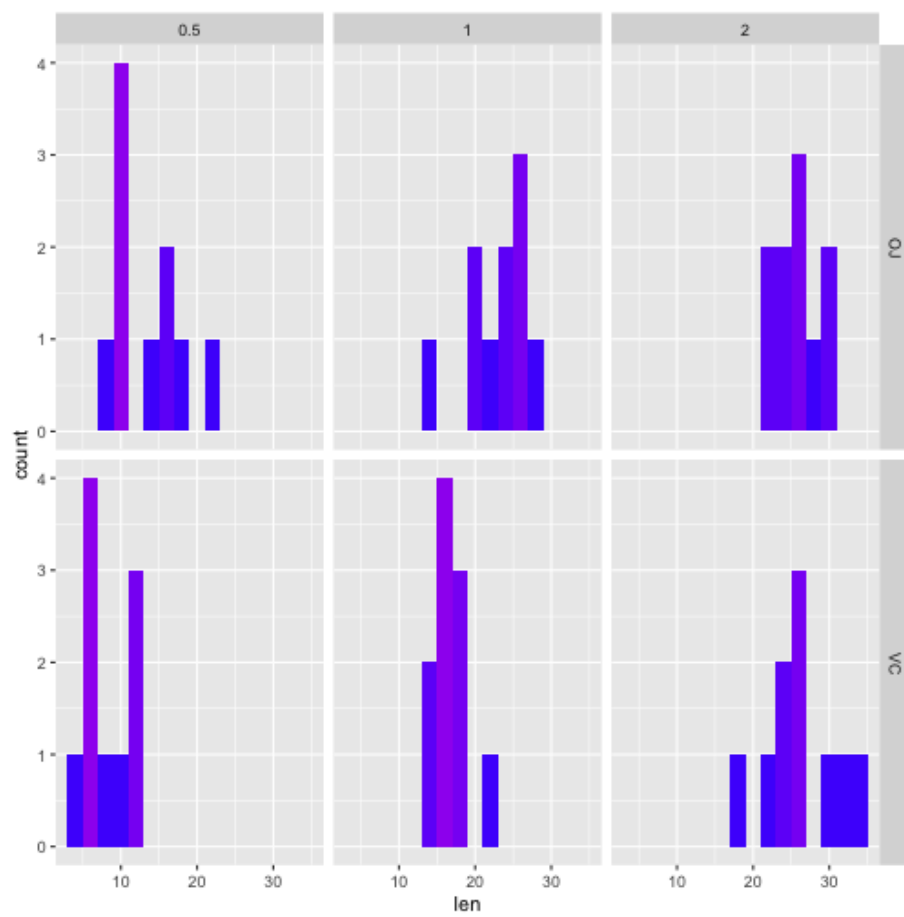


Figure 3: plot of chunk plot