

Inference

Synopsis

something about toothgrowth

Data Summary

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

OJ seems to do more.

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 seperate 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

```

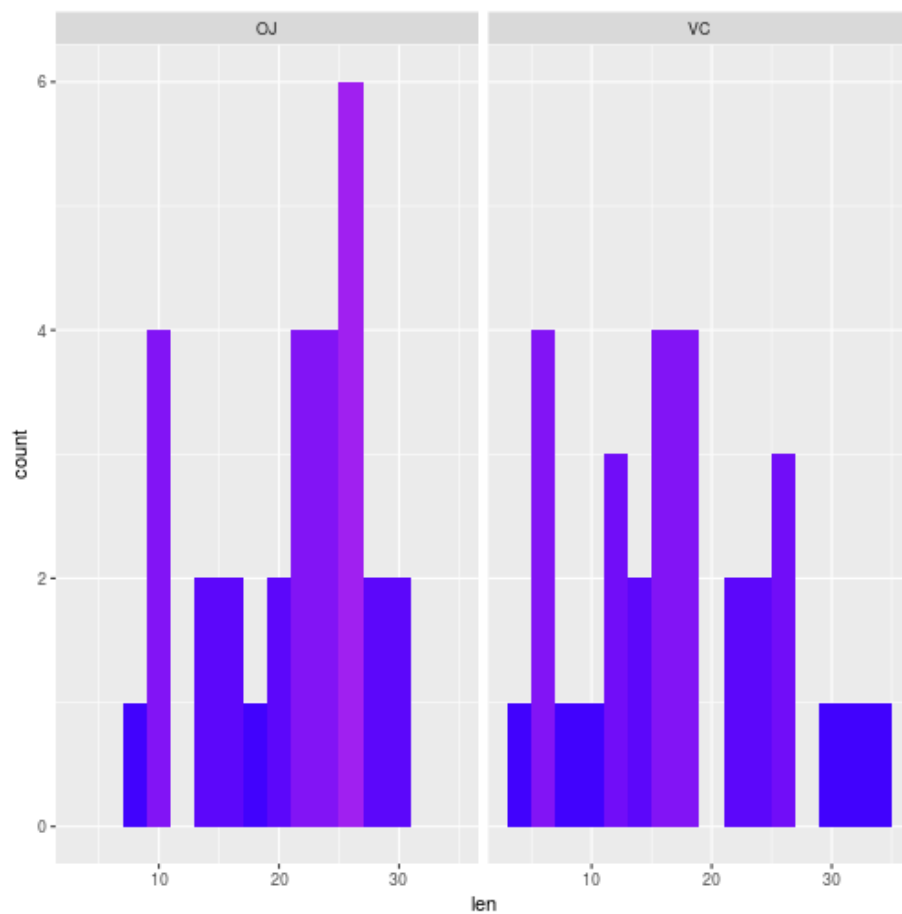


Figure 1: plot of chunk plotdose2

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)
{
  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
for (i in 1:3)

```

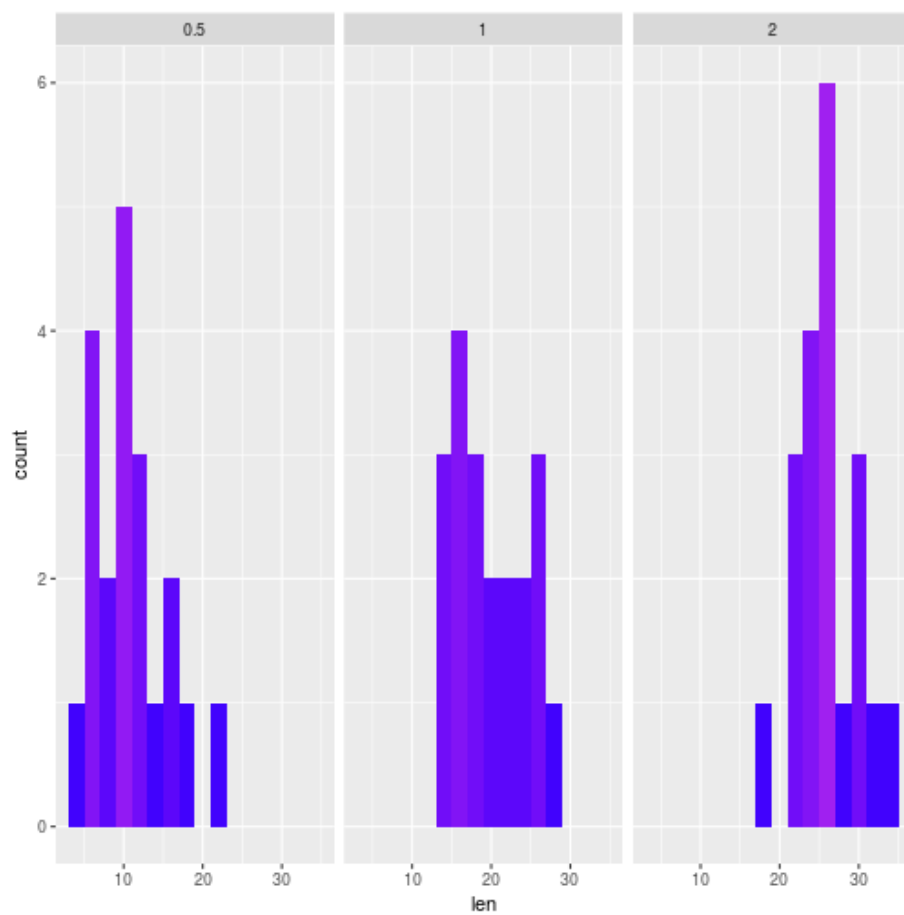


Figure 2: plot of chunk plotdose

```

{
  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 = -0.046136, 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

```

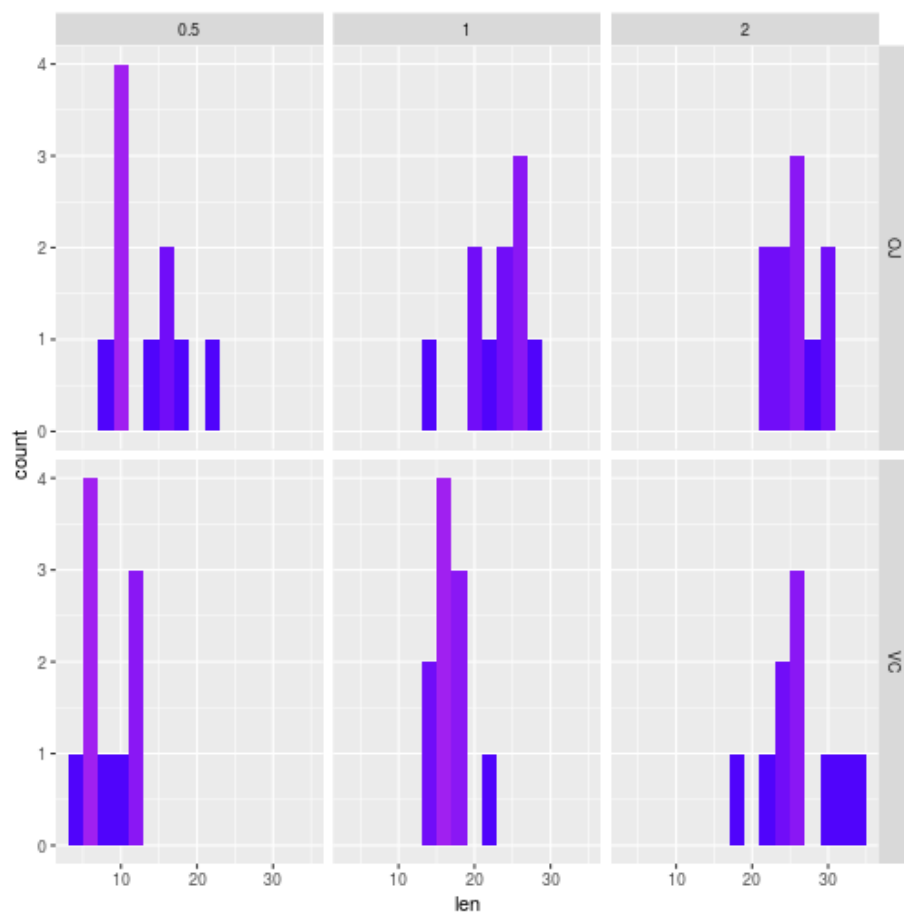


Figure 3: plot of chunk plot