

Vitamin C in Guinea Pigs

CF Hainey

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Basic Inferential Data Analysis on tooth growth

Overview

R has a data set called `ToothGrowth`. This dataset contains the growth of a tooth in Guinea Pigs given two different vitamin C supplements (OJ = orange juice, VC = asorbic acid) at 3 different dosages. The set has 60 objects with 3 variables, length of tooth, supplement and dosage.

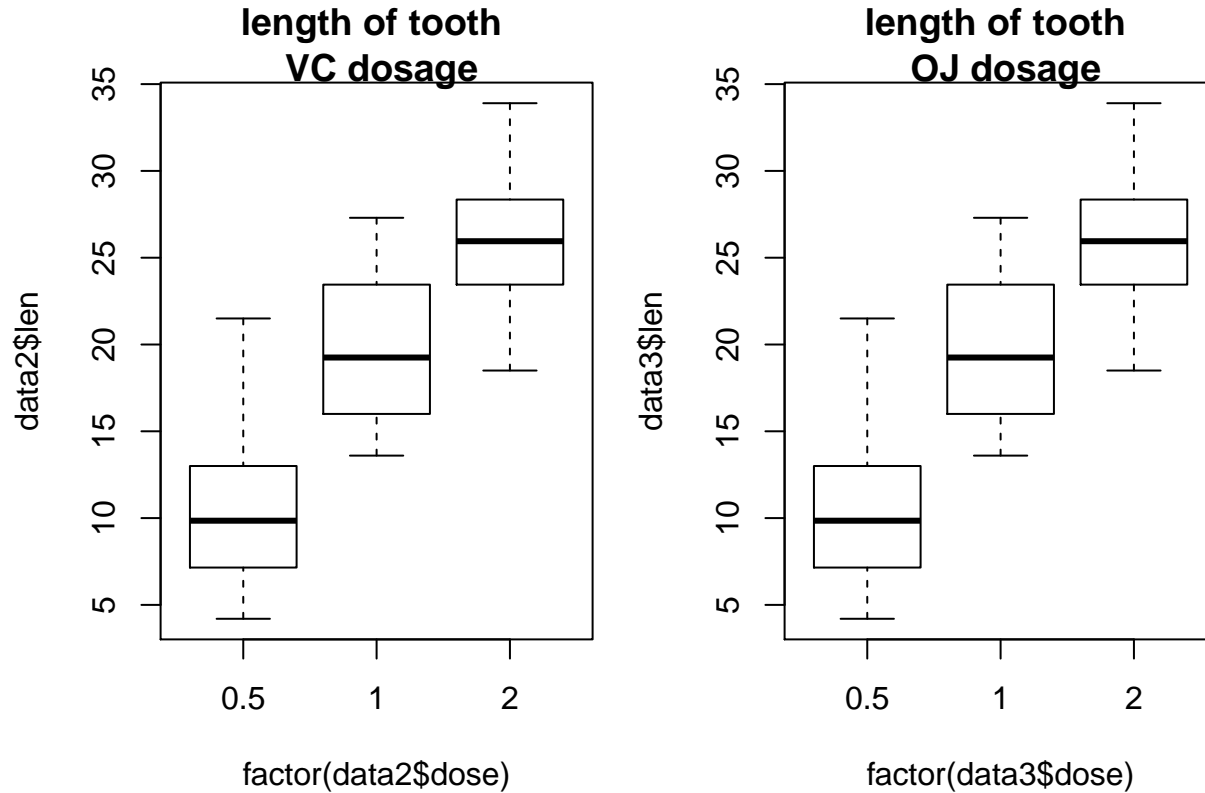
Conclusion

There is not a clear difference between the supplements based on t-test $p = 0.06$. There is also not a difference between the different dosages and the supplements. There is however a difference, based on t-test that the different dosages contribute to length of tooth. The significance range from $e-05$ to $e-14$. The largest significance was from 0.5 dosing to 2.0, regardless of the supplement.

```
data("ToothGrowth"); summary(ToothGrowth); dat1 <- aggregate(.~dose, data=ToothGrowth, mean)
```

```
##      len      supp      dose
## Min.   : 4.20   OJ:30   Min.    :0.500
## 1st Qu.:13.07   VC:30   1st Qu.:0.500
## Median :19.25           Median :1.000
## Mean   :18.81           Mean    :1.167
## 3rd Qu.:25.27           3rd Qu.:2.000
## Max.   :33.90           Max.    :2.000
```

```
data2 <- subset(ToothGrowth, supp="VC"); data3 <- subset(ToothGrowth, supp="OJ")
par(mfrow = c(1, 2), mar = c(4, 4, 2, 1), oma = c(0, 0, 2, 0))
plot(data2$len ~factor(data2$dose), main = "length of tooth \n VC dosage")
plot(data3$len ~factor(data3$dose),main = "length of tooth \n OJ dosage")
```



```

VC <- ToothGrowth[ which(ToothGrowth$supp == "VC"), ]
OJ <- ToothGrowth[ which(ToothGrowth$supp == "OJ"), ]
VC0.5 <-data2[which(data2$dose == 0.5),]; VC1.0 <-data2[which(data2$dose == 1.0),];VC2.0 <-data2[which(
OJ0.5 <-data3[which(data2$dose == 0.5),]; OJ1.0 <-data3[which(data2$dose == 1.0),];OJ2.0 <-data3[which(
t1 <-t.test(VC$len, OJ$len, mu = 0, paired=F, conf.level = 0.95 )
t2 <-t.test(VC0.5$len, OJ0.5$len, mu = 0, paired=F, conf.level = 0.95 );t3 <-t.test(VC1.0$len, OJ1.0$len, mu = 0, paired=F, conf.level = 0.95 );
t4 <-t.test(VC2.0$len, OJ2.0$len, mu = 0, paired=F, conf.level = 0.95 );t5 <-t.test(VC0.5$len, VC1.0$len, mu = 0, paired=F, conf.level = 0.95 );
t6 <-t.test(VC0.5$len, VC2.0$len, mu = 0, paired=F, conf.level = 0.95 );
t8 <-t.test(OJ0.5$len, OJ1.0$len, mu = 0, paired=F, conf.level = 0.95 );t9 <-t.test(OJ0.5$len, OJ2.0$len, mu = 0, paired=F, conf.level = 0.95 );
jj<- c("VC_OJ", "VC0.5_OJ0.5","VC1.0_OJ1.0","VC2.0_OJ2.0","VC0.5_VC1.0","VC0.5_VC2.0","VC1.0_VC2.0","OJ0.5_OJ1.0","OJ0.5_OJ2.0","OJ1.0_OJ2.0")
jj <- cbind(t1$p.value, t2$p.value,t3$p.value,t4$p.value,t5$p.value,t6$p.value,t8$p.value,t9$p.value)
hh <- cbind(t1$conf.int, t2$conf.int,t3$conf.int,t4$conf.int,t5$conf.int,t6$conf.int,t8$conf.int,t9$conf.int)
note <- c("VC_OJ", "VC0.5_OJ0.5", "VC1.0_OJ1.0", "VC2.0_OJ2.0", "VC0.5_VC1.0","VC0.5_VC2.0","OJ0.5_OJ1.0","OJ0.5_OJ2.0","OJ1.0_OJ2.0")
note2 <-c("CI lower", "upper","p-value")
x <- rbind( hh, jj); dat2 <- as.data.frame(x, row.names = note2); colnames(dat2) <- note; print(dat2, d

```

```

##          VC_OJ VC0.5_OJ0.5 VC1.0_OJ1.0 VC2.0_OJ2.0 VC0.5_VC1.0
## CI lower -7.571         -2.9         -2.8         -2.4        -1.2e+01
## upper     0.171          2.9          2.8          2.4         -6.3e+00
## p-value   0.061          1.0          1.0          1.0         1.3e-07
##          VC0.5_VC2.0 OJ0.5_OJ1.0 OJ0.5_OJ2.0
## CI lower  -1.8e+01    -1.2e+01    -1.8e+01
## upper     -1.3e+01    -6.3e+00    -1.3e+01
## p-value    4.4e-14     1.3e-07     4.4e-14

```