

# data\_analysis\_toothgrowth

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{r setup, include=FALSE} knitr::opts_chunk$set(echo = TRUE)

data(ToothGrowth)

str(ToothGrowth)

head(ToothGrowth)

summary(ToothGrowth)
library(ggplot2)

t = ToothGrowth
levels(t$supp) <- c("Orange Juice", "Ascorbic Acid")
ggplot(t, aes(x=factor(dose), y=len)) +

  facet_grid(.~supp) +

  geom_boxplot(aes(fill = supp), show_guide = FALSE) +

  labs(title="Guinea pig tooth length by dosage for each type of supplement",
        x="Dose (mg/day)",
        y="Tooth Length")

hypoth1<-t.test(len ~ supp, data = t)

hypoth1$conf.int

hypoth1$p.value
hypoth2<-t.test(len ~ supp, data = subset(t, dose == 0.5))

hypoth2$conf.int

hypoth2$p.value

hypoth3<-t.test(len ~ supp, data = subset(t, dose == 1))

hypoth3$conf.int

hypoth3$p.value

hypoth4<-t.test(len ~ supp, data = subset(t, dose == 2))

hypoth4$conf.int

hypoth4$p.value
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