Pengenalan R, RStudio, Git, PCA, ggplot, sogosurvey.com

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#package

```
knitr::opts_chunk$set(echo = TRUE)
library(knitr) # untuk R markdown
library(Rmisc) # untuk fungsi summarySE
```

```
## Loading required package: lattice
```

```
## Loading required package: plyr
```

```
library(agricolae)# untuk fungsi HSD.test
library(ggplot2) #untuk fungsi grafik dengna ggplot
library(cowplot) #untuk membuat grafik grid
```

```
##
## ********************************************************
```

```
## Note: As of version 1.0.0, cowplot does not change the
```

```
##   default ggplot2 theme anymore. To recover the previous
```

```
##   behavior, execute:
##   theme_set(theme_cowplot())
```

```
## ********************************************************
```

#data

```
data(ToothGrowth)
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
## 7  11.2   VC  0.5
## 8  11.2   VC  0.5
## 9   5.2   VC  0.5
## 10  7.0   VC  0.5
## 11 16.5   VC  1.0
## 12 16.5   VC  1.0
## 13 15.2   VC  1.0
## 14 17.3   VC  1.0
## 15 22.5   VC  1.0
## 16 17.3   VC  1.0
```

```
## 17 13.6   VC   1.0
## 18 14.5   VC   1.0
## 19 18.8   VC   1.0
## 20 15.5   VC   1.0
## 21 23.6   VC   2.0
## 22 18.5   VC   2.0
## 23 33.9   VC   2.0
## 24 25.5   VC   2.0
## 25 26.4   VC   2.0
## 26 32.5   VC   2.0
## 27 26.7   VC   2.0
## 28 21.5   VC   2.0
## 29 23.3   VC   2.0
## 30 29.5   VC   2.0
## 31 15.2   OJ   0.5
## 32 21.5   OJ   0.5
## 33 17.6   OJ   0.5
## 34  9.7   OJ   0.5
## 35 14.5   OJ   0.5
## 36 10.0   OJ   0.5
## 37  8.2   OJ   0.5
## 38  9.4   OJ   0.5
## 39 16.5   OJ   0.5
## 40  9.7   OJ   0.5
## 41 19.7   OJ   1.0
## 42 23.3   OJ   1.0
## 43 23.6   OJ   1.0
## 44 26.4   OJ   1.0
## 45 20.0   OJ   1.0
## 46 25.2   OJ   1.0
## 47 25.8   OJ   1.0
## 48 21.2   OJ   1.0
## 49 14.5   OJ   1.0
## 50 27.3   OJ   1.0
## 51 25.5   OJ   2.0
## 52 26.4   OJ   2.0
## 53 22.4   OJ   2.0
## 54 24.5   OJ   2.0
## 55 24.8   OJ   2.0
## 56 30.9   OJ   2.0
## 57 26.4   OJ   2.0
## 58 27.3   OJ   2.0
## 59 29.4   OJ   2.0
## 60 23.0   OJ   2.0
```

summarySE

```r
ToothGrowth_sum<-summarySE(data = ToothGrowth, "len", groupvars = c("supp", "dose"), na.rm = FALSE,
          conf.interval = 0.95, .drop = TRUE)
```

statistik

linier model

```
tx_supp_dose <- with(ToothGrowth, interaction(supp, dose))
lm_supp_dose <- lm(len~tx_supp_dose, data = ToothGrowth)
summary(lm_supp_dose)
```

```
##
## Call:
## lm(formula = len ~ tx_supp_dose, data = ToothGrowth)
##
## Residuals:
##    Min    1Q Median    3Q    Max
##  -8.20  -2.72  -0.27   2.65   8.27
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          13.230      1.148  11.521 3.60e-16 ***
## tx_supp_doseVC.0.5   -5.250      1.624  -3.233  0.00209 **
## tx_supp_doseOJ.1      9.470      1.624   5.831 3.18e-07 ***
## tx_supp_doseVC.1      3.540      1.624   2.180  0.03365 *
## tx_supp_doseOJ.2     12.830      1.624   7.900 1.43e-10 ***
## tx_supp_doseVC.2     12.910      1.624   7.949 1.19e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.631 on 54 degrees of freedom
## Multiple R-squared:  0.7937, Adjusted R-squared:  0.7746
## F-statistic: 41.56 on 5 and 54 DF,  p-value: < 2.2e-16
```

anova test

```
anova(lm_supp_dose)
```

```
## Analysis of Variance Table
##
## Response: len
##              Df  Sum Sq Mean Sq F value    Pr(>F)
## tx_supp_dose  5 2740.10  548.02  41.557 < 2.2e-16 ***
## Residuals    54  712.11   13.19
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

HSD test group

```
HSD_supp_dose<-HSD.test(lm_supp_dose, trt = "tx_supp_dose", group = TRUE, console=TRUE)
```

```
##
## Study: lm_supp_dose ~ "tx_supp_dose"
##
## HSD Test for len
##
## Mean Square Error:  13.18715
##
## tx_supp_dose,  means
##
```

```
##          len       std  r  Min  Max
## OJ.0.5 13.23 4.459709 10  8.2 21.5
## OJ.1   22.70 3.910953 10 14.5 27.3
## OJ.2   26.06 2.655058 10 22.4 30.9
## VC.0.5  7.98 2.746634 10  4.2 11.5
## VC.1   16.77 2.515309 10 13.6 22.5
## VC.2   26.14 4.797731 10 18.5 33.9
##
## Alpha: 0.05 ; DF Error: 54
## Critical Value of Studentized Range: 4.178265
##
## Minimun Significant Difference: 4.798124
##
## Treatments with the same letter are not significantly different.
##
##          len groups
## VC.2   26.14      a
## OJ.2   26.06      a
## OJ.1   22.70      a
## VC.1   16.77      b
## OJ.0.5 13.23      b
## VC.0.5  7.98      c
```

HSD test group p value

```
HSD_supp_doseP<-HSD.test(lm_supp_dose, trt = "tx_supp_dose", group = FALSE, console=TRUE)
```

```
##
## Study: lm_supp_dose ~ "tx_supp_dose"
##
## HSD Test for len
##
## Mean Square Error:  13.18715
##
## tx_supp_dose,  means
##
##          len       std  r  Min  Max
## OJ.0.5 13.23 4.459709 10  8.2 21.5
## OJ.1   22.70 3.910953 10 14.5 27.3
## OJ.2   26.06 2.655058 10 22.4 30.9
## VC.0.5  7.98 2.746634 10  4.2 11.5
## VC.1   16.77 2.515309 10 13.6 22.5
## VC.2   26.14 4.797731 10 18.5 33.9
##
## Alpha: 0.05 ; DF Error: 54
## Critical Value of Studentized Range: 4.178265
##
## Comparison between treatments means
##
##                 difference pvalue signif.        LCL        UCL
## OJ.0.5 - OJ.1        -9.47 0.0000     *** -14.2681238  -4.671876
## OJ.0.5 - OJ.2       -12.83 0.0000     *** -17.6281238  -8.031876
## OJ.0.5 - VC.0.5       5.25 0.0243       *   0.4518762  10.048124
## OJ.0.5 - VC.1        -3.54 0.2640          -8.3381238   1.258124
```

```
## OJ.0.5 - VC.2       -12.91 0.0000     *** -17.7081238  -8.111876
## OJ.1 - OJ.2          -3.36 0.3187         -8.1581238   1.438124
## OJ.1 - VC.0.5        14.72 0.0000     ***  9.9218762  19.518124
## OJ.1 - VC.1           5.93 0.0074      **  1.1318762  10.728124
## OJ.1 - VC.2          -3.44 0.2936         -8.2381238   1.358124
## OJ.2 - VC.0.5        18.08 0.0000     *** 13.2818762  22.878124
## OJ.2 - VC.1           9.29 0.0000     ***  4.4918762  14.088124
## OJ.2 - VC.2          -0.08 1.0000         -4.8781238   4.718124
## VC.0.5 - VC.1        -8.79 0.0000     *** -13.5881238  -3.991876
## VC.0.5 - VC.2       -18.16 0.0000     *** -22.9581238 -13.361876
## VC.1 - VC.2          -9.37 0.0000     *** -14.1681238  -4.571876
```

grafik

base

```r
plot(ToothGrowth_sum$dose,ToothGrowth_sum$len)
```
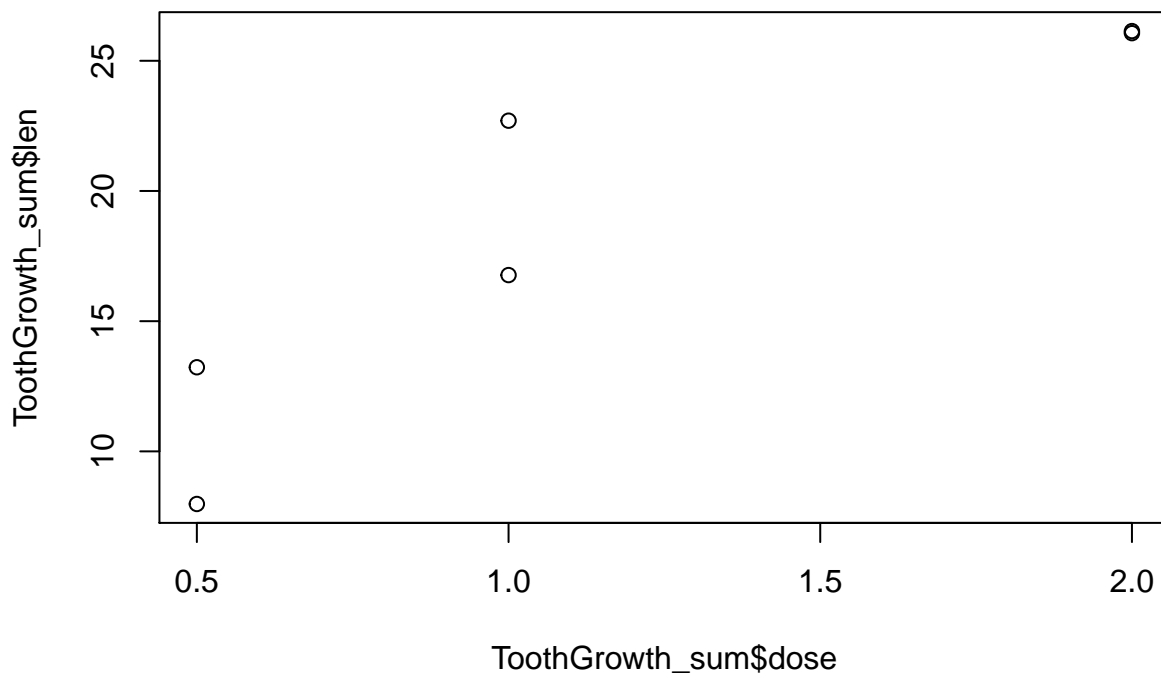


```
#fungsi plot dasar pada R tidak dapat melakukan gruping, sehingga jenis suplemen tidak dapat diamati
```
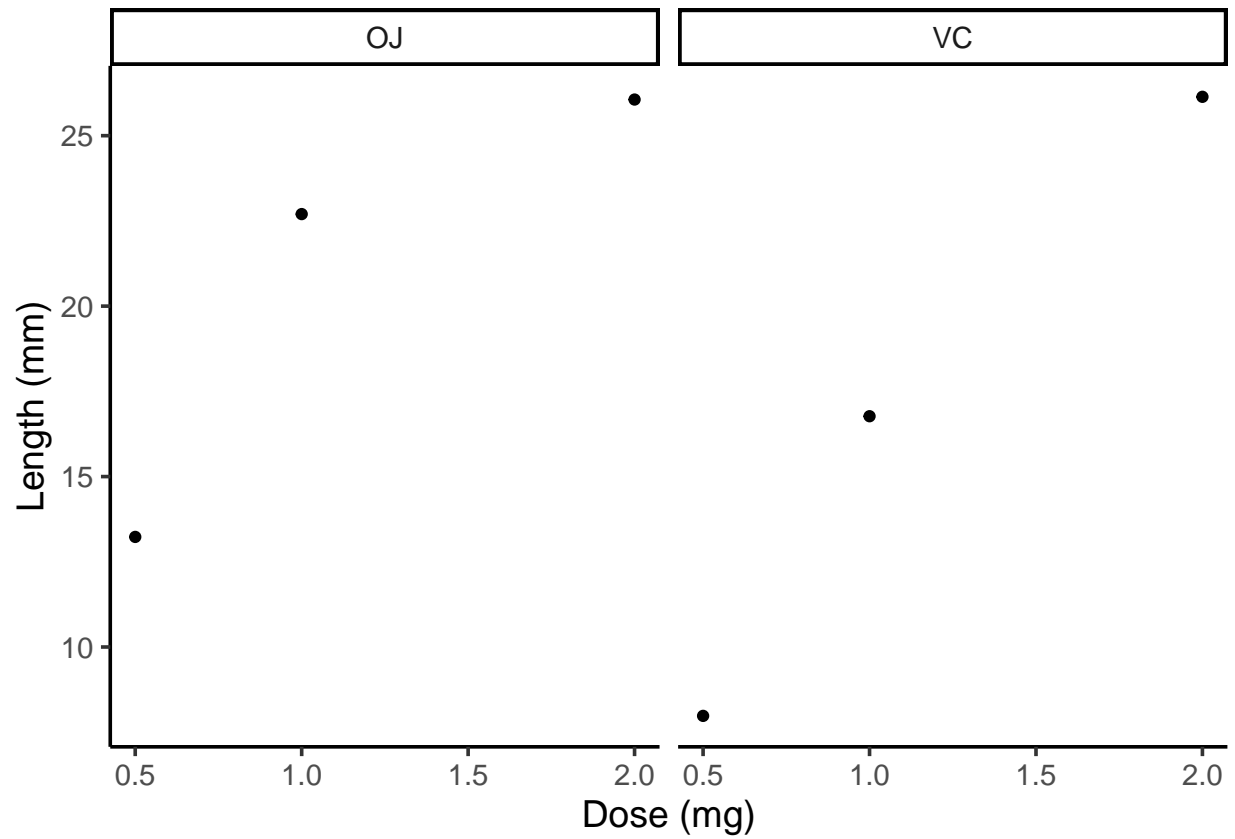
##grafik ggplot ###grafik ggplot dalam 1 plot

```r
g.ToothGrowth<-
  ggplot(data = ToothGrowth_sum,aes(x = dose,y=len), na.rm = FALSE) +
    geom_point(data = ToothGrowth_sum, aes(color=supp), size=4)+
  theme_classic(base_size = 14)+
  xlab("Dose (mg)") +
```
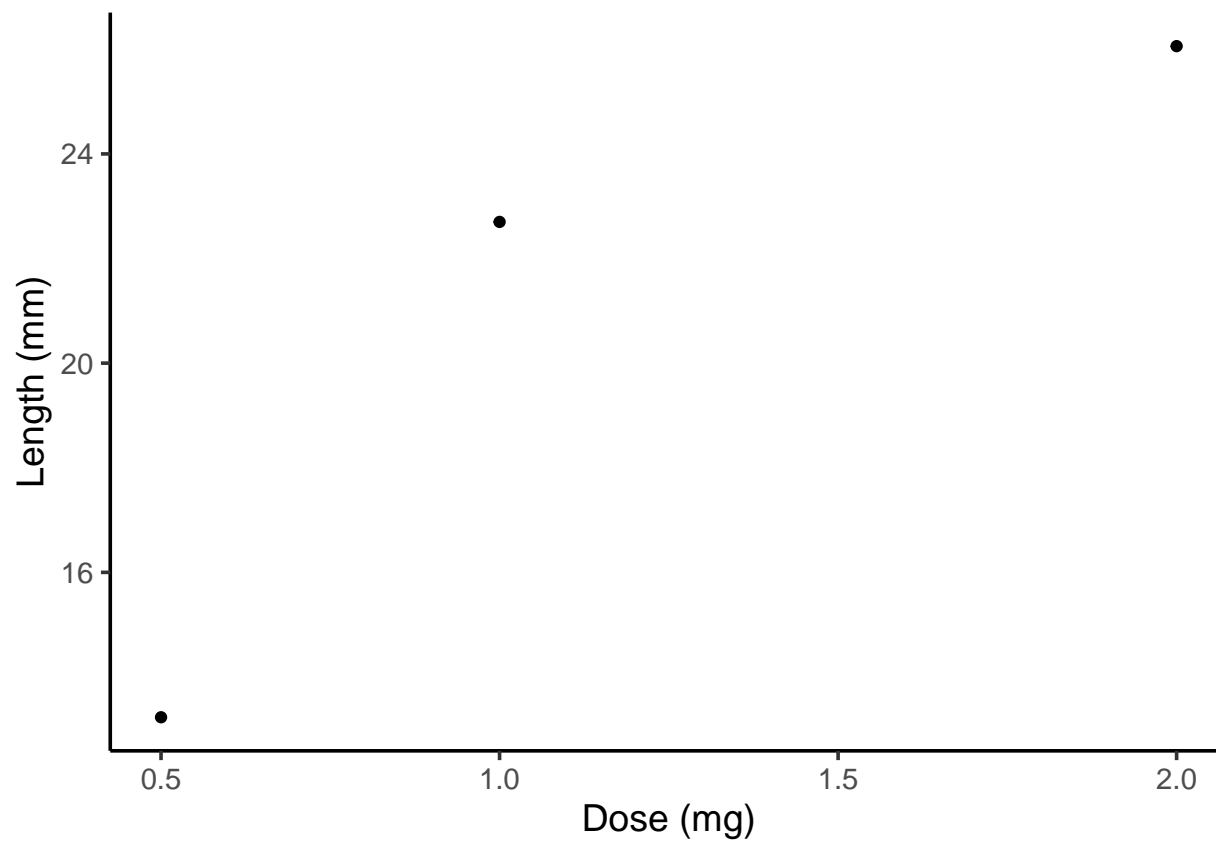
```
  ylab("Length (mm)")
g.ToothGrowth
```
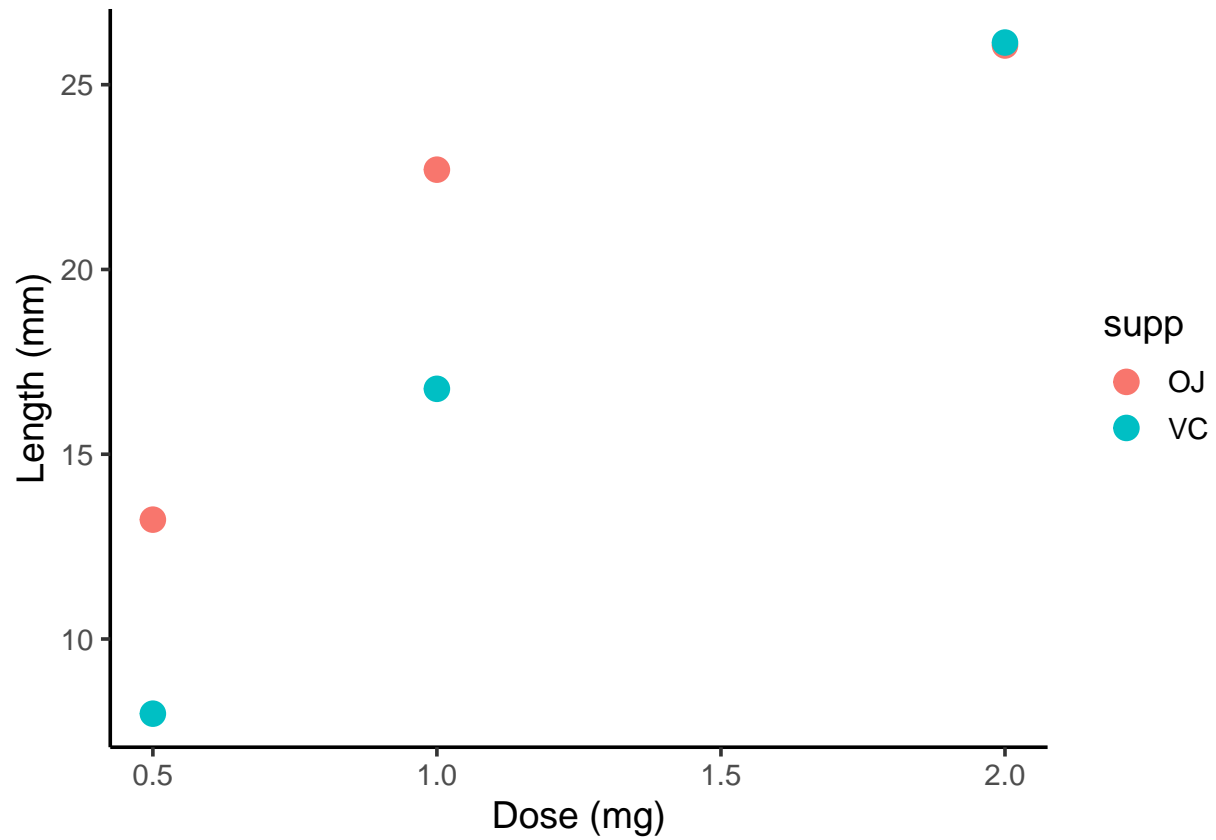

grafik ggplot dalam 2 plot bersusun

```
g.ToothGrowth_grid<-
  ggplot(data = ToothGrowth_sum,aes(x = dose,y=len), na.rm = FALSE) +
    geom_point()+
  theme_classic(base_size = 14)+
  xlab("Dose (mg)") +
  ylab("Length (mm)")+
  facet_grid(cols = vars(supp))
g.ToothGrowth_grid
```

grafik ggplot dalam 2 plot manual

```r
g.ToothGrowth_OJ<-
  ggplot(data = ToothGrowth_sum[ToothGrowth_sum$supp=="OJ",],aes(x = dose,y=len), na.rm = FALSE) +
    geom_point()+
  theme_classic(base_size = 14)+
  xlab("Dose (mg)") +
  ylab("Length (mm)")
g.ToothGrowth_OJ
```
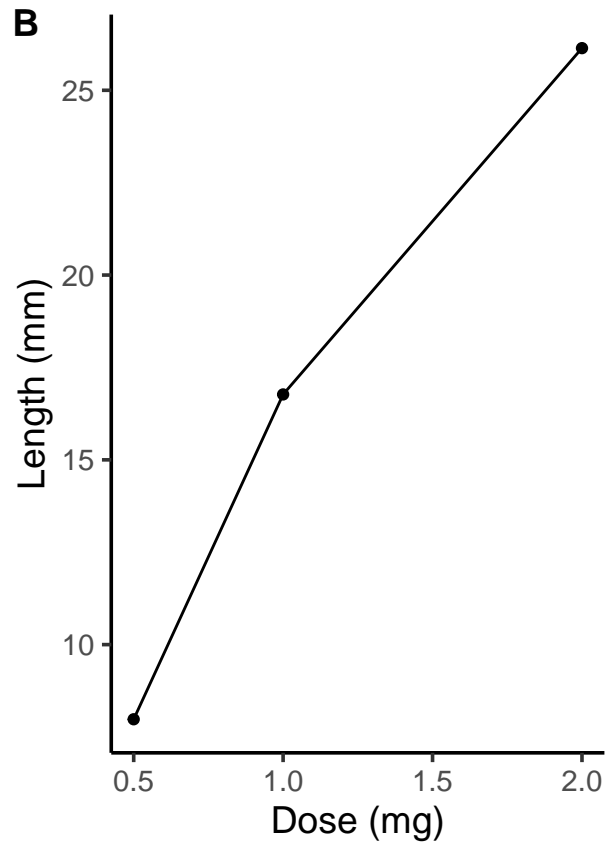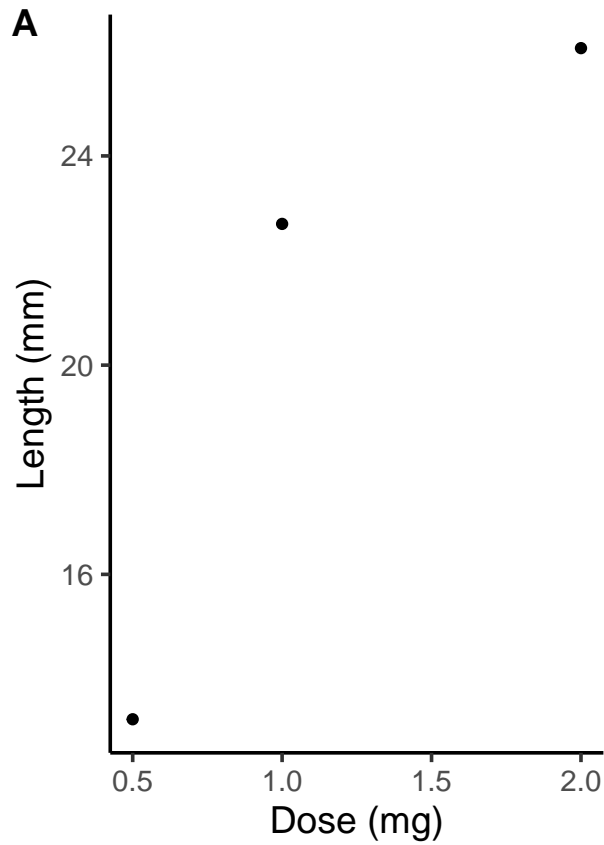
```
g.ToothGrowth_VC<-
  ggplot(data = ToothGrowth_sum[ToothGrowth_sum$supp=="VC",],aes(x = dose,y=len), na.rm = FALSE) +
    geom_line()+
  geom_point()+
  theme_classic(base_size = 14)+
  xlab("Dose (mg)") +
  ylab("Length (mm)")
g.ToothGrowth_VC
```
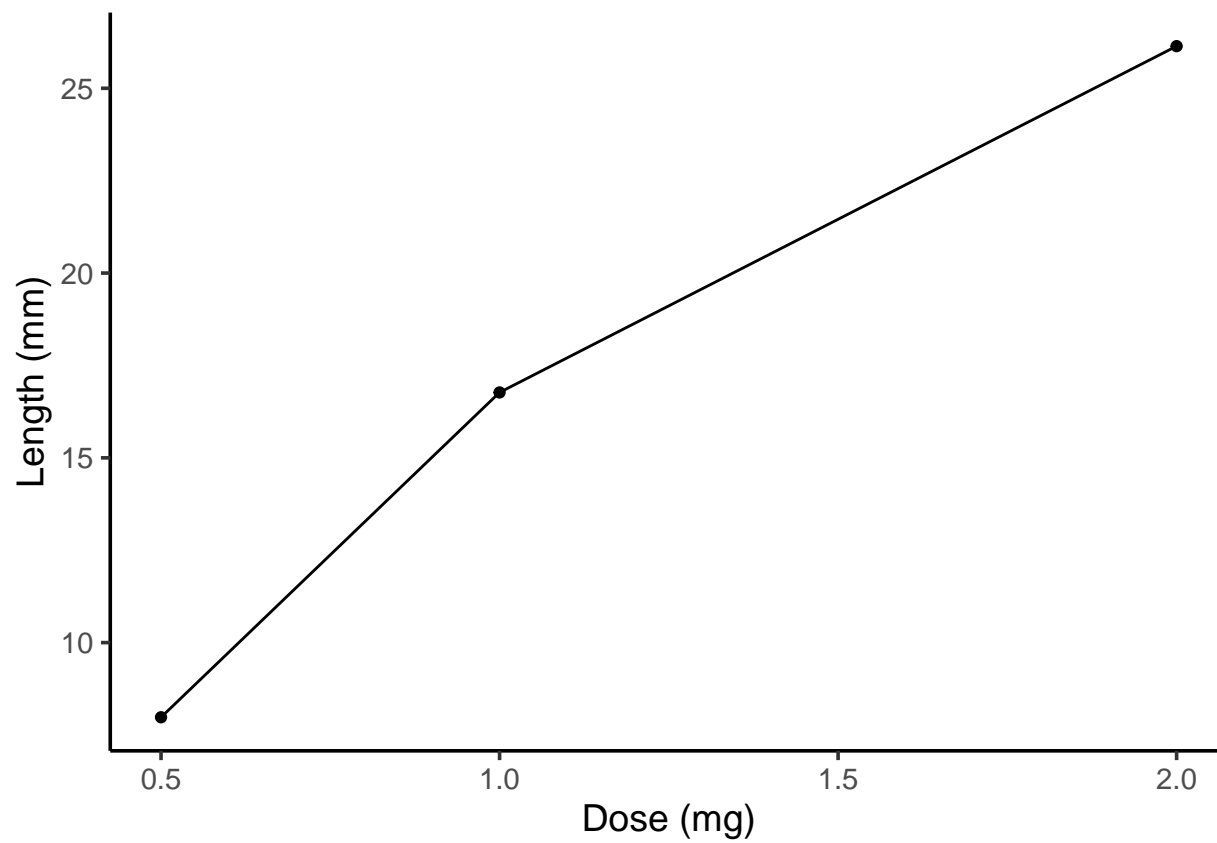
```
g.ToothGrowth_grid<-plot_grid(g.ToothGrowth_OJ, g.ToothGrowth_VC,                    ncol=2,  align =
                              labels = c('A', 'B'))
g.ToothGrowth_grid
```

```
ggsave("g.ToothGrowth_grid.pdf", plot= g.ToothGrowth_grid,  width = 200, height = 130, units = "mm")
#untuk menyimpan dalam bentuk pdf
ggsave("g.ToothGrowth_grid.png", plot= g.ToothGrowth_grid,  width = 200, height = 130, units = "mm")
#untuk menyimpan dalam bentuk png
```