

Growth on PDA

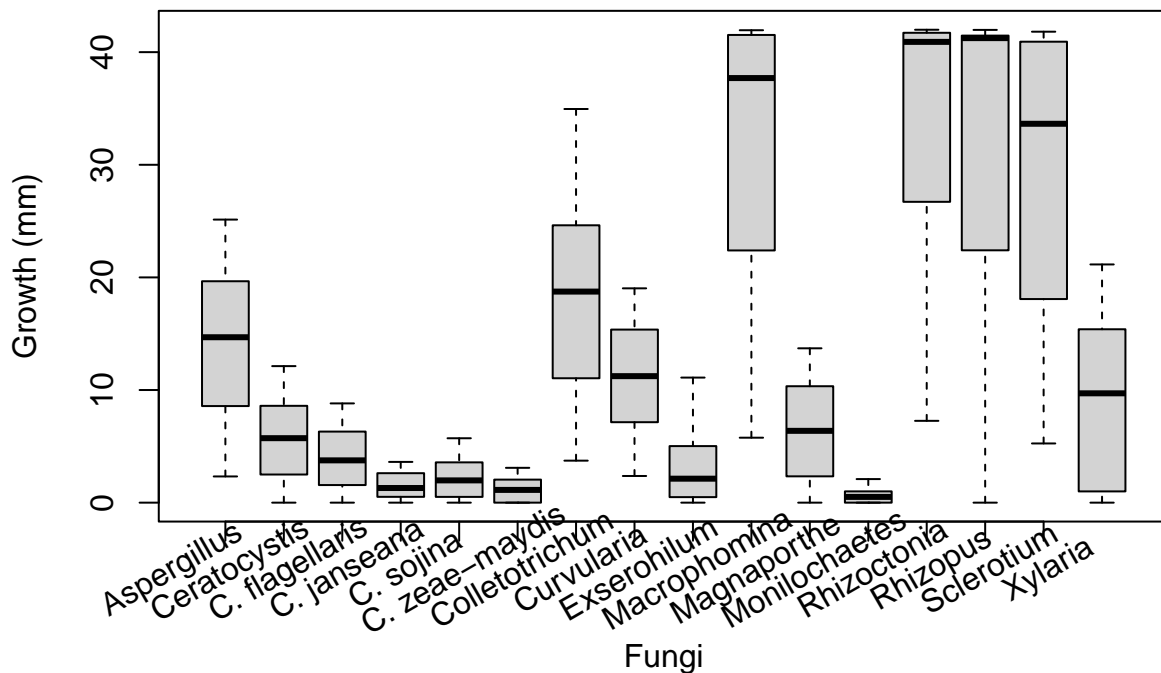
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```
grfungi <- read.csv("growthallassaypda.txt")
str(grfungi)
```

```
## 'data.frame':    720 obs. of  6 variables:
## $ Count      : int  1 1 1 1 1 1 1 1 1 2 ...
## $ plate_number: int  74 73 76 75 78 81 77 79 80 74 ...
## $ fungi      : chr  "Colletotricum" "Colletotricum" "Colletotricum" "Colletotricum" ...
## $ day        : int  1 1 1 1 1 1 1 1 1 2 ...
## $ mean       : num  4.04 4.11 4.36 4.01 3.73 ...
## $ days       : chr  "day1" "day1" "day1" "day1" ...
```

Growth differences among fungi (PDA)

```
#boxplot
colnames <- c("Aspergillus", "Ceratocystis",
              "C. flagellaris", "C. janseana", "C. soja",
              "C. zeae-maydis", "Colletotrichum", "Curvularia",
              "Exserohilum", "Macrophomina", "Magnaporthe", "Monilochaetes",
              "Rhizoctonia", "Rhizopus", "Sclerotium", "Xylaria")
boxplot(mean ~ fungi,
        data = grfungi,
        ylab = "Growth (mm)",
        xlab = "Fungi",
        pars = list(xaxt = "n"))
axis(1, at=c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15),
     labels = FALSE)
text(c(0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15),
     par("usr")[3] - 1.8, labels = colnames, srt = 30, pos = 1, xpd = TRUE, adj = 0.965,)
```



calculate mean and sd of each group

Get packages

```
#install.packages("tidyverse")
library("tidyverse")
library("ggplot2")
```

Get sd (make a function)

```
data_summary <- function(data, varname, groupnames){
  require(plyr)
  summary_func <- function(x, col){
    c(mean = mean(x[[col]], na.rm=TRUE),
      sd = sd(x[[col]], na.rm=TRUE))
  }
  data_sum<-ddply(data, groupnames, .fun=summary_func,
                  varname)
  data_sum <- rename(data_sum, c("mean" = varname))
  return(data_sum)
}
df3 <- data_summary(grfungi, varname="mean",
                    groupnames=c("fungi", "day"))
```

Loading required package: plyr

You have loaded plyr after dplyr - this is likely to cause problems.
If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
library(plyr); library(dplyr)

Attaching package: 'plyr'

The following objects are masked from 'package:dplyr':

arrange, count, desc, failwith, id, mutate, rename, summarise,
summarize

The following object is masked from 'package:purrr':

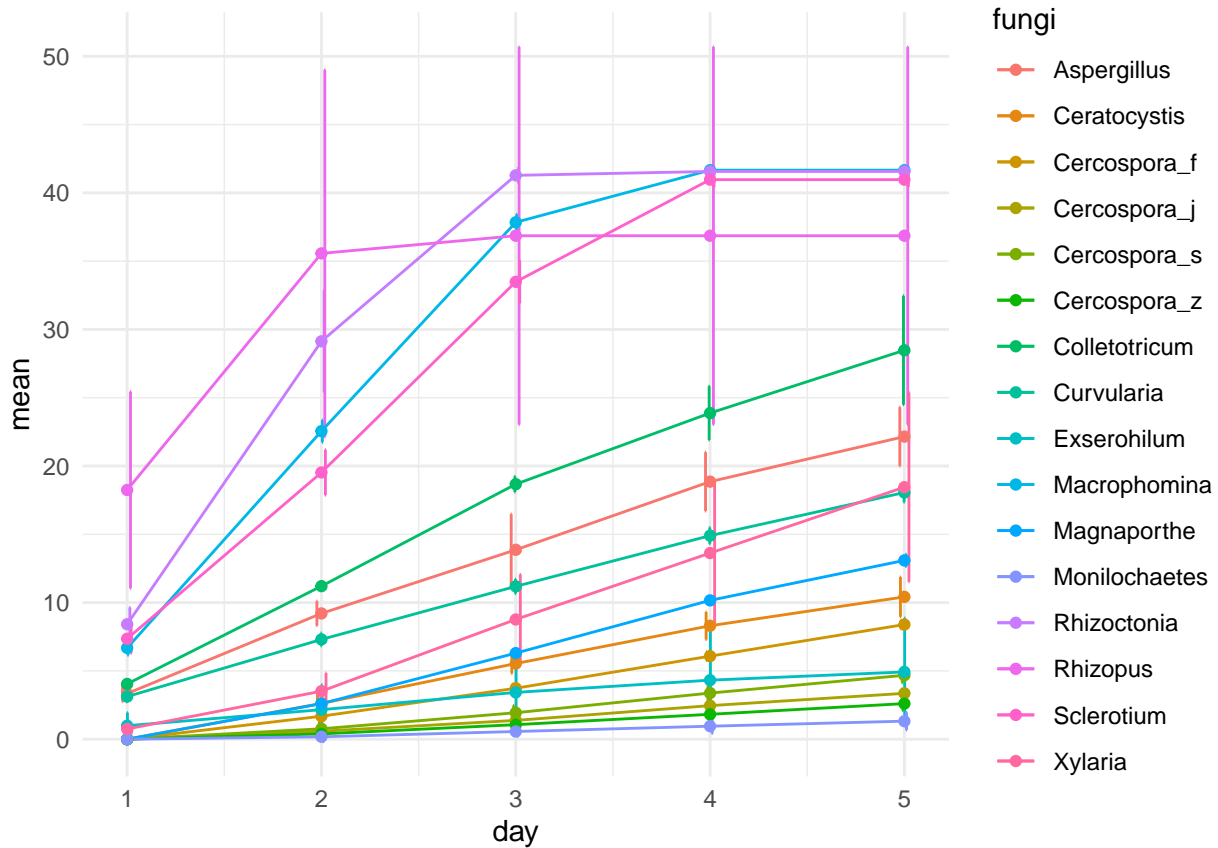
compact

head(df3)

```
##      fungi day      mean      sd
## 1 Aspergillus  1  3.341111 0.5837155
## 2 Aspergillus  2  9.207000 0.8909454
## 3 Aspergillus  3 13.865389 2.6185641
## 4 Aspergillus  4 18.856583 2.1538097
## 5 Aspergillus  5 22.153972 2.1523630
## 6 Ceratocystis 1  0.000000 0.0000000
```

Make a colorful graph

```
ggplot(df3, aes(x=day, y=mean, group=fungi, color=fungi)) +  
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,  
                 position=position_dodge(0.05)) +  
  geom_line() + geom_point()+theme_minimal()
```



well...

Lets do a subset of all of them

```
gr1 <-df3[which(df3$fungi %in% c("Xylaria", "Colletotricum")),]  
gr2 <-df3[which(df3$fungi %in% c("Xylaria", "Cercospora_s")),]  
gr3 <-df3[which(df3$fungi %in% c("Xylaria", "Rhizoctonia")),]  
gr4 <-df3[which(df3$fungi %in% c("Xylaria", "Curvularia")),]  
gr5 <-df3[which(df3$fungi %in% c("Xylaria", "Sclerotium")),]  
gr6 <-df3[which(df3$fungi %in% c("Xylaria", "Exserohilum")),]  
gr7 <-df3[which(df3$fungi %in% c("Xylaria", "Cercospora_f")),]  
gr8 <-df3[which(df3$fungi %in% c("Xylaria", "Macrophomina")),]  
gr9 <-df3[which(df3$fungi %in% c("Xylaria", "Ceratokystis")),]  
gr10 <-df3[which(df3$fungi %in% c("Xylaria", "Magnaporthe")),]  
gr11 <-df3[which(df3$fungi %in% c("Xylaria", "Rhizopus")),]  
gr12 <-df3[which(df3$fungi %in% c("Xylaria", "Monilochaetes")),]  
gr13 <-df3[which(df3$fungi %in% c("Xylaria", "Cercospora_z")),]  
gr14 <-df3[which(df3$fungi %in% c("Xylaria", "Cercospora_j")),]  
gr15 <-df3[which(df3$fungi %in% c("Xylaria", "Aspergillus")),]
```

Make the graphs

```
#install.packages("mdthemes") #add italics  
library("mdthemes")
```

```
#1_comparison  
p1 <- ggplot(gr1, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +  
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,  
                position=position_dodge(0.05)) +  
  geom_line() +  
  geom_point()+  
  labs(title="X & *Colletotricum gloeosporioides*",x="Days", y = "Growth (mm)")+  
  mdthemes::md_theme_classic()  
  
#2_comparison  
p2 <- ggplot(gr2, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +  
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,  
                position=position_dodge(0.05)) +  
  geom_line() +  
  geom_point()+  
  labs(title="X & *Cercospora soja*",x="Days", y = "Growth (mm)")+  
  mdthemes::md_theme_classic()  
  
#3_comparison  
p3 <- ggplot(gr3, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +  
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,  
                position=position_dodge(0.05)) +  
  geom_line() +  
  geom_point()+  
  labs(title="X & *Rhizoctonia solani*",x="Days", y = "Growth (mm)")+  
  mdthemes::md_theme_classic()  
  
#4_comparison  
p4 <- ggplot(gr4, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +  
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,  
                position=position_dodge(0.05)) +  
  geom_line() +  
  geom_point()+
```

```

labs(title="X & *Curvularia lunata*",x="Days", y = "Growth (mm)")+
mdthemes::md_theme_classic()
#5_comparison
p5 <- ggplot(gr5, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Sclerotium rolfsii*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#6_comparison
p6 <- ggplot(gr6, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Exserohilum turcicum*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#7_comparison
p7 <- ggplot(gr7, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Cercospora flagellaris*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#8_comparison
p8 <- ggplot(gr8, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Macrophomina phaseolina*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#9_comparison
p9 <- ggplot(gr9, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Ceratomyxa fimbriata*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#10_comparison
p10 <- ggplot(gr10, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Magnaporthe oryzae*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#11_comparison
p11 <- ggplot(gr11, aes(x=day, y=mean, group=funghi, shape=funghi, linetype=funghi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,

```

```

        position=position_dodge(0.05)) +
geom_line() +
geom_point()+
labs(title="X & *Rhizopus stolonifer*",x="Days", y = "Growth (mm)")+
mdthemes::md_theme_classic()
#12_comparison
p12 <- ggplot(gr12, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Monilochaetes* sp.",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#13_comparison
p13 <- ggplot(gr13, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Cercospora zeae-maydis*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#14_comparison
p14 <- ggplot(gr14, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Cercospora janseana*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()
#15_comparison
p15 <- ggplot(gr15, aes(x=day, y=mean, group=fungi, shape=fungi, linetype=fungi)) +
  geom_errorbar(aes(ymin=mean-sd, ymax=mean+sd), width=.1,
    position=position_dodge(0.05)) +
  geom_line() +
  geom_point()+
  labs(title="X & *Aspergillus flavus*",x="Days", y = "Growth (mm)")+
  mdthemes::md_theme_classic()

```

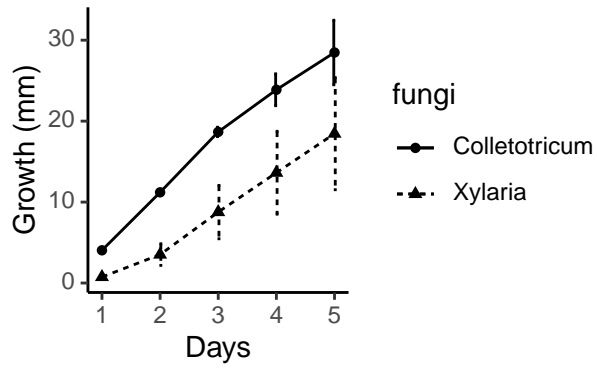
Group them?

```
#install.packages("ggpubr")  
library("ggpubr")
```

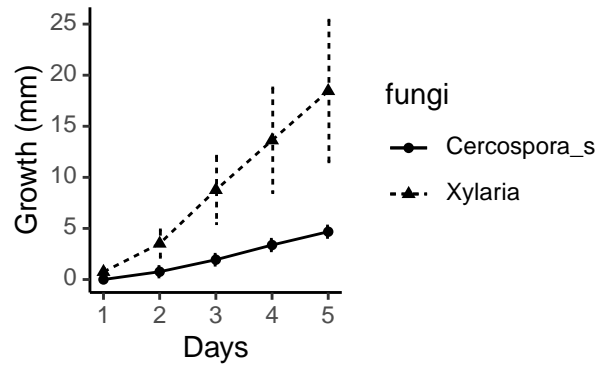
```
group1 <- ggarrange(p1, p2, p3, p4,  
  labels = c("A.", "B.", "C.", "D."),  
  ncol = 2, nrow = 2)  
group2 <- ggarrange(p5, p6, p7, p8,  
  labels = c("E.", "F.", "G.", "H."),  
  ncol = 2, nrow = 2)  
group3 <- ggarrange(p9, p10, p11, p12,  
  labels = c("I.", "J.", "K.", "L."),  
  ncol = 2, nrow = 2)  
group4 <- ggarrange(p13, p14, p15,  
  labels = c("M.", "N.", "O."),  
  ncol = 2, nrow = 2)
```


group1

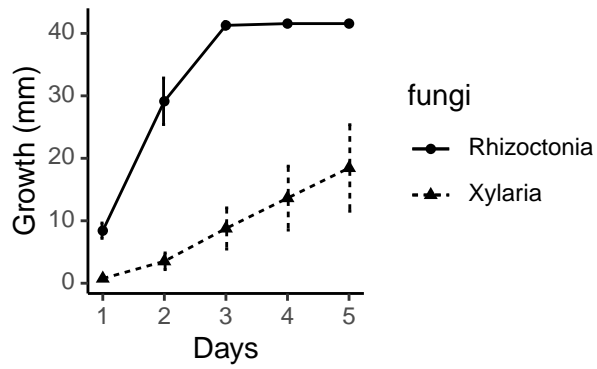
A. X & *Colletotricum gloeosporioides*



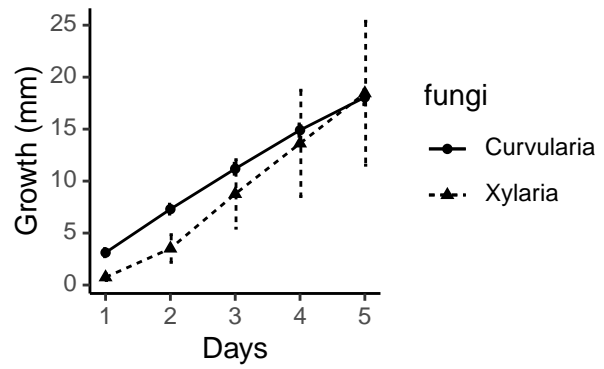
B. X & *Cercospora sojae*

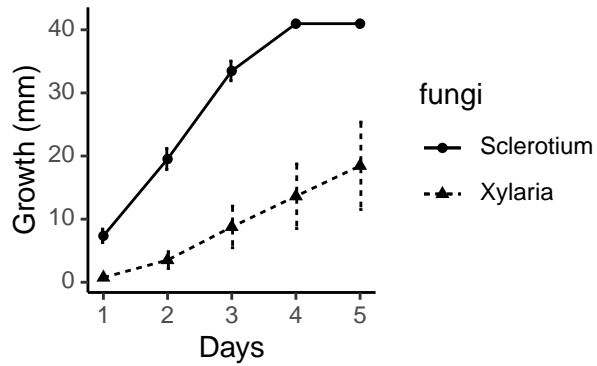
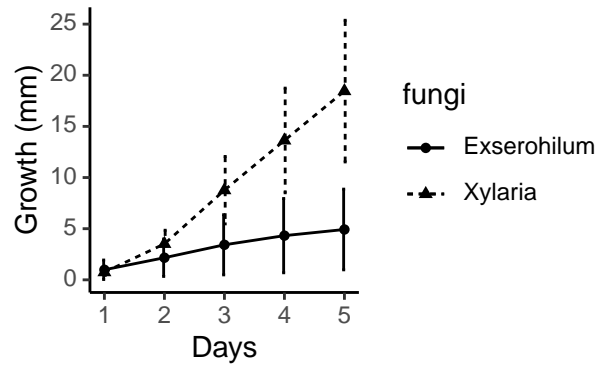
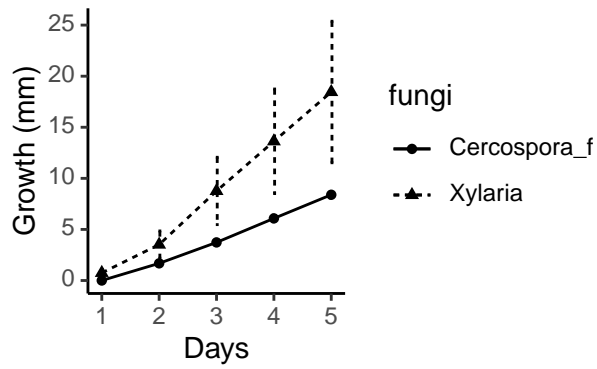
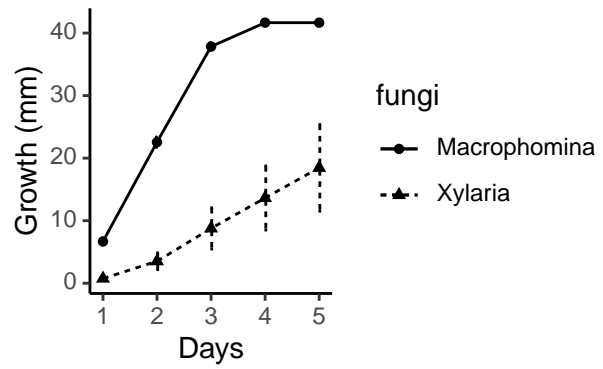


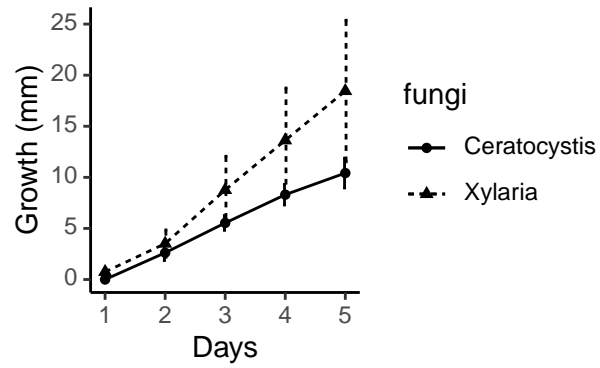
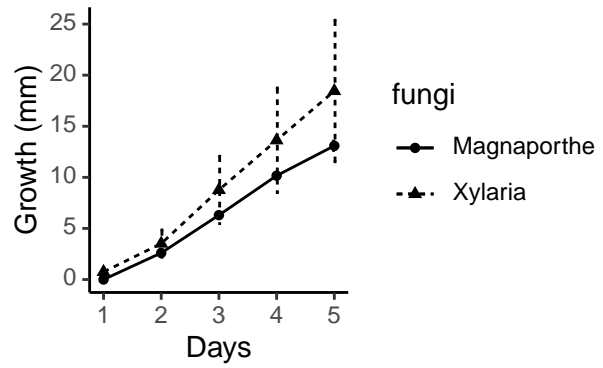
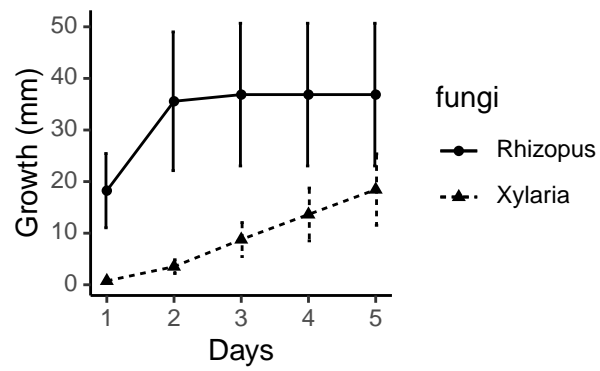
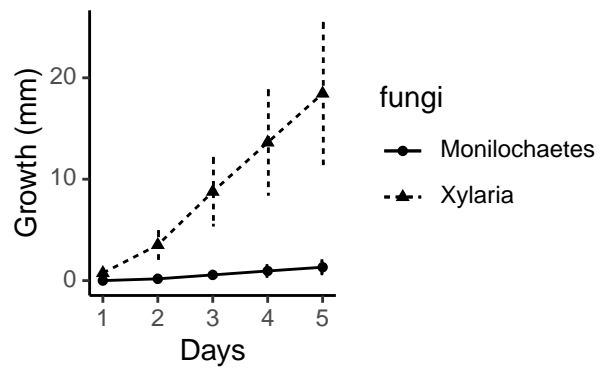
C. X & *Rhizoctonia solani*

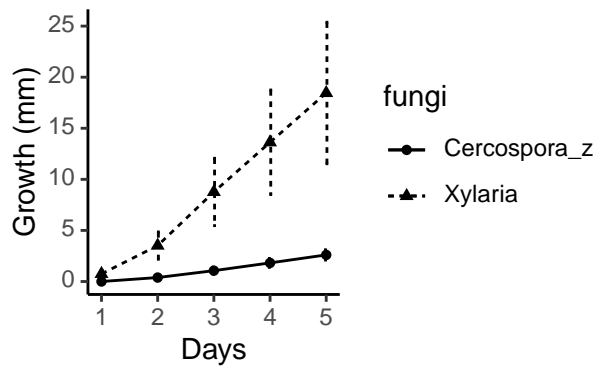
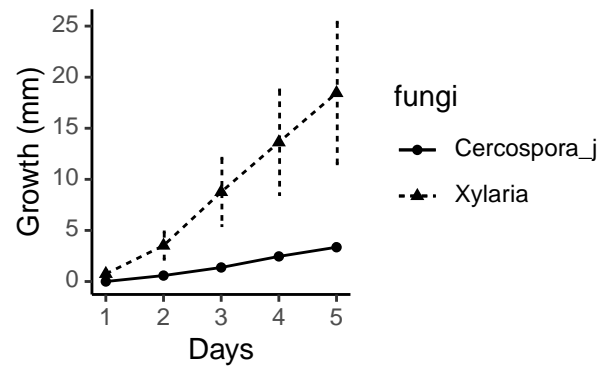


D. X & *Curvularia lunata*



E. X & *Sclerotium rolfsii***F.** X & *Exserohilum turcicum***G.** X & *Cercospora flagellaris***H.** X & *Macrophomina phaseolina*

I. X & *Ceratocystis fimbriata***J. X & *Magnaporthe oryzae*****K. X & *Rhizopus stolonifer*****L. X & *Monilochaetes* sp.**

M. X & *Cercospora zeae-maydis***N. X & *Cercospora janseana*****O. X & *Aspergillus flavus***