

Growth on PDA

Jose Solorzano

```
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)

calculate mean and sd of each group

Get packages

Get sd (make a function)

Make a colorful graph

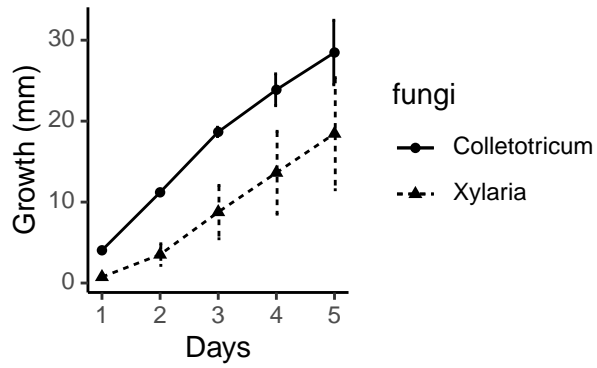
well...

Lets do a subset of all of them
Make the graphs

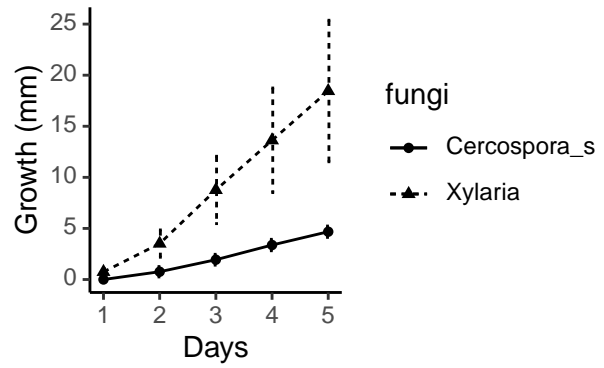
Group them?

group1

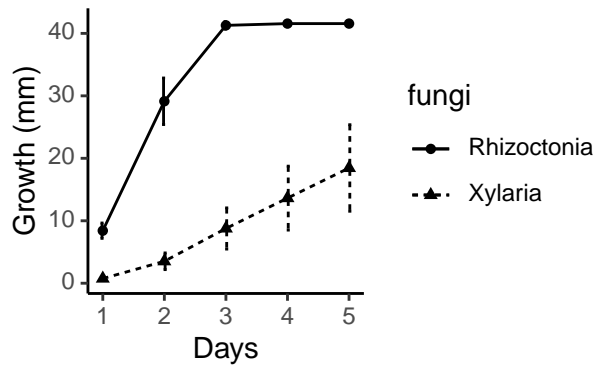
A. X & *Colletotricum gloeosporioides*



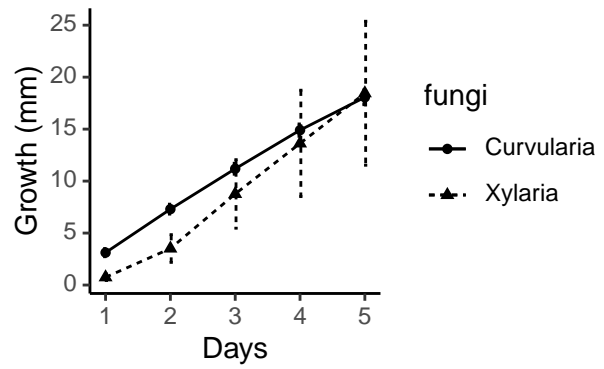
B. X & *Cercospora sojae*

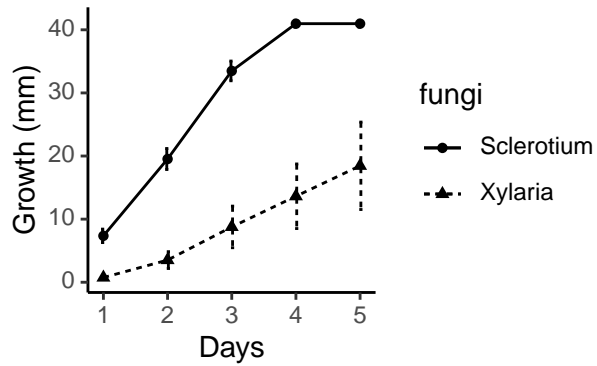
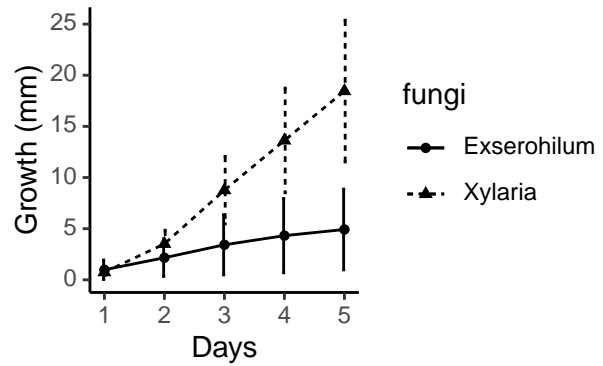
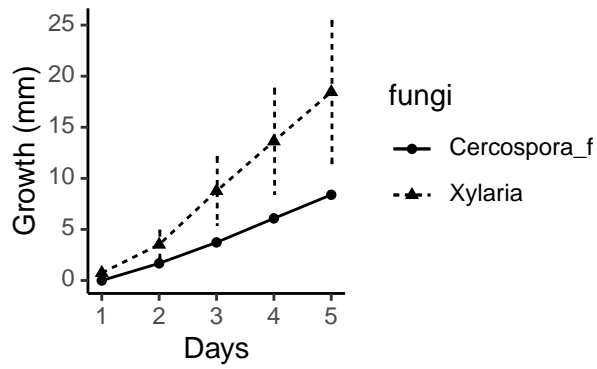
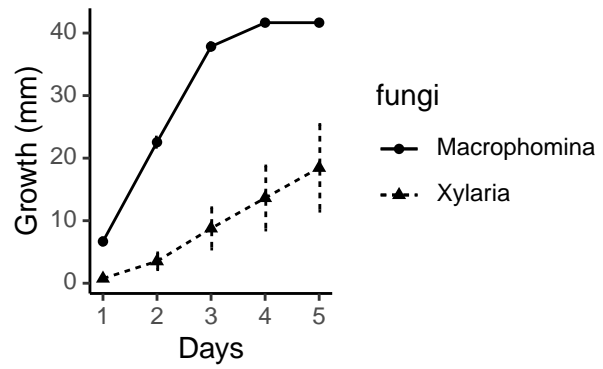


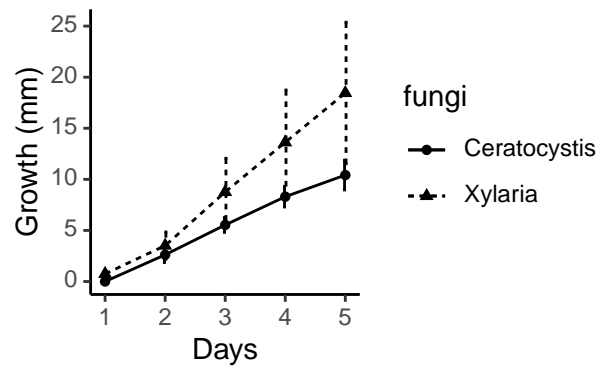
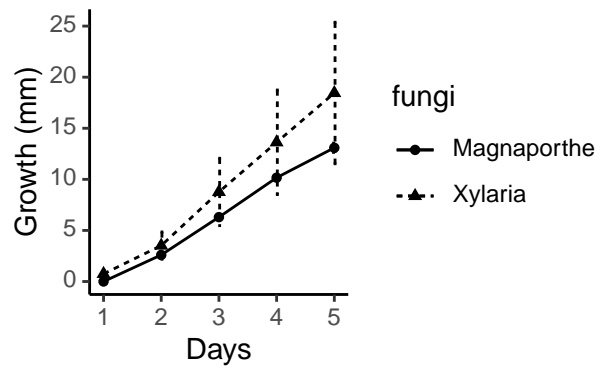
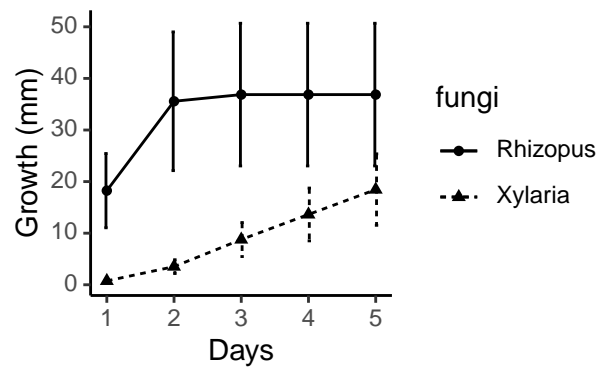
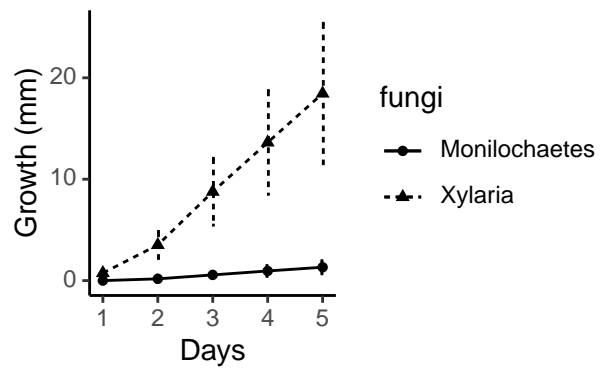
C. X & *Rhizoctonia solani*

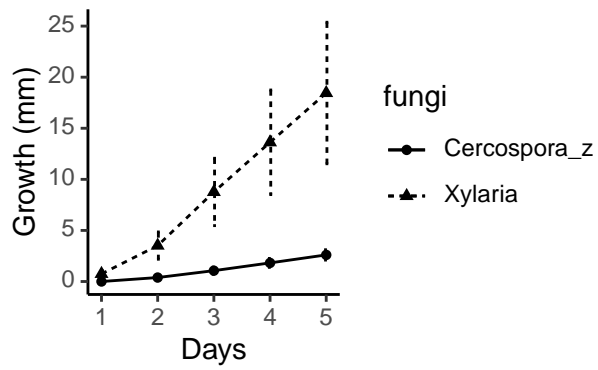
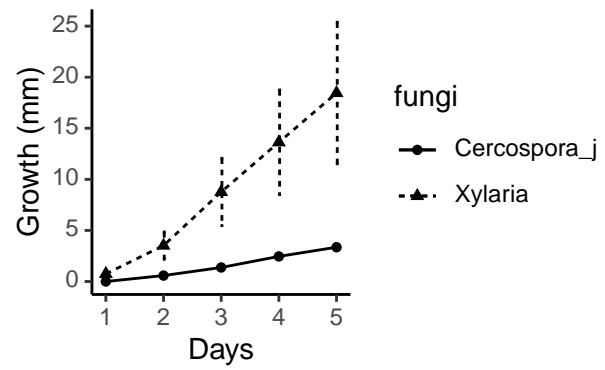


D. X & *Curvularia lunata*



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***