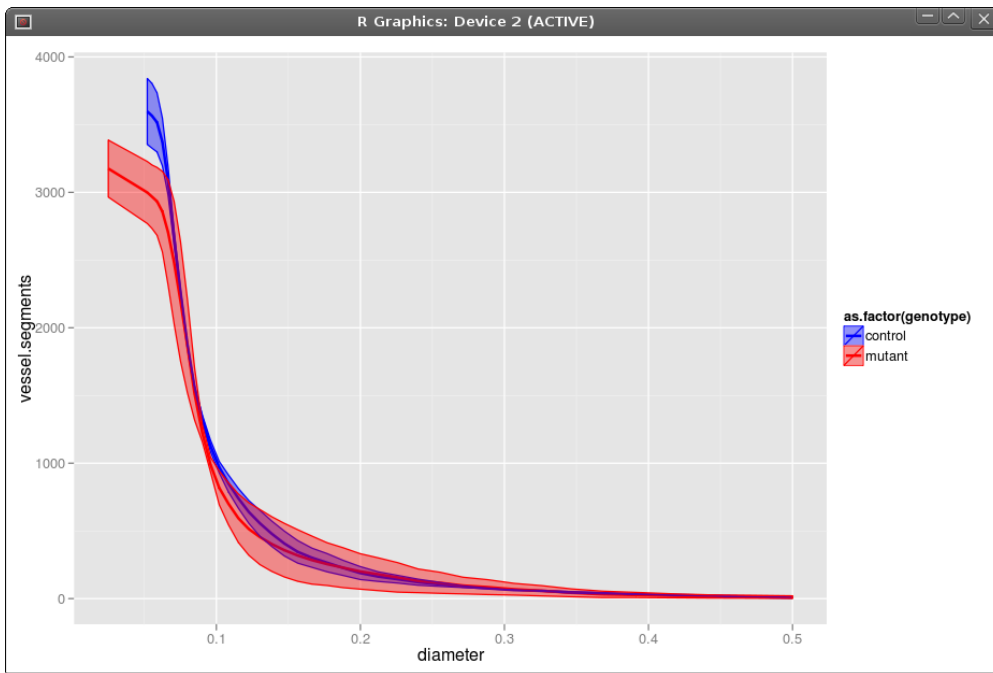


ggplot2

This page will contain example plots and the commands that were used to create them using ggplot2. For now little details might be given about what everything exactly means, but you might be able to deduce how to create similar plots of your data given the examples.

Ribbons

```
ggplot(offset , aes(x = diameter,y = vessel.segments,colour=as.factor(genotype),fill=as.factor(genotype)))  
+ geom_line(size=1, aes(colour=as.factor(genotype)))  
+ geom_ribbon(data=offset, aes(ymin = vessel.segments-sem,ymax=vessel.segments+sem), alpha=0.4)  
+ scale_colour_manual(values=c("blue", "red","black"))  
+ scale_fill_manual(values=c("blue", "red", "black"))
```



Bar plots with confidence intervals

(For more see [Plotting means and error bars \(ggplot2\)](#))

```
ggplot(range_data_factor, aes(x=change_induced, y=abs(effect_size_sd_wt), fill=brainstructure))  
+ geom_bar(position=position_dodge())  
+ geom_errorbar(aes(ymin=range_data$lowend_effect_size, ymax=highest_effect_size), width=0.3,  
position=position_dodge(.9), colour="black")  
+ opts(title="Effect size of recovery at varying amounts of change induced")  
+ xlab("Induced change in percentage of structure")  
+ ylab("Effect size with 95% confidence interval")  
+ expand_limits(y=c(0,3), x=c(-0.5,3))
```

Effect size of recovery at varying amounts of change induced

