```
#If you don't have drc downloaded, this code will download it from CRAN
install.packages("drc")

#These lines of code generate the logistic fit. Must be in a data frame format. e intercept is your IC50.
library(drc)
curve<-data.frame(conc=c(100, 50, 25, 12.5, 6.25, 3.12, 1.56, .78, 0.39 ), death=c(0.05, 0.05, 0.7, 1, 25,
75, 98, 100, 105 ))
curve
drm(death ~ conc, data = curve, fct = LL.4())
#change death or conc to be the columns you want to use in your dataframe.
GraphA<-drm(death ~ conc, data = curve, fct = LL.4())

#These lines of code generate the plot
plot(GraphA, xlab="concentration (uM)",main="Representative IC50 (4 parameter-Logistic)",
ylab="cytotoxicity (percent)", cex.axis=1.5, cex.lab=1.5, col="blue")
```