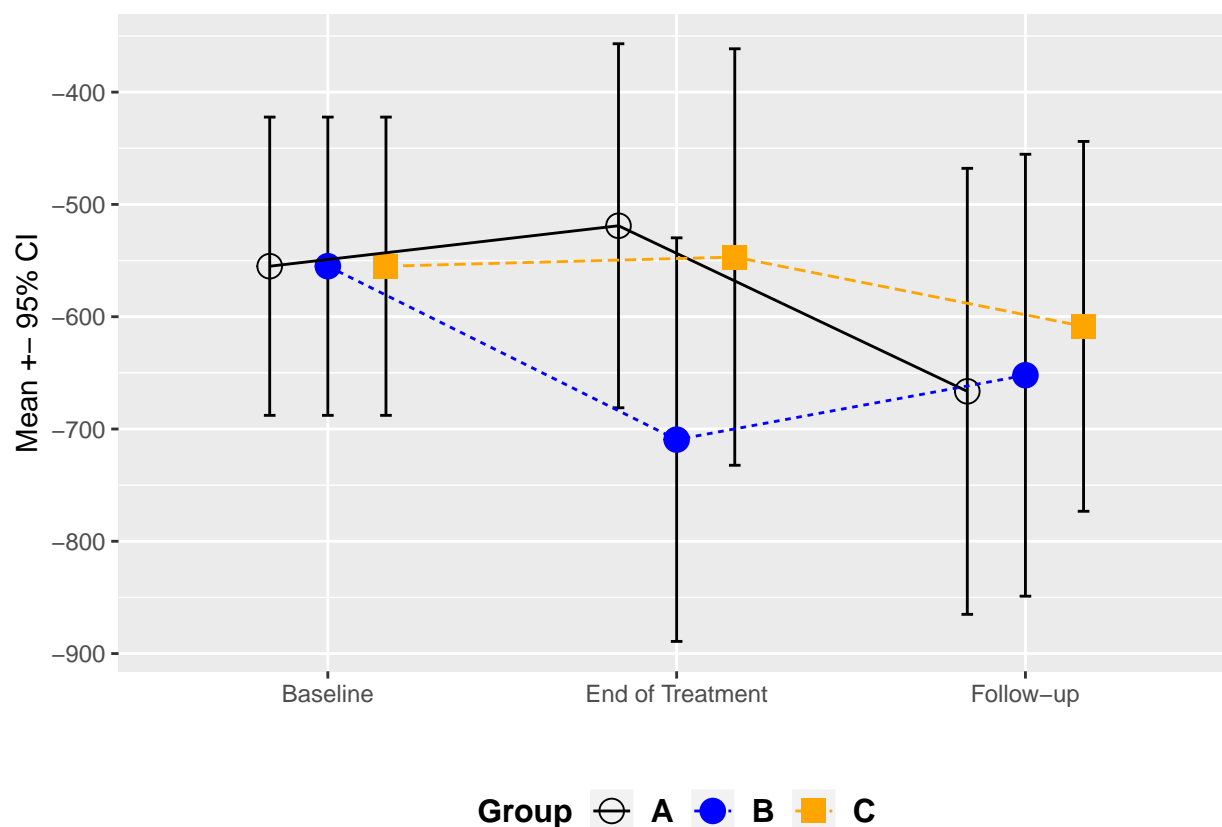


plots

```
library(ggplot2)

file <- read.csv("biocarta_inflamm_pathway_summary2.csv",header=TRUE)
file$Group <- as.factor(file$Group)

pd <- position_dodge(0.5)
ggplot(file, aes(x=Timeline, y=Value,color=Group,shape=Group,group=Group)) +
  geom_errorbar(aes(ymin=Value-ci, ymax=Value+ci), width=.1, position=pd,color="black") +
  scale_shape_manual(values=c(1, 19, 15,3))+
  scale_color_manual(values=c('black','blue','orange','green'))+
  geom_point(position=pd,size=4)+
  geom_line(aes(linetype=Group),position=pd) +
  theme(legend.position="bottom",legend.text = element_text(colour="black", size=12,
                                                             face="bold")) +
  theme(legend.position="bottom",legend.title = element_text(colour="black", size=12,
                                                             face="bold"))+
  labs(x="",y="Mean +- 95% CI")
```



```
file <- read.csv("hallmark_oxid_phospho_summary2.csv",header=TRUE)
file$Group <- as.factor(file$Group)

pd <- position_dodge(0.5)
ggplot(file, aes(x=Timeline, y=Value,color=Group,shape=Group,group=Group)) +
  geom_errorbar(aes(ymin=Value-ci, ymax=Value+ci), width=.1, position=pd,color="black") +
```

```

scale_shape_manual(values=c(1, 19, 15,3))+
scale_color_manual(values=c('black','blue','orange','green'))+
geom_point(position=pd,size=4)+
geom_line(aes(linetype=Group),position=pd) +
theme(legend.position="bottom",legend.text = element_text(colour="black", size=12,
                                                            face="bold")) +

theme(legend.position="bottom",legend.title = element_text(colour="black", size=12,
                                                            face="bold"))+

labs(x="",y="Mean +- 95% CI")

```

