```
rm(list=ls())
library(MASS)



cv <- read.csv("covid_ant.csv")
cv$PRNT80 <- factor(cv$PRNT80,levels=sort(unique(cv$PRNT80)),
                    ordered=TRUE)
cv$SAMPLE.DAYS.POST.SYMP <- as.numeric(cv$SAMPLE.DAYS.POST.SYMP)
fit <-
polr(PRNT80 ~ IgG + IgM + SAMPLE.DAYS.POST.SYMP,data=cv)
s <- summary(fit)
ci <- confint(fit)
tab <- exp(cbind(s$coefficients[1:3,1],ci))
round(tab,3)

fit <-
polr(PRNT80 ~ IgG ,data=cv)

n.sim <- 1000
IgG.obs <- cv$IgG
PRNT80.set <- levels(cv$PRNT80)
cv.sim <- cv[complete.cases(cv[,c("PRNT80","IgG")]),]
prob.set <- predict(fit,newdata=data.frame(IgG=cv$IgG),type="probs")

beta.sim <- rep(NA,n.sim)
zeta.sim <- matrix(NA,nrow=n.sim,ncol=length(levels(cv$PRNT80))-1)
for(i in 1:n.sim) {
  cv.sim$PRNT80 <- apply(prob.set,1,function(r) PRNT80.set[as.numeric(rmultinom(1,1,r))==1])
  cv.sim$PRNT80 <- factor(cv.sim$PRNT80,levels = levels(cv$PRNT80))
  fit.sim <- polr(PRNT80 ~ IgG ,data=cv.sim)
  beta.sim[i] <- fit.sim$coefficients
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  zeta.sim[i,] <- fit.sim$zeta
}

IgG.med <- median(cv$IgG)
n.cl <- length(levels(cv$PRNT80))
n.pr <- n.cl-1
prev.samples.med <- matrix(NA,nrow=n.sim,ncol=n.cl)
for(i in 1:n.sim) {
  cum.prob.i <- 1/(1+exp(-(zeta.sim[i,]-beta.sim[i]*IgG.med)))
  prev.samples.med[i,] <- c(cum.prob.i[1],cum.prob.i[2:n.pr]-cum.prob.i[1:(n.pr-1)],
      1-cum.prob.i[n.pr])
}

med.p <- apply(prev.samples.med,2,function(x) c(quantile(x,0.025),
                                  mean(x),
                                  quantile(x,0.975)))
xlab <- c("<1:20",paste("1:",levels(cv$PRNT80)[-1],sep=""))
matplot(t(med.p),type=c("l","b","l"),pch=20,col=1,
      lty=c("dashed","solid","dashed"),
      axes=FALSE,ylab = "Probability",xlab="PRNT80",
      main="Median IgG")
axis(1,1:10,xlab)
axis(2,seq(0,1,0.05),seq(0,1,0.05))


IgG.1stq <- quantile(cv$IgG,0.25)
n.cl <- length(levels(cv$PRNT80))
n.pr <- n.cl-1
prev.samples.1stq <- matrix(NA,nrow=n.sim,ncol=n.cl)
for(i in 1:n.sim) {
  cum.prob.i <- 1/(1+exp(-(zeta.sim[i,]-beta.sim[i]*IgG.1stq)))
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  prev.samples.1stq[i,] <- c(cum.prob.i[1],cum.prob.i[2:n.pr]-cum.prob.i[1:(n.pr-1)],
                        1-cum.prob.i[n.pr])
}

first.qr.p <- apply(prev.samples.1stq,2,function(x) c(quantile(x,0.025),
                                    mean(x),
                                    quantile(x,0.975)))
xlab <- c("<1:20",paste("1:",levels(cv$PRNT80)[-1],sep=""))
matplot(t(first.qr.p),type=c("l","b","l"),pch=20,col=1,
      lty=c("dashed","solid","dashed"),
      axes=FALSE,ylab = "Probability",xlab="PRNT80",
      main="1st Quartile IgG")
axis(1,1:10,xlab)
axis(2,seq(0,1,0.05),seq(0,1,0.05))

IgG.2stq <- quantile(cv$IgG,0.75)
n.cl <- length(levels(cv$PRNT80))
n.pr <- n.cl-1
prev.samples.2stq <- matrix(NA,nrow=n.sim,ncol=n.cl)
for(i in 1:n.sim) {
  cum.prob.i <- 1/(1+exp(-(zeta.sim[i,]-beta.sim[i]*IgG.2stq)))
  prev.samples.2stq[i,] <- c(cum.prob.i[1],cum.prob.i[2:n.pr]-cum.prob.i[1:(n.pr-1)],
                        1-cum.prob.i[n.pr])
}

second.qr.p <- apply(prev.samples.2stq,2,function(x) c(quantile(x,0.025),
                                    mean(x),
                                    quantile(x,0.975)))
xlab <- c("<1:20",paste("1:",levels(cv$PRNT80)[-1],sep=""))
matplot(t(second.qr.p),type=c("l","b","l"),pch=20,col=1,
      lty=c("dashed","solid","dashed"),
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      axes=FALSE,ylab = "Probability",xlab="PRNT80",
      main="2nd Quartile IgG")
axis(1,1:10,xlab)
axis(2,seq(0,1,0.05),seq(0,1,0.05))
```