diabetes<- read.csv("diabetes.csv")

par(mfcol=c(3,3))

#(1)

plot(diabetes$Insulin,diabetes$Glucose,xlab="Insulin Concentration",ylab="Glucose",main="Relation between Glucose and Insulin",col="blue")

# (2)

hist(diabetes$Glucose,xlab="Glucose Value",xlim = c(50,150),breaks = 20,main="Glucose value in blood",col="Green")

#(3)

boxplot(diabetes$BloodPressure,main="Blood Pressure Measurements",col="blue")

#(4)

maxmum<- aggregate(diabetes$Insulin, list(diabetes$Age) , max)

barplot(maxmum$x , names.arg =maxmum$Group.1 ,main = "maxmum insulin per age", col="red" )

#(5)

tabl <- table(diabetes$Pregnancies)

barplot(tabl,col="Gold",main = "Pregnancies")

#(6)

slices<- c( mean(diabetes$Insulin),max(diabetes$Insulin), median(diabetes$Insulin), min(diabetes$Insulin))

Lbl <- c ("mean" , "max" , "median" , "min")

r <- slices/sum(slices)\*100

Lbl <- paste(Lbl,r)

pie(slices,labels = Lbl,col= rainbow(5))

#(7)

plot(density(diabetes$DiabetesPedigreeFunction),main ="Diabetes Pedigree Function Distribution" )

plot(density(diabetes$Age),main ="Age Distribution" )

#(8)

dotchart(diabetes$DiabetesPedigreeFunction ,groups = diabetes$Outcome ,xlab = "Diabetes Pedigree Function per Diabetes outcome")

#(9)

colors <- c("purple","Gold","red","blue","brown")

plot(diabetes[c(5,8,2,3,7)])

pairs(diabetes[c(5,8,2,3,7)],main="diabates",pch=22,bg=c("purple","Gold","red","blue","brown"))

par(xpd=TRUE)

legend(0,1,horiz =TRUE ,as.vector(c("Insulin","Age","Glucose","Blood","Diabetes" )),fill= c("purple","Gold","red","blue","brown"))

#(10)