1. Code for the visualisation of chordal graphs

```
library(statnet)
library(circlize)
data=read.table( "Butterfly_Season.txt")
my.data<-as.matrix(data)
grid.col[c("Winter","Autumn","Summer","Spring")]=
        c("#402E32","#006B5D","#9A0000","#F35700")
grid.col[rownames(my.data)]=
        c("#FFFFFF","#B87333","#6D6968","#D1D0CE","#FFFFFF","#FBF6D9","#CD7F32","#FFF
        8C6","#FFEBCD","#C88141","#FFDB58","#FFFF00","#737CA1","#FFFFFF","#FAEBD7","#
        9A0000","#CCFB5D","#FF7F50","#C48189","#F2BB66","#C19A6B","#F5F5DC","#6D7B8D
        ","#FFE5B4","#B5EAAA","#657383","#E9CFEC","#BCC6CC","#82CAFA","#FFF8C6","#F
        FFFFF","#F9966B","#43C6DB","#F0F8FF","#DEB887","#7FE817","#98AFC7","#FC6C85","
        #FFEBCD","#CFECEC","#FBB117","#EDE275","#FFF380","#C2B280","#006B5D","#EE9A
        4D","#827B60","#95B9C7","#FFFFFF","#FFF8C6","#616D7E","#FFFFFF","#FFCBA4","#FF
        FFC2","#C3FDB8","#F87431")
circos.par(canvas.xlim =c(-0.8,-1.5),canvas.ylim = c(1.5,-2.5),cell.padding = c(0.01,0,0.01,0))
circos.par(gap.degree = c(rep(2, nrow(my.data)-1), 10, rep(2, ncol(my.data)-1), 10),
            start.degree = 190,clock.wise=TRUE)
chordDiagram(my.data,
              grid.col = grid.col, link.sort = TRUE, link.decreasing = TRUE, reduce = 0)
circos.clear()

data=read.table( "Butterfly_Habitat.txt")
my.data<-as.matrix(data)
grid.col[c("SH","RH")]=
        c("#9A0000","#F35700")
grid.col[rownames(my.data)]=
        c("#FFFFFF","#B87333","#6D6968","#D1D0CE","#FFFFFF","#FBF6D9","#CD7F32","#FFF
        8C6","#FFEBCD","#C88141","#FFDB58","#FFFF00","#737CA1","#FFFFFF","#FAEBD7","#
        9A0000","#CCFB5D","#FF7F50","#C48189","#F2BB66","#C19A6B","#F5F5DC","#6D7B8D
        ","#FFE5B4","#B5EAAA","#657383","#E9CFEC","#BCC6CC","#82CAFA","#FFF8C6","#F
        FFFFF","#F9966B","#43C6DB","#F0F8FF","#DEB887","#7FE817","#98AFC7","#FC6C85","
        #FFEBCD","#CFECEC","#FBB117","#EDE275","#FFF380","#C2B280","#006B5D","#EE9A
        4D","#827B60","#95B9C7","#FFFFFF","#FFF8C6","#616D7E","#FFFFFF","#FFCBA4","#FF
        FFC2","#C3FDB8","#F87431")
circos.par(canvas.xlim =c(-0.8,-1.5),canvas.ylim = c(1.5,-2.5),cell.padding = c(0.01,0,0.01,0))
circos.par(gap.degree = c(rep(2, nrow(my.data)-1), 10, rep(2, ncol(my.data)-1), 10),
            start.degree = 190,clock.wise=TRUE)
chordDiagram(my.data,
              grid.col = grid.col, link.sort = TRUE, link.decreasing = TRUE, reduce = 0)
circos.clear()
```

2. Code for iNEXT model prediction

```
library(iNEXT)
library(ggplot2)
library(ggthemes)
library(patchwork)
data=read.table( "Butterfly_Habitat.txt")
out<iNEXT(data,q=0,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRUE,c
onf=0.95,nboot=200)
g <- ggiNEXT(out, type=1)
g
g1 <- g + theme_few() + xlim(c(0,6500))+theme(
   axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
   axis.text.y=element_text(size=20)) + labs(x="Number of individuals", y= "Species richness")
+ scale_colour_manual(values=c("#F35700","#9A0000"))+
   scale_fill_manual(values =c("#F35700","#9A0000"))+
theme(legend.position=c(0.8,0.2),legend.background=element_blank(),legend.text=element_te
xt(size=18))
g1

out1<iNEXT(data,q=1,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRUE,
conf=0.95,nboot=200)
g <- ggiNEXT(out1, type=3)
g
g2 <- g + theme_few() +theme(
   axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
   axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Shannon diversity") +
scale_colour_manual(values=c("#F35700","#9A0000"))+
   scale_fill_manual(values =c("#F35700","#9A0000"))+
   theme(legend.position="none")
g2

out2<iNEXT(data,q=2,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRUE,
conf=0.95,nboot=200)
g <- ggiNEXT(out2, type=3)
g
g3 <- g + theme_few() +theme(
   axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
  axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Simpson diversity") +
scale_colour_manual(values=c("#F35700","#9A0000"))+
  scale_fill_manual(values =c("#F35700","#9A0000"))+
  theme(legend.position="none")
g3

data1=read.table("Butterfly_Season.txt")
out4<iNEXT(data1,q=0,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out4, type=1)
g
g4 <- g + theme_few() +theme(
                     axis.title.x=element_text(size=22),
                     axis.title.y=element_text(size=22),
                     axis.text.x=element_text(size=20),
                     axis.text.y=element_text(size=20)) + labs(x="Number of individuals",
y=                     "Species                    richness")                    +
scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+

scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+
theme(legend.position=c(0.8,0.2),legend.background=element_blank(),
legend.text=element_text(size=18))
g4

Out5<iNEXT(data1,q=1,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out5, type=3)
g
g5 <- g + theme_few() +theme(
  axis.title.x=element_text(size=22),
  axis.title.y=element_text(size=22),
  axis.text.x=element_text(size=20),
  axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Shannon diversity") +
scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+
  scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+
  theme(legend.position="none")
g5

Out6<iNEXT(data1,q=2,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out6, type=3)
g
g6 <- g + theme_few() +theme(
  axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
   axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Simpson diversity") +
scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+
   scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32"))+
theme(legend.position="none")
g6

ggarrange(g1,g2,g3,g4,g5,g6,ncol = 3, nrow = 2, labels = c("A","B","C","D","E","F"))

data3=read.table("Butterfly_Family.txt")
out7<iNEXT(data3,q=0,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out7, type=1)
g
g7 <- g + theme_base() +theme(
   axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
   axis.text.y=element_text(size=20)) + labs(x="Number of individuals", y= "Species richness")
+ scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
   scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
   theme(legend.position=c(0.8,0.2),legend.background=element_blank(),
legend.text=element_text(size=18))
g7

out8<iNEXT(data3,q=1,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out8, type=3)
g
g8 <- g + theme_base() +theme(
   axis.title.x=element_text(size=22),
   axis.title.y=element_text(size=22),
   axis.text.x=element_text(size=20),
   axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Shannon diversity") +
scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
   scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
   theme(legend.position="none")
g8

out9<iNEXT(data3,q=2,datatype="abundance",size=NULL,endpoint=NULL,knots=40,se=TRU
E,conf=0.95,nboot=200)
g <- ggiNEXT(out9, type=3)
g
```

```
g9 <- g + theme_base() +theme(
  axis.title.x=element_text(size=22),
  axis.title.y=element_text(size=22),
  axis.text.x=element_text(size=20),
  axis.text.y=element_text(size=20)) + labs(x="Sample coverage", y= "Simpson diversity") +
scale_colour_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
  scale_fill_manual(values=c("#F35700","#9A0000","#006B5D","#402E32","#21BDDD"))+
  theme(legend.position="none")
g9
```

3. Code for NMDS and ANOSIM analysis

```
library(tidyverse)
library(vegan)
library(ggpubr)
library(ggthemes)
library(ggplot2)
windowsFonts(A=windowsFont("Times New Roman"),
             B=windowsFont("Arial"))
df <- read.csv(file.choose(),header = T)
nmds <- metaMDS(select(df, starts_with("SPECIES")),k=2,trymax=100)
df.dist <- vegdist(subset(df,select = -Group))
ppp <- anosim(df.dist, df$Group, permutations = 999, distance = "bray", strata = NULL,
              parallel = getOption("mc.cores"))
ppp
plot(ppp)

p1<- scores(nmds)$sites %>%
  cbind(df) %>%
  ggplot(aes(x = NMDS1, y = NMDS2)) +
  geom_point(aes(size = 0.5, color = Group)) +
  stat_chull(geom = "polygon", aes(group = Group, color = Group, fill = Group), alpha = 0.3) +
  annotate("text", x = 1.0, y = 0.5, label = paste0("Stress = ", format(nmds$stress, digits = 4)),
hjust = 0,size = 6) +
  theme(text=element_text(family="B",size=20))+theme_few()+
  theme(legend.position=c(0.8, 0.2), legend.background=element_blank(),
legend.text=element_text(size=18))+
  theme(axis.title.x=element_text(size=22),
        axis.title.y=element_text(size=22,angle=90),
        axis.text.y=element_text(size=20),
        axis.text.x=element_text(size=20),
        panel.grid=element_blank())+
  scale_fill_manual(values =c("#FFC995","#ECA297"))+
scale_colour_manual(values=c("#FFC995","#ECA297"))+
  annotate("text",x = 1.2, y= 0.43, label="R = 0.309",color="black",size = 6)+
  annotate("text",x = 1.2, y= 0.36, label="p =0.012",color="black",size = 6)
p1


df <- read.csv(file.choose(),header = T)
nmds <- metaMDS(select(df, starts_with("OTU")),k=2,trymax=100)
df.dist <- vegdist(subset(df,select = -Group))
ppp <- anosim(df.dist, df$Group, permutations = 999, distance = "bray", strata = NULL,
              parallel = getOption("mc.cores"))
ppp
plot(ppp)

p2<- scores(nmds)$sites %>%
  cbind(df) %>%
  ggplot(aes(x = NMDS1, y = NMDS2)) +
  geom_point(aes(size = 0.5, color = Group)) +
  stat_chull(geom = "polygon", aes(group = Group, color = Group, fill = Group), alpha = 0.3) +
  annotate("text", x = -1.0, y = 0.5, label = paste0("Stress = ", format(nmds$stress, digits = 4)),
hjust = 0,size = 6) +
  theme(text=element_text(family="B",size=20))+theme_few()+
  theme(legend.position=c(0.2, 0.15), legend.background=element_blank(),
legend.text=element_text(size=18))+
  theme(axis.title.x=element_text(size=22),
        axis.title.y=element_text(size=22,angle=90),
        axis.text.y=element_text(size=20),
        axis.text.x=element_text(size=20),
        panel.grid=element_blank())+
scale_colour_manual(values=c("#FFC995","#ECA297","#3CAE9E","#DFE0DF"))+
  scale_fill_manual(values=c("#FFC995","#ECA297","#3CAE9E","#DFE0DF"))+
  annotate("text",x =- 1.0, y= 0.43, label="R = 0.664",color="black",size = 6)+
  annotate("text",x = -1.0, y= 0.36, label="p =0.001",color="black",size = 6)
p2
```