Appendix 2

R code

Description

The following code can be used to reproduce the figures of "Systemic Analysis of a Developing Plant Community on the Island of Surtsey" (Schrenk et al. 2021). It is based on the R-package QtAC (Schreiber and Schrenk, 2020).

Prerequisites

- R >= 3.6
- RStudio >= 1.3 (optional)
- Java (JDK) >= 1.8

Install packages

```
source("install_packages_QtAC.R")
install.packages("QtAC_1.0.tar.gz", repos = NULL, type = "source")
```

Load libraries

```
library("rJava")
library("igraph")
library("rgl")
library("pracma")
library("RColorBrewer")
library("gplots")
library("ggplot2")
library("dplyr")
library("plotrix")
library("stringr")
library("gridExtra")
library("xlsx")
library("QtAC")
```

Set paths

Save "Surtsey_precipitation.xlsx", "Surtsey_GPP.xlsx", and "Surtsey_abundances.txt" in the working directory.

Path to the working directory

```
work_folder <- "/path/to/the/working/directory/"
setwd(work_folder)
```

Path to MTinfodynamics.jar

```
infodyn_path <- "dist/MTinfodynamics.jar"
```

NOTE: A certain amount of additional random Gaussian noise is required to guarantee the functioning of the KSG-estimator as being incorporated in the JIDT toolkit (see Kraskov 2008, Lizier 2014). Hence, results usually cannot be identically reproduced. However, the amount of random noise added is chosen small enough to guarantee very similar results.

```
observ_data <- "Surtsey_abundances.txt"
Data <- QtAC.TXT.reader(observ_data,col_names=TRUE,row_names = FALSE)
years <- colnames(Data)
years_short <- c("90","92","94","96","98","00","02","04","06","08","10","12","14","16","18")
names_short <- c('CF', 'CO', 'FR', 'HP', 'LA', 'MM', 'PA', 'PP', 'PD', 'SP', 'SM', 'T')
names_short_all <- c('CF', 'CO', 'FR', 'HP', 'LA', 'MM', 'PA', 'PP', 'PD', 'SP', 'SM', 'T', 'ND')
```

Estimating information transfer

Mean and standard deviation of the systemic variables

NOTE: The computation of one repetition can take up to 45 minutes.

```
 year <- 1:30
sysvar <- 1:30
mean <- 1:30
sd <- 1:30

develops <- array(NA,c(50,10,3))
for(rep in 1){
  result_mtx <- QtAC(Data,num_timepoints = 6, k = 3L, l = 3L, javapath = infodyn_path, noise_level = "1e-20")
  save(result_mtx,file = paste("result_mtx_",rep,".Rdata",sep=""))
  result_mtx2 <- QtAC.signfactor(result_mtx,0.1)
  maturation <- QtAC.maturation(result_mtx2)
  save(maturation,file = paste("maturation_",rep,".Rdata",sep=""))
  develops[rep,,1] <- t(maturation[,1])
  develops[rep,,2] <- t(maturation[,2])
  develops[rep,,3] <- t(maturation[,3])
}

sysvars <- c("pot","con","res")

r <- 1
for(y in 1:10){
  for(sv in 1:3){
    year[r] <- years[y+5]
    sysvar[r] <- sysvars[sv]
    data <- develops[,y,sv]
    mean[r] <- mean(data)
    sd[r] <- sd(data)
    r <- r+1
  }
}

df <- data.frame(year,sysvar,mean,sd)

pdf("Boxplot_Surtsey.pdf",paper = "a4r")
p1 <-   qplot(x    =  year,
              y    =  mean,
              data =  df[df$sysvar=="pot",],
              ylab = "potential") +

  geom_errorbar(aes(ymin = mean - sd,
                    ymax = mean + sd,
                    width = 0.15),
                color = "darkgreen") +
  geom_point(color='darkgreen') +
  theme(axis.title.y = element_text(size = 15),
        axis.title.x = element_text(size = 15),
        axis.text.x = element_text(size = 12),
        axis.text.y = element_text(size = 12))

p2 <-   qplot(x    =  year,
              y    =  mean,
              data =  df[df$sysvar=="con",],
              ylab = "connectedness") +

  geom_errorbar(aes(ymin = mean - sd,
                    ymax = mean + sd,
                    width = 0.15),
                color = "blue") +
  geom_point(color='blue')+
  theme(axis.title.y = element_text(size = 15),
        axis.title.x = element_text(size = 15),
        axis.text.x = element_text(size = 12),
        axis.text.y = element_text(size = 12))

p3 <-   qplot(x    =  year,
              y    =  mean,
              data =  df[df$sysvar=="res",],
              ylab = "resilience") +

  geom_errorbar(aes(ymin = mean - sd,
                    ymax = mean + sd,
                    width = 0.15),
                color = "red") +
  geom_point(color='red')+
  theme(axis.title.y = element_text(size = 15),
        axis.title.x = element_text(size = 15),
        axis.text.x = element_text(size = 12),
        axis.text.y = element_text(size = 12))

grid.arrange(p1,p2,p3,nrow = 3)
dev.off()
```

Distribution of resilience

```
res <- 1:500
year <- 1:500
r <- 1
for(rep in 1:50){
  maturation <- get(load(paste("maturation_",rep,".Rdata",sep="")))
  for(i in 1:10){
    res[r] <- maturation[i,3]
    year[r] <- i
    r <- r+1
  }
}

df <- data.frame(resi = as.numeric(res), group = as.numeric(year))

pdf("Scatterplot_surtsey.pdf")
par(cex.axis = 1.5, cex.lab = 2)
plot(as.numeric(year),as.numeric(res), cex = 2, lwd = 2, col = "red", xaxt = "n", ylab = "resilience", xlab = "year")
axis(side = 1, at= seq(1,10,1), labels= years[6:15])
dev.off()
```

Development of the systemic variables

NOTE: The following computations should be executed for a representative of the above repetitions. Here, "result_mtx_1.Rdata" is chosen exemplarily.

```
maturation <- get(load("maturation_1.Rdata"))
```

2-dimensional plot

NOTE: A plain version of this plot can be created via QtAC.2dplot.

```
p <- maturation[,1]
c <- maturation[,2]
r <- maturation[,3]

steps <- seq(1,10,0.01)
steps1 <- seq(1,3,0.01)
steps2 <- seq(3,6,0.01)
steps3 <- seq(6,7,0.01)
steps4 <- seq(7,10,0.01)

pdf("2d_Surtsey.pdf")
par(fig = c(0,1,0.5,1), new = TRUE, xpd=NA, cex.lab = 1.5, cex.axis = 1.25)
par(fig = c(0,1,0.5,1), new = TRUE, xpd=NA, cex.lab = 1.5, cex.axis = 1.25)

plot(1:10,p,pch=19,cex=0.5,col="white",xlab="",xaxt="n",ylab="potential", ylim = c(10,90))
cc <- pchip(1:10,p,seq(1,10,0.01))

color.scale.lines(steps1,cc[1:201],col = smoothColors("green",201,"green"),lwd=6)
color.scale.lines(steps2,cc[201:501], col = smoothColors("green",100,"red",50,"red",50,"orange",50,"orange",50,"green"), lwd=6)
color.scale.lines(steps3,cc[501:601],col= smoothColors("green",100,"green"),lwd=6)
color.scale.lines(steps4,cc[601:901],col = smoothColors("green",300,"red"),lwd=6)
points(1:10,p,pch=19,cex=0.5,col="grey48")

text(2,110,"r",col="black",cex =2)
text(3.5,110,"K",col="black",cex =2)
text(5,110,expression(Omega/alpha),col="black",cex =2)
text(6.5,110,"r",col="black",cex =2)

par(xpd = FALSE)

abline(v=3, lty = "dotted")
abline(v=4, lty = "dotted")
abline(v=6, lty = "dotted")
abline(v=7, lty = "dotted")

par(fig = c(0,1,0.263,0.763),new=TRUE, xpd = FALSE)

plot(1:10,c,pch=19,cex=0.25,col="white",xlab="",xaxt="n",ylab="connectedness", ylim = c(3,19))
cc <- pchip(1:10,c,seq(1,10,0.01))

color.scale.lines(steps1,cc[1:201],col = smoothColors("green",201,"green"),lwd=6)
color.scale.lines(steps2,cc[201:501], col = smoothColors("green",100,"red",50,"red",50,"orange",50,"orange",50,"green"), lwd=6)
color.scale.lines(steps3,cc[501:601],col= smoothColors("green",100,"green"),lwd=6)
color.scale.lines(steps4,cc[601:901],col = smoothColors("green",300,"red"),lwd=6)
points(1:10,p,pch=19,cex=0.5,col="grey48")

abline(v=3, lty = "dotted")
abline(v=4, lty = "dotted")
abline(v=6, lty = "dotted")
abline(v=7, lty = "dotted")

par(fig=c(0,1,0.0261,0.5261),new=TRUE, xpd= FALSE)

plot(1:10,r,pch=19,cex=0.25,col="white",xaxt="n",ylab="resilience", xlab = "year")
cc <- pchip(1:10,r,seq(1,10,0.01))

color.scale.lines(steps1,cc[1:201],col = smoothColors("green",201,"green"),lwd=6)
color.scale.lines(steps2,cc[201:501], col = smoothColors("green",100,"red",50,"red",50,"orange",50,"orange",50,"green"), lwd=6)
color.scale.lines(steps3,cc[501:601],col= smoothColors("green",100,"green"),lwd=6)
color.scale.lines(steps4,cc[601:901],col = smoothColors("green",300,"red"),lwd=6)
points(1:10,p,pch=19,cex=0.5,col="grey48")

abline(v=3, lty = "dotted")
abline(v=4, lty = "dotted")
abline(v=6, lty = "dotted")
abline(v=7, lty = "dotted")

axis(1, at=1:10, labels=years_short[6:15])
dev.off()
```

3-dimensional plot

NOTE: A plain version of this plot can be created via QtAC.3dplot.

```
 axis <- seq(1,dim(maturation)[1],1)
steps <- seq(1,dim(maturation)[1],0.01)

xa <- maturation[,1]
ya <- maturation[,2]
za <- maturation[,3]

steps <- seq(1,10,0.01)
steps1 <- seq(1,3,0.01)
steps2 <- seq(3,6,0.01)
steps3 <- seq(6,7,0.01)
steps4 <- seq(7,10,0.01)

x <- pchip(1:10,xa,seq(1,10,0.01))
y <- pchip(1:10,ya,seq(1,10,0.01))
z <- pchip(1:10,za,seq(1,10,0.01))

x1 <- x[1:201]
y1 <- y[1:201]
z1 <- z[1:201]
x2 <- x[201:501]
y2 <- y[201:501]
z2 <- z[201:501]
x3 <- x[501:601]
y3 <- y[501:601]
z3 <- z[501:601]
x4 <- x[601:901]
y4 <- y[601:901]
z4 <- z[601:901]

plot3d(ya, xa, za, pch=19, cex=0.25, size=0.5 ,type = "s", col="black",xlab = "connectedness", ylab = "potential",zlab = "resilience
lines3d( y1, x1, z1, col=smoothColors("green",201,"green"),lwd=6)
lines3d( y2, x2, z2, col=smoothColors("green",100,"red",50,"red",50,"orange",50,"orange",50,"green"), lwd=6)
lines3d( y3, x3, z3, col=smoothColors("green",100,"green"),lwd=6)
lines3d( y4, x4, z4, col=smoothColors("green",300,"red"),lwd=6)
text3d(ya,xa,za, rownames(maturation))
arrow3d(c(y4[280],x4[280],z4[280]),c(y4[300],x4[300],z4[300]), type="lines",s=2/3, col = "#EC1200",lwd=6)
```

Species abundance

Abundances

```
 data <- read.table('Surtsey_abundances.txt')
data <- data[-c(1,14),]

steps <- seq(1,15,0.01)

pos <- matrix(0,1,15)
for(i in 1:15){
  pos[1,i] <- (i-1)* 100+ 1
}

l <- length(steps)
sm <- matrix(0,12,l)

for(i in 1:12){
  x <- seq(1,15,1)
  y <- as.numeric(data[i,])
  pchip(x,y,seq(1,15,by = 0.01))
  fp <- pchipfun(x,y)
  fp(seq(1,6,by = 0.5))
  xs <- seq(1, 15, by = 0.01)
  yp <- pchip(x, y, xs)
  sm[i,] <- yp
}
cols <- c("red","black",
          "yellow", "lightgreen",
          "forestgreen",  "cyan",
          "purple", "blue",
          "orange", "brown",
          "magenta", "lightblue")
pdf('Abundances_Surtsey.pdf', paper = "a4r", width = 28)
par(mar = c(5,6,4,2))
plot(xs,
     sm[1,],
     type = "l",
     lwd = 2,
     lty = 1,
     col = cols[1],
     ylim = c(0,100),
     xlim = c(1,15),
     xlab = "year",
     ylab = "% of plot covered",
     xaxt = "n",
     cex.axis = 1.5,
     cex.lab = 2)
for(i in 2:12){
  lines(xs,sm[i,], type = "l", lwd = 2, lty = 1, col = cols[i])
}
axis(1, at=xs[pos], labels=years, cex.axis = 1.5)
legend("topleft", names_short, lty = 1, lwd = 2, col = cols, ncol = 2, cex = 1.5)

text(xs[pos[7]],95,"r",col="black",cex =2)
text(xs[pos[8.2]]+0.5,95,"K",col="black",cex =2)
text(xs[pos[9.7]]+0.9,95,expression(Omega/alpha),col="black",cex =2)
text(xs[pos[11.2]]+0.5,95,"r",col="black",cex =2)

par(xpd = FALSE)

abline(v=xs[pos[6]], lty = "dotted")
abline(v=xs[pos[8]], lty = "dotted")
abline(v=xs[pos[9]], lty = "dotted")
abline(v=xs[pos[11]], lty = "dotted")
abline(v=xs[pos[12]], lty = "dotted")
dev.off()
```

Information transfer of individual species

```
 pdf("Netflow_Surtsey.pdf", onefile = TRUE, paper = "a4r", width = 20)
for(s in 1:13){
  flows <- matrix(NA,10,2)
  for(i in 1:10){
    network <- result_mtx2[[1]][[i]]
    flows[i,1] <- sum(network[,s])
    flows[i,2] <- sum(network[s,])
  }
  par(cex.lab = 2, cex.axis = 1.5, cex.main = 2, mar = c(5,4.5,5,15))
  barplot(t(flows),
          ylim = c(0,5.25),
          col = c("mediumvioletred", "mediumturquoise"),
          legend.text = c("inflow","outflow"),
          args.legend = list(cex = 2, x = "right", bty="n", inset=c(-0.25,0), xpd = TRUE),
          main = paste("Information transfer ",names_short_all[s],sep = ""),
          beside = TRUE,
          ylab = "information [nats]",
          xlab = "year",
          names.arg = t(years[6:15]))
  abline(v=9, lty = "dotted")
  abline(v=12, lty = "dotted")
  abline(v=18, lty = "dotted")
  abline(v=21, lty = "dotted")
  text(4,5,"r",cex =2)
  text(10,5,"K",cex =2)
  text(15,5,expression(Omega/alpha),cex =2)
  text(19,5,"r",cex =2)
}
dev.off()
```

Heatmap of eigencentrality

```
 eigs <- matrix(0,13,10)
for(u in 1:10){
  adj_mtx <- result_mtx2[[1]][[u]]
  graph_adj_mtx <- igraph::graph.adjacency(adj_mtx, mode="directed", weighted=TRUE)
  eigen <- eigen_centrality(graph_adj_mtx, directed = FALSE, scale = FALSE)
  eigs[,u] <- eigen$vector
}
pdf(file= "Heatmap_Surtsey.pdf" , onefile=T, paper = "a4r",width = 28)
par(mar=c(10,6,15,1)+.1, cex.lab = 2, cex.axis = 1.5)
heatmap.2(eigs,
          Colv = FALSE,
          dendrogram = "none",
          key = "TRUE",
          key.xlab = "eigencentrality",
          density.info = "none",
          trace= "none",
          labCol = years[6:15],
          labRow = names_short_all,
          srtCol = 90,
          cexCol = 1.5,
          cexRow = 1.5)
dev.off()
```

Precipitation on Surtsey

```
 data <- read.xlsx("Surtsey_precipitation.xlsx",1, rowNames = TRUE)
mj <- as.numeric(data[2,12:30])

pdf("Precipitation_Surtsey.pdf", onefile = TRUE, paper = "a4r", width = 20)
par(cex.lab = 2, cex.axis = 1.5, cex.main = 2, mar = c(5,4.5,5,15))
barplot(as.numeric(as.matrix(mj)),
        ylim = c(0,170),
        col = "cornflowerblue",
        ylab = "Mean Rainfall May-July [mm]",
        xlab = "year",
        names.arg = c("00","","02","","04","","06","","08","","10","","12","","14","","16","","18"))

abline(v=5.5, lty = "dotted")
abline(v=7.9, lty = "dotted")
abline(v=12.7, lty = "dotted")
abline(v=15.1, lty = "dotted")
text(3,150,"r",cex =2)
text(6.7,150,"K",cex =2)
text(10,150,expression(Omega/alpha),cex =2)
text(14,150,"r",cex =2)
dev.off()
```

Gross primary production

```
 data <- read.xlsx('Surtsey_GPP.xlsx',1, rowNames = TRUE)
data1 <- as.numeric(data[2,2:14])
data_se <- as.numeric(data[3,2:14])
time <- seq(1,13,1)
pdf("GPP_Surtsey.pdf", paper = "a4r", width = 28)
q <- qplot(time,
           data1,
           size = 3,
           color = "green",
           xlab = "year",
           ylab = expression(paste("GPP [", mu,"mol CO"[2],"m"^{-2}, "sec"^{-1}, "]"))) +
  geom_errorbar(aes(x=time, ymin=data1-data_se, ymax=data1+data_se),
                width=0.5,
                size = 1.5,
                color = "darkgreen")
q <- q + scale_colour_manual(values = "darkgreen")
q <- q + scale_x_discrete(limits= c("06","07","08","09","10","11","12","13","14","15","16","17","18"))
q <- q + theme(axis.text.y = element_text(size=20))
q <- q + theme(axis.text.x = element_text(size=20))
q <- q + theme(axis.title.y = element_text(size=20))
q <- q + theme(axis.title.x = element_text(size=20))
q <- q + theme(legend.position = "none")
q
dev.off()
```