

ELECTRONIC SUPPLEMENTARY MATERIAL

SPATIAL EPIDEMICS DYNAMICS: SYNCHRONIZATION


MODEL STUDENTS

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CONTENTS

1	Introduction	1
2	Bifurcation Diagram	1
3	Deterministic Solution	2
4	Stochastic Simulation	7
4.1	Gillespie Algorithm	7
4.2	Adaptive Tau-Leaping Algorithm	11
5	Coherence Dependence on Parameters	15
5.1	3D Plot with Deterministic Solution	17
5.2	Four Panel Plot with Adaptive Tau	18
	Bibilography	20

1 INTRODUCTION

This is a supplementary document for the report “Spatial epidemics dynamics: Synchronization” created for reproducibility. This supplement was created using `knitr`, an  package that merges output languages such as \LaTeX with coding languages, allowing for dynamic reproducible report generation [1]. Other packages used are `deSolve`, `tikzDevice`, and `adaptivetau`.

```
library("deSolve")
library("tikzDevice")
library("adaptivetau")
```

Output is currently suppressed during compile in the interest of speed - some code chunks take hours to run - but code can still be run using the uncompiled document `SupplementaryMaterial.Rnw`.

2 BIFURCATION DIAGRAM

The bifurcation diagram was created using `XPPAUT` following the script described in the supplementary by Krylova and Earn [2]. In the script, equations for the single patch model with sinusoidal forcing were passed to the argument. The program was then instructed to solve the ODE by evaluating the equations with given initial conditions and parameters ranging over the parameter \mathcal{R}_0 from 0-30 using Poincaré maps with period one year.

```

1 ## Equations:
  f(x,y)=mu-R0*(gamma+mu)*(1 + a*cos(2*pi*t))*x*y-mu*x
3 g(x,y)=R0*(gamma+mu)*(1 + a*cos(2*pi*t))*x*y-(gamma+mu)*y
  x(t+1)=f(x,y)
5 y(t+1)=g(x,y)
  R0(t+1)=R0
7
8 ## Auxiliary Output Variables
9 aux R0
10
11 ## Initial Conditions
  init x=0.058824,y=0.00067043,R0=0
13 par a=0.1,mu=0.02,gamma=28.077
  ## auxiliary parameters to corresponding with
15 ## deterministic/stochastic models
16
17 ## Plotting in XPPAUT
  @ xp=R0, yp=y
19 @ xlo=0,xhi=40,yhi=0.008,ylo=-0.008
20
21 ## Range over R0
  @ rangeover=R0, rangestep=5000
23 @ rangelow=0,rangehigh=30,rangereset=no
  @ rangeoldic=yes, lt=0
25
26 ## Storing variables
27 @ total=650,trans=0
  @ maxstor=10000000
29 @ meth=discrete
  @ output=bifurcation.dat
31 done

```

bifurcation ode

When run using XPPAUT, this code outputs a file containing the values of time, susceptibles, infecteds, and \mathcal{R}_0 for all specified iterations of \mathcal{R}_0 .

This file can be generated and read by  via the following console commands:

```

system("xppaut bifurcation.ode -silent")

bfd <- read.table("bifurcation.dat", col.names=c("time", "S", "I", "R0"))

```

The bifurcation diagram can be generated using the following command:

```
plot(I$bfd, R0$bfd)
```

3 DETERMINISTIC SOLUTION

The SIR meta-patch vector field function, `SIRmeta.vector.field`, returns the values of $\frac{dS_i}{dt}$, $\frac{dI_i}{dt}$, and $\frac{dR_i}{dt}$ for all patches (i.e. $1 \leq i \leq n$) at a given time, given the values of S_i , I_i , and R_i for all patches and the values of parameters \mathcal{R}_0 (the basic reproductive number), μ (the death/birth rate), γ (the recovery rate), α (the strength of seasonal forcing), m (the mixing parameter) and EC (a switch: if **TRUE** use equal coupling, otherwise use nearest neighbour coupling).

It creates the beta matrix:

$$\beta(t) = \langle \beta \rangle (1 + \alpha \cos(2\pi t))M \quad (1)$$

where M is the mixing matrix. If equal coupling is used then

$$M = \begin{bmatrix} 1-m & \frac{m}{n-1} & \frac{m}{n-1} & \frac{m}{n-1} \\ \frac{m}{n-1} & 1 & \frac{m}{n-1} & \frac{m}{n-1} \\ \frac{m}{n-1} & \frac{m}{n-1} & 1 & \frac{m}{n-1} \\ \frac{m}{n-1} & \frac{m}{n-1} & \frac{m}{n-1} & 1 \end{bmatrix}$$

Otherwise nearest neighbour coupling is used.

$$M = \begin{bmatrix} 1-m & \frac{m}{2} & 0 & 0 & \dots & \frac{m}{2} \\ \frac{m}{2} & 1-m & \frac{m}{2} & 0 & & \vdots \\ 0 & \frac{m}{2} & 1-m & & & \\ 0 & 0 & & \ddots & & \\ \vdots & & & & \ddots & \frac{m}{2} \\ \frac{m}{2} & & & \dots & \frac{m}{2} & 1-m \end{bmatrix}$$

The proportional dynamics of a single patch in the meta-patch SIR model are given by

$$\begin{aligned} \frac{dS_i}{dt} &= \mu - S_i \sum_{j=1}^n \beta_{ij}(t) I_j - \mu S_i \\ \frac{dI_i}{dt} &= S_i \sum_{j=1}^n \beta_{ij}(t) I_j - \gamma I_i - \mu I_i \\ \frac{dR_i}{dt} &= \gamma I_i - \mu R_i \end{aligned} \tag{2}$$

```
SIRmeta.vector.field <- function(t,vars,parms=NULL) {
  ##parms should be of form (R_0,gamma,mu,alpha,m,EC)
  ##vars should be of form (S,I,R)
  with(as.list(c(parms,vars)), { #So that it can call variables stored in parms
    ##vars contains the values of S, I, and R at time t
    n <- length(vars)/3
    S <- vars[1:n]
    I <- vars[(n+1):(2*n)]
    R <- vars[(2*n+1):(3*n)]

    #Equal Coupling
    if (EC==TRUE){
      ##mixing matrix
      M <- matrix(m/(n-1),n,n)+(1-m*(1+1/(n-1)))*diag(n)
      ##beta matrix
      betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*t))*M
    }else{
      #Nearest Neighbors
      ##mixing matrix
      M <- (1-m)*diag(n)
      M[row(M)%n==(col(M)+1)%n] <- m/2
      M[row(M)%n==(col(M)-1)%n] <- m/2
      ##beta matrix
      betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*t))*M
    }
  }
}
```

```

dS <- NULL
dI <- NULL
dR <- NULL
for (i in 1:n){
  dS[i] <- mu*(1-S[i]) - S[i]*sum(betam[i,]*I) ##dS_i/dt
  dI[i] <- S[i]*sum(betam[i,]*I) - (mu+gamma)*I[i] ## dI_i/dt
  dR[i] <- gamma*I[i] -mu*R[i]
}
vec.fld <- c(dS=dS,dI=dI,dR=dR)
return(list(vec.fld))
})
}

```

The `run.soln` function returns the values of S_i , I_i , and R_i for all patches at times given in `times`, given the initial conditions, the vector field function, and parameter to pass to the vector field function. It also returns the value of “coherence” at all times. A state is said to be coherent at time step t when $I_1(t) = I_2(t) = \dots = I_n(t)$ for all n patches [3]. The measure used here of “how coherent” a state is is the coefficient of variation, also called the relative standard deviation, of $\{I_i(t)\}_{i=1}^n$. It is the standard deviation of these values divided by the mean. The smaller it is the closer all states are to the mean and the more coherent the state is.

$$\begin{aligned}
c_v(t) &= \frac{SD(I_i(t))}{\overline{I_i(t)}} \\
&= \frac{\sqrt{\frac{1}{n} \sum_{i=1}^n (I_i(t) - \overline{I_i(t)})^2}}{\overline{I_i(t)}}
\end{aligned} \tag{3}$$

This is calculated using \mathbb{R} ’s native `sd` and `mean` functions.

```

## Get Solutions and coherence measure
run.soln <- function(n,ic=c(S=rep(0,n),I=rep(0,n),R=rep(1,n)),tmax=1,
                      times=seq(0,tmax,
                                by=tmax/1000),
                      func,parms) {
  soln <- ode(ic,times,func,parms)

  #Measure of coherence: the coefficient of variation/relative standard deviation of
  #all the patches at each time step
  coherence <- rep(0,length(times))
  for(tims in 1:length(times)){
    coherence[tims]<- sd(soln[tims,paste0('I',1:n)])/mean(soln[tims,paste0('I',1:n)])
    if(is.nan(coherence[tims])){
      coherence[tims]<- 0
    }
  }
  return(list("times"=times, "soln" = soln, "coherence"= coherence))
}

```

Function `plot.SIRmeta` uses `run.soln` to get the solution of the deterministic model with the given initial conditions and parameters, and plots the results. It should be noted that when outputting the images, they were run through the `tikzDevice` package for \mathbb{R} to enable the use of \LaTeX within figures. The images were also saved to PDF through `tikzDevice`.

```

#Given ics and paramters, plot the det soln of the SIR meta model to pdf
plot.SIRmeta <- function(n,ic=c(S=rep(0,n),I=rep(0,n),R=rep(1,n)),tmax=1,
                        parms,...){
  ##parms should be of form (R_0,gamma,mu,alpha,m,EC)
  with(as.list(c(parms)), { #So that it can call variables stored in parms
    ## get solutions
    run <- run.soln(n=n,ic=ic,tmax=tmax,
                   func=SIRmeta.vector.field,
                   parms=parms)
    times<-run$times
    soln<-run$soln
    coherence<-run$coherence

    #Print to pdf using tikz
    filename <- paste0("images/det",if(EC) "EC" else "NN", "R0", R_0, "m", m, ".tex")
    if(file.exists(filename)){ #If the filename is already used
      filename <- paste0("images/det",if(EC) "EC" else "NN", "R0", R_0, "m", m, "(1).tex")
    }
    if(file.exists(filename)){ #If the filename(1) is already used
      filename <- paste0("images/det",if(EC) "EC" else "NN", "R0", R_0, "m", m, "(2).tex")
    }

    tikz(filename,standAlone=TRUE,width=6,height=6)

    #leave room on right margin for coherence label
    par(mar = c(5,5,2,5))
    #Calculates I* to estimate how high the y-axis needs to be
    IEE <- (1 - 1/R_0)*mu/gamma
    ## draw box for plot
    plot(0,0,xlim=c(0,tmax),ylim=c(0,IEE*5),type="n",xlab="Time (years)",
         ylab="Prevalence (I)",las=1)

    #Plot I for all patches with different colours and lty
    for (i in 1:n){
      lines(times,soln[,paste0('I',i)],col=i,lty=i)
    }

    #Plot coherence over top
    par(new = T)
    plot(times,coherence,type='l',lwd=2,axes=F,xlab=NA, ylab=NA,ylim=c(0,1))
    axis(side=4)
    #Label left axis
    mtext(side = 4, line = 3, 'Coherence')

    #Make legend
    labels <- c(1:n)
    for(i in 1:n){
      labels[i]<-paste('$I_{',i,'}$',collapse=NULL)
    }
    legend("topright",legend=labels,col=1:n,lty=1,bty='n')
    dev.off()
    tools::texi2dvi(filename,pdf=T)
  })

```

}

The following chunk of code uses `plot.SIRmeta` to plot solutions to the meta-patch model for different parameters and with initial conditions within $\pm 30\%$ of the Endemic Equilibrium (EE) to preserve asymptotic local stability of the system[4]. This is so that the solutions converge quickly to a stable solution. The endemic equilibrium is

$$\begin{aligned} S^* &= \frac{1}{\mathcal{R}_0} \\ I^* &= \frac{\mu}{\gamma} \left(1 - \frac{1}{\mathcal{R}_0} \right) \\ R^* &= 1 - S^* - I^* \end{aligned} \tag{4}$$

```
#Parameters
R_0 <- 17    ##basic reproduction rate (if the system had no forcing)
gamma <- 365/13  ##inverse of mean infectious period
mu <- 1/50    ##death and birth rate
alpha <- 0.1   ##strength of seasonal forcing
n <- 10       ## Number of patches
m <- 0.2      ##Connectivity matrix parameter
EC <- FALSE   ##if true use equal coupling, if false use nearest neighbors

##Initial conditions
#Want ICs near EE for stability. Find EE values:
SEE <- 1/R_0
IEE <- (1 - 1/R_0)*mu/gamma
REE <- 1-SEE-IEE
#Use random initials conditions within +/-30% of EE values
set.seed(34) #For reproducibility
percent <- 0.3
S0 <- runif(SEE*(1-percent), SEE*(1+percent), n)
I0 <- runif(IEE*(1-percent), IEE*(1+percent), n)
R0 <- 1-S0-I0

tmax<-15

#### Plotting lots of solutions to pdf ####
#Making detNNR017m0.2
plot.SIRmeta(n=n,ic=c(S=S0,I=I0,R=R0),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detNNR010m0.2
R_0<-10
plot.SIRmeta(n=n,ic=c(S=S0,I=I0,R=R0),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detNNR025m0.2
R_0<-25
plot.SIRmeta(n=n,ic=c(S=S0,I=I0,R=R0),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detECR017m0.2s
R_0<-17
tmax<-5
EC<-TRUE
plot.SIRmeta(n=n,ic=c(S=S0,I=I0,R=R0),tmax=tmax,
```

```

        parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detNNR017m0.2s
EC<-FALSE
plot.SIRmeta(n=n,ic=c(S=S0,I=IO,R=RO),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detNNR017m0.01
tmax<-15
m<-0.01
plot.SIRmeta(n=n,ic=c(S=S0,I=IO,R=RO),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))
#Making detNNR017m0.01wider
percent <- 0.4
S0 <- runif(SEE*(1-percent), SEE*(1+percent), n)
IO <- runif(IEE*(1-percent), IEE*(1+percent), n)
RO <- 1-S0-IO
plot.SIRmeta(n=n,ic=c(S=S0,I=IO,R=RO),tmax=tmax,
             parms=c(R_0=R_0,gamma=gamma,mu=mu,alpha=alpha,m=m,EC=EC))

```

4 STOCHASTIC SIMULATION

Stochastic simulations of the model were also used.

4.1 Gillespie Algorithm

The Gillespie algorithm is a method of exactly simulating a stochastic process. Consider a process involving transitions between different states. The rate for a given transition i is labelled a_i . The total transition rate is defined as

$$a_0 = \sum a_i \quad (5)$$

If we assume that the time spent in a given state is exponentially distributed, then by sampling from an exponential distribution with rate a_0 (using \mathbb{R} 's `rexp` function) we can simulate how much time was spent in a given state before the next transition.

The probability that transition i occurred is $\frac{a_i}{a_0}$. By sampling from a uniform distribution over $[0, a_0]$ we can simulate which transition occurred in the following way: if the sampled value is in the i^{th} interval from the list

$$[0, a_1), [a_1, a_1 + a_2), \dots, [a_1 + a_2 + \dots + a_{i-1}, a_1 + a_2 + \dots + a_i), \dots \quad (6)$$

than say transition i occurred.

For this problem, the states are the values of $\{(S_i, I_i, R_i)\}_{i=1}^n$. The state space is all possible set of n triplets of non-negative integers. Possible transitions are:

- A birth ($S_i \rightarrow S_i + 1$)
- A transmission ($S_i \rightarrow S_i - 1$ and $I_i \rightarrow I_i + 1$)
- A recovery ($I_i \rightarrow I_i - 1$ and $R_i \rightarrow R_i + 1$)
- A death of a susceptible ($S_i \rightarrow S_i - 1$)
- A death of an infected ($I_i \rightarrow I_i - 1$)
- A death of a recovered ($R_i \rightarrow R_i - 1$)

for $1 \leq i \leq n$. The transition rates are:

- The birth rate $\mu(S_i + I_i + R_i)$

- The transmission rate $\frac{S_i}{S_i+I_i+R_i} \sum_{j=1}^n \beta_{ij}(t)I_j$
- The recovery rate γI_i
- The susceptible death rate μS_i
- The infected death rate μI_i
- The recovered death rate μR_i

for $1 \leq i \leq n$.

The function `SIRmeta.Gillespie` implements a stochastic simulation of the meta-patch SIR model using the Gillespie algorithm. It returns a list of times (starting at zero and ending near the input variable `tmax` with non-uniform step sizes) and the values of S_i , I_i , and R_i for all patches at these times given initial conditions and parameter values.

```
SIRmeta.Gillespie <- function(tmax,ic=c(S0,I0,R0),
                             parms=c(R_0=2,gamma=0.25,mu=4e-5,
                                       alpha=0.1,m=0.2,EC=TRUE)){
  times <- 0

  n <- length(ic)/3
  #S, I, R matrices: column index is patch index and rows (added later in while loop)
  #are values at different time steps
  S <- matrix(0,1,n)
  I <- matrix(0,1,n)
  R <- matrix(0,1,n)
  #Initial Coniditions
  S[1,] <- ic[1:n]
  I[1,] <- ic[(n+1):(2*n)]
  R[1,] <- ic[(2*n+1):(3*n)]

  index <- 1
  while(times[index] < tmax){
    #A matrix of all rates
    rates <- matrix(0,n,6)
    #the first column is all birth rates
    rates[,1] <- mu*(S[index,]+I[index,]+R[index,])
    #thrid column are recovery rates
    rates[,3] <- gamma*I[index,]
    #last three columns are death rates from S and I
    rates[,4] <- mu*S[index,]
    rates[,5] <- mu*I[index,]
    rates[,6] <- mu*R[index,]
    #Second column are transmission rates
    #Equal Coupling
    if(EC){
      M <- matrix(m/(n-1),n,n)+(1-m*(1+1/(n-1)))*diag(n) ##connectivity matrix
      betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*times[index]))*M ##beta matrix
    }else{
      #Nearest Neighbors
      M <- (1-m)*diag(n)
      M[row(M)%n==(col(M)+1)%n] <- m/2
      M[row(M)%n==(col(M)-1)%n] <- m/2
      betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*times[index]))*M ##beta matrix
    }
  }
}
```



```

}
rates[,2] <- S[index,]*colSums(t(betam[1:n,])*I[index,])/(S[index,]+I[index,]+R[index,])
totalrate <- sum(rates)

#Getting a timestep using R's exp distribution
timestep <- rexp(n=1, rate= totalrate)
times <- rbind(times, times[index]+timestep)

#Adding new row to S, I, R
S <- rbind(S, S[index,])
I <- rbind(I, I[index,])
R <- rbind(R, R[index,])

#Getting which compartment transistion occurred
#TO DO: Do a bisection search (or some other faster method) instead
#Get a random number from a uniform distribution
randomvar <- runif(n=1,min=0,max=totalrate)
interval <- 1
#Make the rates matrix into a vector for convinence
rateslisted <- c(0,as.vector(t(rates)))
#Find which interval randomval is in from list:
#[0,a_1), [a_1, a_1+a_2), etc
#If in interval [a_1 + .. + a_(i-1), a_1 + ... + a_i),
#transition given by rate a_i occurred
while(interval < (6*n)){
  if(randomvar >= sum(rateslisted[1:interval]) &
    randomvar < sum(rateslisted[1:(interval+1)])){
    break
  }else{
    interval<- interval+1
  }
}
#Get row, col indices of a_i in rates matrix
#row index says in which patch a transition occurred
#col index says what type of transition occurred
colInd <- interval%%6
rowInd <- ceiling(interval/6)
if(colInd ==1){ ##A birth occurred
  S[index+1,rowInd] <- S[index,rowInd]+1
}else if(colInd ==2){ ##An infection occurred
  S[index+1,rowInd] <- S[index,rowInd]-1
  I[index+1,rowInd] <- I[index,rowInd]+1
}else if(colInd ==3){ ##A recovery occurred
  I[index+1,rowInd] <- I[index,rowInd]-1
  R[index+1,rowInd] <- R[index,rowInd]+1
}else if(colInd ==4){ ##A death in S occurred
  S[index+1,rowInd] <- S[index,rowInd]-1
}else if(colInd ==5){ ##A death in I occurred
  I[index+1,rowInd] <- I[index,rowInd]-1
}else if(colInd ==0){ ##A death in R occurred
  R[index+1,rowInd] <- R[index,rowInd]-1
}
}

```

```

    index <- index+1
  }
  return(cbind(times, S, I, R))
}

```

The following code uses the `SIRmeta.Gillespie` function to plot a stochastic simulation of the model.

```

#For reproducibility set the seed
set.seed(899)

tmax <- 10
n <- 10

#Parameters
R_0 <- 17 ##basic reproduction rate (if the system had no forcing)
gamma <- 365/13 ##inverse of mean infectious period
mu <- 1/50 ##death and birth rate
alpha <- 0.1 ##strength of seasonal forcing
n <- 10 ## Number of patches
m <- 0.5 ##Connectivity matrix parameter
EC <- TRUE ##if true use equal coupling, if false use nearest neighbors

##Initial conditions
#Want ICs near EE for stability. Find EE values:
SEE <- 1/R_0
IEE <- (1 - 1/R_0)*mu/gamma
REE <- 1-SEE-IEE
#Sample from initials conditions within +/-10% of EE values
#convert from proportions to numbers and convert to integers
percent <- 0.1
population <- 3000
possibleS0 <- seq(as.integer(population*SEE*(1-percent)),
                  as.integer(population*SEE*(1+percent)),1)
possibleI0 <- seq(as.integer(population*IEE*(1-percent)),
                  as.integer(population*IEE*(1+percent)),1)
S0 <- sample(possibleS0, n,replace=TRUE)
I0 <- sample(possibleI0, n,replace=TRUE)
R0 <- population-S0-I0

#Get simulation results
results <- SIRmeta.Gillespie(tmax,ic=c(S0,I0,R0),
                             parms=c(R_0,gamma,mu,alpha,m,EC))
times<-results[,1]
I <- results[, (n+2):(2*n+2)]

#Save data for later use and plot to pdf and png
write.table(results,file="GillIECR017m0.2.pdf")
pdf(file="images/GillIECR017m0.2.pdf")
copy <- dev.cur()
png(file="images/GillIECR017m0.2.png")
dev.control("enable")

## draw box for plot
plot(0,0,xlim=c(0,tmax),ylim=c(0,population*IEE*2),xlab="Time (years)",

```

```

      ylab="Prevalence (I)")
    #Plot all I_i using a differnt line colour and lty for each patch
  for (i in 1:n) {
    lines(times, I[,i],col=i,lwd=0.2)
  }
  #Make legend
  legend("topright",legend=1:n,fill="white",title="Patch",col=1:n,lty=1,cex=0.5)

dev.copy(which=copy)
dev.off
dev.off

```

This code runs very slowly for large populations. For a 250,000 person per patch population it took 3 hours. This method for simulating the stochastic realization of the model is thus not practical.

4.2 Adaptive Tau-Leaping Algorithm

To simulate a stochastic process efficiently, an approximate method can be used. The adaptive tau-leaping algorithm works by

The `runadapttau` function contains a list of all possible transitions and `rateFct`, a function that returns the values of all transition rates given the time and current state. `runadapttau` passes these, along with the input initial conditions and parameters, to the `ssa.adaptivetau` function. It returns a list of times (starting at zero and ending near input `tmax` with non-uniform step size) and the values of the state at all these times.

```

run.adapttau <-function(tmax,ic=c(S0,I0,R0),
                      params=c(R_0,gamma,mu,alpha,m,EC)){
  #Get the # of patches from the ics
  n <- length(ic)/3

  #TO DO: This should be changed so that it works with different n values
  #and is less ugly
  #A list of all possible transitions
  transitions <- list(c(S1 = +1), c(S1 = -1, I1= +1), c(I1 = -1, R1= +1), c(S1 = -1),
                    c(I1 = -1), c(R1 = -1),
                    c(S2 = +1), c(S2 = -1, I2= +1), c(I2 = -1, R2= +1), c(S2 = -1),
                    c(I2 = -1), c(R2 = -1),
                    c(S3 = +1), c(S3 = -1, I3= +1), c(I3 = -1, R3= +1), c(S3 = -1),
                    c(I3 = -1), c(R3 = -1),
                    c(S4 = +1), c(S4 = -1, I4= +1), c(I4 = -1, R4= +1), c(S4 = -1),
                    c(I4 = -1), c(R4 = -1),
                    c(S5 = +1), c(S5 = -1, I5= +1), c(I5 = -1, R5= +1), c(S5 = -1),
                    c(I5 = -1), c(R5 = -1),
                    c(S6 = +1), c(S6 = -1, I6= +1), c(I6 = -1, R6= +1), c(S6 = -1),
                    c(I6 = -1), c(R6 = -1),
                    c(S7 = +1), c(S7 = -1, I7= +1), c(I7 = -1, R7= +1), c(S7 = -1),
                    c(I7 = -1), c(R7 = -1),
                    c(S8 = +1), c(S8 = -1, I8= +1), c(I8 = -1, R8= +1), c(S8 = -1),
                    c(I8 = -1), c(R8 = -1),
                    c(S9 = +1), c(S9 = -1, I9= +1), c(I9 = -1, R9= +1), c(S9 = -1),
                    c(I9 = -1), c(R9 = -1),
                    c(S10 = +1), c(S10 = -1, I10= +1), c(I10 = -1, R10= +1), c(S10 = -1),
                    c(I10 = -1), c(R10 = -1))

```

```

#A function that outputs the transition rates given parameters, S,I,R, and t
rateFct <- function(x,params,time){
  #x should be of form: x=c(S,I,R)
  #params should be of form: paarms=c(R_0,gamma,mu,alpha,m,EC)

  with(
    as.list(c(params)),
    {
      n <- length(x)/3
      S <- as.vector(x[1:n])
      I <- as.vector(x[(n+1):(2*n)])
      R <- as.vector(x[(2*n+1):(3*n)])

      #A matrix of all rates
      rates <- matrix(0,n,6)
      #the first column is all birth rates
      rates[,1] <- mu*(S+I+R)
      #third column are recovery rates
      rates[,3] <- gamma*I
      #last three columns are death rates from S and I
      rates[,4] <- mu*S
      rates[,5] <- mu*I
      rates[,6] <- mu*R
      #Second column are transmission rates
      #Equal Coupling
      if (EC==TRUE){
        M <- matrix(m/(n-1),n,n)+(1-m*(1+1/(n-1)))*diag(n) ##connectivity matrix
        betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*time))*M ##beta matrix
      }else{
        #Nearest Neighbors
        M <- (1-m)*diag(n)
        M[row(M)%%n==(col(M)+1)%%n] <- m/2
        M[row(M)%%n==(col(M)-1)%%n] <- m/2
        betam <- R_0*(gamma+mu)*(1+alpha*cos(2*pi*time))*M ##beta matrix
      }
      rates[,2] <- S*colSums(t(betam[1:n,])*I)/(S+I+R)

      return(as.vector(t(rates)))
    }
  )
}

init.values <- c(S=S0,I=I0,R=R0)
#Get approximate simulation
simResults <- ssa.adaptivetau(init.values,transitions, rateFct, params, tf=tmax)
I <- simResults[, (12:21)]

#Measure of coherence: the coefficient of variation/relative
#standard deviation of all the patches at each time step
coherence <- rep(0,length(simResults[,1]))
for(tims in 1:length(simResults[,1])){
  coherence[tims] <- sd(I[tims,])/mean(I[tims,])
  #In case the mean is zero (and thus the coefficient of variation becomes nan or inf)

```

```

    if(is.nan(coherence[tims]) | is.infinite(coherence[tims])){
      coherence[tims]<- 0
    }
  }

  #Is the disease extinct (I pop below 20% of IEE for awhile) in any of the patches?
  #Store 1s for yes, 0 for nos
  localextinction<-c(1:n)
  for(i in 1:ncol(I)){
    if(mean(I[(nrow(I)-50):nrow(I),i])<= IEE*population*0.2){
      localextinction[i]<-1
    }else{
      localextinction[i]<-0
    }
  }
  localext<-mean(localextinction)

  #If the disease is extinct in all patches there is global extinction
  if(all(localextinction==1)){
    globalextinction<-1
  }else{
    globalextinction<-0
  }

  return(list("sim" = simResults, "coherence"= coherence,"localext"=localext,
            "globalext"=globalextinction))
}

```

The following function, `plot.adapttau`, uses `runadapttau` to approximately simulate the meta-patch SIR model and plot the results.

```

plot.adapttau <- function(tmax,init.values,params,IEE,population){
  with(as.list(c(parms)), {
    n<-10
    run <- run.adapttau(tmax,init.values,params)

    simResults <- run$sim
    coherence <- run$coherence

    ##Saving the data and the print plot to pdf
    filename <- paste0("adapttau",if(EC==TRUE) "EC" else "NN", "R0", R_0, "m", m)
    if(file.exists(filename)){ #If the filename is already used
      filename <- paste0("adapttau",if(EC==TRUE) "EC" else "NN", "R0", R_0, "m", m, "(1)")
    }
    if(file.exists(filename)){ #If the filename(1) is already used
      filename <- paste0("images/adapttau",if(EC==TRUE) "EC" else "NN", "R0", R_0, "m", m,
                        "(2)")
    }
    write.table(run,file=paste0(filename,".csv"))
    pdf(file=paste0("images/",filename,".pdf"))

    ## draw box for plot
    #leave room on right margin for Coherence label
    par(mar = c(5,5,2,5))
  }
}

```

```

#Solutions should oscillate around IEE so ylim should go to around twice
#that so solns are in the middle of plot
plot(0,0,xlim=c(0,tmax),ylim=c(0,population*IEE*4),xlab="Time (years)",
     ylab="Prevalence (I)")

##plot I_i for each patch
j<-1:n
for (i in 1:n) {
  if(i%%8==1) j[i] <- i+3 #indices so that black and solid lines are
  #skipped; saved for legend
  lines(simResults[,1], simResults[,11+i],col=j[i],lty=j[i],lwd=0.5)
  # use a different line colour and line type for each patch
}

#Currently unused code for plotting the det soln over this sim
# draw.single.soln(n,ic=c(S=SEE,I=IEE,R=(1-SEE-IEE)),tmax=tmax,
#                  func=SIR.vector.field,
#                  parms=c(R_0,gamma,mu,alpha,population))

#Plot coherence onto of pre-existing plot
par(new = T)
plot(simResults[,1],coherence,type='l',axes=F,xlab=NA, ylab=NA, ylim=c(0,1))
#y axis and coherence label on right axis
axis(side=4)
mtext(side = 4, line = 3, 'Coherence')

#Make legends
legend("topright",legend=1:n,title="Patch",bg='white',col=j,lty=j,lwd=0.5,cex=0.8)
legend("bottomright", legend="Relative Standard Deviation",bg='white',
      col=1,lty=1, cex=0.8)

dev.off()
}

```

Using `plot.adapttau` to simulate the model with different parameter values:

```

#Parameters
R_0 <- 17 ##basic reproduction rate (if the system had no forcing)
gamma <- 365/13 ##inverse of mean infectious period
mu <- 1/50 ##death and birth rate
alpha <- 0.1 ##strength of seasonal forcing
n <- 10 ## Number of patches
m <- 0.2 ##Connectivity matrix parameter
EC <- TRUE ##if true use equal coupling, if false use nearest neighbors
parms<-c(R_0,gamma,mu,alpha,m,EC)

##Initial conditions
#Want ICs near EE for stability. Find EE values:
SEE <-1/R_0
IEE <-(1 - 1/R_0)*mu/gamma
REE <-1-SEE-IEE
#Sample ics from points +/-10% from the EE values
percent <- 0.1

```

```

population <- 5000000
possibleS0 <- seq(as.integer(population*SEE*(1-percent)),
                  as.integer(population*SEE*(1+percent)),1)
possibleI0 <- seq(as.integer(population*IEE*(1-percent)),
                  as.integer(population*IEE*(1+percent)),1)
S0 <- sample(possibleS0, n,replace=TRUE)
I0 <- sample(possibleI0, n,replace=TRUE)
R0 <- population-S0-I0
init.values <- c(S=S0,I=I0,R=R0)

tmax <- 15

plot.adapttau(tmax,init.values,params,IEE,population)
m<-0.01
plot.adapttau(tmax,init.values,params,IEE,population)

```

5 COHERENCE DEPENDENCE ON PARAMETERS

The dependence of a meta-patch solution becoming “coherent” on the parameters used in the model was explored. A system is considered coherent when the mean value of $c_v(t)$ from $t = 9$ years to $t = 10$ years is below a threshold value. We will refer to this value as the coherence threshold.

A list of \mathcal{R}_0 (the basic reproductive number) values from 1.1 to 30 was made, along with a list of m (the mixing parameter) values. For each set of \mathcal{R}_0 and m values, a solution or simulation of the model was run ten times each with different initial conditions (all within 10% of the Endemic Equilibrium values). It was stored whether or not each solution or simulation became coherent; a one was saved if it did and a zero was saved otherwise. By taking the mean of these values for all runs, the probability of becoming coherent for a given \mathcal{R}_0 and m value was found.

If parameter DetOrAdap is **TRUE** this is done using deterministic solutions to the model, created by the `run.soln` function. Otherwise, this is done using adaptive tau simulations in the `runadapttau` function.

```

coherenceGrid <- function(params=c(gamma,mu,alpha,EC),
                             R_0list,mlist,nsample,DetOrAdap,population=1){
  with(
    as.list(c(params)),
    {
      n <- 10 ## Number of patches
      ##Param for Initial conditions
      percent <- 0.1
      tmax <- 10
      gridsize<-length(mlist)
      gridsizeR_0 <- length(R_0list)
      avgCoherence<- matrix(0, gridsize,gridsizeR_0)
      avgLE<- matrix(0, gridsize,gridsizeR_0)
      avgGE<- matrix(0, gridsize,gridsizeR_0)

      index2 <- 1
      for (R_0 in R_0list){
        index1 <- 1
        #Want ICs near EE for stability. Find EE values:
        #Note: They depend on R_0
        SEE <-1/R_0
        IEE <-(1 - 1/R_0)*mu/gamma

```

```

if(!DetOrAdap){ #Only need these for adapttau sim
  possibleS0 <- seq(as.integer(population*SEE*(1-percent)),
                    as.integer(population*SEE*(1+percent)),1)
  possibleI0 <- seq(as.integer(population*IEE*(1-percent)),
                    as.integer(population*IEE*(1+percent)),1)
}

for (m in mlist){
  coherenceProb <- rep(0, nsample)
  coherenceProb <- rep(0, nsample)
  localextProb <- rep(0, nsample)
  globalextProb <- rep(0, nsample)
  for (sampler in 1:nsample){
    #Get det soln nsample times with different ICs
    #Take mean of coherence near end of soln
     #(since coherence can be somewhat oscillatory)

    if(DetOrAdap){
      S0 <- runif(n,SEE*(1-percent),SEE*(1+percent))
      I0 <- runif(n,IEE*(1-percent),IEE*(1+percent))
      R0 <- 1-S0-I0
      coherenceRun <- run.soln(n,ic=c(S=S0,I=I0,R=R0),tmax=tmax,
                               func=SIRmeta.vector.field,
                               parms=c(R_0,gamma,mu,alpha,m,EC))$coherence
    }else{
      S0 <- sample(possibleS0, n,replace=TRUE)
      I0 <- sample(possibleI0, n,replace=TRUE)
      R0 <- population-S0-I0
      run <- run.adapttau(tmax,init.values=c(S=S0,I=I0,R=R0),
                         params=c(R_0,gamma,mu,alpha,m,EC))
      coherenceRun<-run$coherence
      localextProb[sampler] <- run$localext
      globalextProb[sampler] <- run$globalext
    }

    mean <- mean(coherenceRun[length(coherenceRun)-(100:0)])
    if(mean<threshold){
      coherenceProb[sampler] <- 1
    }else{
      coherenceProb[sampler] <- 0
    }
  }
  #Take mean of all coherence for all runs with these parameters
  avgCoherence[index1,index2]<- mean(coherenceProb)
  avgLE[index1,index2]<- mean(localextProb)
  avgGE[index1,index2]<- mean(globalextProb)

  index1<-index1+1
}
index2<-index2+1
}
#Save data
filename<-paste0("grid",if(DetOrAdap) "det" else "adap",if(EC) "EC" else "NN",".csv")

```



```

if(file.exists(filename)){ #If the filename is already used
  filename <-paste0("grid",if(DetOrAdap) "det" else "adap",if(EC) "EC" else "NN",
                    "(1).csv")
}
cohdata <- cbind.data.frame(avgCoherence,avgLE,avgGE)
write.table(cohdata,file=filename)
return(list("coherence"=avgCoherence, "LE"=avgLE,"GE"=avgGE))
})
}

```

5.1 3D Plot with Deterministic Solution

A 3D plot showing the probability of coherence vs \mathcal{R}_0 and m is created in the function `coherence3DPlot`.

```

coherence3DPlot <- function(avgCoherence,params=c(gamma,mu,alpha,EC),R_0list,
                           mlist,nsample,DetOrAdap,population){
  with(
    as.list(c(params)),
    {

      #3D plot:
      filename<-paste0("images/",if(DetOrAdap) "det" else "adap","3D",if(EC) "EC" else "NN",
                      ".pdf")
      pdf(file=filename)
      #Making a colour gradient for the plot
      nbcol <- 100
      #You can change start and end to get different parts of the rainbow
      color <- rev(rainbow(nbcol, start = 3/6, end = 3.5/6))
      #The colour gradient will correspond to the 'height' of the plot
      zcol <- cut(t(avgCoherence), nbcol)
      persp( R_0list,mlist, t(avgCoherence), theta = 30, phi = 30, expand = 0.5,
            col = color[zcol],ltheta = 120, shade = 0.75, ticktype = "detailed",
            xlab = "Basic Reproduction Number", ylab = "Mixing Parameter",
            zlab = "Probability of Coherence")
      dev.off()
    })
}

```

The following code calls `coherence3DPlot` to make a plot.

```

#Use the det soln if TRUE or adaptau sim if FALSE
DetOrAdap <- TRUE

#The value at which things are considered coherent
threshold <- 0.05
#threshold <- 0.15 #for adaptau higher tol needed

#Parameter values for grid
gridsizeR_0 <- 100
gridsizeM <- 100
nsample <- 10 #Number of runs per grid pt
mlist <- seq(0.0001, 0.15, (0.15-0)/(gridsizeM-1))
R_0list <- seq(1.1,30,(30-1.1)/(gridsizeR_0-1))

```

```

#Parameters
gamma <- 365/13 ##inverse of mean infectious period
mu <- 1/50 ##death and birth rate
alpha <- 0.1 ##strength of seasonal forcing
EC <- FALSE ##if true use equal coupling, if false use nearest neighbors

#Get data
data <- coherenceGrid(params=c(gamma=gamma,mu=mu,alpha=alpha,EC=EC),
                        R_Olist,mlist,nsample,DetOrAdap,population)
avgCoherence <- data$avgCoherence
#Plot
coherence3DPlot(avgCoherence,params=c(gamma=gamma,mu=mu,alpha=alpha,EC=EC),
                R_Olist,mlist,nsample,DetOrAdap,population=1)

data <- coherenceGrid(params=c(gamma=gamma,mu=mu,alpha=alpha,EC=TRUE),
                        R_Olist,mlist,nsample,DetOrAdap,population)
avgCoherence <- data$avgCoherence
coherence3DPlot(avgCoherence,params=c(gamma=gamma,mu=mu,alpha=alpha,EC=TRUE),
                R_Olist,mlist,nsample,DetOrAdap,population=1)

```

5.2 Four Panel Plot with Adaptive Tau

The function `fourPanPlot` makes a four panel plot showing the probability of coherence, the probability of local and global extinction, overtop of the bifurcation diagram of the single patch forced SIR model.

```

fourPanPlot <- function(avgCoherence,avgLE,avgGE,
                        params=c(gamma,mu,alpha,EC),R_Olist,mlist,
                        nsample,DetOrAdap,population){

  with(
    as.list(c(params)),
    {
      if(length(mlist)!=4){
        print("Warning: mlist should have length 4 for 4 panel plot
              \\ The first 4 elements of mlist will be used")
      }
    }

  #Save plot to pdf
  filename<-paste0("images/",if(DetOrAdap) "det" else "adap","4pan",
                  if(EC) "EC" else "NN",".pdf")
  pdf(file=filename)

  #Get bifur data for backgrounds
  bfd <- read.table("bifurcation.dat",
                   col.names=c("time","S","I","R0","log10S","log10I"))

  #Get max probs for y lim
  maxExt <- max(avgLE,avgGE)
  maxCoh <- max(avgCoherence)

  #To fit bifur data to probability plot
  bfdI <- maxExt*(1.1/max(bfd$I))*bfd$I

```

```

#leave room on outside margins for labels on righth, left and bottom
#par(mar = c(5,5,2,5))
par(oma=c(4,4,2,4))
#A four panel plot
par(mfrow=c(2,2))
par(mar = c(2, 3, 1, 2))
par(tcl = -0.25)
for(ind in 1:4){
  #Make an empty plot
  plot(0,0,xlim=c(1,30),
       ylim=c(0,maxExt*1.1),xlab=NA, ylab=NA,type='n')

  #Plot the bifur background
  points(bfd$R0,bfdI, pch=20, col="grey90", xpd=FALSE)
  #Plot LE, GE probs
  lines(R_Olist, avgLE[ind,],col=4)
  lines(R_Olist, avgGE[ind,],col=2)
  #Plot coherence prob overtop of current panel
  par(mfg = c(ceiling(ind/2),(ind-1)%2 +1))
  plot(R_Olist, avgCoherence[ind,],type='l',col=3,axes=F,xlab=NA,
       ylab=NA,ylim=c(0,maxCoh*1.1))
  axis(side=4)
  #Label m values on each plot
  mtext(paste0("m=",mlist[ind]), side = 3, line = -2, adj = 0.1,
       cex = 0.8, col = 1)
}

#Axes labels:
mtext("Basic Reproduction Number", side = 1, outer = TRUE, line = 1)

#Left axis label has multiple colors
mtext(expression("Probability of ")*phantom("Local/ Global Extinction")),
       side = 2, outer = TRUE, line = 1, col = 1)
mtext(expression(phantom("Probability of ")*"Local"*phantom("/ Global Extinction")),
       side = 2, outer = TRUE, line = 1, col = 4)
mtext(expression(phantom("Probability of Local")*"/"*phantom(" Global Extinction")),
       side = 2, outer = TRUE, line = 1, col = 1)
mtext(expression(phantom("Probability of Local/")*" Global"*phantom(" Extinction")),
       side = 2, outer = TRUE, line = 1, col = 2)
mtext(expression(phantom("Probability of Local/ Global")*" Extinction"),
       side = 2, outer = TRUE, line = 1, col = 1)

mtext("Probability of Coherence", side = 4, outer = TRUE, line = 1, col = 3)

dev.off()
}

```

Using fourPanPlot:

```

#The value at which things are considered coherent
threshold <- 0.15
#Parameter values for grid
gridsizeR_0 <- 200

```

```

gridsizeM <- 4
nsample <- 20
mlist <- c(0.2,0.45,0.7,0.9)
R_Olist <- seq(1.1,30,(30-1.1)/(gridsizeR_0-1))
DetOrAdap <- FALSE

#Parameters
gamma <- 365/13 ##inverse of mean infectious period
mu <- 1/50 ##death and birth rate
alpha <- 0.1 ##strength of seasonal forcing
n <- 10 ## Number of patches
EC <- FALSE ##if true use equal coupling, if false use nearest neighbors

population <- 250000

#Get data
data <- coherenceGrid(params=c(gamma=gamma,mu=mu,alpha=alpha,EC=EC),
                           R_Olist,mlist,nsample,DetOrAdap,population)
avgCoherence <- data$avgCoherence
avgLE <- data$avgLE
avgGE <- data$avgGE

#Plot
fourPanPlot(avgCoherence,avgLE,avgGE,
             params=c(gamma=gamma,mu=mu,alpha=alpha,EC=EC),
             R_Olist,mlist,nsample,DetOrAdap,population)

```

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