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**Mestrado:**

Epidemiologia Experimental Aplicada às Zoonoses, Faculdade de Medicina Veterinária e Zootecnia, USP.

Título da tese de mestrado:

“Modelagem da dinâmica de doenças infecciosas em redes de movimentação de animais”.

Orientador: Marcos Amaku.

Links Interessantes

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Meus Exercícios

Link para a página com os meus exercícios resolvidos [exec](#)

Proposta de Trabalho Final

Principal

Uma função que simula o espalhamento de uma doença em uma rede estática. Pode-se simular um modelo Suscetível-Infectado (SI) ou Suscetível-Infectado-Suscetível (SIS), dependendo dos parâmetros fornecidos pelo usuário.

Parâmetros da função:

- Matriz de adjacência (Matriz que representa como os nós estão conectados na rede) [M_adj]
- Vetor com o tempo que cada nó ficará infectado (Condição inicial) [tI]
- Probabilidade de um nó ser infectado por outro [pspread]
- Tempo mínimo de infecção [tImin]
- Tempo máximo de infecção [tImax]
- Tempo de simulação [tSim]

Retorna uma matriz onde cada coluna representa os nós que estavam infectados no tempo $t(x)$, $x=1, \dots$.

Aplicações dos resultados:

- Cálculo da prevalência num dado momento $t(x)$
- Número de vezes que um certo nó foi infectado durante a simulação

OBS.: Apesar de descrito como espalhamento de doenças (AIDS, Vírus de Computador, etc), a função também pode ser usada em outras áreas, como por exemplo, para simular o espalhamento de idéias

em redes sociais. Utilizando-se da interpretação do pesquisador.

Comentários da Proposta Principal

Legal, é generalizável. Você pode plotar seu output num gráfico para observar o espalhamento também. Parece factível no prazo.

Gabriel

Comentários do autor sobre a versão final

Acabo de postar a versão final de minha função.

Nela, eu tentei colocar um pouco de cada conceito visto nas aulas da disciplina(desde funções pré-prontas até programação mais bruta).

E atendendo ao comentário do Gabriel eu incluí umas opções mais gráficas. Que poderiam muito bem ser funções separadas da função final. Deu um pouco de trabalho, mas tudo bem, digamos que foi uma promoção pague 1 função e leve 3 hehehe.

Raul

Página de Ajuda

simulationSIS

package:bie5782_2011

R Documentation

Simulates the spread of diseases on a static directed network

Description:

Simulates the spread of diseases on a static directed network, returning the simulation matrix for user analysis.

Optionally, the function returns some analysis of the simulation and an animation representing step by step the simulation of the spread on the network, for a more visual analysis.

Usage:

simulationSIS (M_adj, tI, psread, tImin, tImax, tSim, analysis=TRUE, animation=TRUE)

Arguments:

M_adj: A numeric matrix. Adjacency matrix which represents the network. Where $M_adj(i,j)=1$ if there is a connection between two nodes, or 0 with no connection exists.
tI: A numeric vector. Vector of the initial 'infected' nodes.

Where each position represents the t times steps that a node will be 'infected' from the beginning of the simulation.

pspread: Numeric value ($0 \leq \text{pspread} \leq 1$). The probability that a node will get 'infected'.

tImin: Numeric value ($0 \leq \text{tImin} \leq \text{tImax}$). The minimum time that a new 'infected' node will be in this state.

tImax: Numeric value ($0 \leq \text{tImin} \leq \text{tImax}$). The maximum time that a new 'infected' node will be in this state.

tSim: Numeric value ($\text{tSim} \geq 1$). The t time steps to simulate.

analysis: Logical. If TRUE, shows the network and the prevalence; also returns a list with the simulation matrix, the proportion of 'infected' at each time step t , total time that each node was 'infected', nodes that most stayed 'infected', nodes that least stayed 'infected'.

Requires the igraph package.

animation: Logical. If TRUE, opens the web-browser and shows the simulation of spread on the network. Requires the animation and igraph packages.

Details:

Although described as a function to simulate the spread of a disease on a network, its usage can be expanded to other areas like social analysis when one would be interested in how an idea spread on a social network.

The function requires that the user inputs the network where the simulation will be done.

The initial state of each node (in time steps of the 'infected' state).

The probability of a node becoming 'infected'. Used in the expression:

$$\text{prob_i} = 1 - (1 - \text{pspread})^{(\text{Number of 'infected' nodes connected to node } i)}$$

The range of the 'infected' state, expressed in time steps [tImin , tImax]

The number of times steps to simulate.

If the option `analysis=TRUE`, the function automatically return some analysis that might interest the user.

If the option `animation=TRUE`, the function generates an animation of the simulation for visual inspection. (See `Warning[*]`)

Value:

By default, the function returns:

M_Sim: Simulation matrix where each entrie represents for how long will a node be 'infected', at a time step t .

If `analysis=TRUE`, returns a list with:

M_Sim: See above.

proportion_tT (vector): Proportion of 'infected' nodes at a time step t .

total_tI (vector): Sum of the total time that each node was in

the 'infected' state.

 max_total_tI (vector): Nodes that stayed the most at the 'infected' state.

 min_total_tI (vector): Nodes that stayed the least at the 'infected' state.

 and prints on screen the network representation and a graphic with the proportion of 'infected' nodes at each time step simulated.

Warning:

 This function supposes that you have the animation and the igraph packages installed.

 Also it considers the input adjacency matrix as a representation of a directed network, what shouldn't be a problem if your input represents an undirected one.

 This function was developed disconsidering autoloops and multiple edges in the network. So, check your network before using this function on it.

 [*] If animation=TRUE, after each simulation it is strongly recommended that the user cleans his actual working directory, so that no previous simulation results disturbs the next ones. Also it is recommended deactivating the animation option for long times of simulation (tSim>100) which will decrease the processing time.

Author(s):

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References:

 Ossada, R.; Amaku, M.; Grisi-Filho J.H.H.; Ferreira, F. - Modelagem da dinâmica de doenças infecciosas em redes complexas - Resumos do XXXIII CNMAC, 2010. p.39

<http://ecologia.ib.usp.br/bie5782/doku.php>

<http://www.leb.fmvz.usp.br/>

Example:

```
# Defining the arguments/parameters.  
M_adj = matrix(data=c(0,1,0,0,0, 0,0,0,0,1, 1,0,0,0,0, 0,1,0,0,1,  
1,0,0,0,0), nrow=5, ncol=5);  
tI = c(0, 5, 0, 0, 2);  
pspread = 1;  
tImin = 1;  
tImax = 10;  
tSim = 10;  
analysis=TRUE;  
animation=TRUE;  
# Executing the simulation.
```

```
TEST = simulationSIS (M_adj, tI, psread, tImin, tImax, tSim,  
analysis=TRUE, animation=TRUE);  
TEST;
```

Código da Função

```
simulationSIS <- function(M_adj, tI, psread, tImin, tImax, tSim,  
analysis=TRUE, animation=TRUE)  
{  
  # Load the packages igraph and animation  
  library(igraph);  
  library(animation);  
  
  # Builds the simulation matrix where each row represents a node and  
  # each column represents a time step of the simulation  
  M_Sim = matrix(data=NA, nrow=nrow(M_adj), ncol=(tSim+1) );  
  
  # For each time step...  
  for( i in 1:tSim )  
  {  
    # ... assembles the tI vector to the corresponding column of  
    # the simulation matrix  
    M_Sim[,i] = tI;  
  
    # Identify the nodes that are at the 'infected' and  
    # 'susceptible' state  
    I = as.numeric(tI>0);  
    S = as.numeric(!I);  
  
    # Multiply the 'infected' vector by the adjacency matrix,  
    # generating the potential infection vector  
    Pvector = I %*% M_adj;  
  
    # Vector with the probability of each node getting infected  
    Pnode = 1 - (1-psread)^Pvector;  
    # Generating a vector with random numbers based on a uniform  
    # distribution [0,1]  
    Prand = runif(n=length(M_adj[1,]), min=0, max=1);  
  
    # If Prand(i) <= Pnode(i), the node becomes 'infected'  
    Pinfection = as.numeric(Prand<=Pnode);  
  
    # Creating the new 'infected' vector: S=(0,1) AND  
    Pinfection=(0,1)  
    Inew = as.numeric(S & Pinfection);  
  
    # Update the 'tI vector' decreasing 1 for each element in  
    # it, denoting the passage of 1 time step  
    temp_tI = tI-1;
```

```
# Check if any node got a negative time duration and if that
happened turn it back to zero
tInew = as.numeric(temp_tI<0) + temp_tI;

# Give a random duration to the new infected nodes
aux_tI = rep( 0, length(Inew) );
# Check which model is been simulated (SIS or SI)
if( tImin != tImax )
{
    aux_tI[ Inew>0 ] = sample(x=(tImin:tImax), size=length(
which(Inew!=0) ), replace=TRUE);
}
else
{
    aux_tI[ Inew>0 ] = rep(x=tImax, times=length( which(Inew!=0) )
);

}

# Merge the new infected nodes with the new ones
tI = tInew + aux_tI; tI
}

# Inputs the results of the last time step of the simulation, in the
simulation matrix
M_Sim[,i+1] = tI;

# Assigns the simulation matrix to the variable to be returned, case
no options were selected
answer = M_Sim;

# If any optional was selected, make the preparations
if(animation==TRUE || analysis==TRUE)
{
    # Name the rows and columns of the adjacency matrix
    rownames(M_adj) = 1:nrow(M_adj)
    colnames(M_adj) = 1:ncol(M_adj)
    # Transforms the adjacency matrix into an igraph network
object
    igraph_network = graph.adjacency(M_adj);
    # Generates coordinates for plotting the network
    coordinates = layout.kamada.kawai(igraph_network);
    # Makes a matrix where each non-zero position of the
simulation matrix is equal to 1 and 0 otherwise.
    M_Result = matrix(data=as.numeric(M_Sim>0), nrow=nrow(M_Sim),
ncol=ncol(M_Sim) );
}
if(animation==TRUE)
{
    # Plot the network, for visual inspection of the user
    plot( x=igraph_network, layout=coordinates, vertex.size=10,
vertex.label=rownames(M_adj), edge.arrow.size=0.6, main="Network Plot" )
}
```

```

        # Calculates the proportion of 'infected' nodes at each time
step
    infected_tT = apply(X=M_Result, MARGIN=2, FUN=sum);
    proportion_tT = infected_tT/nrow(M_Sim);
    # Opens a new device and plots the proportion of the
'infected' nodes at each time step
    x11();
    plot(proportion_tT, pch=16, cex=0.5, xlab="Time (t)",
ylab="Proportion", main="Proportion x Time" );
    lines(x=1:(tSim+1), y=proportion_tT);

    # Calculates for how long each node stayed 'infected'
    total_tI = apply(X=M_Result, MARGIN=1, FUN=sum);
    # Gets the nodes that stayed 'infected' longer and less
    max_total_tI = which(total_tI==max(total_tI));
    min_total_tI = which(total_tI==min(total_tI));

    # Assigns the previous results on a list
    analysis_list = list( M_Sim, proportion_tT, total_tI, max_total_tI,
min_total_tI );
    names(analysis_list) = c( "Simulation Matrix", "Proportion of
'infected' at time(t)", "Total time that each node got 'infected'", "Nodes
that most stayed 'infected'", "Nodes that least stayed 'infected'" );

    # Assigns the list to be returned to the user
    answer = analysis_list;
}

if(animation==TRUE)
{
    # Assigns the colors to be used on the animation 2-
red=infected, 3-green=susceptible
    M_Sim_color = -1 * M_Result + 3;

    # Save the images for the animation on a web-browser
    saveHTML(
    {
        # Plot the network simulations
        for( i in 1:(tSim+1))
        {
            plot( x=igraph_network, layout=coordinates, vertex.size=10,
vertex.label=rownames(M_adj), vertex.color=M_Sim_color[,i],
edge.arrow.size=0.6, main="Animation of the spread on the network" )
            ani.pause();
        }

    }, ani.width=800, ani.height=800, outdir=getwd(),
imgdir="network_dir", img.name="network_plot",
htmlfile="network_animation.html", title="Animation of the spread on the
network", verbose=FALSE, autobrowse=TRUE, autoplay=FALSE );
}

```

```
# Return the answer asked by the user  
return( answer );  
}
```

Arquivo da Função

[simulationSIS.r](#)

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