

# Part II

**CENTER FOR ANIMAL DISEASE MODELING AND SURVEILLANCE (CADMS),  
SCHOOL OF VETERINARY MEDICINE, UC DAVIS**

**Jose Pablo Gomez, Jerome Baron, Jose Manuel Diaz Cao  
Beatriz Martinez Lopez**

Center for Animal Disease Modeling and Surveillance (CADMS)

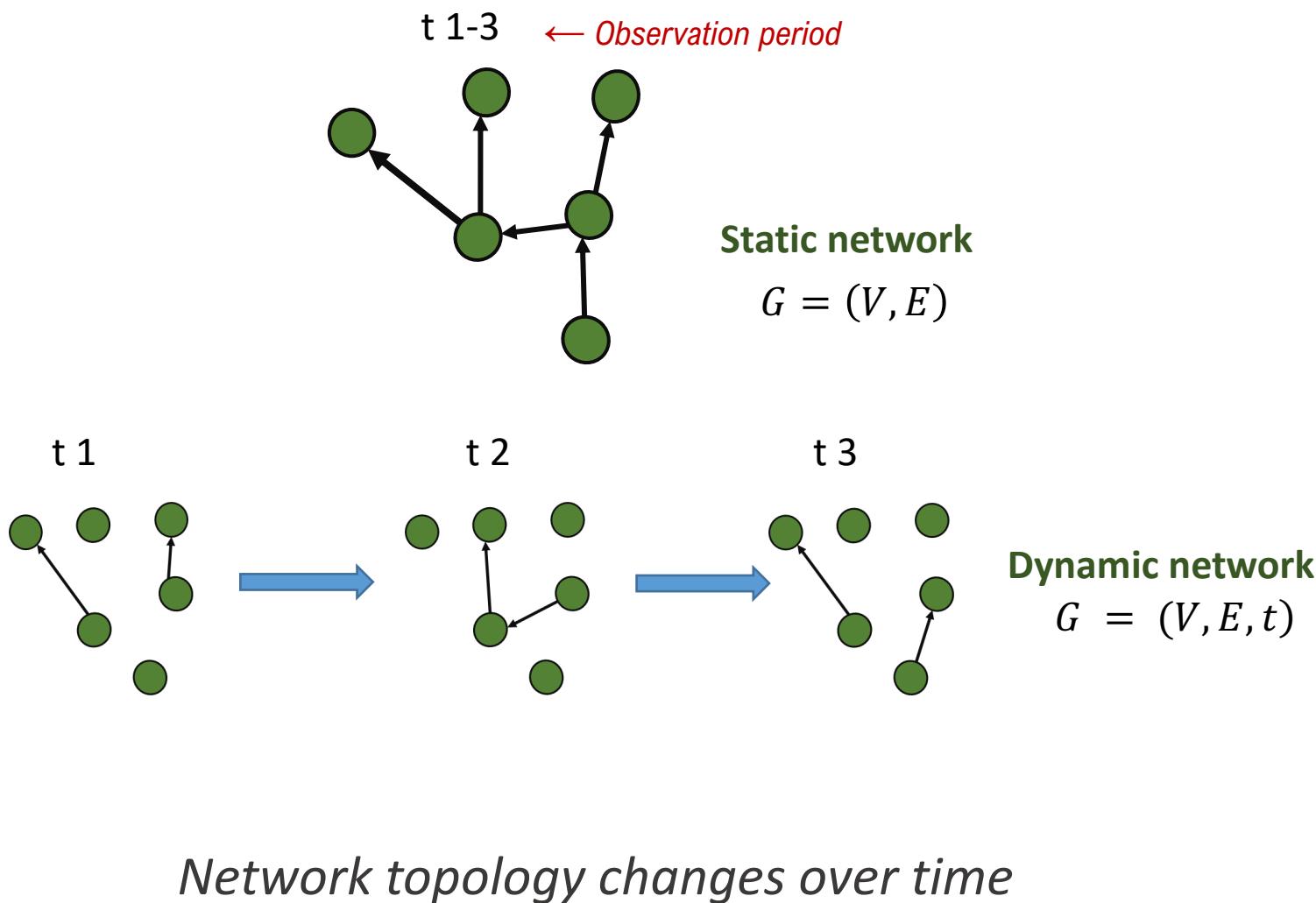
Department of Medicine & Epidemiology  
School of Veterinary Medicine  
University of California, Davis  
\* Contact: [jpgo@ucdavis.edu](mailto:jpgo@ucdavis.edu)

**<https://cadms.vetmed.ucdavis.edu>**

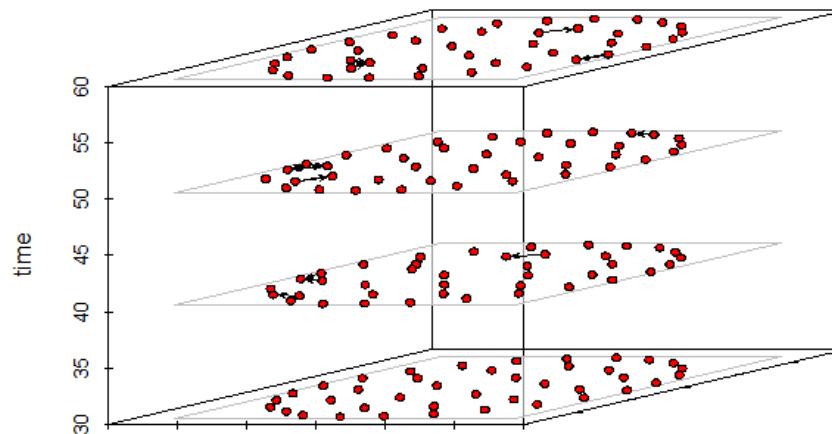
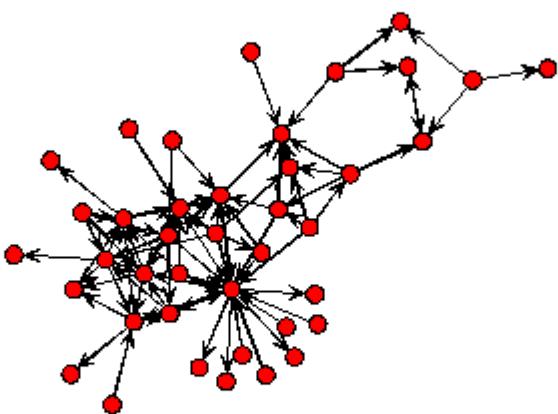
# Outline

- Static vs Dynamic network analysis
- Dynamic network statistics
- Considerations and limitations

# What's the difference between Static and Dynamic analysis?



# Why dynamic networks?

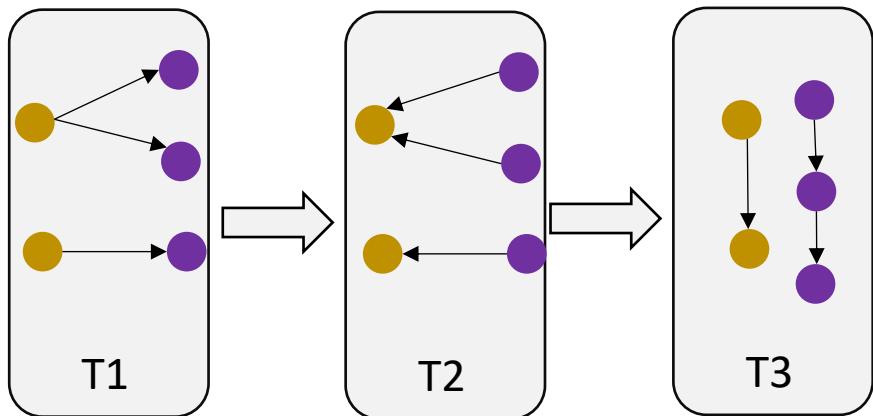


# Why is interesting in epidemiology?

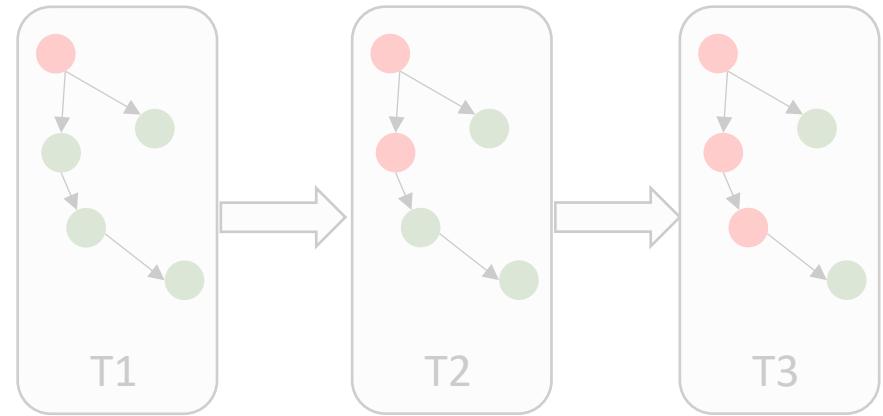
- Contact patterns are usually influenced by extrinsic events (weather conditions, demand, production cycles, etc..)
- Disease transmission has a linear process.
- A static network will always contain edges that were not necessarily present at the time when a transmission event occurred, which could be important for estimating the transmission rates.

# Network dynamics in epidemiology

## Changes on the structure



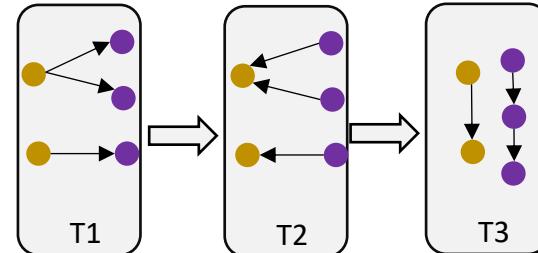
Study disease transmission



# DNA for Changes in the network structure

## Understanding the evolution of the network over time:

As the environment changes, so does the social behavior of individuals.



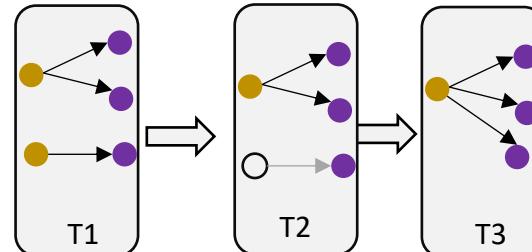
## Understanding how changes in the environment impact the network structure:

Environmental changes such as drought, fires, floods, etc. can have an impact on the way individuals interact.



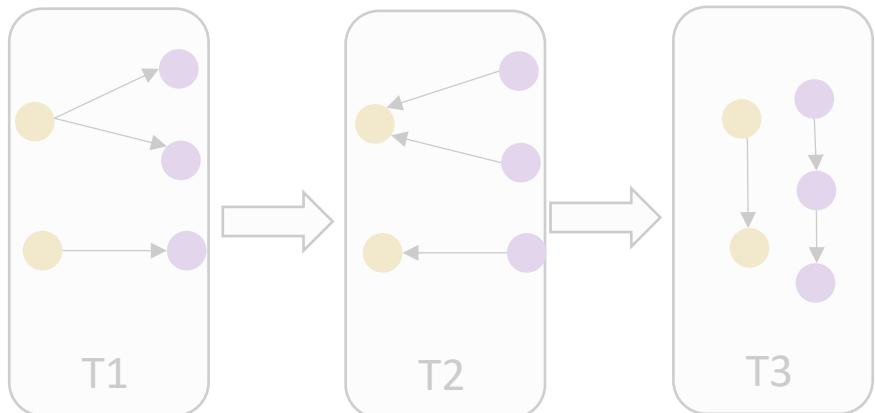
## Understanding how changes in individual traits impact the network structure:

Presence or absence of particular individuals can impact the structure of interactions.

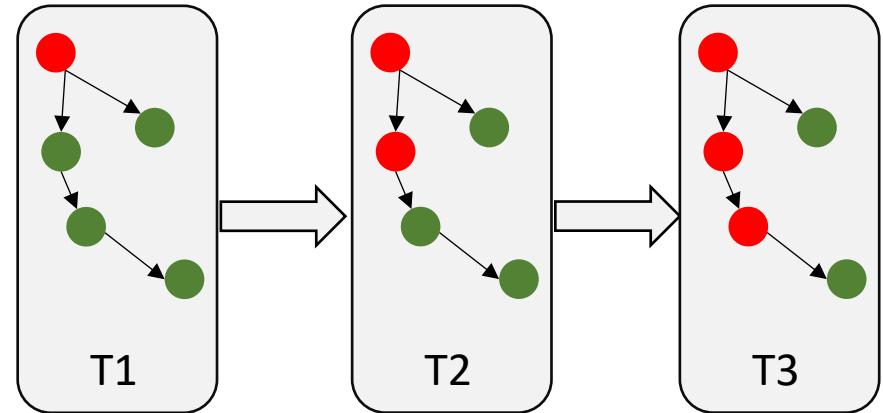


# Network dynamics in epidemiology

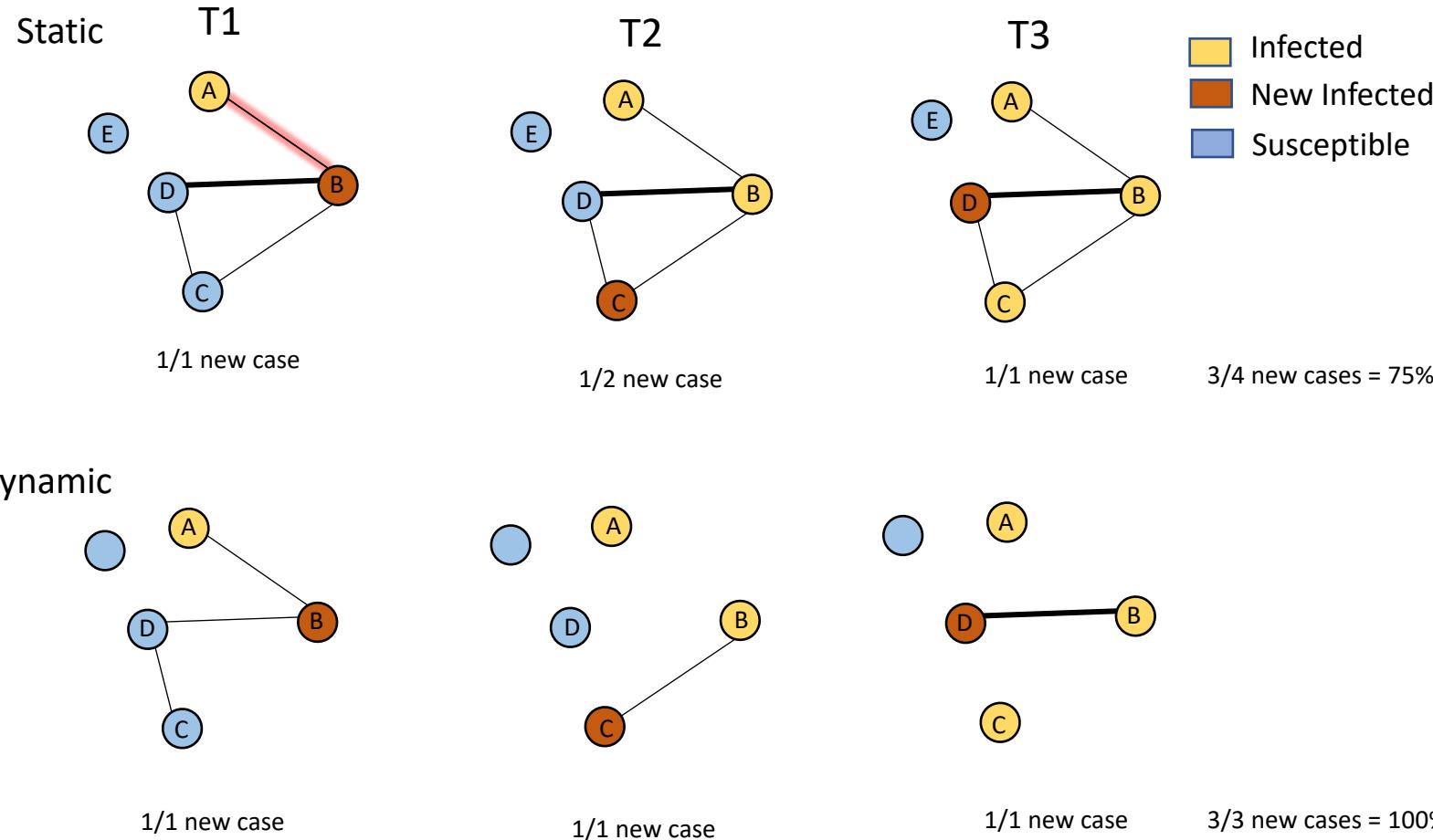
Changes in the structure



Disease transmission



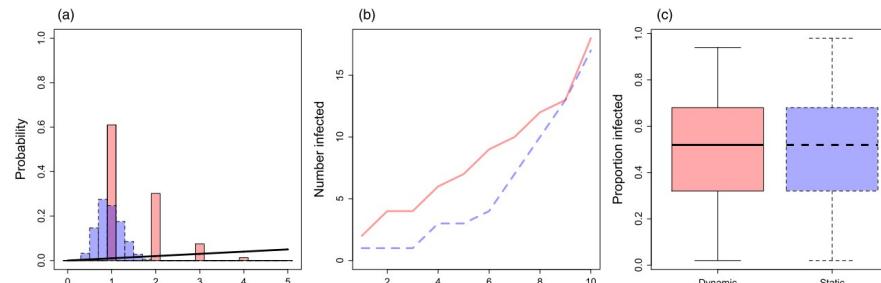
# Understand an observed epidemic



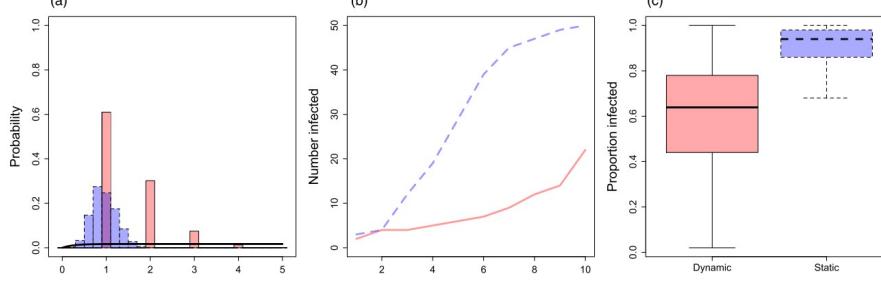
# Making general predictions

- A well designed study that uses DN at a **temporal scale that matches the epidemic transmission profile** will generate the most accurate conclusions.

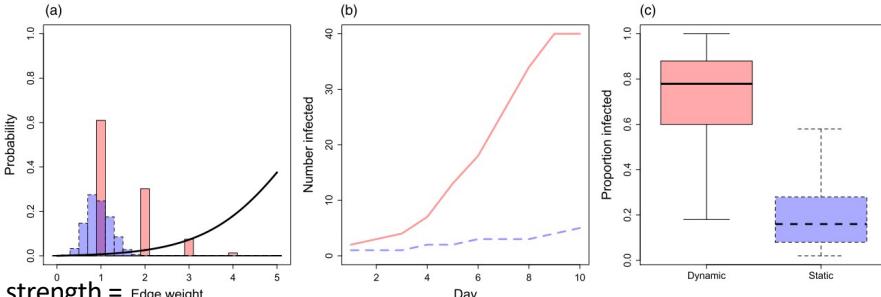
Linear function



Decelerating function



Accelerating function



Transmission rate x Contact strength = Edge weight

# Making general predictions

- When the goal of modelling is to make general predictions such as the epidemic size rather than the pathway it takes, SN is often a better representation of the average population

*Is the observed dynamic network likely to re-occur?*

*Same order of contacts?*

*Same period of time between contacts?*

# Other things to consider

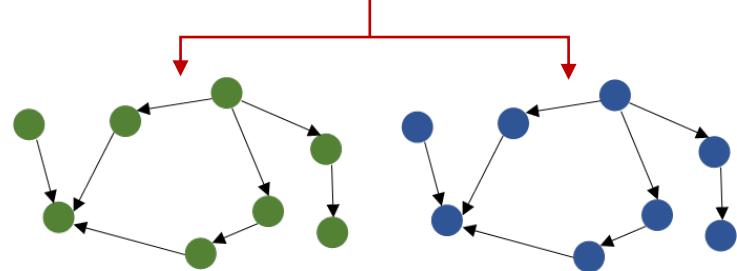
- Is there enough data available to construct each of the temporal snapshots of the network?
- Equal sampling efforts during the study period?

# Dynamic Network Statistics

# How do we know if a network is likely to re-occur?

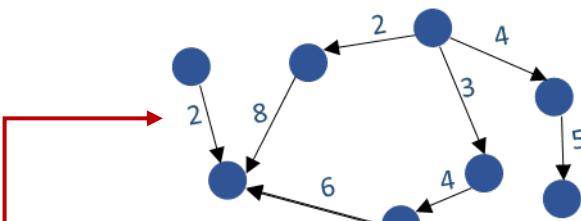
## Network isomorphism

Same adjacency structure

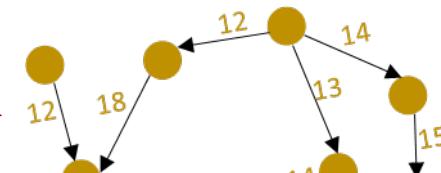


Identify patterns

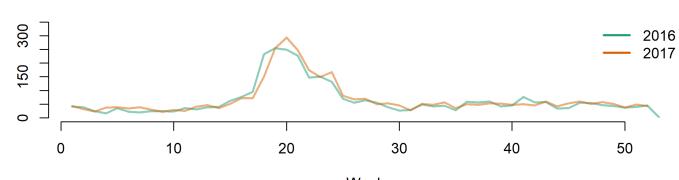
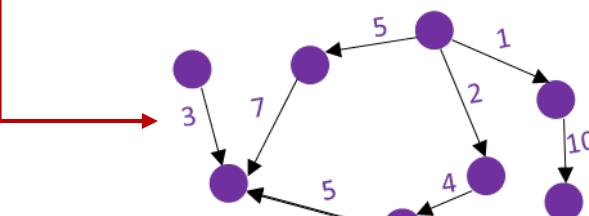
Strictly isomorphic



Temporally isomorphic

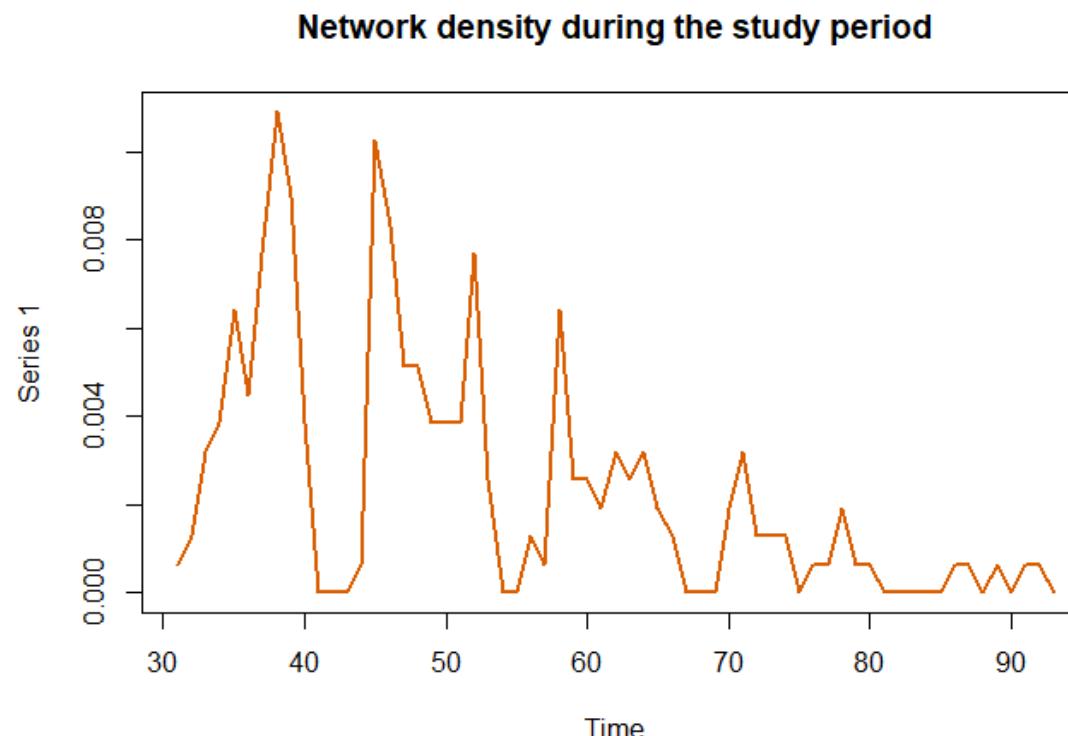


Temporal order isomorphic



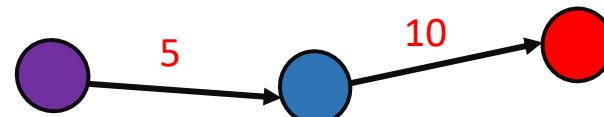
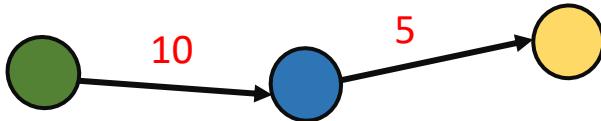
# Why Dynamic network analysis?

- Centrality measures and network statistics used in static networks can be adapted for dynamic network analysis.



# Temporally reachable sets

## Temporally reachable sets



The temporally reachable set of a node, represents the set of other nodes that can be reached following a temporal path.

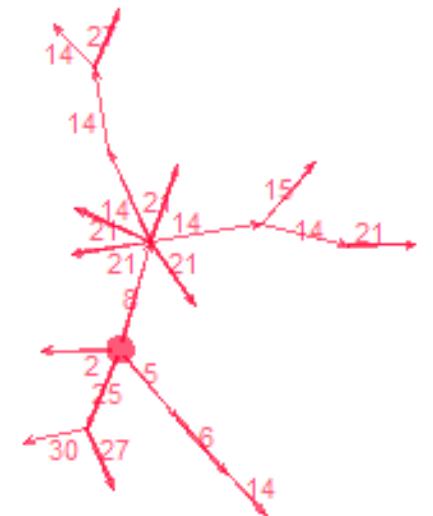
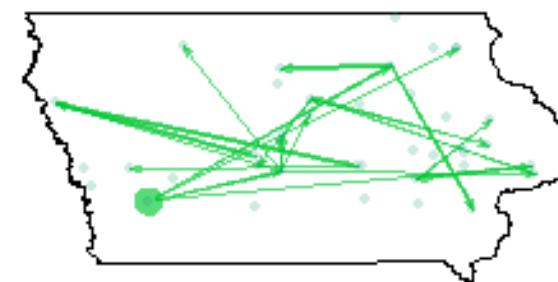
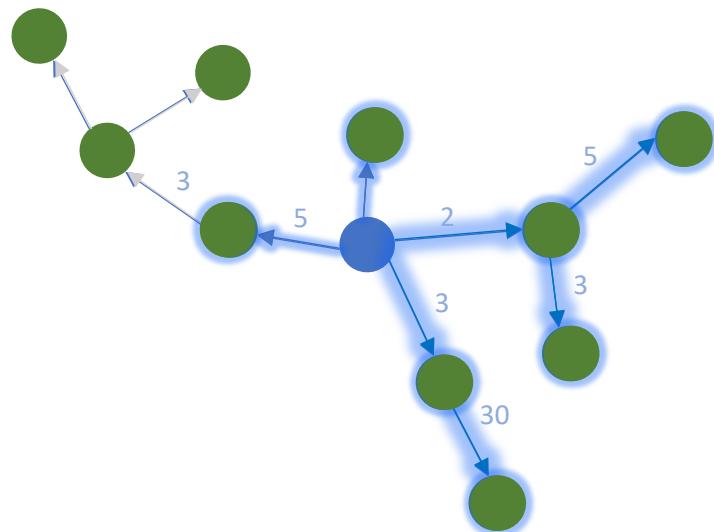
# Temporally reachable sets

$e_1 = (i, j, t_1, \delta t_1)$  Event 1

$e_2 = (j, k, t_2, \delta t_2)$  Event 2

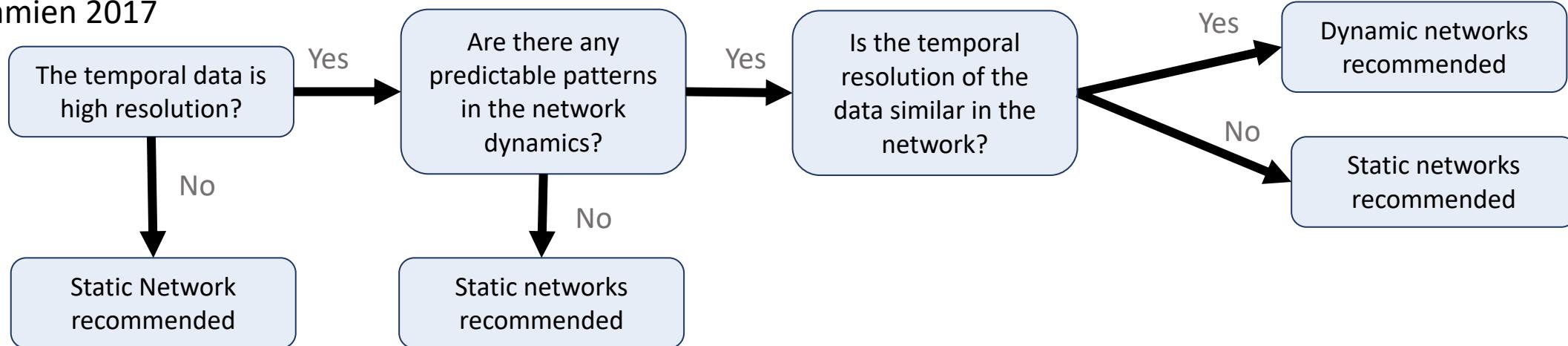
$i \rightarrow j \rightarrow k$  If  $t_2 > t_1 + \delta t_1$

## Reachability of Farm 23



# Recap

Damien 2017



# Limitations

- Time resolution will have an impact on our analysis
- When using dynamic network analysis for modeling or prediction we have to consider how likely is that the observed network will happen again.
- Implementing DN adds complexity to the model, can reduce generality and overinflate the perceived quality of predictions.

# Questions?

# Time for Lab 4!

CADMS

Home

Pre Workshop ▾

Contact ▾

## 1 Introduction to dynamic networks

2 Temporal statistics

3 Plotting the network

4 Temporally reachable sets

5 Animations

## Lab 4

These are the libraries that we will use in this lab:

```
# install.packages("igraph")
# install.packages("maps")
# install.packages("raster")
# install.packages("rgdal")
# install.packages("ggplot2")
# devtools::install_github("GIScience/openrouteservice-r")
# install.packages("sp")
# install.packages("maptools")
# install.packages("spacetime")
# install.packages("plotKML")
# install.packages("scatterplot3d")
```

Let's start by importing the data for edges, node attributes, and the shapefile of the area of study.

We will now use the `graph.data.frame` function to create a directed network.

```
library(igraph)
g1 <- graph.data.frame(net, directed = T)
```

As we have seen earlier, we can add network attributes for both vertices `v()` or edges `E()`. In the next section we will add some attributes related with the location of farms and farm type.

```
# We match the identifiers in the network with the data table
poss<-match(V(g1)$name,node_attrib$idch)
# Add the attributes to the network
V(g1)$lat <- node_attrib$lat[poss]
V(g1)$long <- node_attrib$long[poss]
V(g1)$type <- as.character(node_attrib$farm_type[poss])
V(g1)$fullname <- as.character(node_attrib$name[poss])
# check the correct assignation of the attributes in the object

summary(g1)
```

# Further applications

**CENTER FOR ANIMAL DISEASE MODELING AND SURVEILLANCE (CADMS),  
SCHOOL OF VETERINARY MEDICINE, UC DAVIS**

**Jose Pablo Gomez\*, Jerome Baron,  
Beatriz Martinez-Lopez**

Center for Animal Disease Modeling and Surveillance (CADMS)  
Department of Medicine & Epidemiology  
School of Veterinary Medicine  
University of California, Davis

\* Presenter: Email: [jpdo@ucdavis.edu](mailto:jpdo@ucdavis.edu)  
<https://cadms.vetmed.ucdavis.edu>

# Outline

- Statistical Models
- Simulation Models

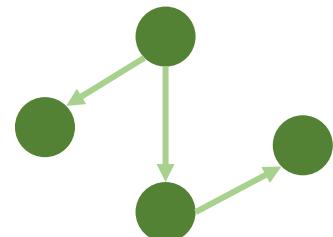
# Network Analysis and Regression

## Regression assumptions:

- Linearity
- Independence
- Normality
- Equal variance

 *i.i.d.*

*SNA recognize the influence of community members on each other.*



## Multilevel Logistic Regression for Repeated measures

$$y_{ij} \sim \text{Binomial}(n_{ij}, \pi_{ij})$$

$$\text{logit}(\pi_{ij}) = \beta_{0j} + \beta_1 X_{1ij} + \beta_2 X_{2ij} \cdots \beta_n X_{nij} + \mu_j$$

$y_{ij}$ : Occurrence of the event  $i$  at time  $j$

$\pi_{ij}$ : Expected probability of PRRS occurrence

$\beta_{0j}$ : The intercept

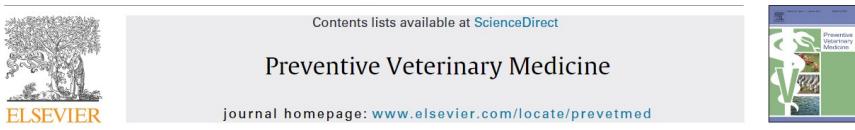
$\beta_1, \beta_2, \dots, \beta_n$ : The slopes

$\mu_j$ : The random effect



Evaluation of the impact of live pig trade network, vaccination coverage and socio-economic factors in the classical swine fever eradication program in Peru

J.P. Gómez-Vázquez<sup>a</sup>, M. Quevedo-Valle<sup>b</sup>,  
<sup>a</sup>Center for Animal Disease Modeling and Surveillance (CADMS), Department of Animal Sciences, University of California, Davis, CA, USA  
<sup>b</sup>Dirección de Sanidad Animal SENASA, Lima, Peru



Unraveling the contact patterns and network structure of pig shipments in the United States and its association with porcine reproductive and respiratory syndrome virus (PRRSV) outbreaks

Kyuyoung Lee<sup>a,\*</sup>, Dale Polson<sup>b</sup>, Erin Lowe<sup>b</sup>, Rodger Main<sup>c</sup>, Derald Holtkamp<sup>c</sup>, Beatriz Martínez-López<sup>a</sup>

<sup>a</sup>Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, CA, USA

<sup>b</sup>Boehringer - Ingelheim Vetmedica, Inc., St. Joseph, MO, USA

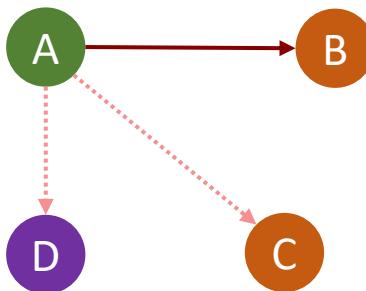
<sup>c</sup>Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA



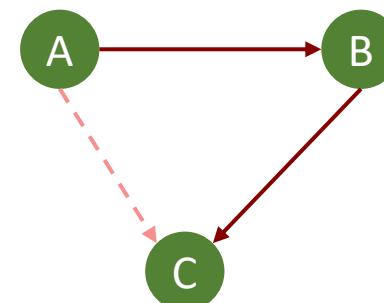
# ERGMs

- **Exponential Random Graph Models:** Predicting dichotomous ties.  
What is the probability of observing our network?
- Evaluate a cross sectional structure

**Individual covariates:** are sow farms more likely to contact GDUs?



**Network structure:** If Farm A contacts Farm B, and Farm B contacts Farm A, what are the chances of farm A contacting Farm B? (Triangles formations)



# Exponential Random Graph Models

```
## =====
## Summary of model fit
## =====
## Formula: n ~ edges + mutual
## Iterations: 2 out of 20
##
## Monte Carlo MLE Results:
##   Estimate Std. Error MCMC % p-value
## edges -1.7634    0.2047    0 <1e-04 ***
## mutual  2.3290    0.4154    0 <1e-04 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Null Deviance: 424.2 on 306 degrees of freedom
## Residual Deviance: 332.3 on 304 degrees of freedom
##
## AIC: 336.3    BIC: 343.7 (Smaller is better.)
```

$$P(Y_{ij} = 1 | y_{ij}^c) = \ln \frac{P(Y = 1 | y_{ij}^c)}{P(Y = 0 | y_{ij}^c)} = \theta' \delta(g(y))_{ij}$$

$Y_{ij}$  is the random variable for the state of the actor pair i,j

$y_{ij}^c$  Is the compliment for  $y_{ij}$  (All the dyads in the network other than  $y_{ij}$ )

$\delta(g(y))_{ij}$  equals  $g(y_{ij}^+) - g(y_{ij}^-)$ , where:

$g(y_{ij}^+)$  is defined as  $y_{ij}^c$  along with  $y_{ij}$  set to 1

$g(y_{ij}^-)$  is defined as  $y_{ij}^c$  along with  $y_{ij}$  set to 0

$g(y)$  is the statistic of the model and  $\delta(g(y))$  the change statistics for actor pair  $y_{ij}$

## RESEARCH ARTICLE

### Modeling the live-pig trade network in Georgia: Implications for disease prevention and control

Esther Andrea Kukielka<sup>1\*</sup>, Beatriz Martínez-López<sup>1</sup>, Daniel Beltrán-Alcrudo<sup>2</sup>

<sup>1</sup> Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine & Epidemiology, School of Veterinary Medicine, University of California, Davis, California, United States of America, <sup>2</sup> Food and Agriculture Organization, FAO Budapest, Hungary

\* These authors contributed equally to this work.

\* [ekukielka@ucdavis.edu](mailto:ekukielka@ucdavis.edu)

## Transboundary and Emerging Diseases



## ORIGINAL ARTICLE

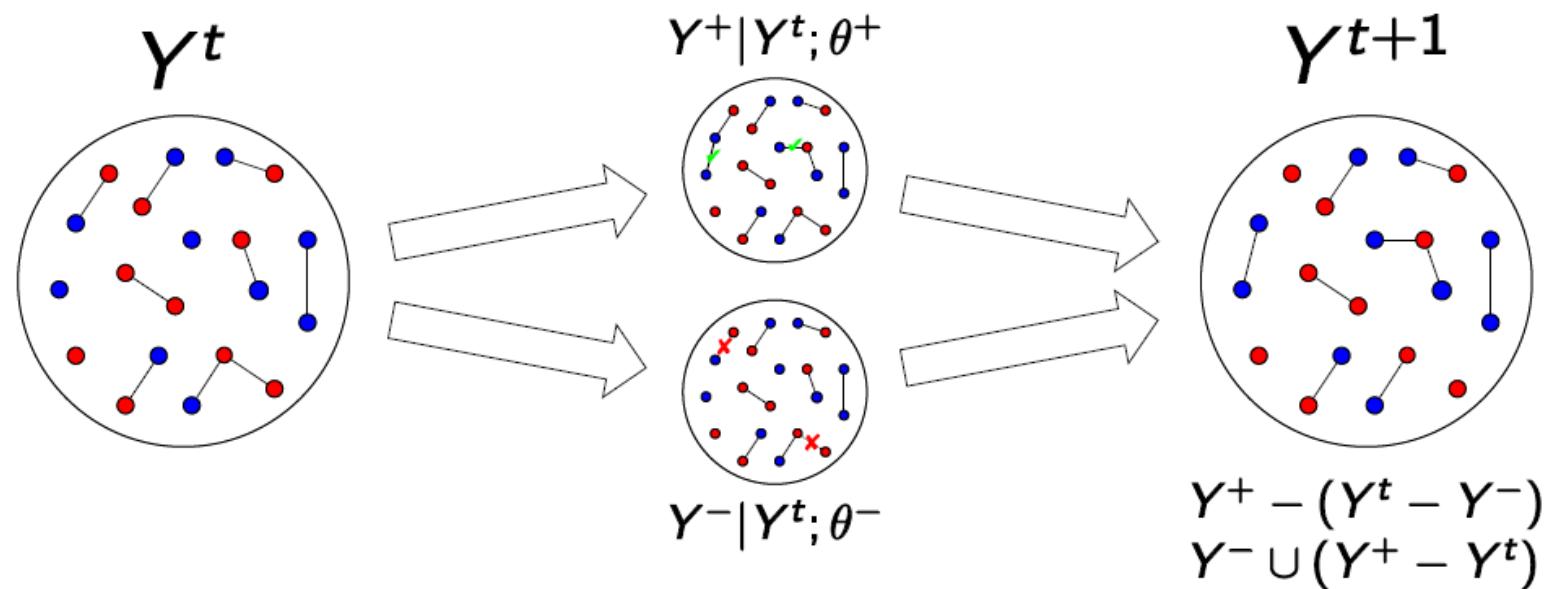
### Application of exponential random graph models to determine nomadic herders' movements in Senegal

Jaber Belkhiria✉, Modou Moustapha Lo, Fafa Sow, Beatriz Martínez-López, Veronique Chevalier

First published: 08 April 2019 | <https://doi.org/10.1111/tbed.13198> | Cited by: 1

# STERGMs

## Separable Temporal ERGM

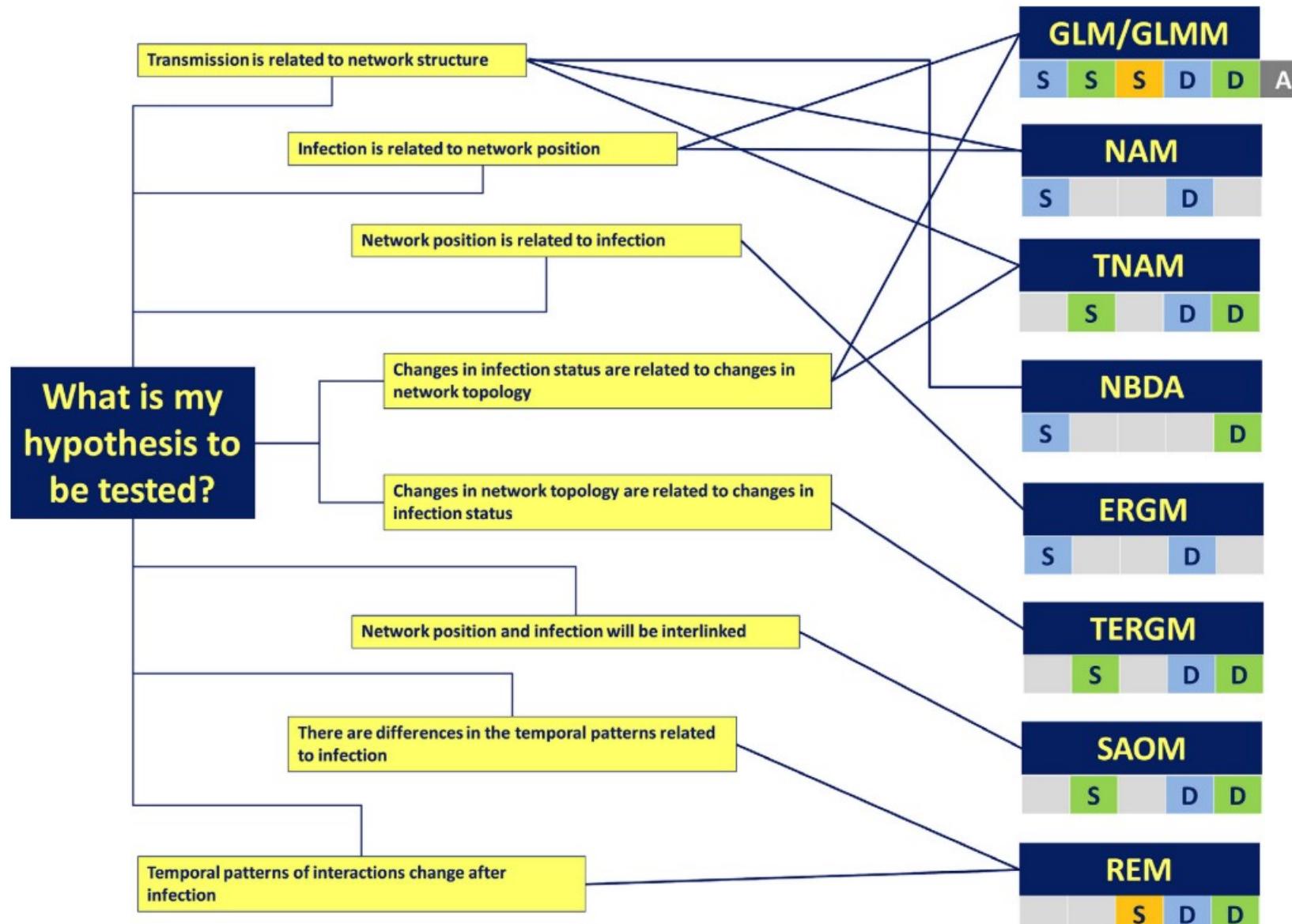


$Y^+$  = network in the formation process after evolution

$Y^-$  = network in the dissolution process after evolution

This is the origin of the “S” in STERGM

# Statistical Models in Network Analysis



**GLM** Generalized linear model  
**GLMM** Generalized linear mixed model  
**NAM** Network autocorrelated model  
**TNAM** temporal autocorrelated model  
**ERGM** exponential random graph model  
**NBDA** Network based diffusion analysis  
**SAOM** stochastic actor-oriented model  
**TERGM** Temporal ERGM  
**REM** Relational events model

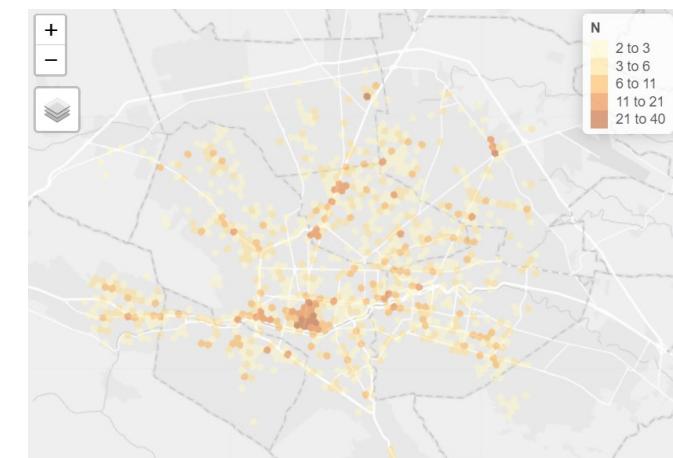
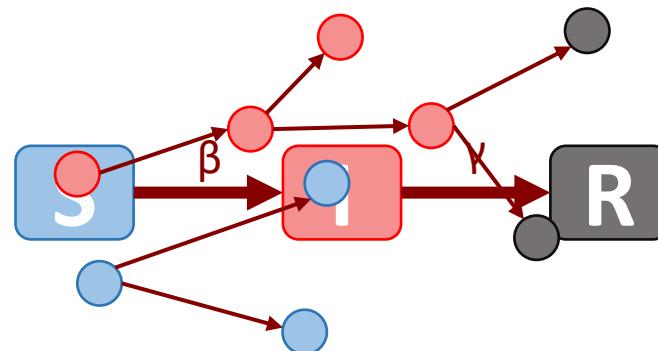
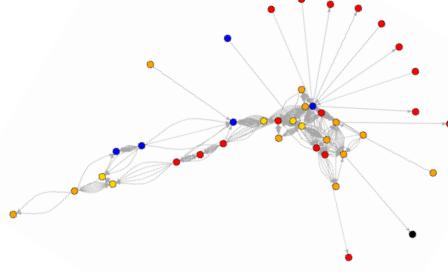
Network data	
S	Static network
S	Temporal snapshots/aggregations
S	Temporally-explicit interaction data
A	Association-based data

**What data am I using?**

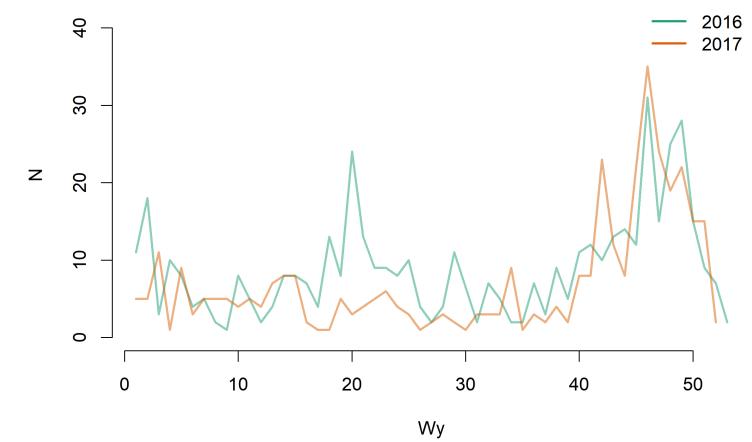
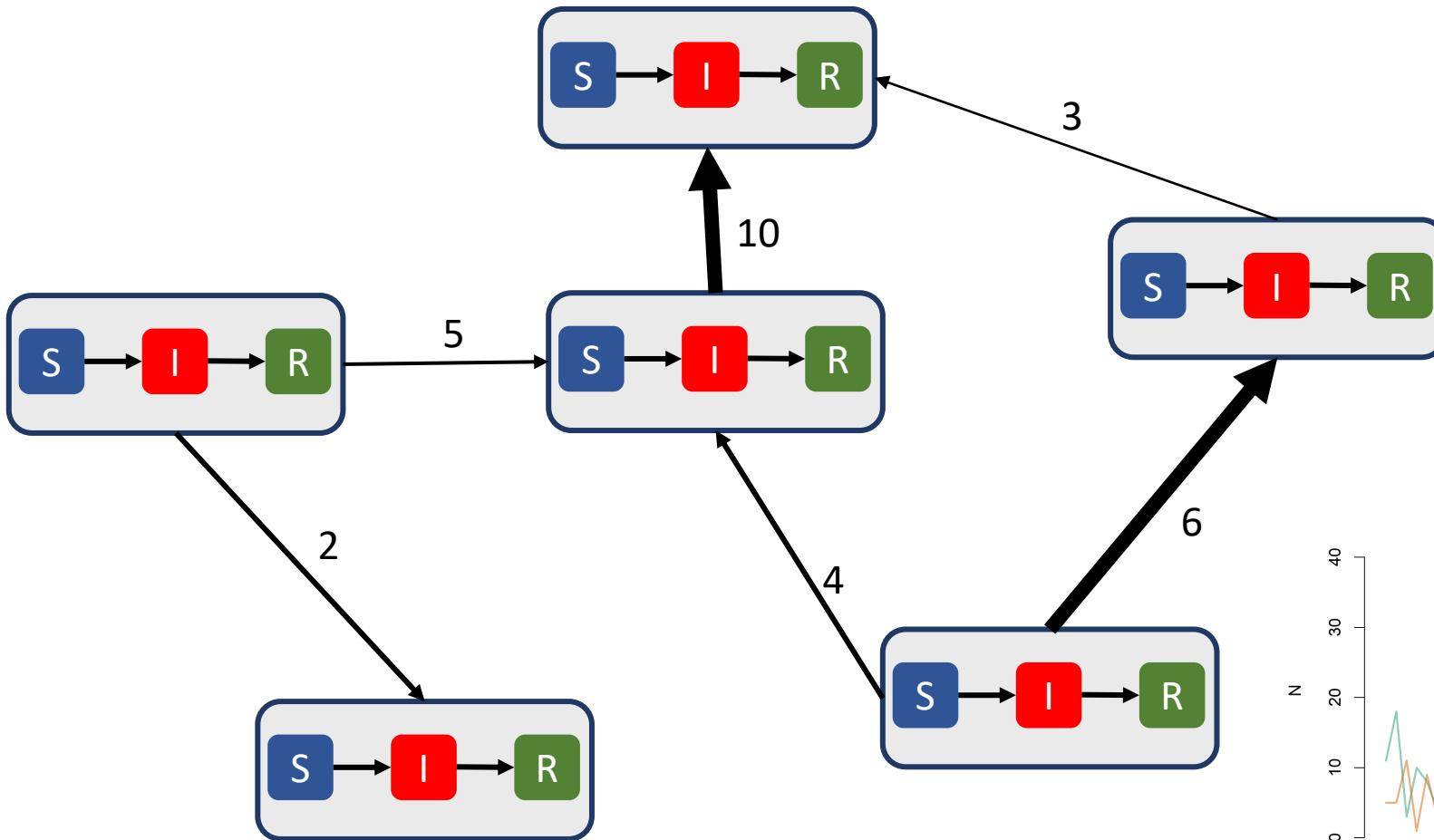
Disease data	
D	Presence/absence or infection load
D	Timing of changes in infection known

# Disease spread models

- Most epidemic models incorporate homogenous mixing assumption (Law of mass action).
- This for some scenarios this assumption is unrealistic but simplifies the mathematical computation of the model.
- Populations are not homogenously mixed, population structure can arise from spatial and social interactions.



# Disease spread models



# Disease spread models

- Using R:

- Statnet
- siminf

Network analyses of transhumance movements and simulations of foot-and-mouth disease virus transmission among mobile livestock in Cameroon

Laura W. Pomeroy<sup>\*,1</sup>, Mark Moritz<sup>2</sup>, Rebecca Garabed<sup>3</sup>

<sup>1</sup> Division of Environmental Health Sciences, College of Public Health, The Ohio State University, Columbus, OH, USA

<sup>2</sup> Department of Anthropology, The Ohio State University, Columbus, OH, USA

<sup>3</sup> Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA

\* corresponding author: pomeroy.26@osu.edu



ORIGINAL RESEARCH  
published: 19 March 2015  
doi: 10.3389/fenvs.2015.00017

## Using Agent-based models:



GAMA Platform

<https://gama-platform.github.io/wiki/Home>



NetLogo

<https://ccl.northwestern.edu/netlogo/>

## A hybrid modeling approach to simulating foot-and-mouth disease outbreaks in Australian livestock

Richard A. Bradhurst<sup>1\*</sup>, Sharon E. Roche<sup>2</sup>, Iain J. East<sup>2</sup>, Paul Kwan<sup>1</sup> and M. Graeme Garner<sup>2</sup>

<sup>1</sup> Discipline of Computer Science, School of Science and Technology, University of New England, Armidale, NSW, Australia,

<sup>2</sup> Epidemiology and One Health Program, Animal Health Policy Branch, Department of Agriculture, Canberra, ACT, Australia

<http://contagion.principiate.org/>

# Questions?