Part II

DYNAMIC NETWORK ANALYSIS

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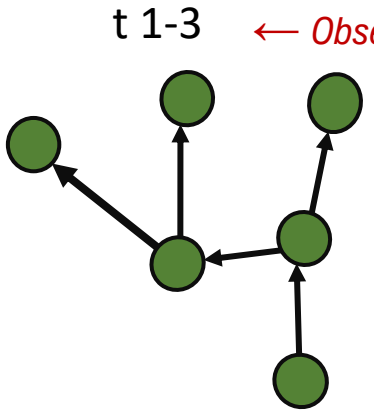
Outline

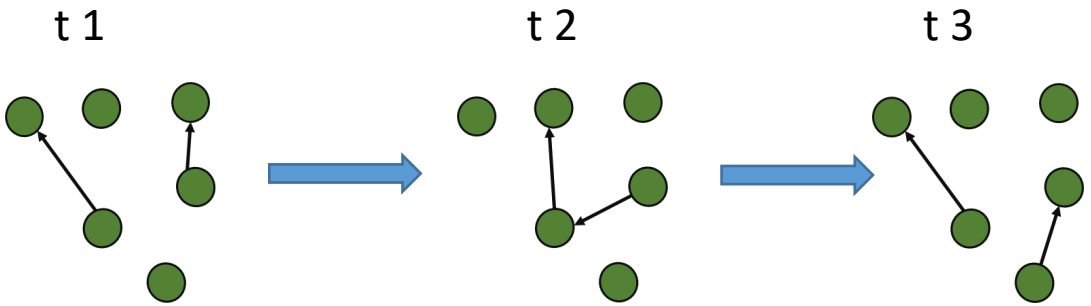
- Static vs Dynamic network analysis
- Dynamic network statistics
- Considerations and limitations

Whats the difference between Static and Dynamic analysis?



Static network

$G = (V, E)$

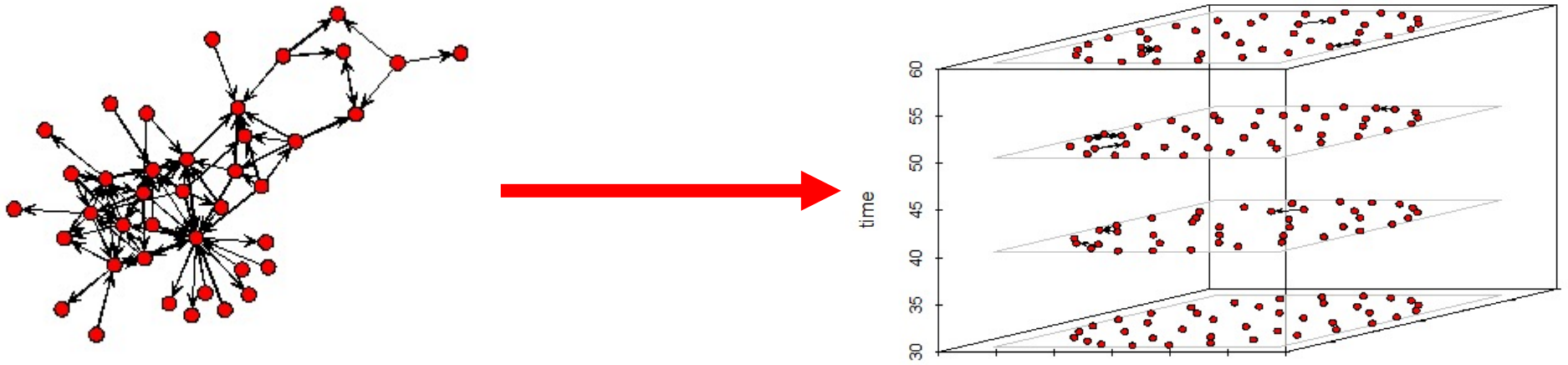


Dynamic network

$G = (V, E, t)$

Network topology changes over time

Why dynamic networks?

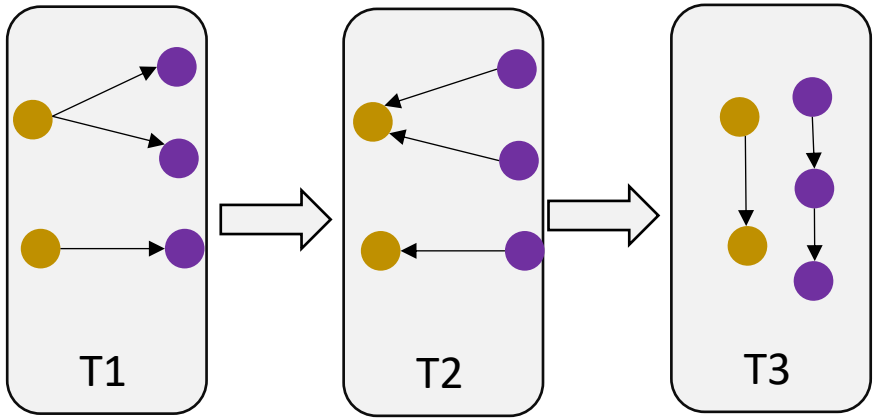


Why is interesting in epidemiology?

- 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

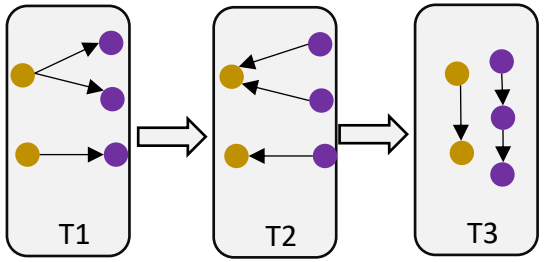
Changes on the structure



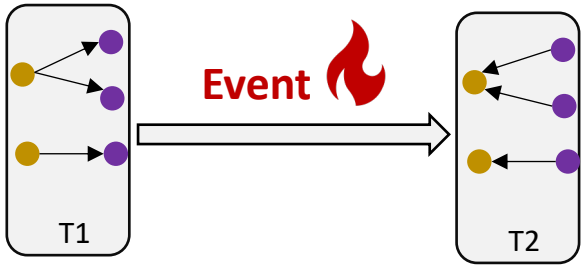
Study disease transmission

DNA for Changes in the network structure

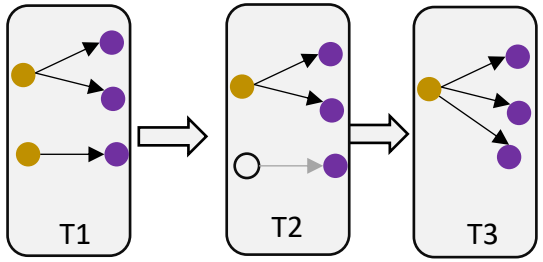
Understanding the evolution of the network over time:
As the environment changes, so does the social behavior of individuals.



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.



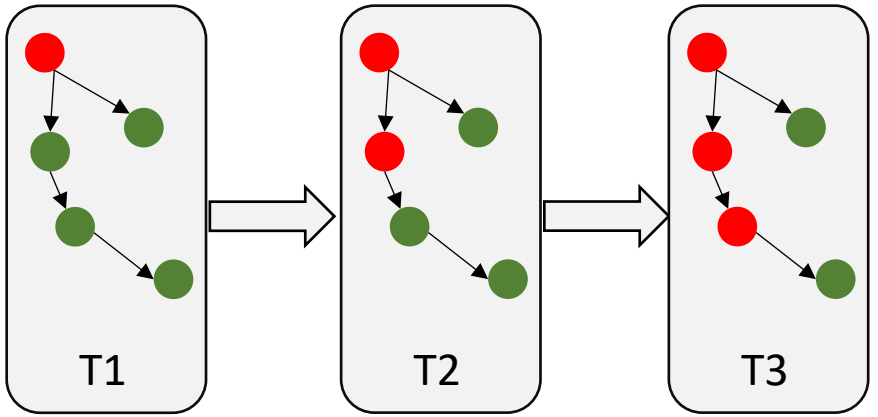
Understanding how changes in individual traits impact the network structure:
Presence or absence of particular individuals can impact the structure of interactions.



Network dynamics in epidemiology

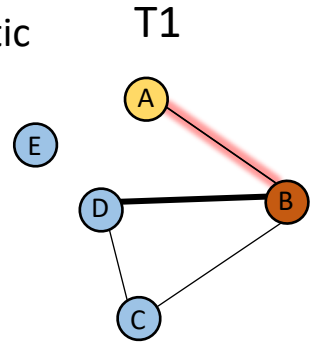
Changes in the structure

Disease transmission

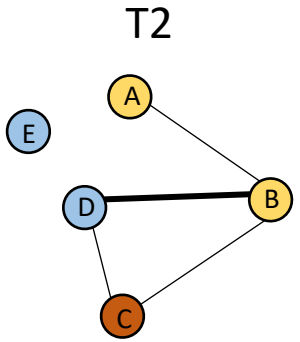


Understand an observed epidemic

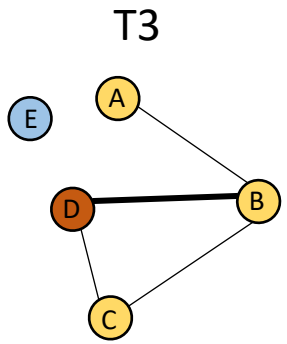
Static



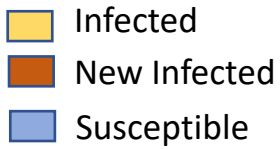
1/1 new case



1/2 new case

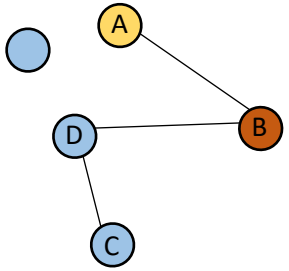


1/1 new case

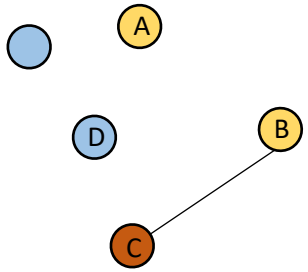


3/4 new cases = 75%

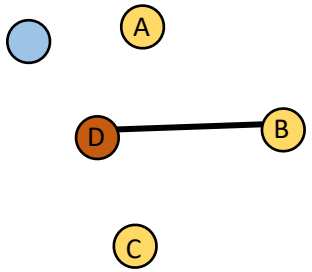
Dynamic



1/1 new case



1/1 new case



1/1 new case

3/3 new cases = 100%

From Damien 2017

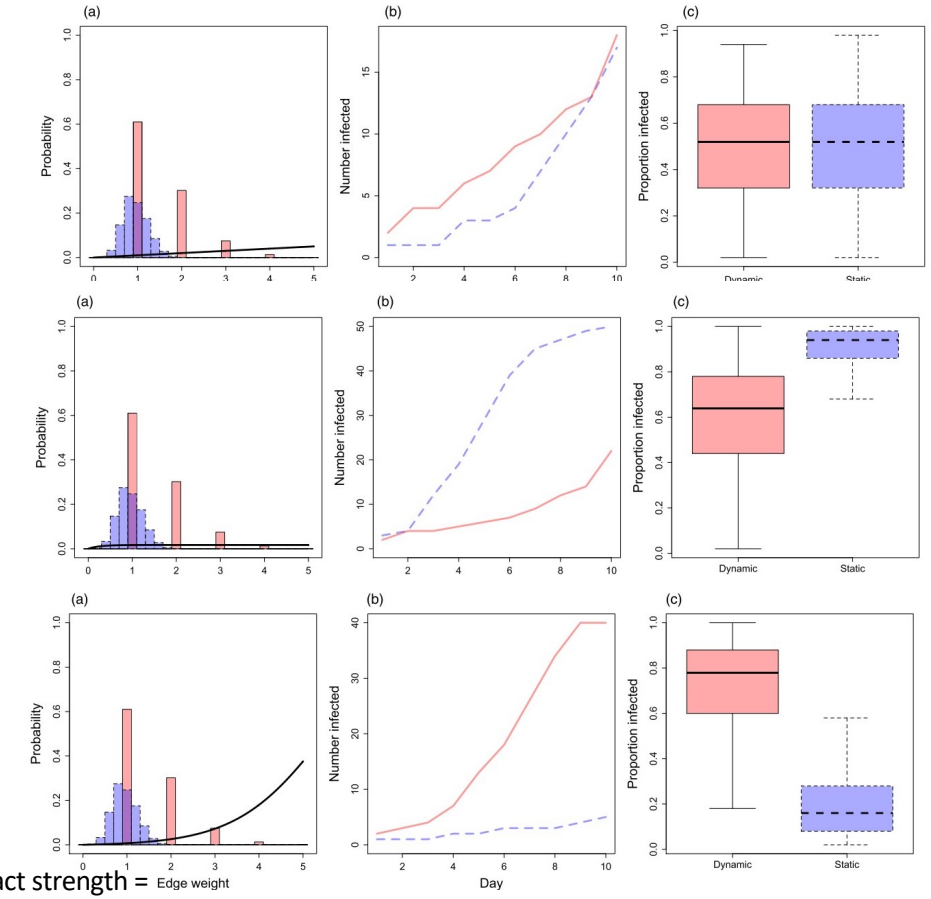
Making general predictions

- 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

Damien 2017

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?

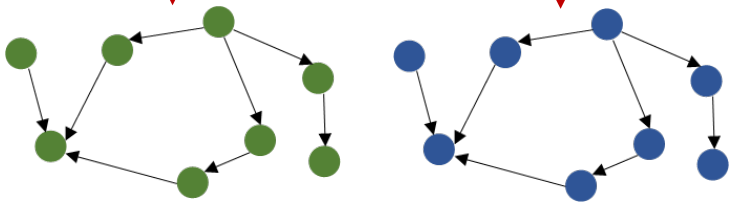
- Equal sampling efforts during the study period?

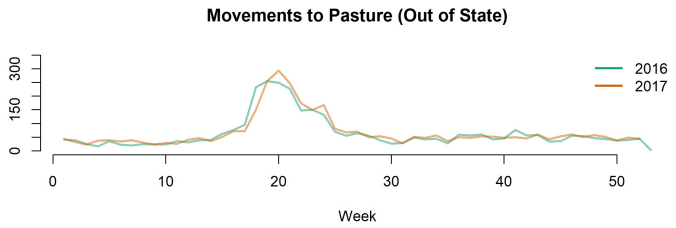
Dynamic Network Statistics

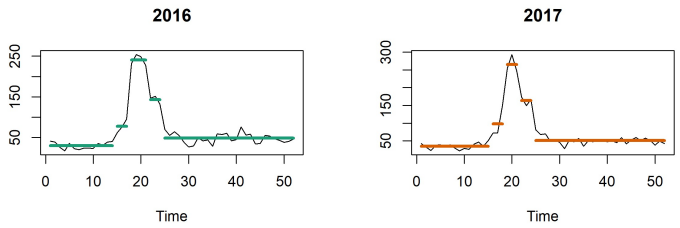
How do we know if a network is likely to re-occur?

Network isomorphism

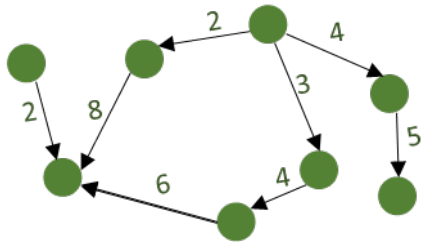
Same adjacency structure

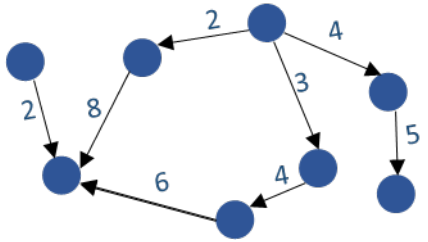




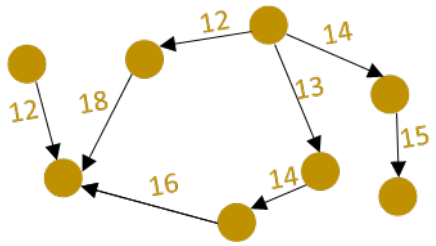


Identify patterns

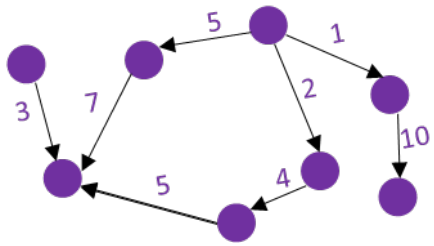




Strictly isomorphic



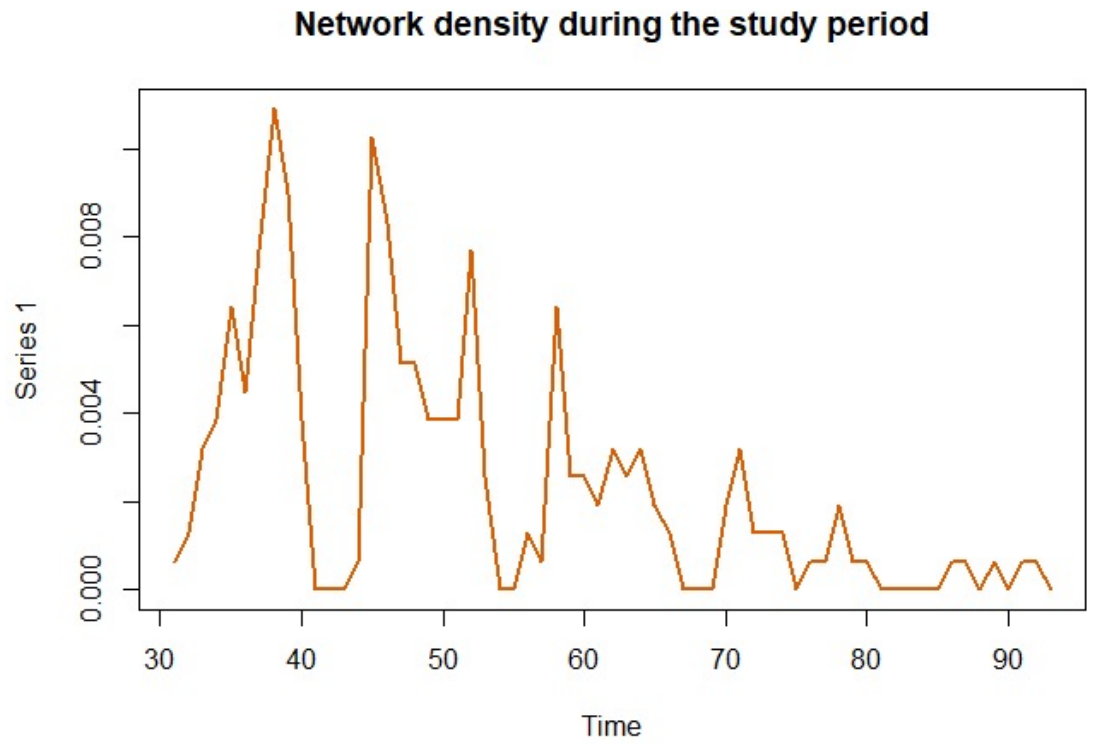
Temporally isomorphic



Temporal order isomorphic

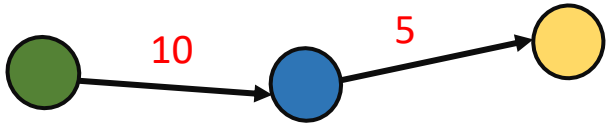
Why Dynamic network analysis?

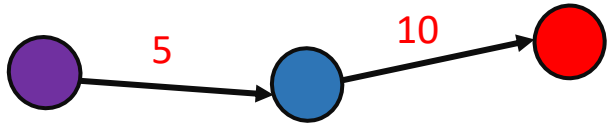
- Centrality measures and network statistics used in static networks can be adapted for dynamic network analysis.



Temporally reachable sets

Temporally reachable sets





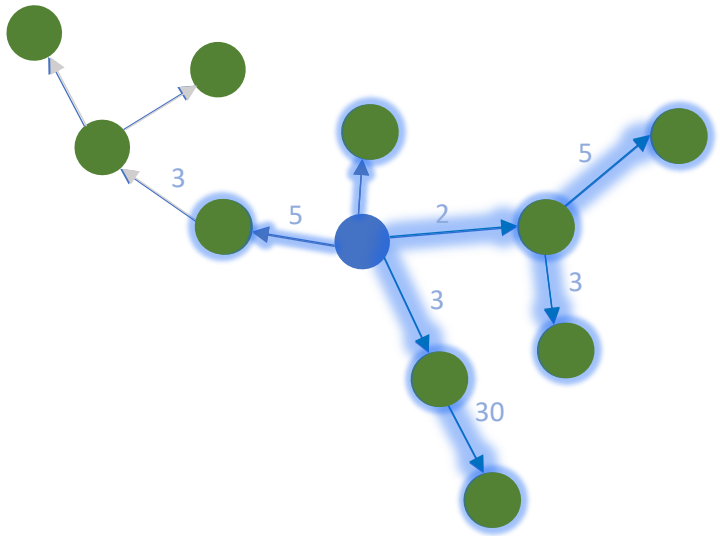
The temporally reachable set of a node, represents the set of other nodes that can be reached following a temporal path.

Temporally reachable sets

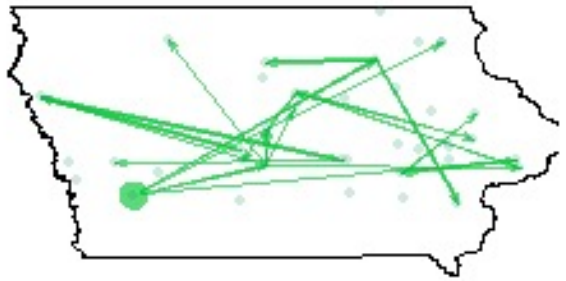
$e_1 = (i, j, t_1, \delta t_1)$ **Event 1**

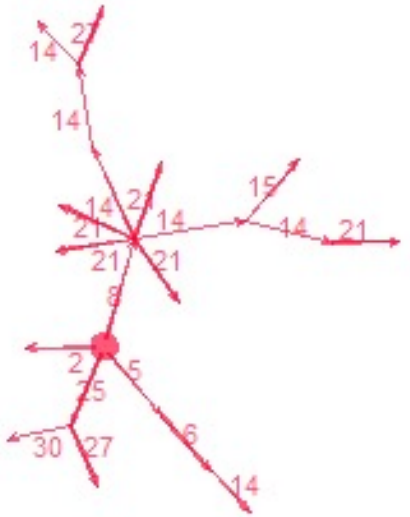
$e_2 = (j, k, t_2, \delta t_2)$ **Event 2**

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

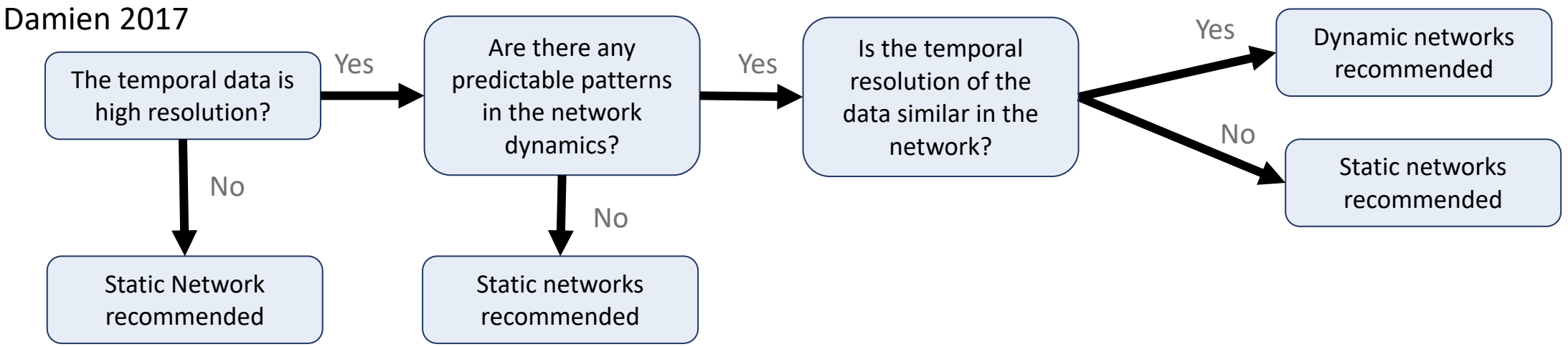


Reachability of Farm 23





Recap


Damien 2017
The temporal data is high resolution?
Yes
No
Static Network recommended
Are there any predictable patterns in the network dynamics?
Yes
No
Static networks recommended
Is the temporal resolution of the data similar in the network?
Yes
No
Dynamic networks recommended
Static networks recommended

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 3!

CADMS Home Pre Workshop Contact

1 Exploratory analysis

2 Species range maps

3 Defining the network:

Lab 3

In this section we will use a different dataset which consist on GPS locations of 3 different species.
We will define our contact network based on proximity between two animals from the GPS location records.

1 Exploratory analysis

```
# libraries we will use
library(dplyr) # for data manipulation
library(sf) # For spatial data manipulation
library(sp) # for spatial data
library(ggplot2) # for making figures
library(purrr) # for network transformation
library(tidygraph) # for network manipulation
library(ggraph) # for plotting networks
# We get the data from the STNet package
GPSc <- STNet::GPSc
```

First we will see how many locations were recorded during the observation period by species:

```
GPSc %>%
  count(species_type) # count by species
```

```
##   species_type     n
## 1       cattle  9309
## 2         deer 11511
## 3          pig  4428
```

Now lets create a dataset for the nodes.

```
Nodes <- GPSc %>%
  mutate(CollarID = as.character(CollarID)) %>% # convert to character
  distinct(CollarID, species_type) # unique IDs
```

Further applications

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

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Outline

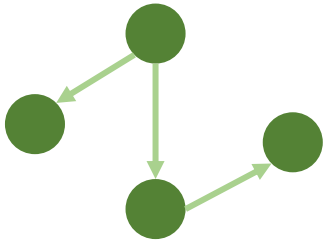
- Statistical Models
- Simulation Models

Network Analysis and Regression

Regression assumptions:

- Linearity
- Independence
- Normality
- Equal variance

SNA recognize the influence of community members on each other.



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Preventive Veterinary Medicine
journal homepage: www.elsevier.com/locate/prevetmed
ELSEVIER

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[a], M. Quevedo-Valle[b], I
[a] Center of Animal Disease Modeling and Surveillance (CADMS), Department United States
[b] Dirección de Sanidad Animal SENASA, Lima, Peru

Contents lists available at ScienceDirect
Preventive Veterinary Medicine
journal homepage: www.elsevier.com/locate/prevetmed
ELSEVIER

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[a,*], Dale Polson[b], Erin Lowe[b], Rodger Main[c], Derald Holtkamp[c], Beatriz Martínez-López[a]

[a] Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, CA, USA
[b] Boehringer - Ingelheim Vetmedica, Inc., St. Joseph, MO, USA
[c] Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA

Multilevel Logistic Regression for Repeated measures

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

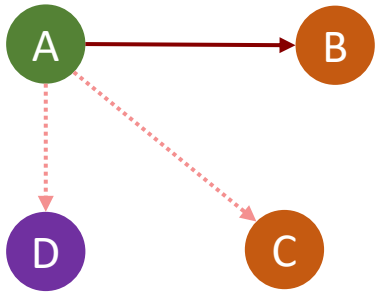
$$logit\ (\pi_{ij}) = \beta_{oj} + \beta_1 X_{1ij} + \beta_2 X_{2ij} \cdots \beta_n X_{nij} + \mu_j$$

y_{ij} : Occurrence of the event *i* at time *j*
π_{ij}: Expected probability of PRRS occurrence
β_{oj}: The intercept
$\beta_1, \beta_2, \cdots \beta_n$: The slopes
μ_j: The random effect

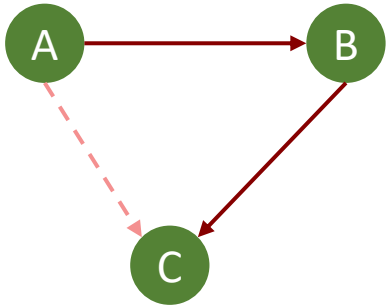
ERGMs

- **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)



`ergm` https://www.jstatsoft.org/article/view/v024i03

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[1☯]*, Beatriz Martínez-López[1☯], Daniel Beltrán-Alcrudo[2☯]

1 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, **2** Food and Agriculture Organization, FAO Budapest, Hungary

☯ These authors contributed equally to this work.
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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

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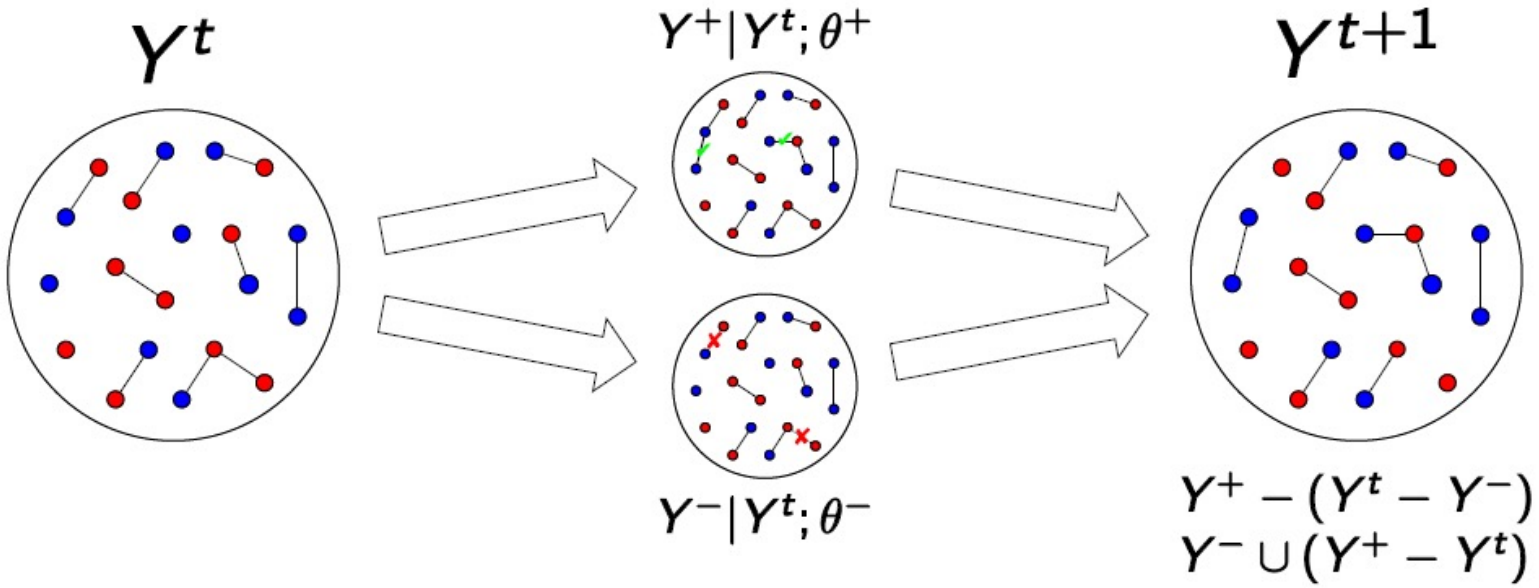
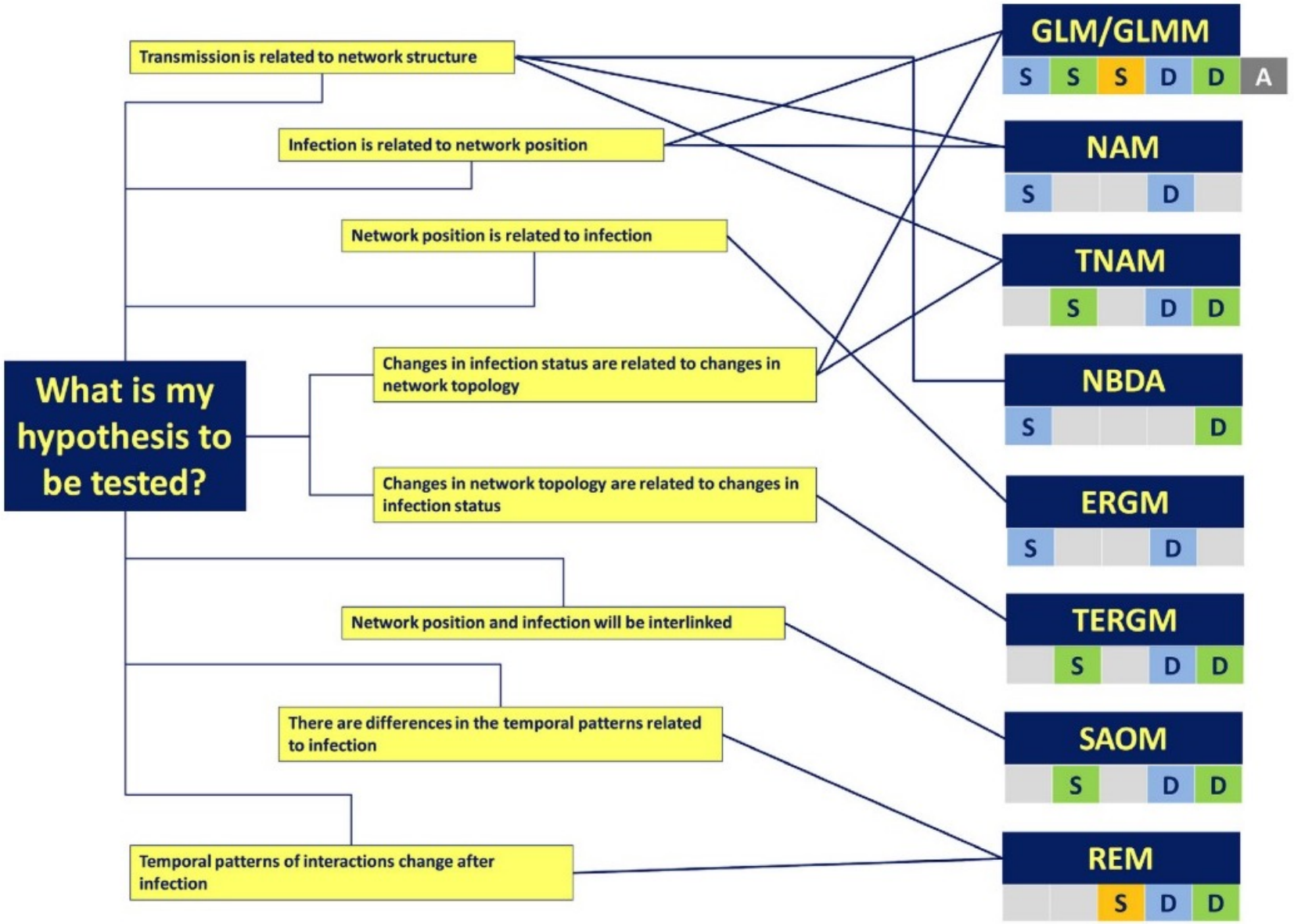
STERGMs

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

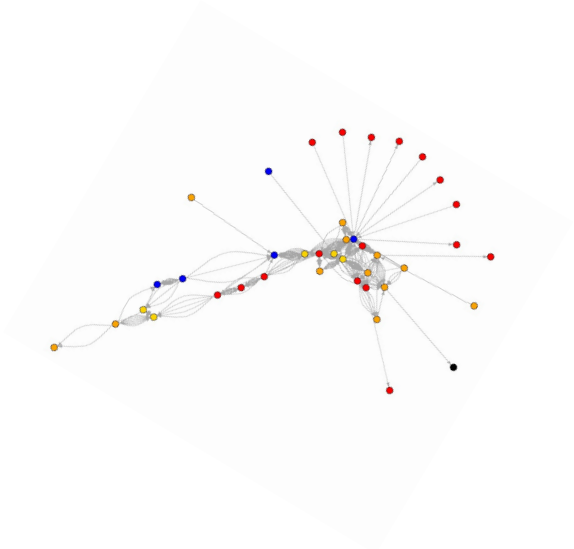
What data am I using?

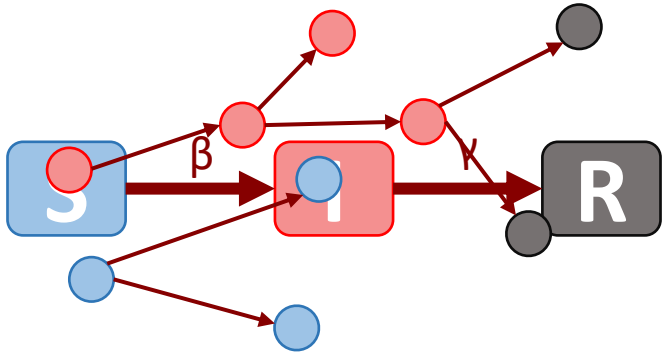
Disease data	
D	Presence/absence or infection load
D	Timing of changes in infection known

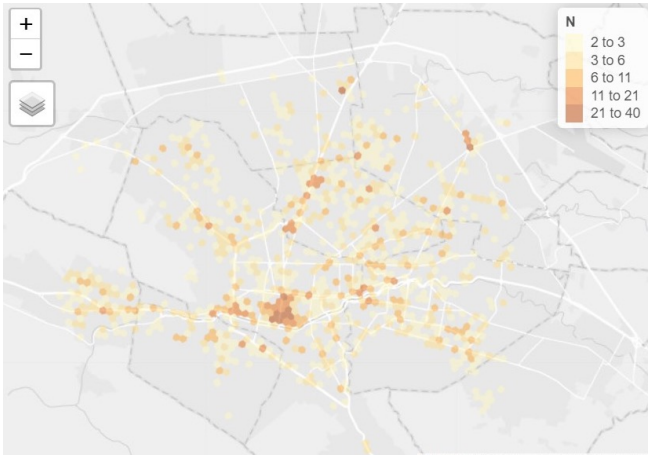
Matthew J. Silk 2017

Disease spread models

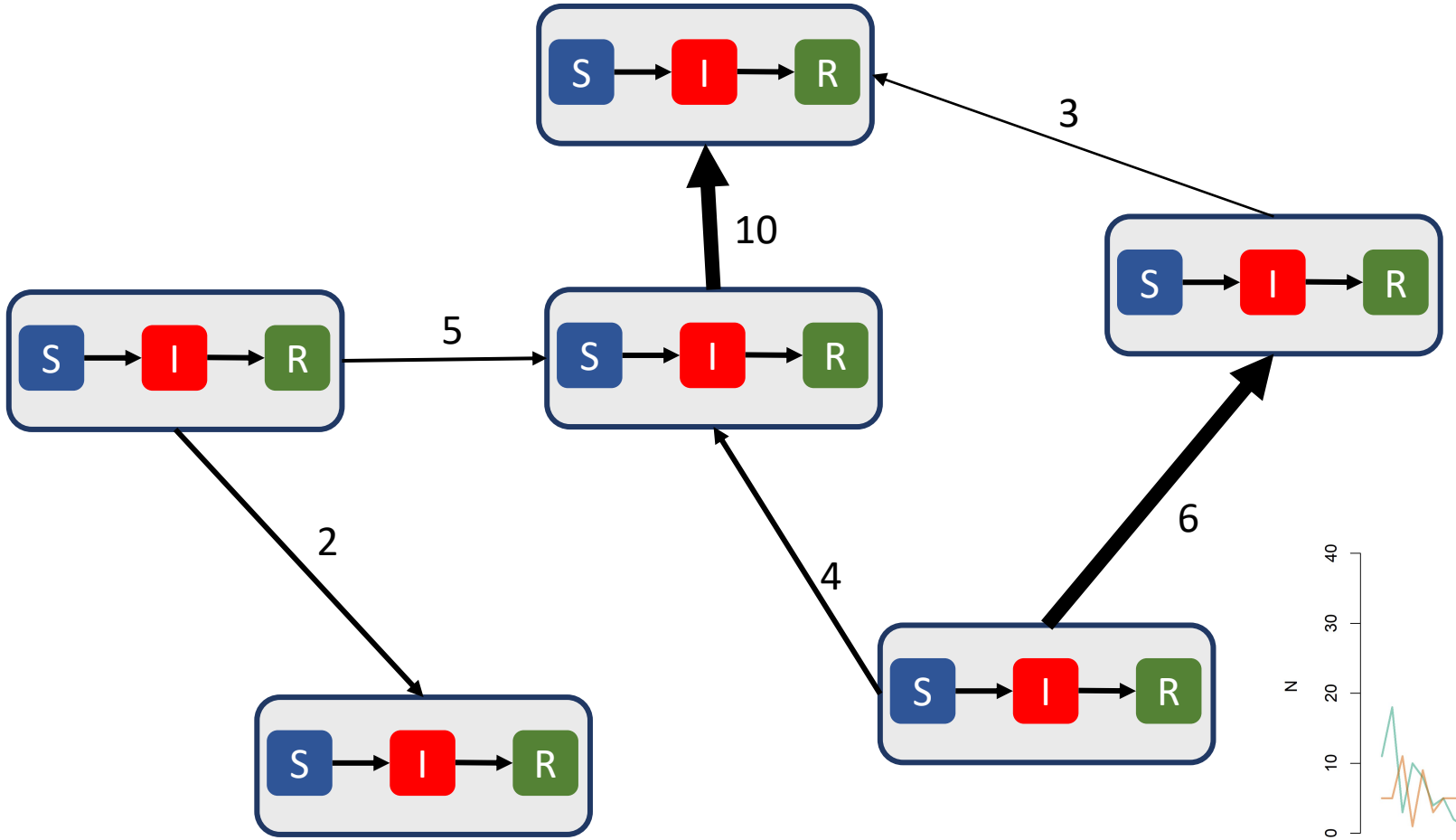
- Most epidemic models incorporate homogenous mixing assumption (Law of mass action).
- This for some scenarios this assumption is unrealistic but simplifies the mathematical computation of the model.
- Populations are not homogenously mixed, population structure can arise from spatial and social interactions.

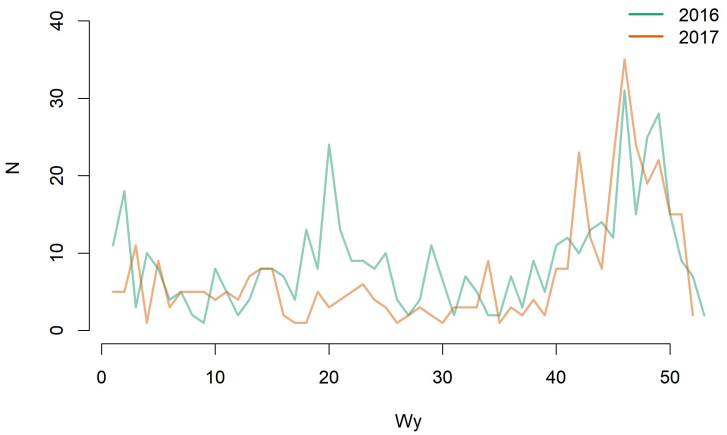






Disease spread models





Disease spread models

- Using R:
  - `Statnet,` http://statnet.org/nme/index.html
  - `GEMFsim` https://ece.k-state.edu/netse/software/index.html

GEMFsim implementations

Language	Author	Manual	Code
MATLAB	Faryad Sahneh	Matlab_Manual	MATLAB
Python	Heman Shakeri	Python_Manual	PYTHON
R	Aram Vajdi	R_Manual	R
C	Futing Fan	C_Manual	C
MATLAB	Haotian Wu	Animation_Manual	

Please email faryad@ksu.edu or caterina@ksu.edu if you are interested in GEMF

Using Agent-based models:

GAMA Platform

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

NetLogo

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

http://contagion.principate.org/

Questions?