Modelos basados en redes

CENTER FOR ANIMAL DISEASE MODELING AND SURVEILLANCE (CADMS),
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www.vetmed.ucdavis.edu/cadms/

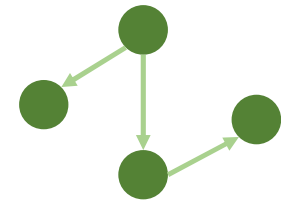- Modelos estadisticos
- Modelos de simulacion

Network Analysis and Regression

Regression assumptions:

- Linearity

- Independence

- Normality

- Equal variance

SNA recognize the influence of community members on each other.

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} : ocurrencia del evento *i* al tiempo *j*
π_{ij}: Probabilidad esperada del evento
β_{oj}: The intercept
$\beta_1, \beta_2, \cdots \beta_n$: Las variables
μ_j: Effecto aleatorio

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

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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

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[c] Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA

ERGMs

- **Exponential Random Graph Models:** Predicen la ocurrencia de conexiones. Cual es la probabilidad de observer nuestra red?
- Evaluan una estructura cros seccional

Individual covariates: are sow farms more likely to contact GDUs?
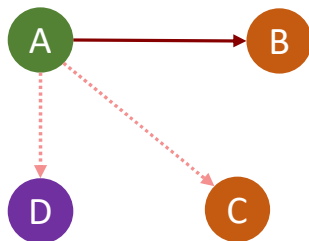
Network structure: If Farm A contacts Farm B, and Farm B contacts Farm A, what are the chances of farm A contacting Farm B? (Triangles formations)

`ergm` https://www.jstatsoft.org/article/view/v024i03
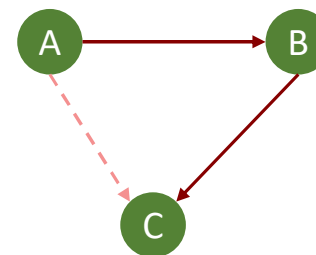
Exponential Random Graph Models

```
## =====================================
## 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}

Separable Temporal ERGM

Y^+ = network in the formation process after evolution
Y^- = network in the dissolution process after evolution
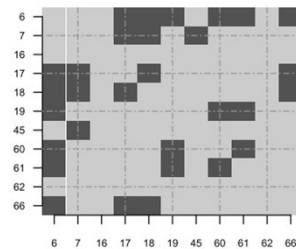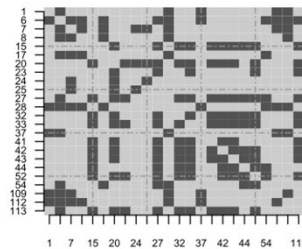This is the origin of the "S" in STERGM

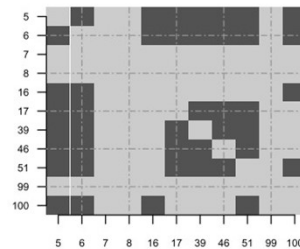# Dynamic Network Regression

Dynamic Network Regression:

https://cran.r-project.org/web/packages/dnr/dnr.pdf
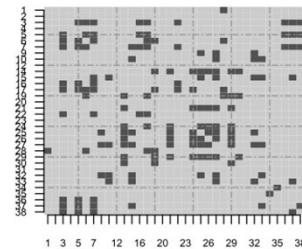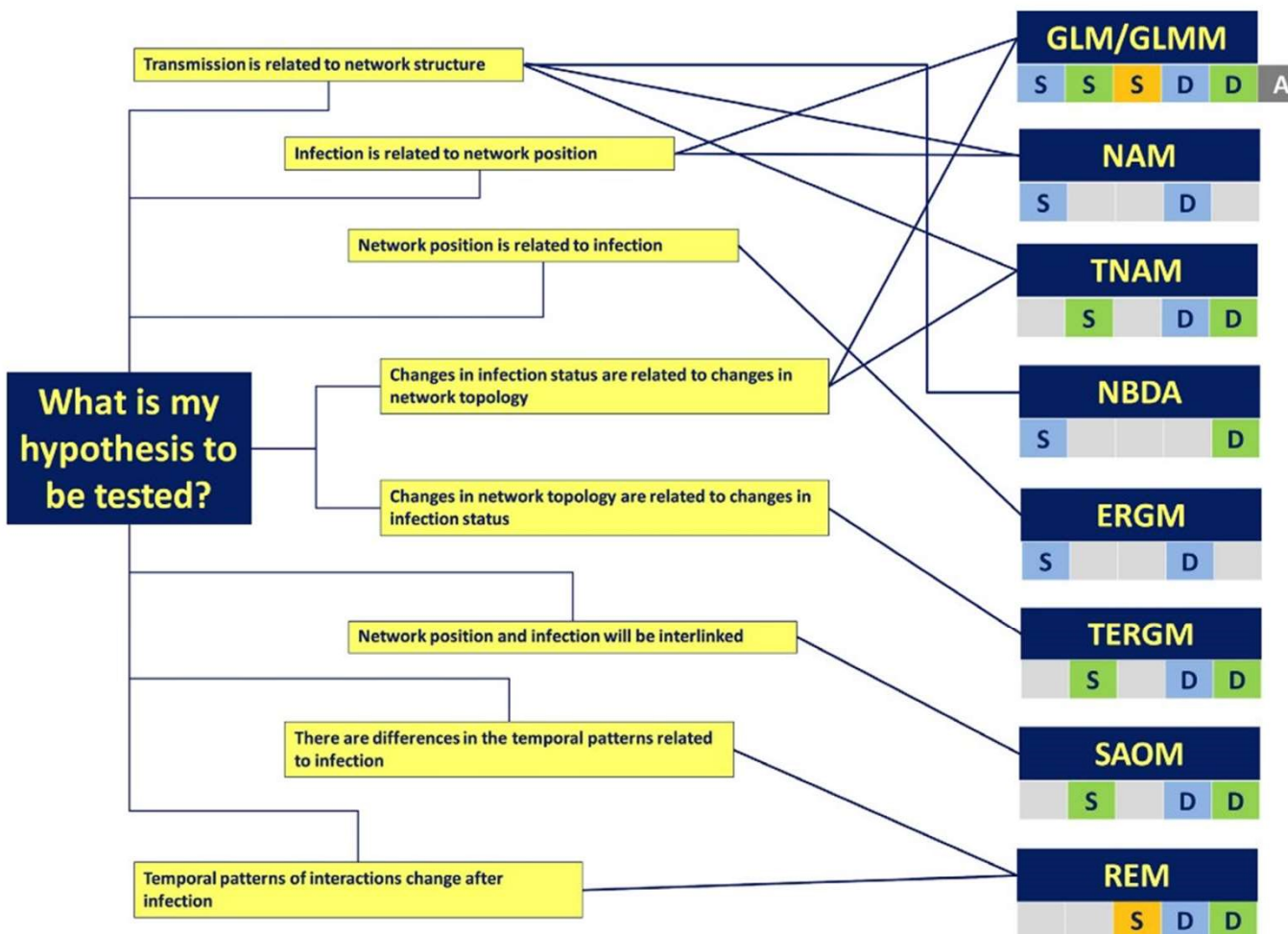
Statistical Models inNetwork Analysis

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

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.
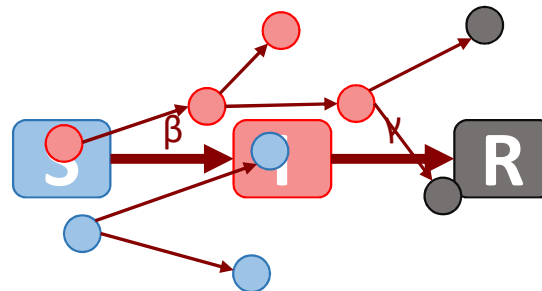
Disease spread models
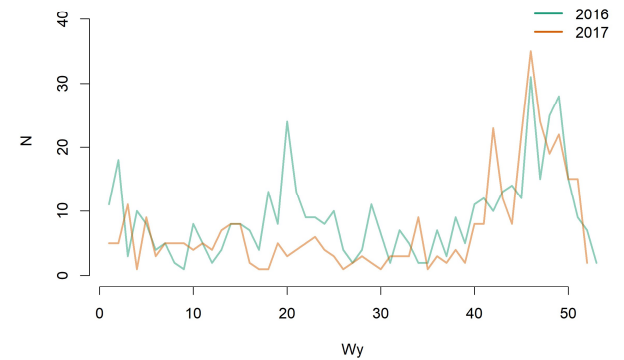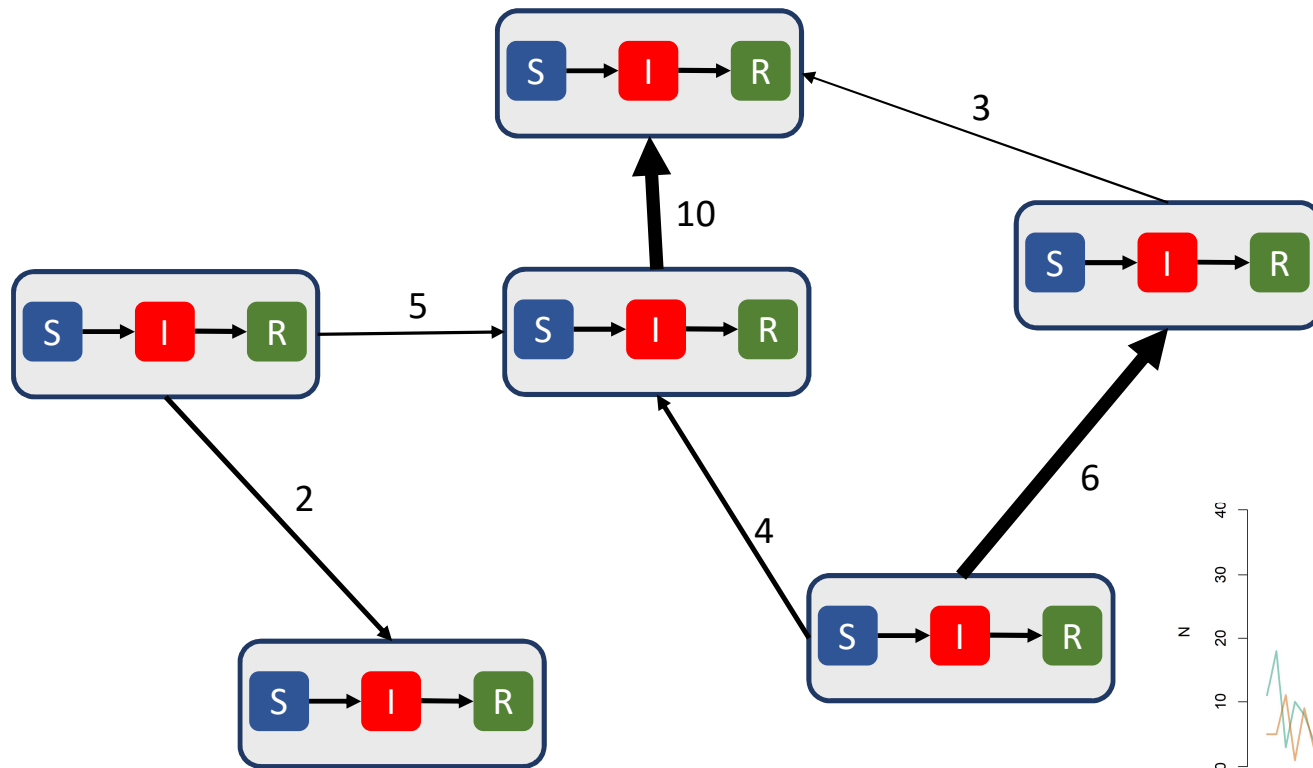
Disease spread models

- Using R:
  - Statnet
  - siminf

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

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Using Agent-based models:

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

Richard A. Bradhurst[1]*, Sharon E. Roche[2], Iain J. East[2], Paul Kwan[1] and M. Graeme Garner[2]

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http://contagion.principate.org/

GAMA Platform

NetLogo

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

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

Questions?