CENTRO DE INVESTIGACIÓN EN COMPLEJIDAD SOCIAL

THE UNIVERSITY OF UTAH®

How does network structure in Agent-Based Models affect epidemiological parameters?

A large simulation study

Aníbal Olivera[1], George Vega Yon[2], Chong Zhang[2], Matthew Samore[2], Karim Khader[2], Alun Thomas[2]

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    a. The context
    b. The goal

2. Simulation study
    a. Methods

3. Results
    a. Peak Prevalence
    b. Peak Time
    c. Generation Time
    d. Reproductive Number

4. Conclusions

Introduction

The context

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Early days of epidemiology → Modelling with continuous mathematics

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- Compartmentalization hypothesis

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  - An individual can be in one of three states: Susceptible (S), Infected (I), Recovered (R), etc.
  - No overlap between states.

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- Compartmentalization hypothesis
  - An individual can be in one of three states: Susceptible (S), Infected (I), Recovered (R), etc.
  - No overlap between states.

- Homogenous Mixing hypothesis
  - Each individual has the same chance of coming into contact with an infected individual.
  - Eliminates the need to know the precise contact network.

The context

If we assume that a typical individual has $\langle k \rangle$ contacts, then

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SI Model

$$i(t) = I(t)/N$$

$$\frac{di}{dt} = \beta\langle k \rangle (1 - i) i$$

$$i(t) = \frac{i_0 e^{\beta\langle k \rangle t}}{1 - i_0 + i_0 e^{\beta\langle k \rangle t}}$$

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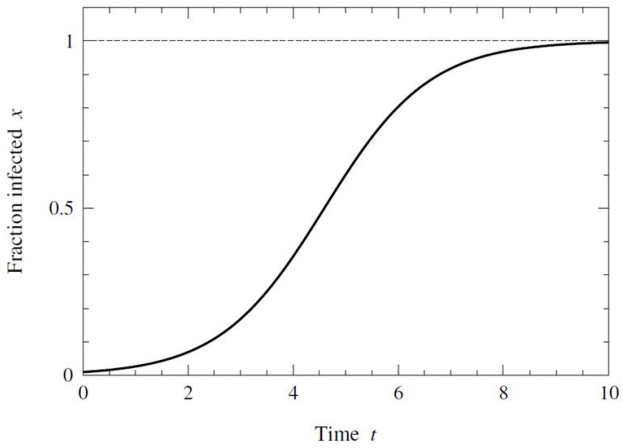

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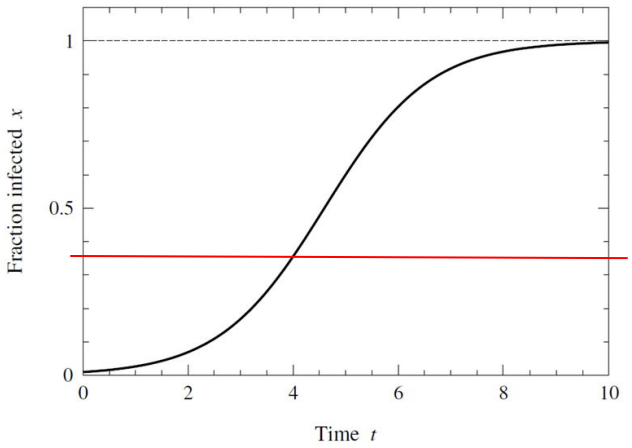

Characteristic time

$$\tau = \frac{1}{\beta \langle k \rangle}$$

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$$\frac{di}{dt} = \beta \langle k \rangle i(1-i) - \mu i$$

$$i(t) = \left[1 - \frac{\mu}{\beta \langle k \rangle}\right] \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$$

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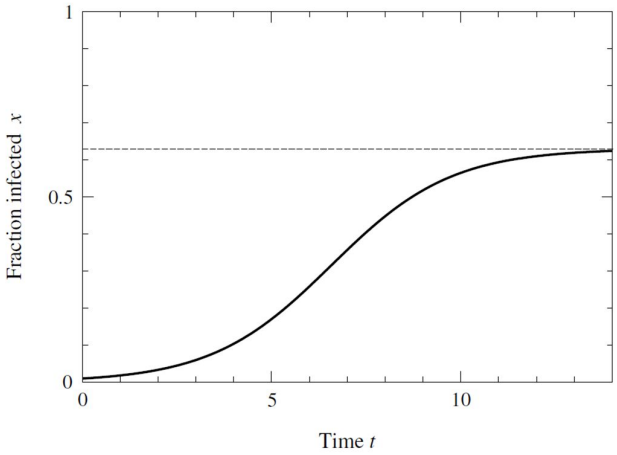

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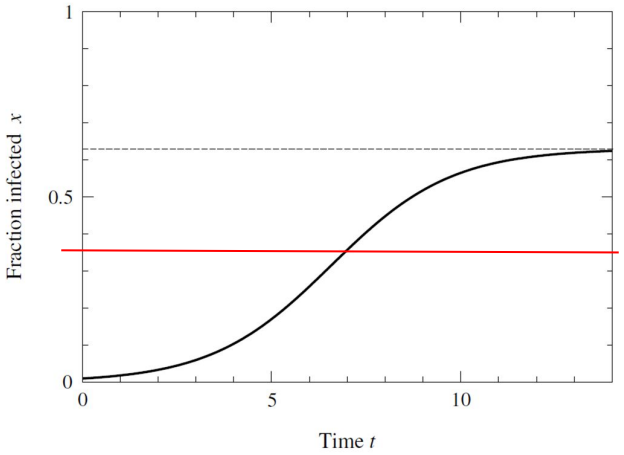

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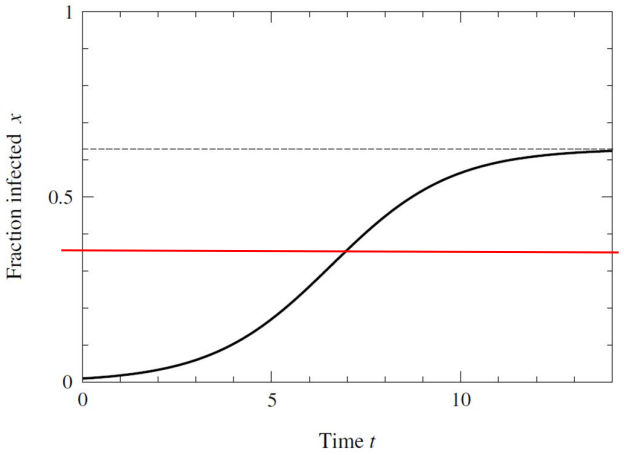

$$\tau = \frac{1}{\mu\left(R_0 - 1\right)}$$

Reproductive Number

$$R_0 = \frac{\beta\langle k \rangle}{\mu}$$

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SIR Model

$$\frac{ds}{dt} = -\beta\langle k\rangle i[1 - r - i]$$
$$\frac{di}{dt} = -\mu i + \beta\langle k\rangle i[1 - r - i]$$
$$\frac{dr}{dt} = \mu i$$

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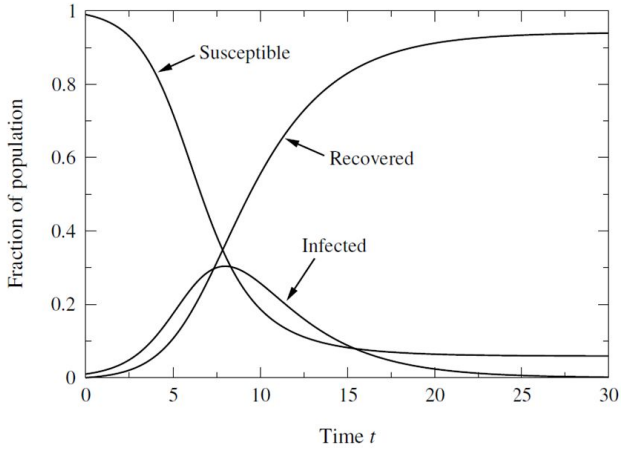

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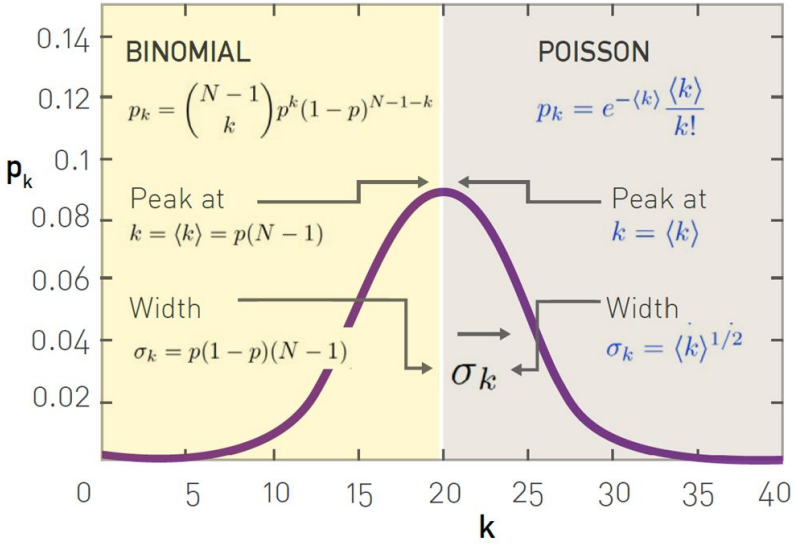

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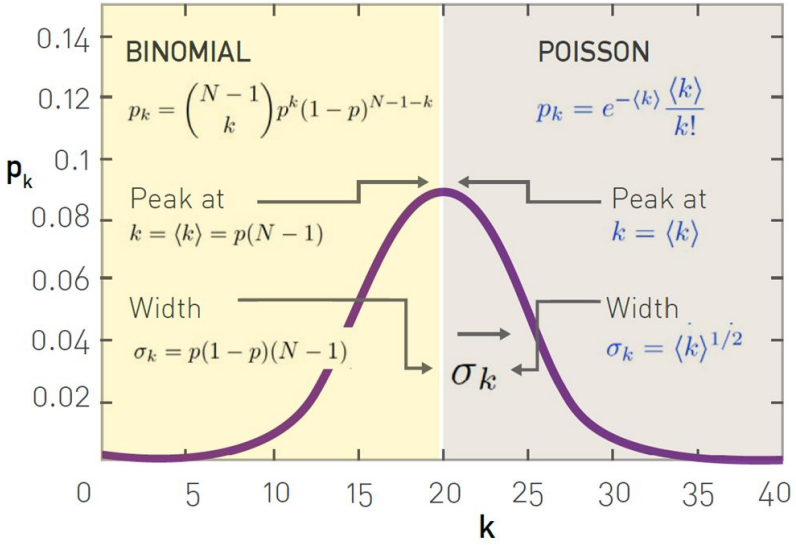

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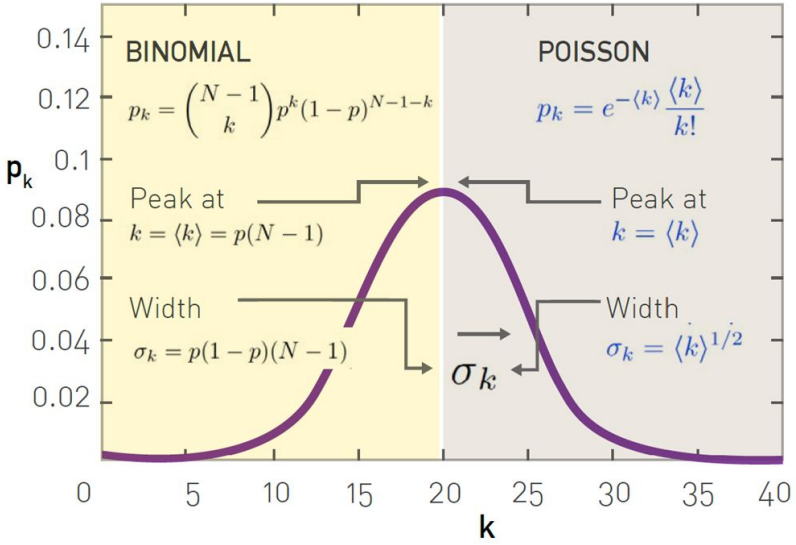

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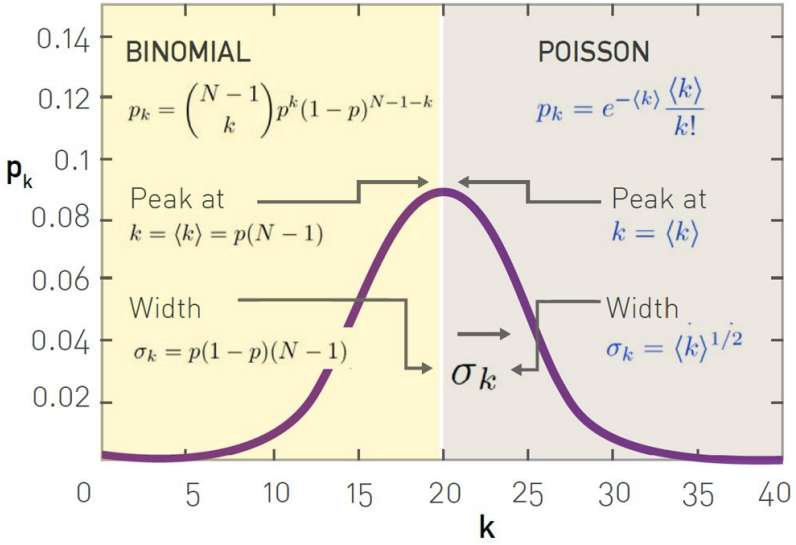

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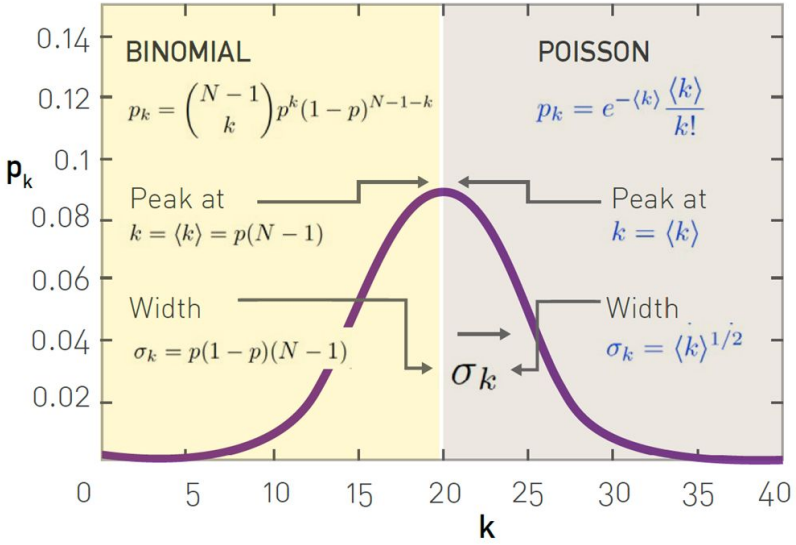

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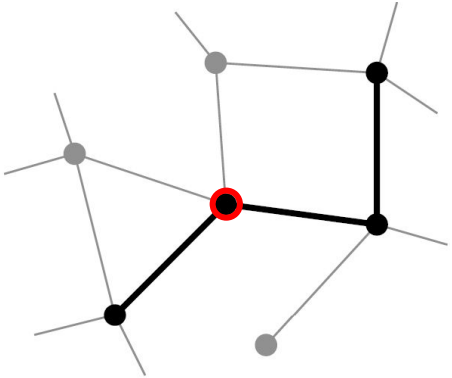
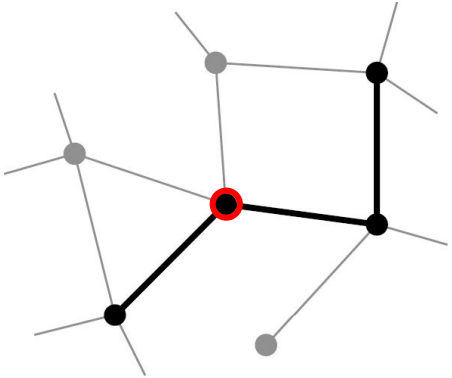


In Agent Based Models, we can add the details of the ego-network of each agent

Rich network-structure

The context



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More accurate predictions

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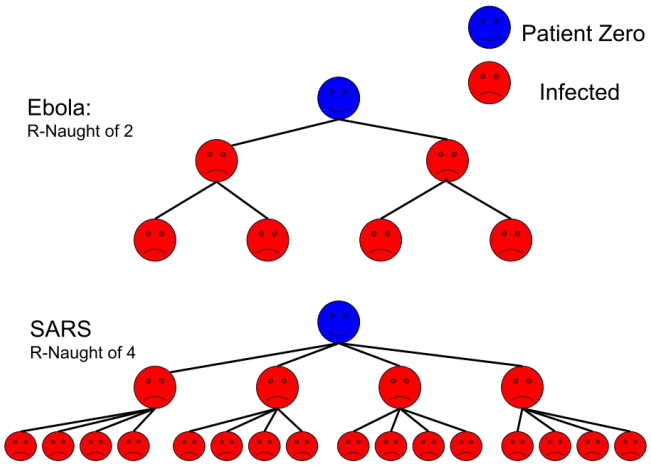
→ ABMs are an important research and policy tool in epidemiology

The context

The idea behind R_0



$R_0 > 1$: Epidemic grows

$R_0 < 1$: Epidemic declines

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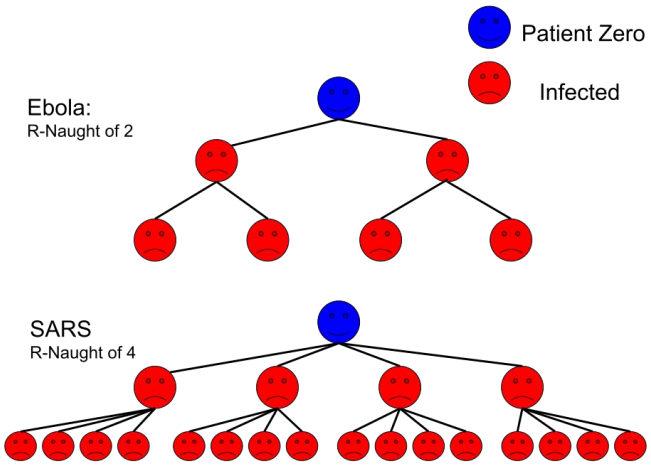

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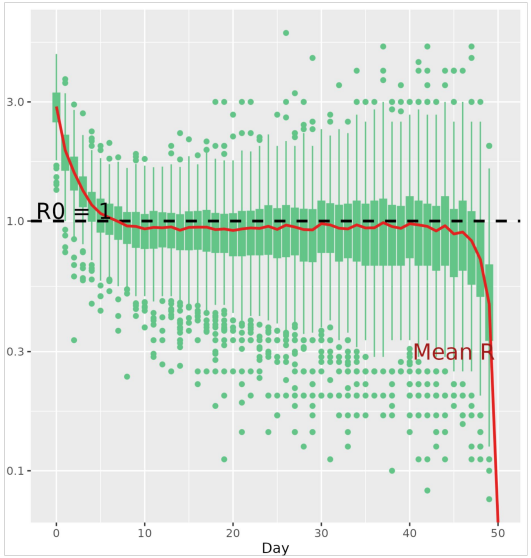
but…



Actually $R_0 < 1$ and still feature full transmission, both in SIR and SEIR! [1, 2]

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- Each network topology is characterized by different levels of local-structures.

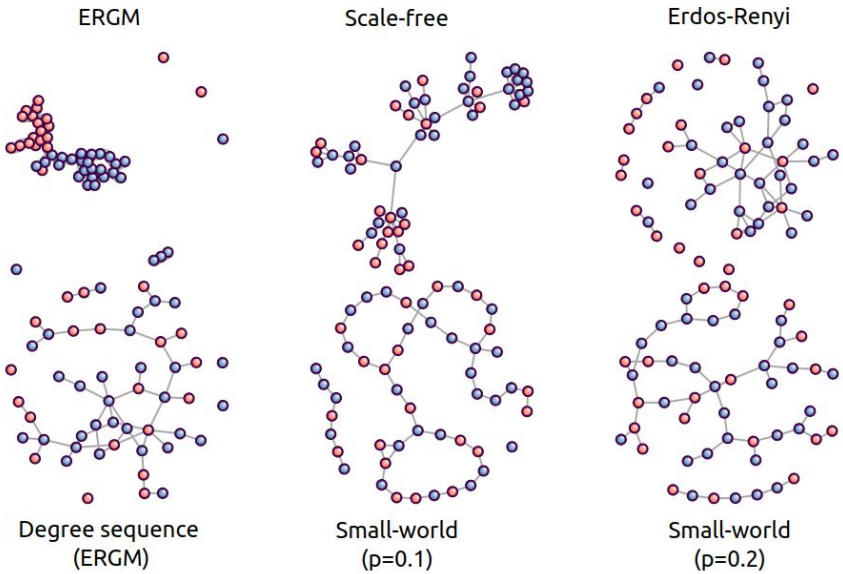
How much do these local structures affect different epidemiological indicators?

Simulation Study

Methods

Based on real-network data:

- We constructed **1,000 networks** of six topologies, all with similar density.



$$N = 534$$

$$\rho \sim 0.029$$

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$$\beta = 1/43$$

Transmission rate
[4]

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Transmission rate [4]

7 Days from Exposed to Infected

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$\beta = 1/43$ — Transmission rate [4]

$a = 1/7$ — 7 Days from Exposed to Infected

$\gamma = 1/7$ — 7 Days from Infected to Recovered

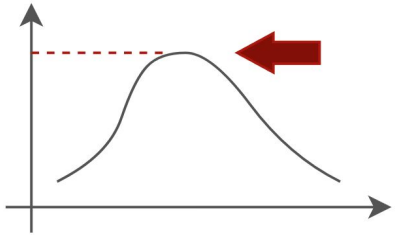
$T = 100$

Methods

From each outbreak, we get:

- Four epidemiological indicators

Peak Prevalence



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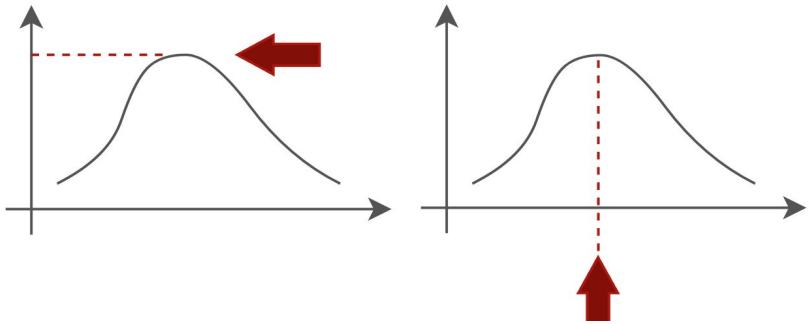
Peak Prevalence - Peak time



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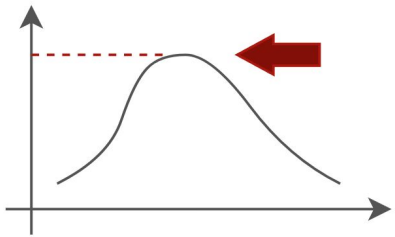

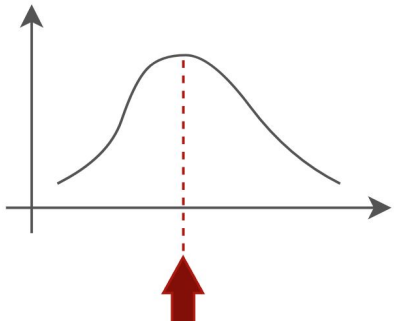

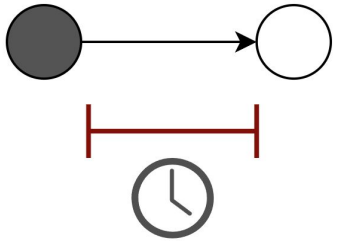

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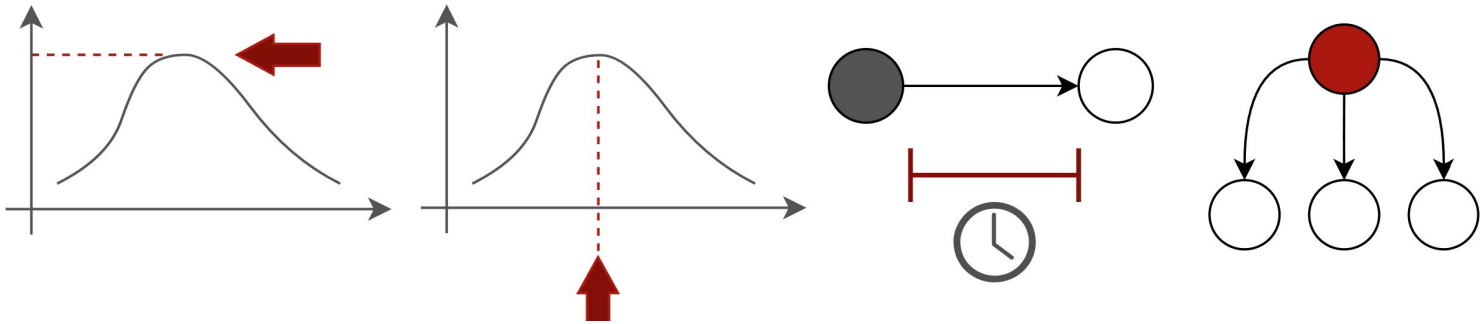

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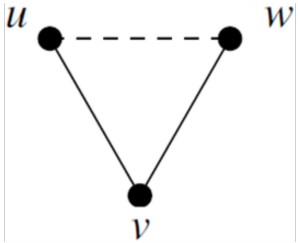
  Peak Prevalence - Peak time - Generation time - Reproductive number

- From the underlying network

  # Two paths - # Balance - # Triangles

  Avg. degree - Avg. path length - Transitivity - Modularity



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$$R_0 \sim \beta_0 + \text{ Net-type } + \beta_2 \text{ Two paths } + \beta_3 \text{ Modularity } + \beta_4 \text{ Modularity }^2$$

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- …or

$$R_0 \sim \beta_0 + \text{ Net-type } + \beta_2 \text{ Two paths } + \beta_3 \text{ log(Modularity)}$$

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4 Dependent Variables $\implies$ $4 \times \text{ Total formulas } = 4,092$

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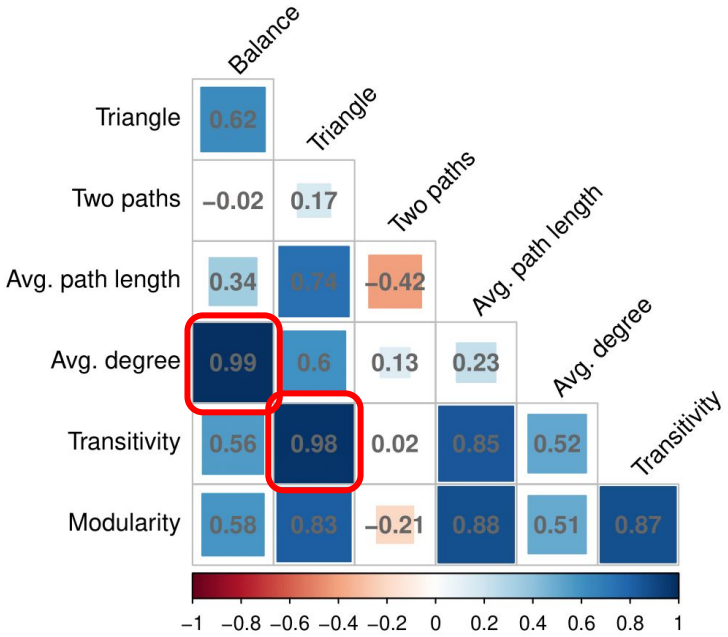
- Unfortunately, there is high correlation between the variables



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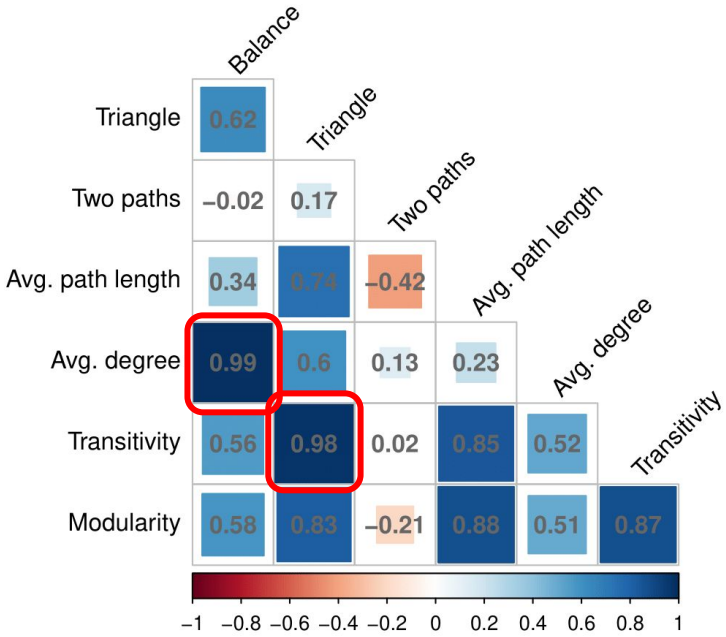

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  Generalized Variance Inflation Factor (GVIF)

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$$\mathrm{GVIF}^{(1/2\mathrm{Df})} > 10$$

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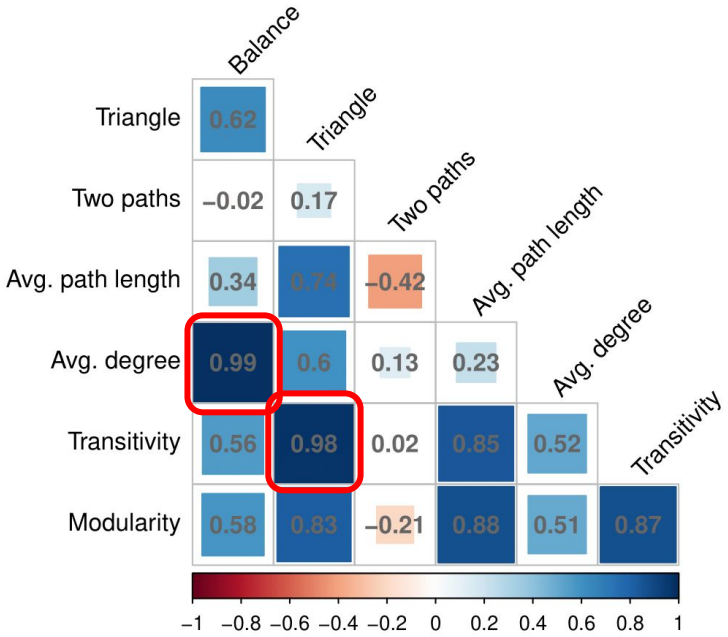

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- This left us with 208 models in total

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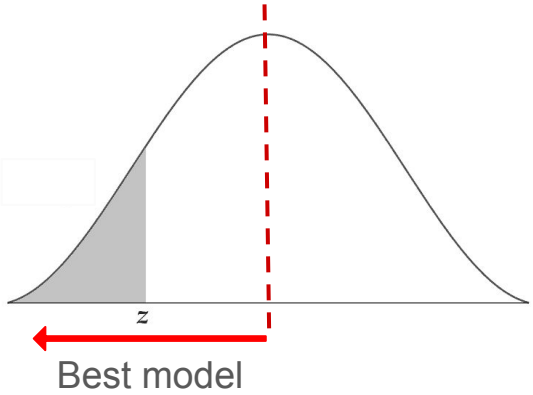

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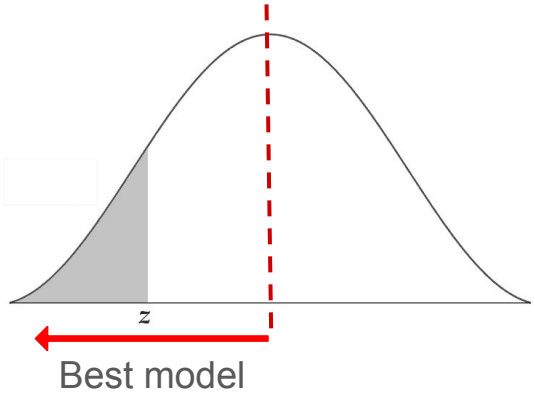
  3. Computed the mean of the z-scores for AIC and BIC
  4. Sort the models according to this number



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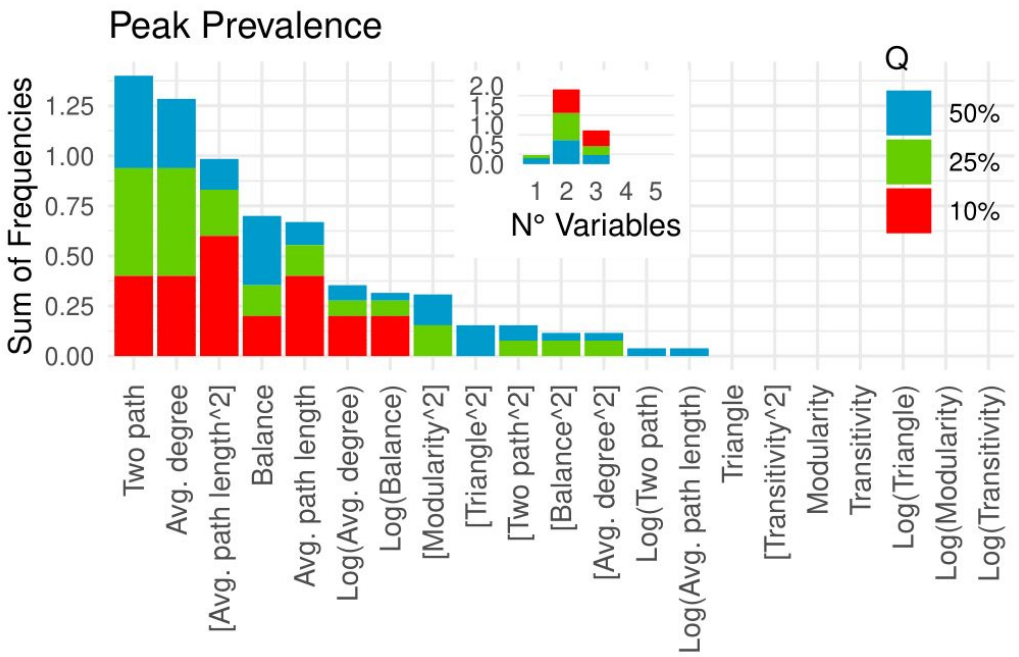
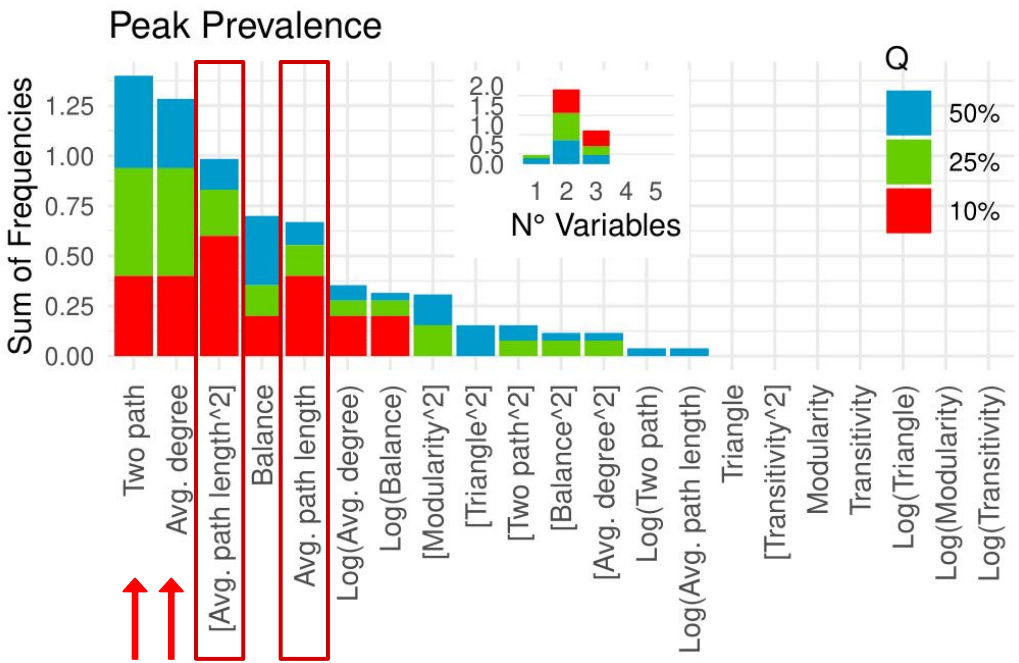
  3. Looked to the **total number of variables** of those models

Results - Peak Prevalence



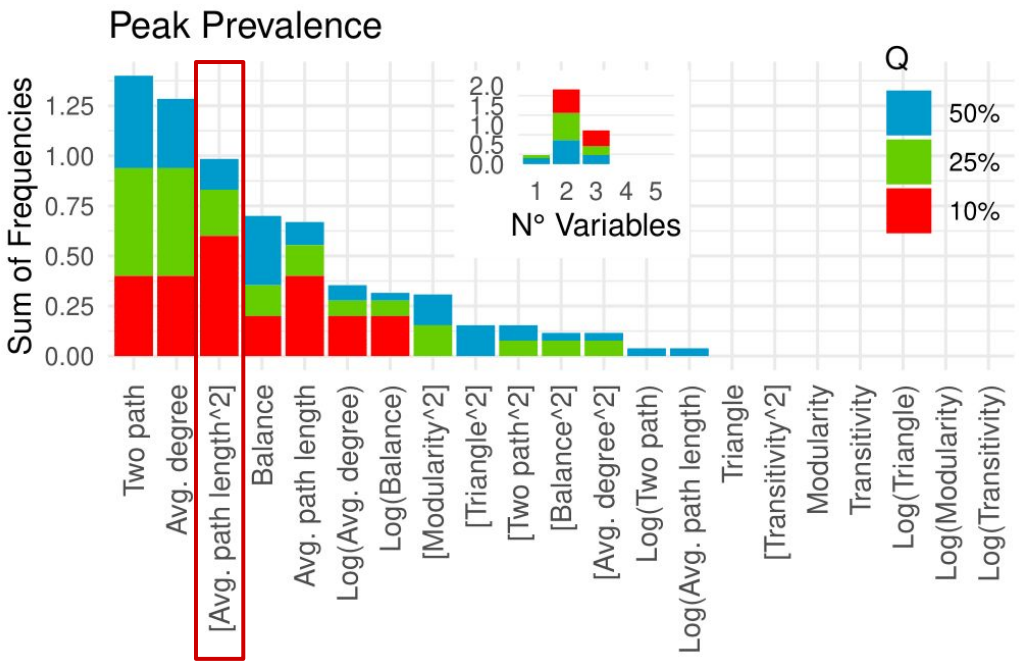
- The best 10% have only **2** or **3** *variables*

Results - Peak Prevalence



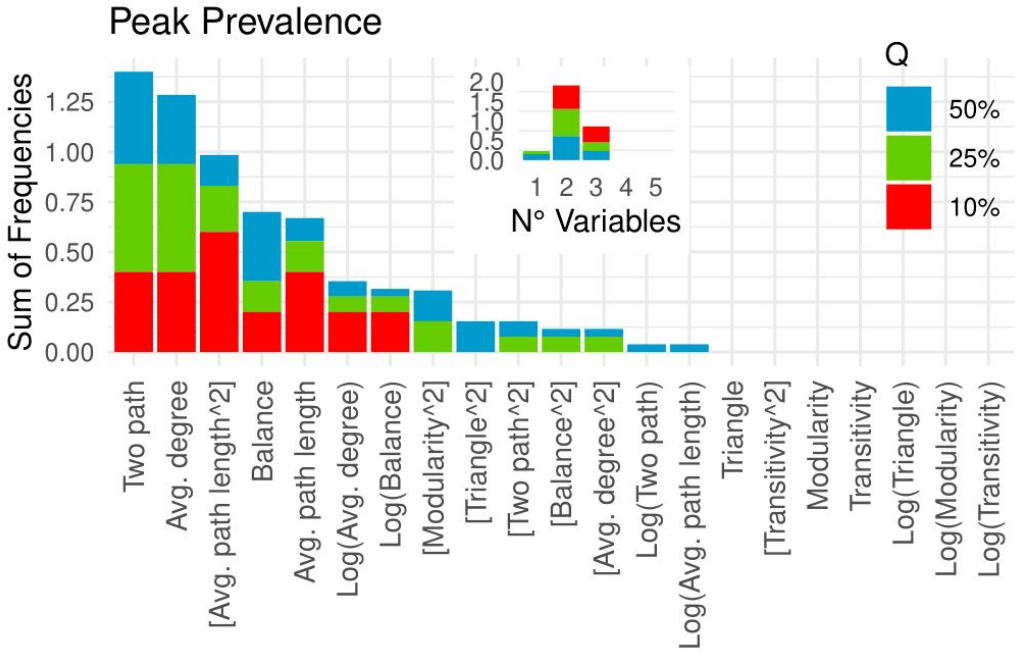
- The best 10% have only **2** or **3** *variables*
- The most prominent variable is **Avg. path length** (linear and quadratic form), along with Two path - Avg. degree

Results - Peak Prevalence



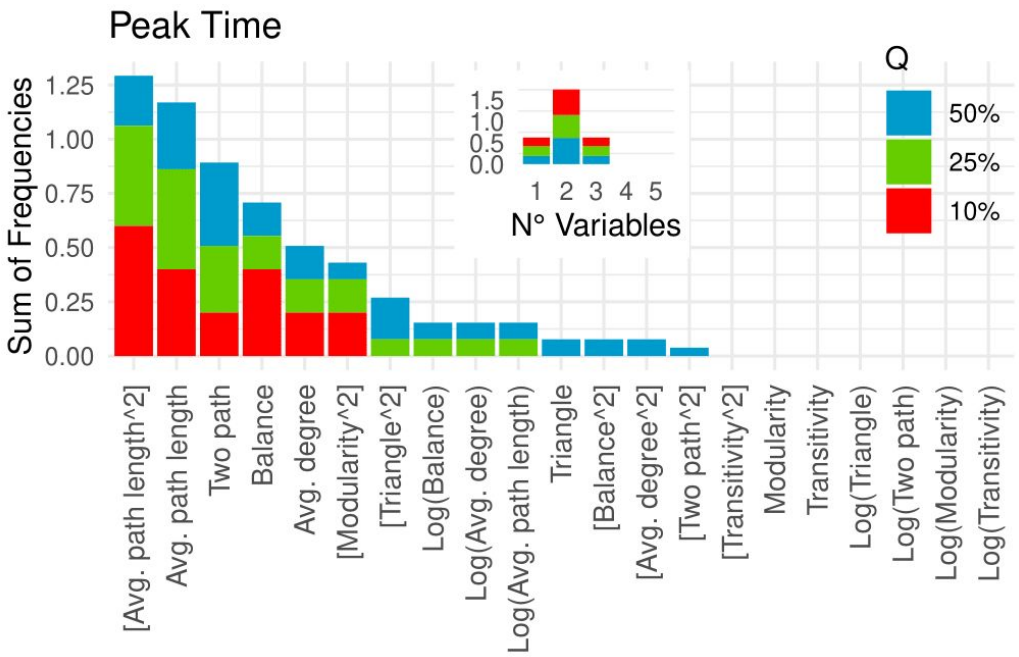
- The best 10% have only **2** or **3** *variables*
- The most prominent variable is **Avg. path length** (linear and quadratic form), along with Two path - Avg. degree
- [Avg. path length^2] has more frequency across all Q

Results - Peak Prevalence



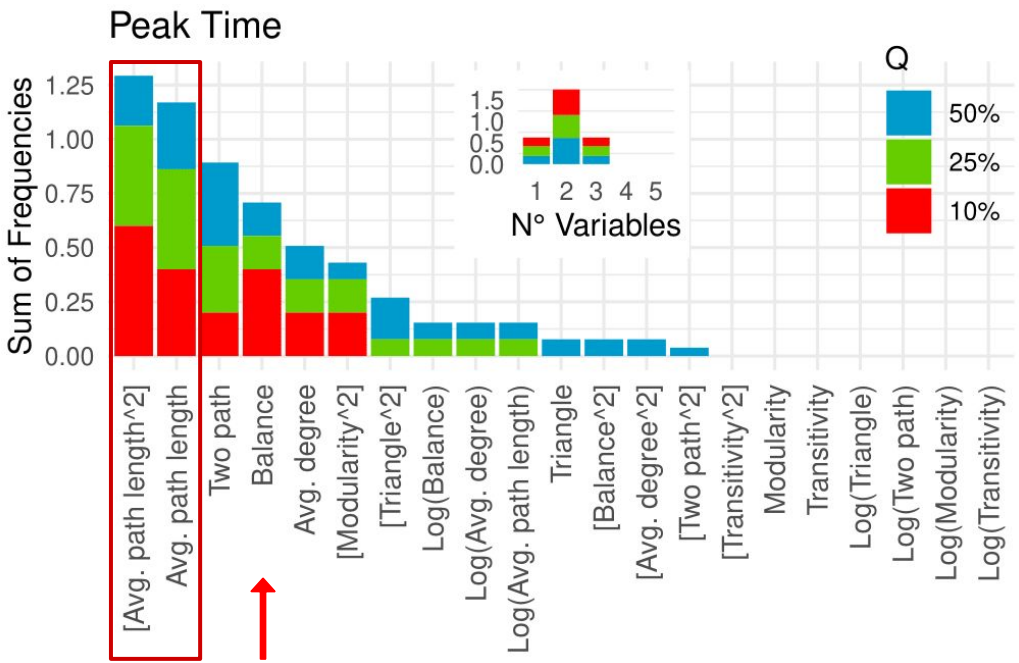
$$\begin{aligned}\text{Peak}_P = \text{Net-type} &+ \beta_0 \text{ two path} \\ &+ \beta_1 \text{ avg. degree} \\ &+ \beta_2 \left[\text{ avg. path length}^2 \right]\end{aligned}$$

Results - Peak Time



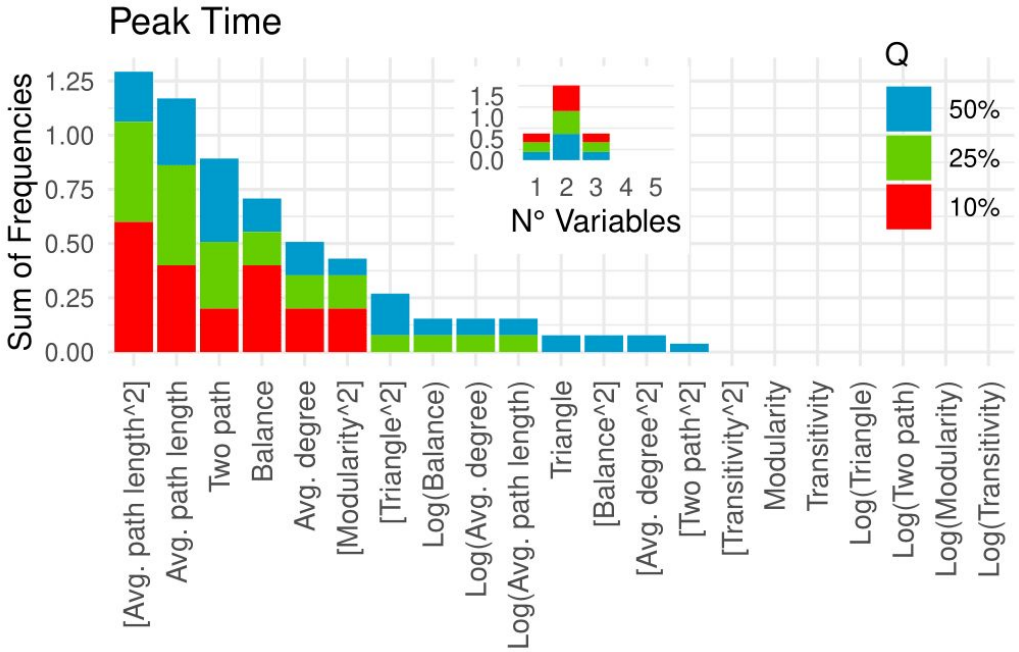
- Models with **2** *variables* performs better

Results - Peak Time



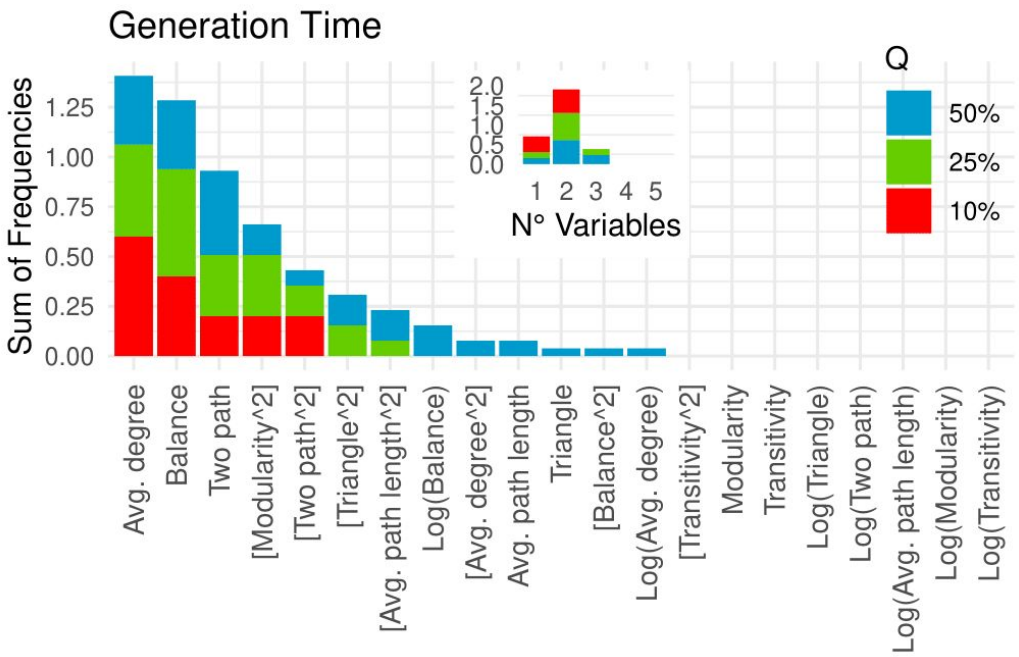
- Models with **2** *variables* performs better
- Once more **Avg. path length** is relevant (linear and quadratic form), along with **Balance**

Results - Peak Time



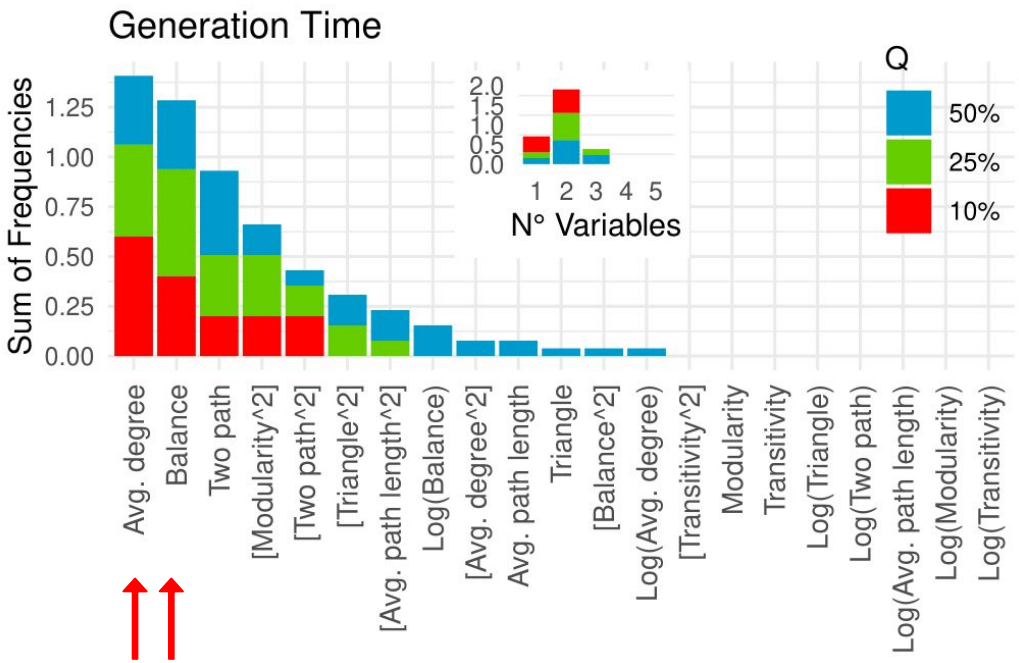
$$\text{Peak}_T = \text{Net-type} + \beta_0 \text{ balance} + \beta_1 [\text{ avg. path length}^2]$$

Results - Generation Time



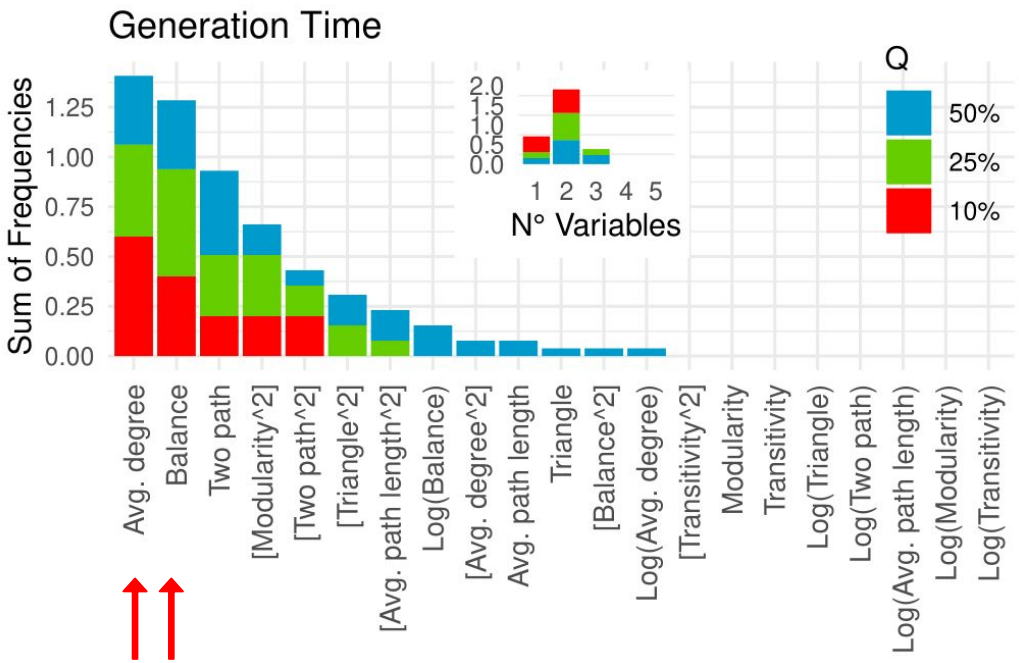
- The best models have only **1** or **2** *variables*

Results - Generation Time



- The best models have only **1** or **2** *variables*
- Clear prominence of **Avg. degree** and **Balance**…

Results - Generation Time



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  … but they shows high correlation

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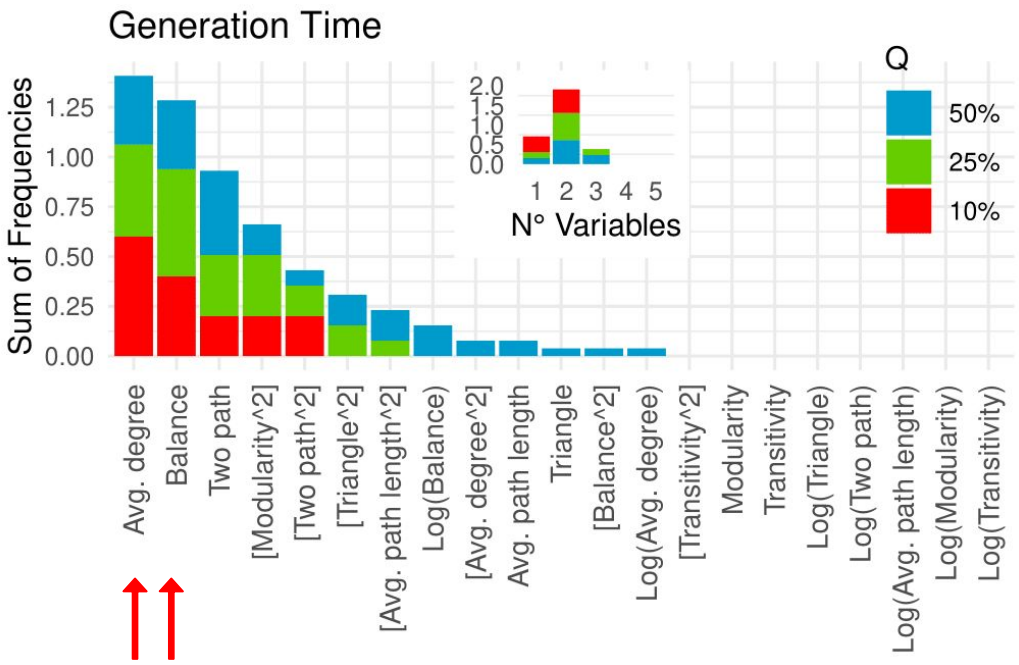
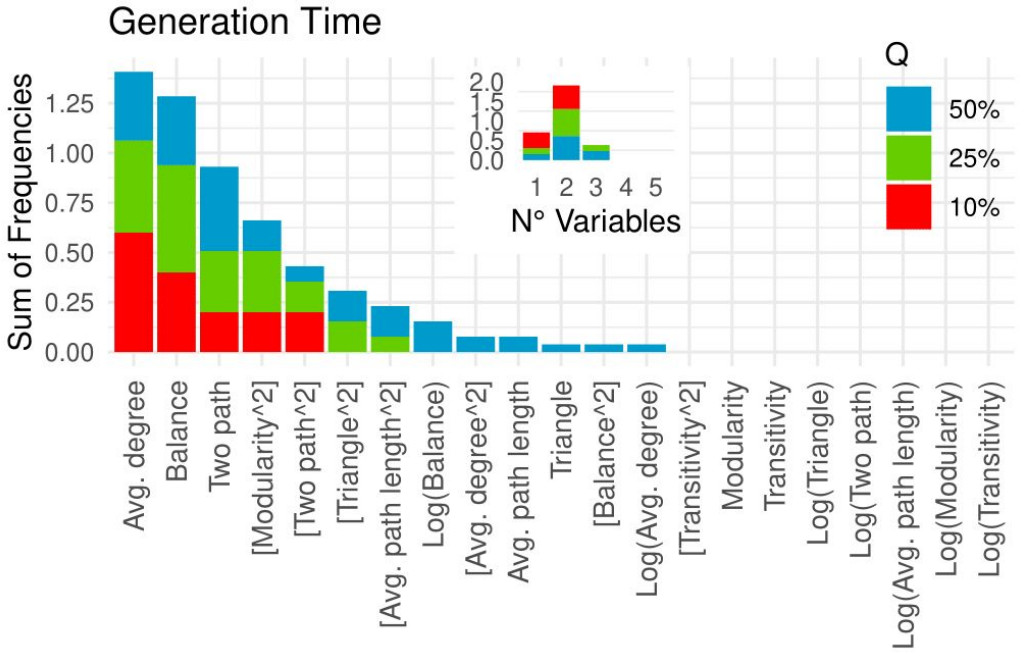


- The best models have only **1** or **2** *variables*
- Clear prominence of **Avg. degree** and **Balance**…

  … but they shows high correlation
- So we get Balance / Avg. degree along (optional) with other relevant variable

Results - Generation Time

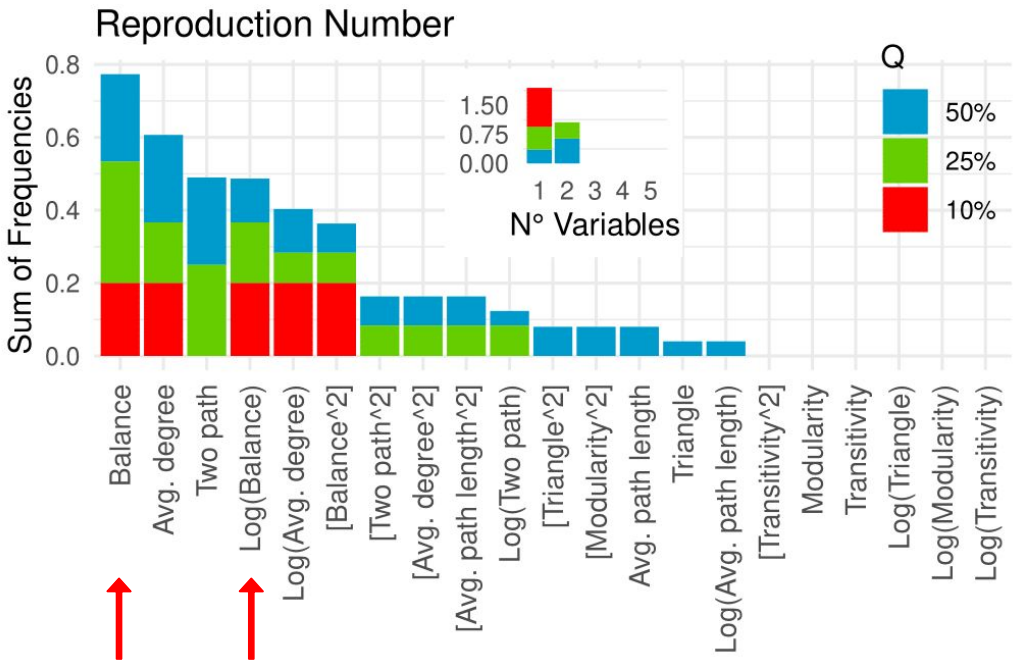


$$\text{Gen. Time} = \text{Net-type} + \beta_0 \text{ balance}$$

or

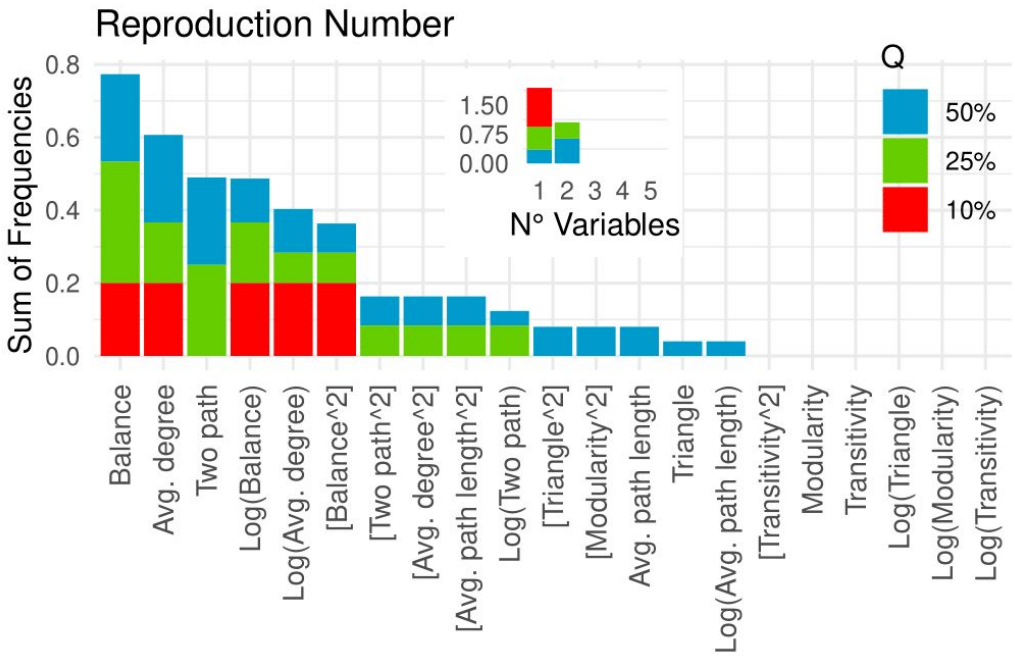
$$\text{Gen. Time} = \text{Net-type} + \beta_0 \text{ balance} + \beta_2 \left[\text{modularity}^2 \right]$$

Results - Reproductive Number



- The best models have only **1** *variable*
- That variable has to be **Balance** or **Avg. degree** (in his logarithmic or quadratic form)

Results - Reproductive Number



$$R_0 = \text{Net-type} + \beta_1 \log(\text{ balance })$$

Results

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$$\begin{aligned}\text{Gen. Time} = \text{Net-type} &+ \beta_0 \text{ balance} \\ &+ \beta_2 \left[\text{ modularity}^2 \right]\end{aligned}$$

$$\begin{aligned}\text{Peak}_T = \text{Net-type} &+ \beta_0 \text{ balance} \\ &+ \beta_1 [\text{ avg. path length}^2]\end{aligned}$$

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Results

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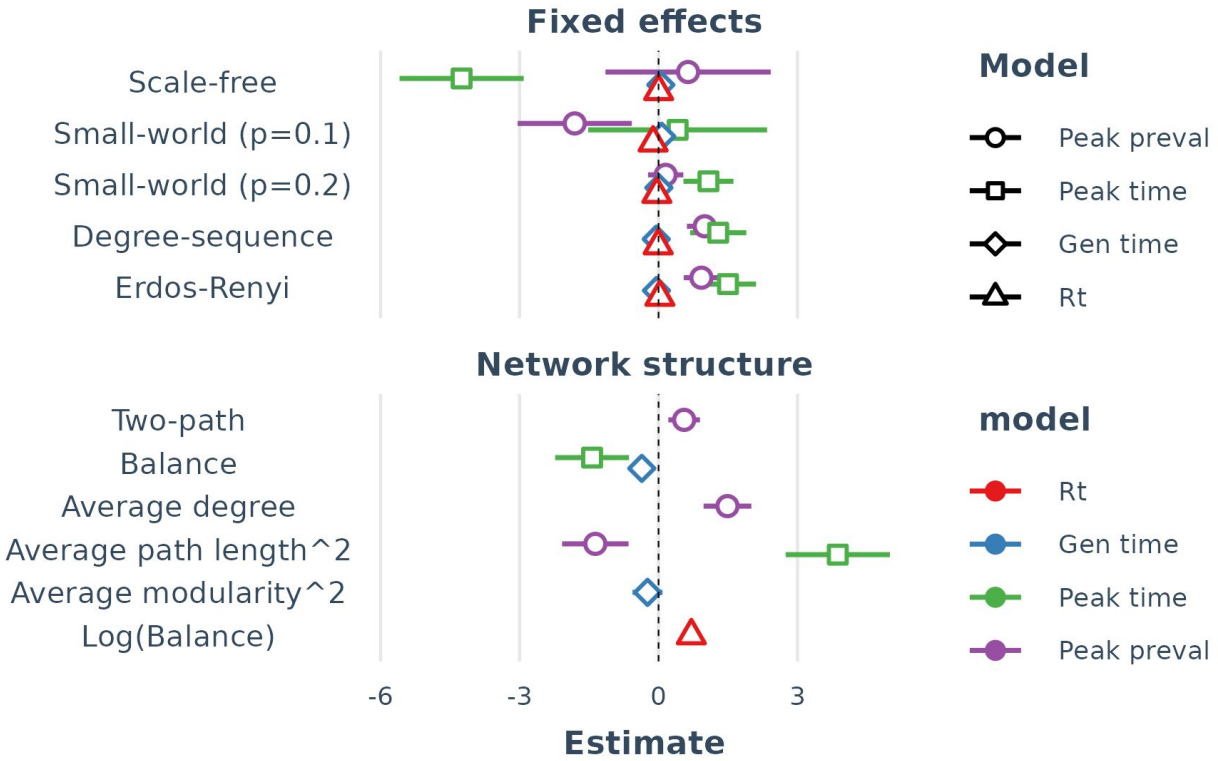

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  2. Have non-trivial forms

  3. Relevant role of Balance and Avg. path length

- Add more variables to **refine the work** $\rightarrow$ $\langle k^2 \rangle$

Thank you!

Reference

[1] C.-H. Li and A. M. Yousef, Bifurcation analysis of a network-based sir epidemic model with saturated treatment function, Chaos: An Interdisciplinary Journal of Nonlinear Science 29, 033129 (2019).

[2] J. Zhou, Y. Zhao, and Y. Ye, Complex dynamics and control strategies of seir heterogeneous network model with saturated treatment 10.2139/ssrn.4151291 (2022).

[4] Derek Meyer and George Vega Yon. "epiworldR: Fast Agent-Based Epi Models". In: The Journal of Open Source Software 8.90 (Oct. 2023). DOI: 10.21105/joss.05781. URL: https://joss.theoj.org/papers/10.21105/joss.05781.

[3] To calculate the transmission rate, we use the following formula: $\beta = \frac{\gamma}{(C/R + \gamma - 1)}$, with contact rate $C = 14$, reproductive $R = 2$, and $\gamma = 1/7$.

	Peak preval	Peak time	Gen time	Rt
Scale-free	0.638	-4.251***	0.050***	0.003
	(0.910)	(0.684)	(0.021)	(0.018)
Small-world (p=0.1)	-1.809***	0.413	0.069***	-0.117***
	(0.628)	(0.985)	(0.028)	(0.017)
Small-world (p=0.2)	0.154	1.078***	0.008	-0.036***
	(0.195)	(0.276)	(0.012)	(0.017)
Degree-sequence	0.997***	1.288***	-0.049***	-0.007
	(0.196)	(0.309)	(0.020)	(0.015)
Erdos-Renyi	0.925***	1.500***	-0.045***	0.029**
	(0.195)	(0.310)	(0.020)	(0.015)
Two-path	0.553***			
	(0.174)			
Balance		-1.434***	-0.361***	
		(0.407)	(0.006)	
Average degree	1.488***			
	(0.263)			
Average path length^2	-1.364***	3.870***		
	(0.366)	(0.574)		
Average modularity^2			-0.238*	
			(0.165)	
Log(Balance)				0.708***
				(0.097)
Num.Obs.	18011	18011	18009	18011
AIC	97940.8	114131.5	1600.7	77572.4
BIC	98018.8	114201.7	1670.9	77634.8

* p < 0.15, ** p < 0.1, *** p < 0.05