

Network Diffusion

Information and Influence

Individuals' choice depend on what other people do

- ▶ Information cascade
- ▶ Network effects
- ▶ Rich-get-richer dynamics

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Who influence whom

- ▶ Population-wide aggregate influence
- ▶ Local influence
 - ▶ Technology for chatting with friends and colleagues
 - ▶ Align political view with your friends

Homophily

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Local aspects of influence can motivate imitative behavior

Choices on a Social Network

Technology Adoption

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Individual behavior is influenced by the social network

Network coordination games

A simple model to study the behavior of individuals on social networks

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 - ▶ Nodes = Individuals
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A	a, a	$0, 0$
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Threshold and Cascade Dynamics

Threshold dynamics

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 - ▶ $d = \text{degree}$
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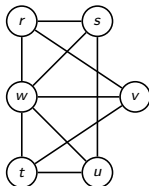
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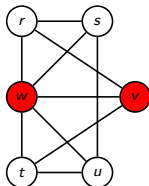
Examples

$$a = 3, b = 2 \rightarrow q = 2/5$$



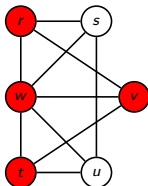
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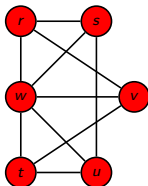
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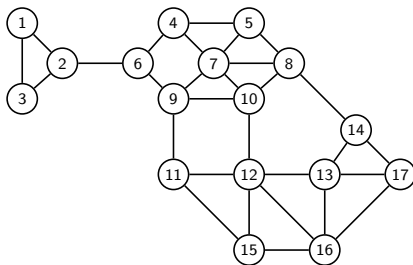
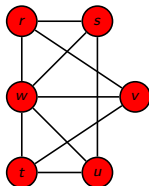
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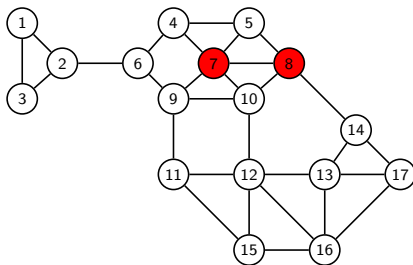
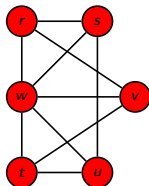
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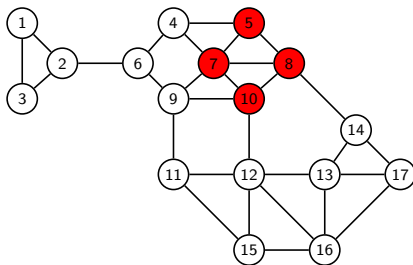
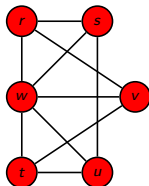
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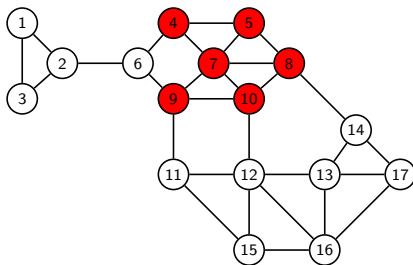
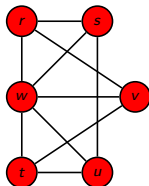
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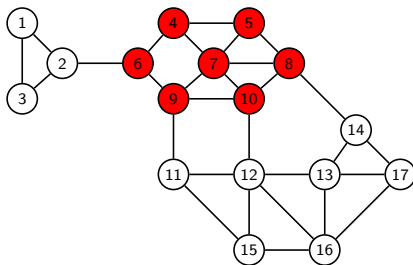
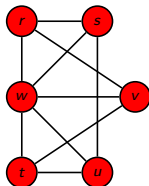
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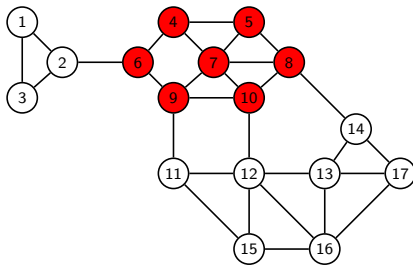
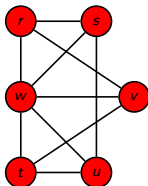
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How to increase influence?

- ▶ Raise the quality of the product (**relative advantage**)
- ▶ Increase the seed (**viral marketing**)

Complete Cascade and Clusters

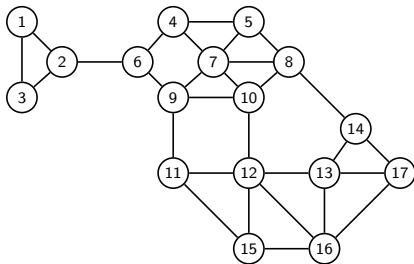
Cluster C of density p

Any node in C has at least a p fraction of neighbors in C

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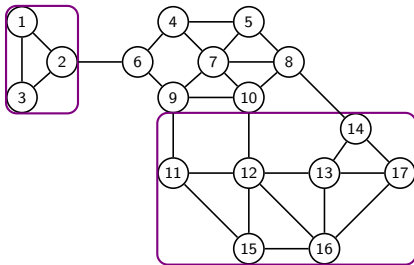
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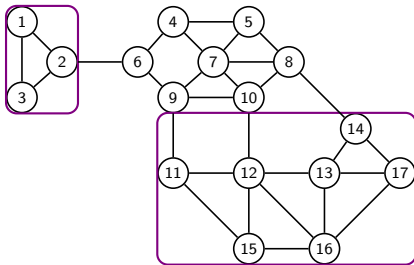
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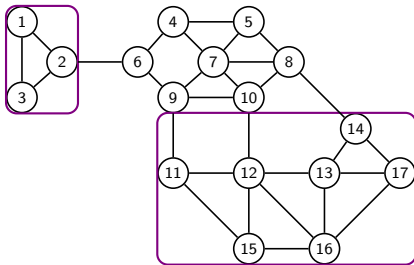


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- ▶ Node in a cluster not necessarily similar

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A cluster of density $1 - q$ is an obstacle to complete cascade

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- ▶ They help to diffuse awareness of an innovation

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Extensions: Personal Thresholds

► Personalized Edge Game Payoffs

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- Diffusion depends on **influenceable** people
- Complete diffusion if and only if no **blocking cluster** C
 - any node in C has a fraction $1 - q_v$ of neighbors in C

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Another Model

Previous Model

- ▶ Social contagion (it requires decision making)

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We define simple random models for the spread of epidemics in contact network

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- ▶ Repeat as long as there is at least one newly infected person

Branching Process

Examples

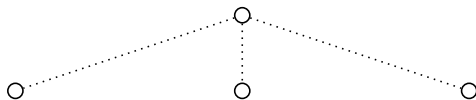
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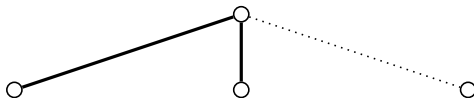
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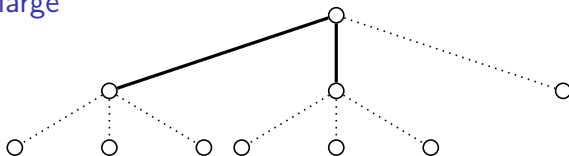
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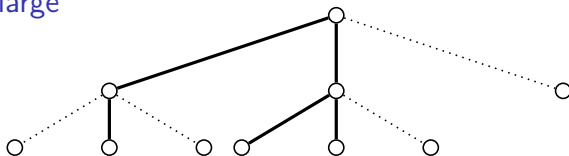
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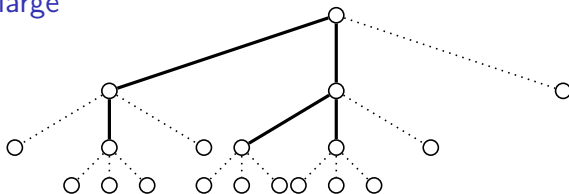
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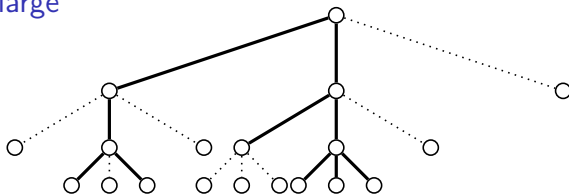
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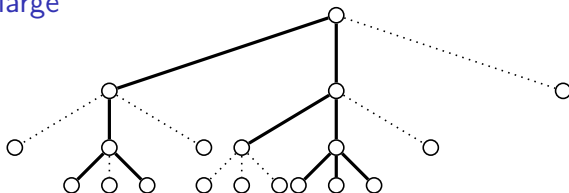
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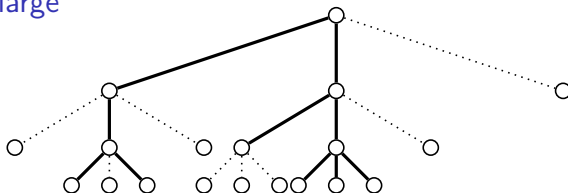
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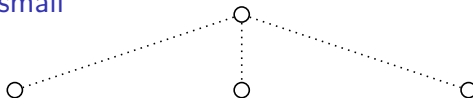
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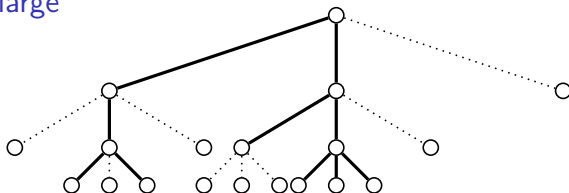
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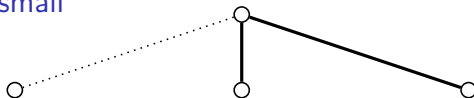
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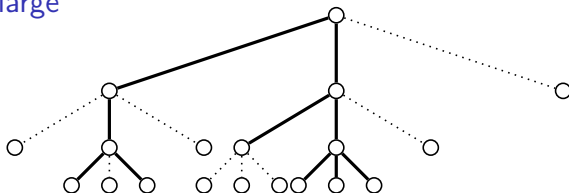
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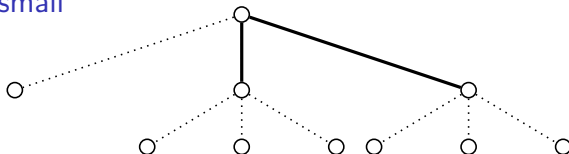
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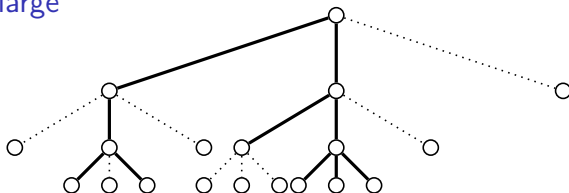
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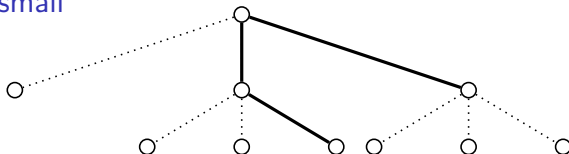
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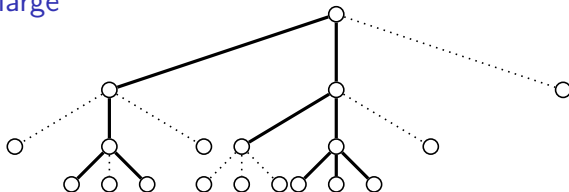
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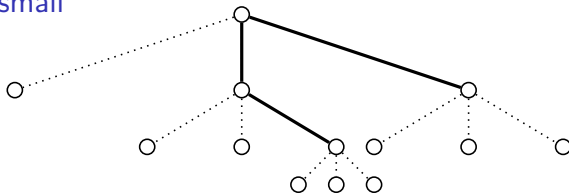
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The basic reproductive number R

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Expected number of new cases caused by a single individual

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The dichotomy for branching process

The dichotomy

- ▶ If $R < 1$, then with probability 1, the disease dies out after a finite number of steps
- ▶ If $R > 1$, then with probability greater than 0 the disease persists by infecting at least one person in each wave

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- ▶ Quarantining individuals (reduces k)
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A more complex model

Node states

- ▶ **Susceptible (S)**: the node has not been infected and it can be infected
- ▶ **Infected (I)**: the node is actually infected and can infect other nodes
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The contact network

Direct graph modeling contacts

- ▶ It allows to represent both mono-directional and bidirectional epidemics

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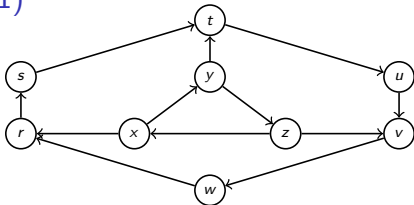
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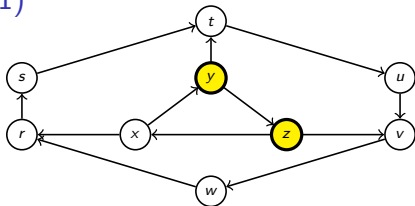


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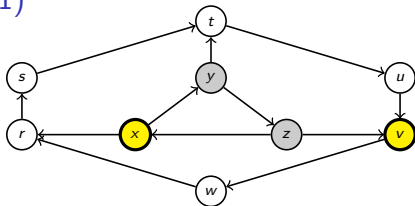


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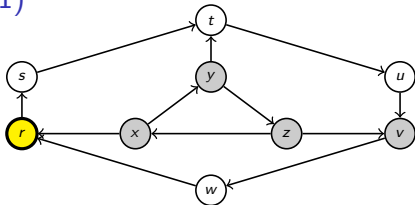


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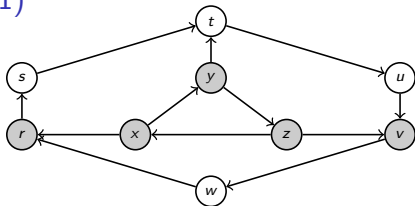


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 - ▶ Early, middle and late periods of infection
- ▶ Time-mutating pathogen
 - ▶ Probabilities and infection periods change during the infection spread

The Basic Reproductive Number reloaded

Definition

The expected number of new cases of the disease caused by a single individual

- ▶ Alternative definition: The expected number of new cases caused by a randomly chosen individual

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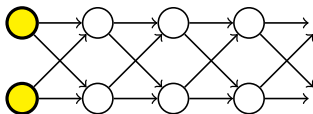
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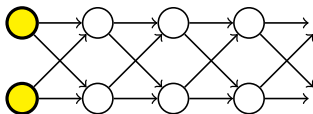
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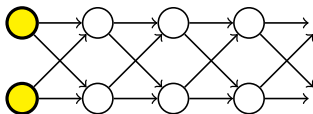
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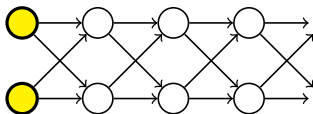
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- ▶ $R = 4/3 > 1$
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- Different network structure can be more or less conductive

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Adding the possibility of being reinfected

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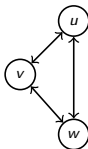
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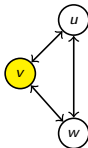
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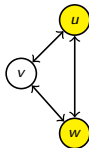
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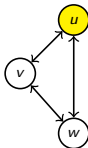
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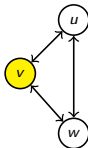
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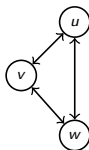
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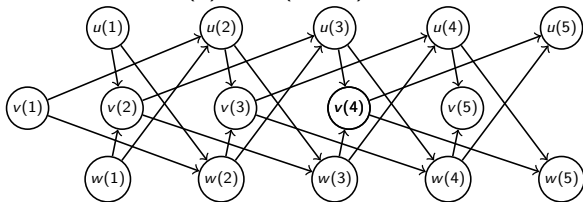
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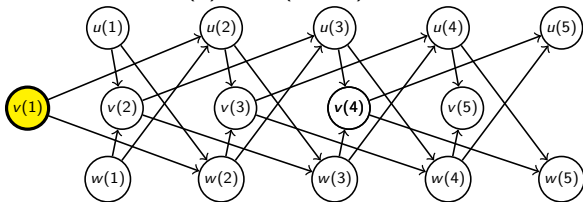
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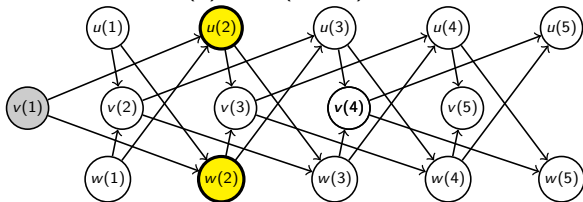
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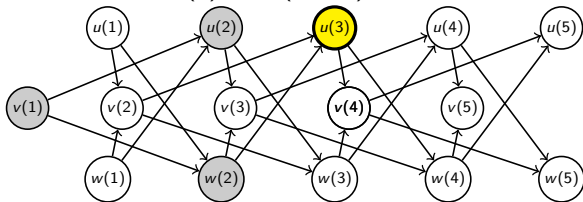
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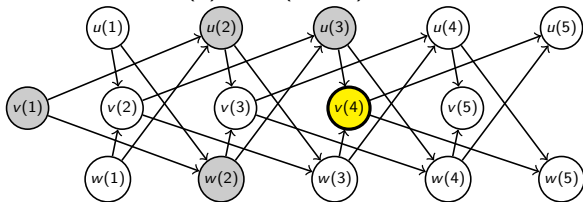
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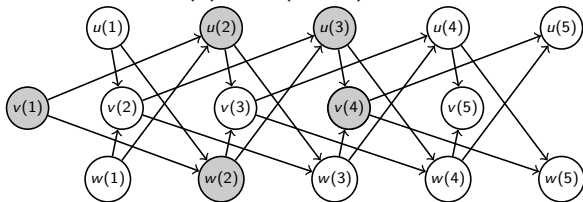
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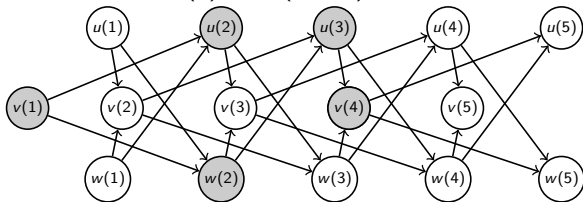
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SIS model = SIR model on the time-expanded contact network

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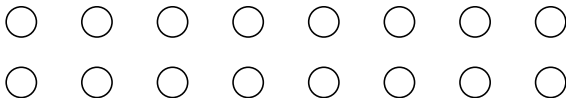
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 - ▶ neutral model (no selective advantage)

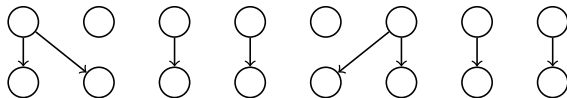
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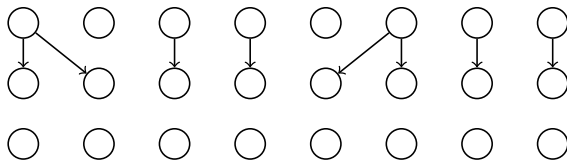
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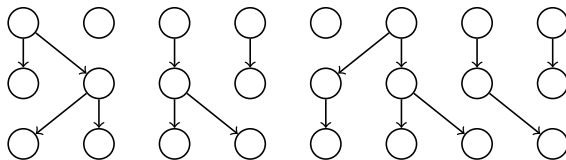
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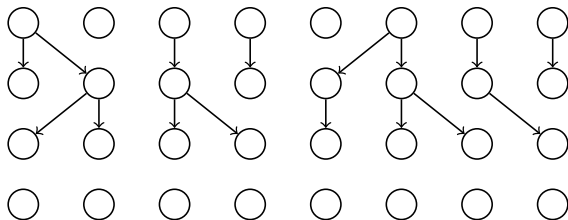
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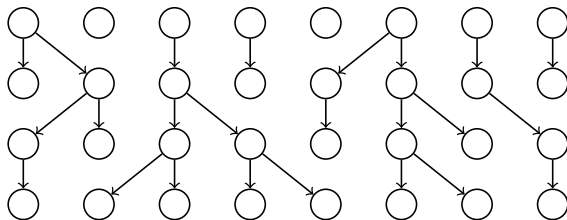
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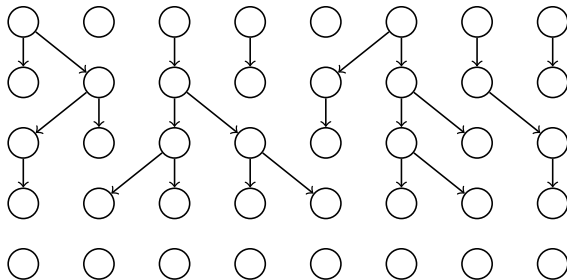
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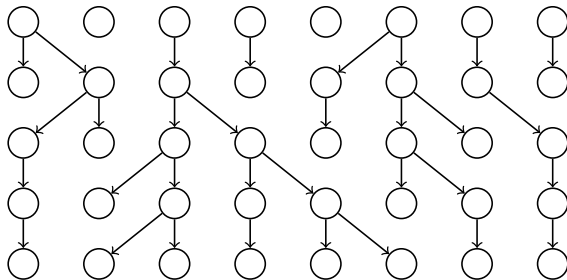
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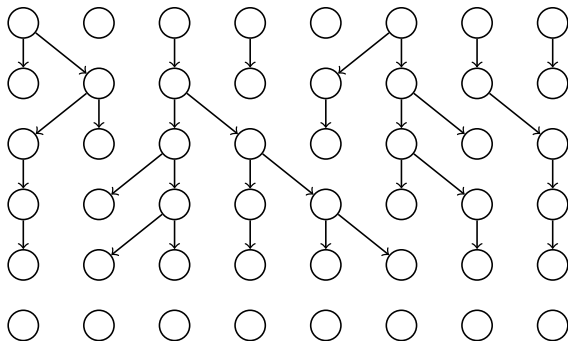
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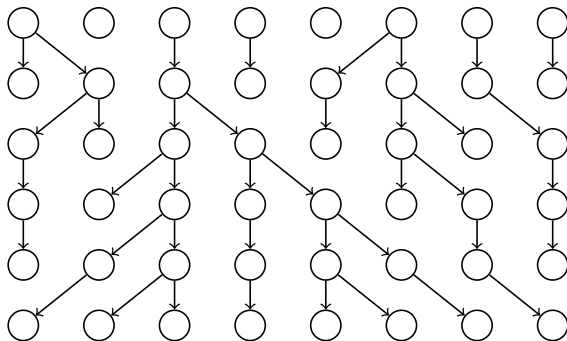
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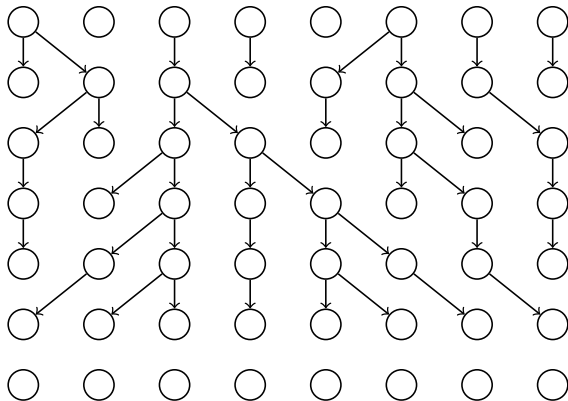
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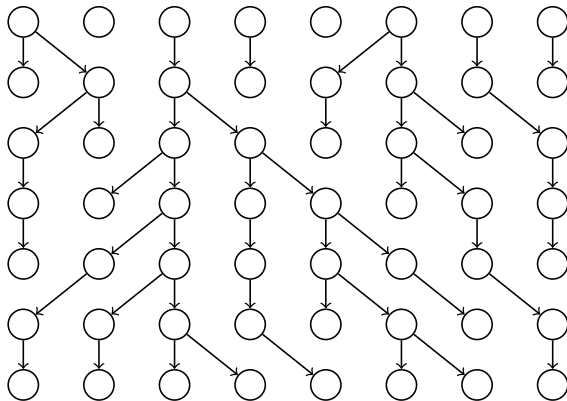
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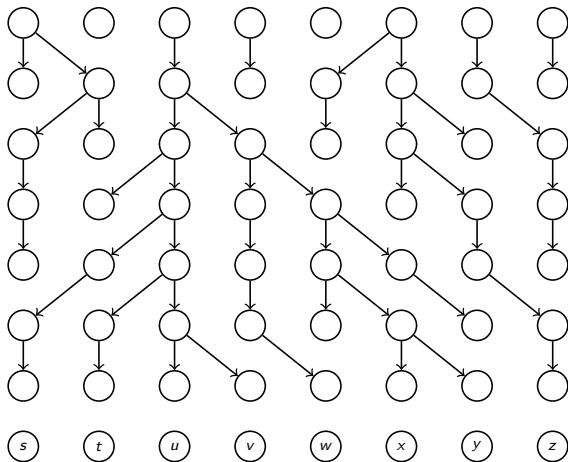
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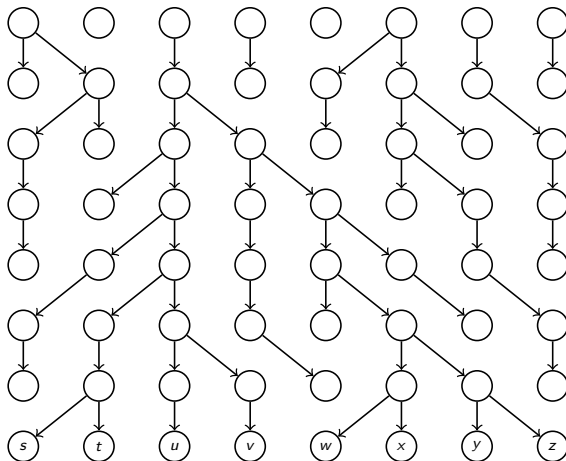
The mitochondrial Eve



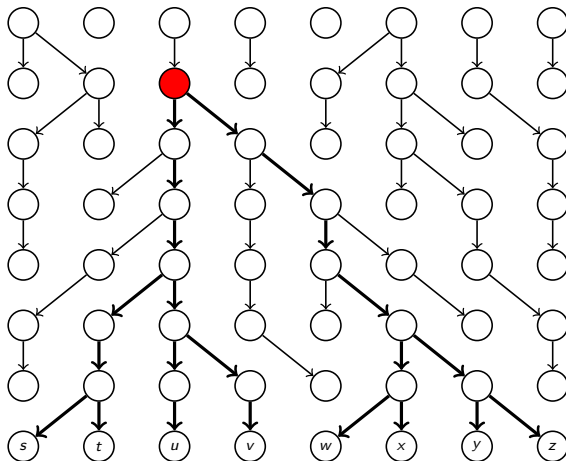
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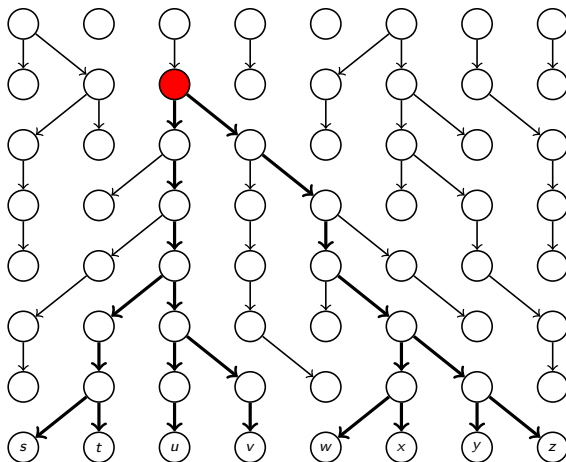
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Does a common ancestor always exist?

The mitochondrial Eve

Wright-Fisher model as a branching process with multiple roots

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- ▶ **Branching process:** from the root and proceed to children
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The coalesce process

- ▶ Start with a population of size N
- ▶ At each time step, every member chooses a parent randomly
- ▶ If two members choose the same parent, their lineage **coalesce**

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There is a mitochondrial Eve that lived 100,000 - 200,000 years ago