Network Modelling

Modern Techniques in Modelling

Overview

Discuss network modelling concepts (~20 min)

Practical 1: Introduction to the igraph package (~40 min)

BREAK (~30 min)

Reed-Frost SIR Model (~10 min)

Practical 2: A network model of mpox transmission (~40 min)

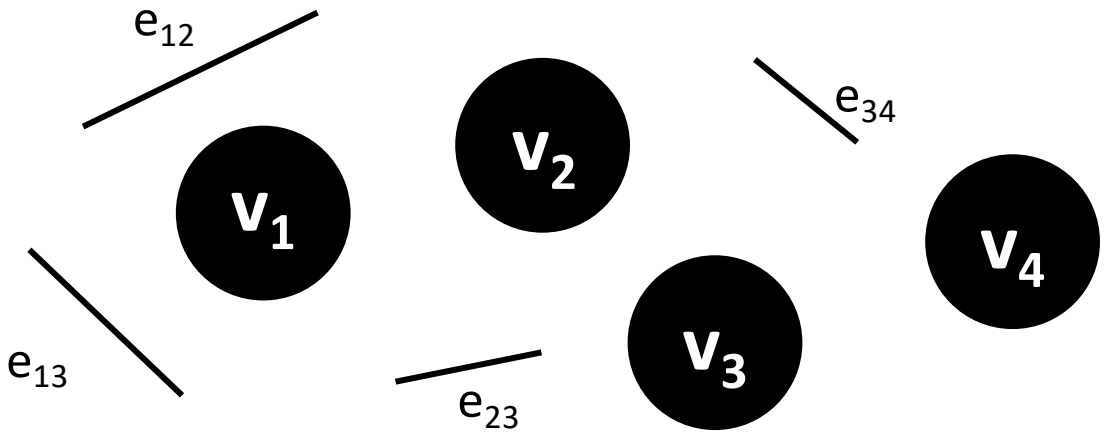
Closing discussion (~10 min)

Part 1:

What are Network Models?
Why Use Networks?

What are Network Models?

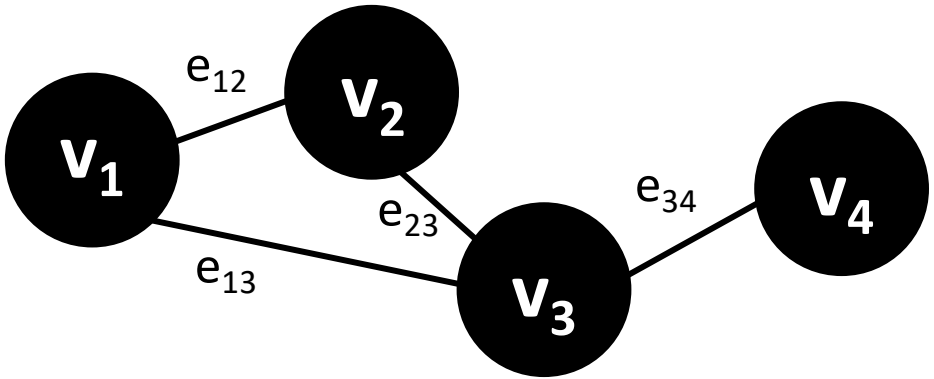
Network = set of vertices ***V*** and edges ***E***



What are Network Models?

Network = set of vertices ***V*** and edges ***E***

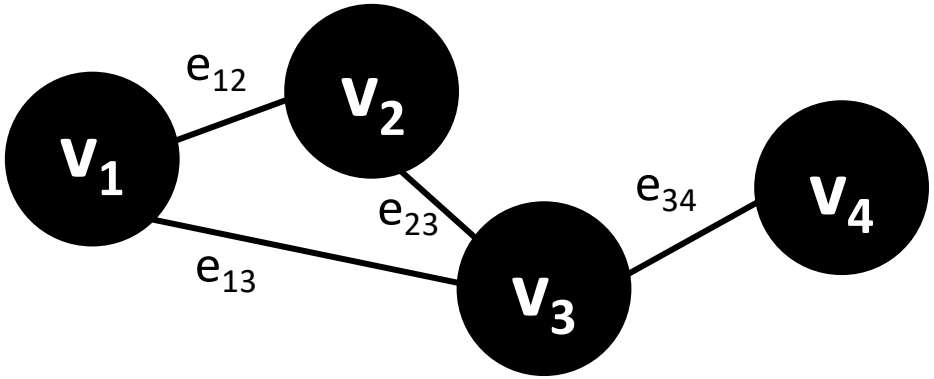
an edge e_{ij} in ***E*** connects two vertices v_i, v_j in ***V***



What are Network *Models*?

Modelling: representing real phenomena by abstractions

How might networks represent infectious disease?



Some possible answers:

Generally: represent process over the *network* (e.g., transmission) + vertex *state* (e.g., SIR)

Useful to think about *contacts*:

- when transmission depends on specific contacts (e.g., STIs)
- if there is heterogeneity / structure to contacts (e.g., influenza in schools *vs* workplaces *vs* households)

Spatial relationships:

- mosquitoes moving between adjacent households
- people migrating from one region to another

Why use networks?

Shared features of those examples:

- “realism” aspect of the model (e.g. vs homogeneous mixing)
- clear translation between observations and model
- generalisation: e.g., why does R_0 vary between contexts? same pathogen & host - but different transmission networks

Practical 1

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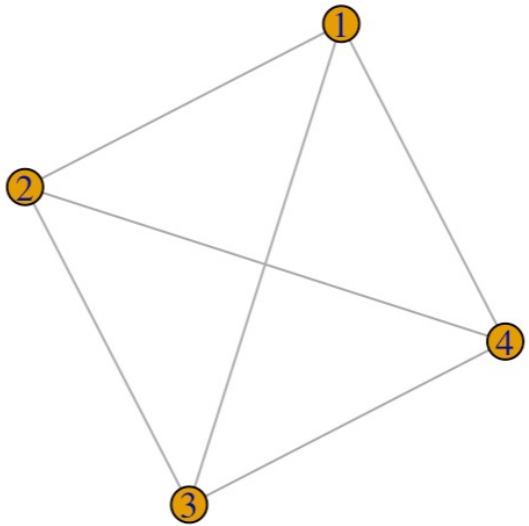
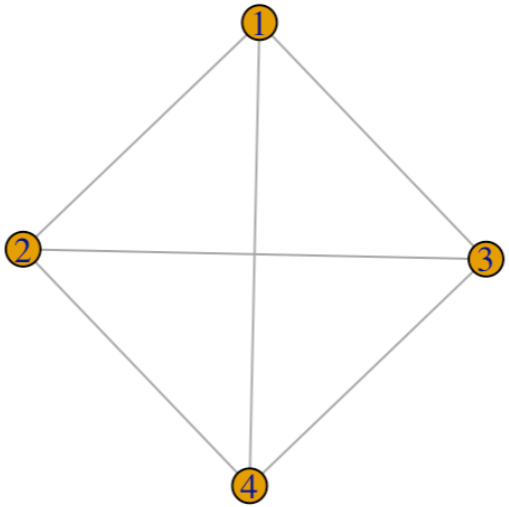
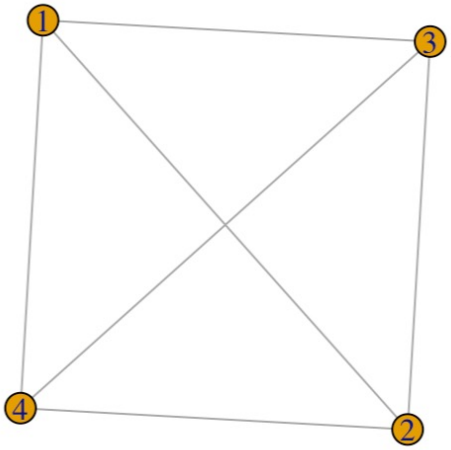
Introduction to the igraph package

Questions from the practical

1. Run the `plot(gr)` line multiple times. The plot changes. Does the graph change?



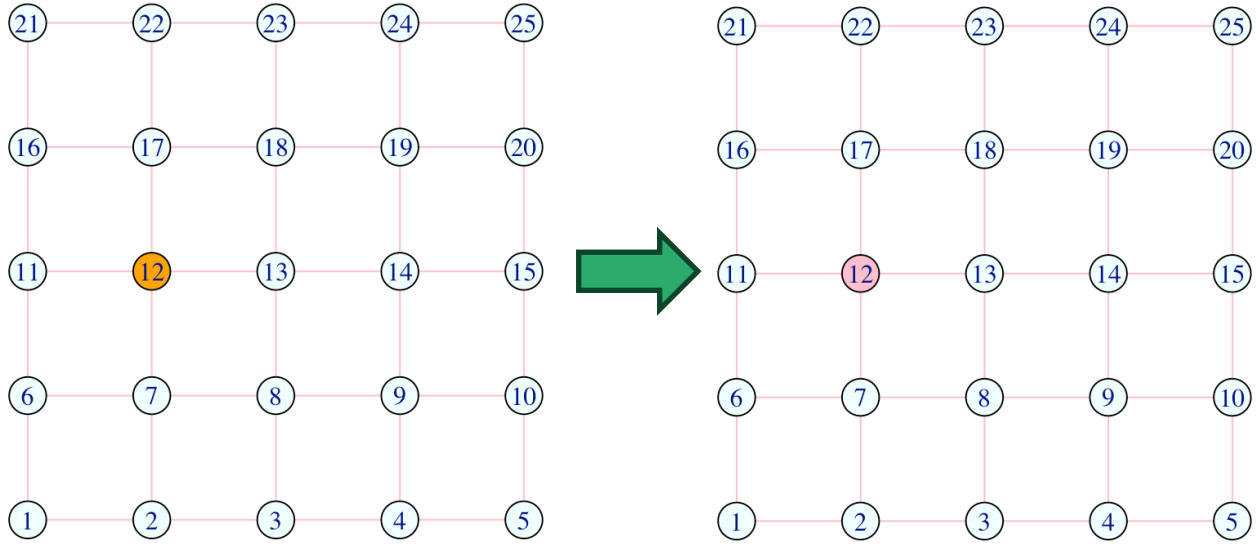




Questions from the practical

```
V(network)[12]$color <- "orange"
V(network)[color == "orange"]$color <- "pink"
```

2. What do the above lines do?



While the first line selects a specific vertex (#12), the second line selects all vertices that have `color == "orange"` — this will be useful when we use vertex properties to represent states (e.g. S, I, R).

Questions from the practical

```
V(network)[.nei(color == "pink")]$color <- "pink"
plot(network)
```

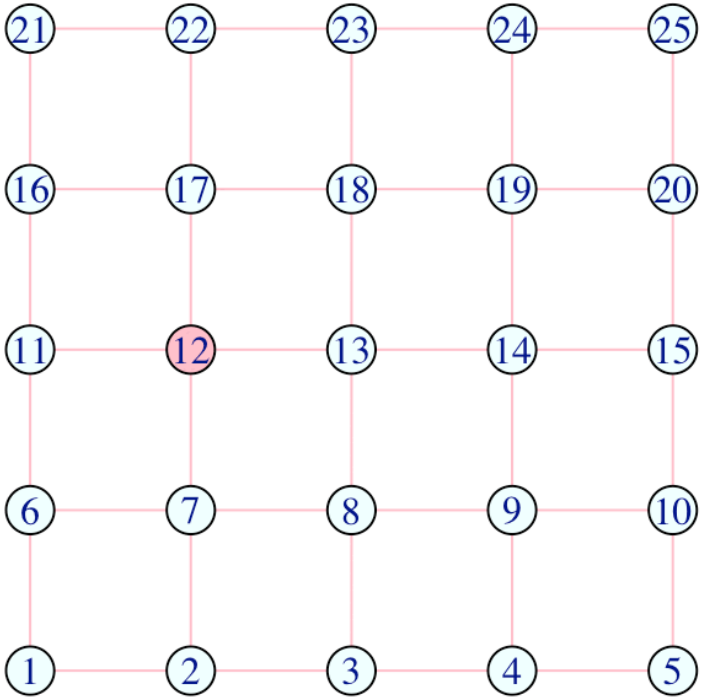
3. What is the code above doing? What happens if you re-run the two lines above several times?

Questions from the practical

```
V(network)[.nei(color == "pink")]$color <- "pink"
plot(network)
```

3. What is the code above doing? What happens if you re-run the two lines above several times?

What relevance might selecting neighbours of vertices have for modelling infectious disease transmission?



Coffee break

Part 2:

A network SIR model for mpox transmission

In this hour…

1. Describe the “Reed-Frost” model
2. Describe how this model can be implemented on a network
3. Practical: Model mpox transmission on a sexual network

The Reed-Frost model

Population, ***N***, of hosts

"Time" in steps (generations): ***t***, ***t+1***, …

Hosts either ***S****usceptible*, ***I****nfectious*, or ***R****emoved*

When ***I*** and ***S*** interact at ***t***,
probability ***p*** that the ***S*** becomes ***I*** at ***t+1***
(i.e., stochastic infection)

All ***I*** hosts at a time step ***t*** become ***R*** at ***t+1***

This can be implemented on a network…

Population, ***N***, of hosts

“Time” in steps: ***t***, ***t+1***, …

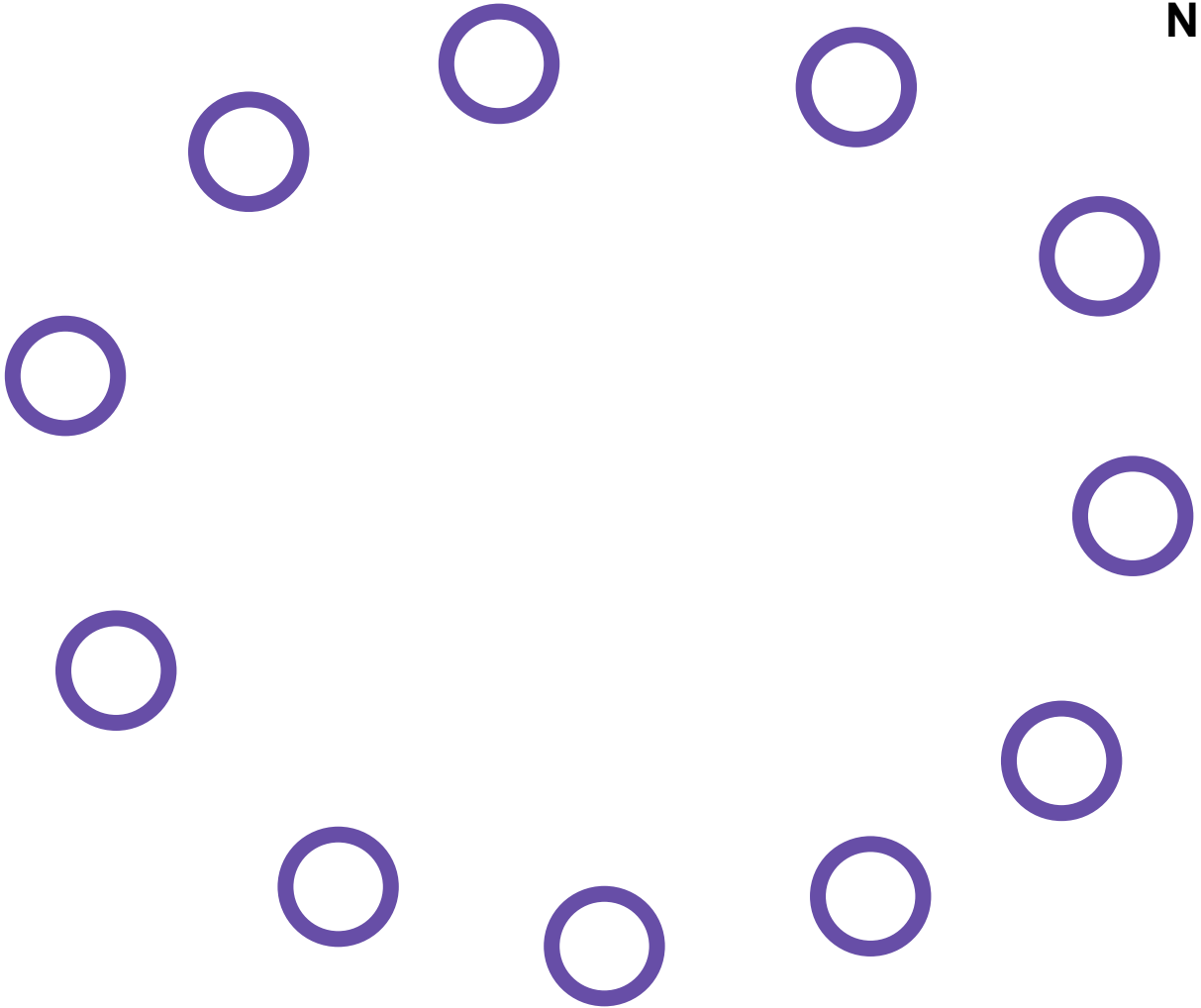
Hosts either ***Susceptible***, ***Infectious***, or ***Removed***

Each time step, ***all*** hosts **interact**

When ***I*** and ***S*** interact at ***t***, probability ***p*** that the ***S*** becomes ***I*** at ***t+1***

All ***I*** hosts at a time step ***t*** become ***R*** at ***t+1***

N = 11



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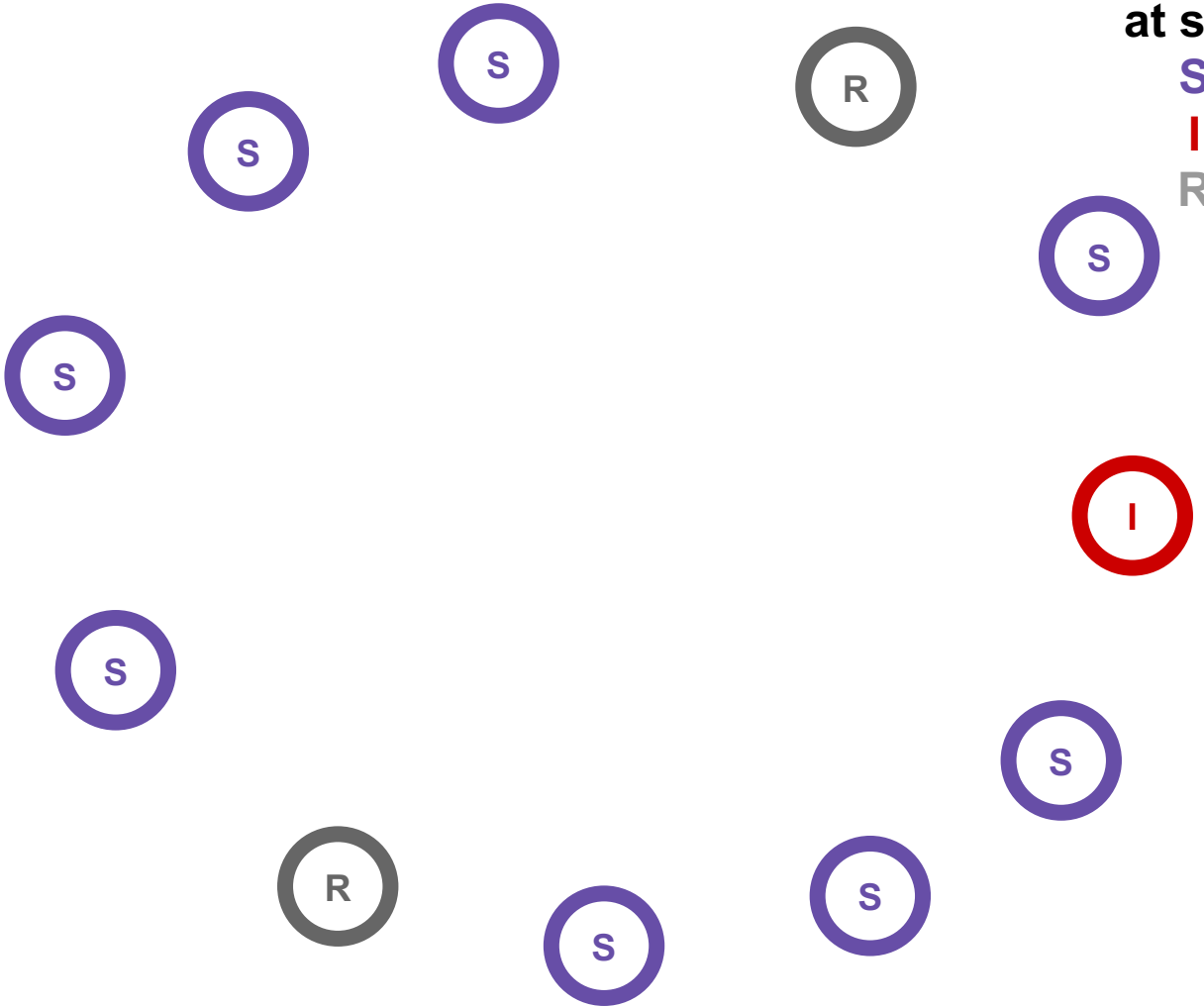
"Time" in steps: ***t***, *t+1*, …

Hosts either ***Susceptible***, ***Infectious***, or ***Removed***

Each time step, ***all*** hosts **interact**

When *I* and *S* interact at *t*, probability *p* that the *S* becomes *I* at *t+1*

All *I* hosts at a time step *t* become *R* at *t+1*



at some *t*,

S = 8

I = 1

R = 2

Population, ***N***, of hosts

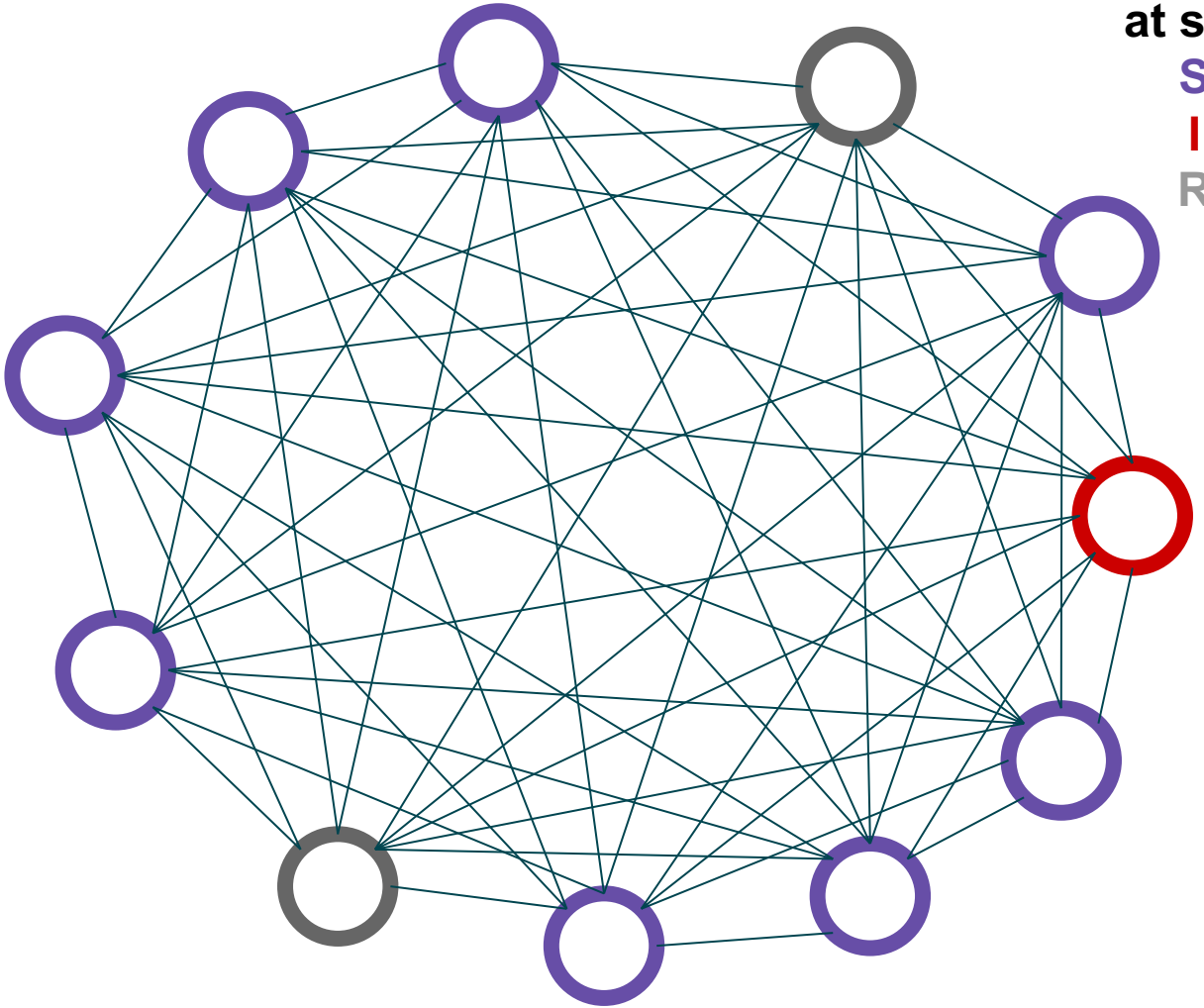
"Time" in steps: ***t***, *t+1*, …

Hosts either ***Susceptible***, ***Infectious***, or ***Removed***

Each time step, ***all neighbours*** **interact**

When *I* and *S* interact at *t*, probability *p* that the *S* becomes *I* at *t+1*

All *I* hosts at a time step *t* become *R* at *t+1*



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When ***I*** and ***S*** **interact** at ***t***, probability ***p*** that the ***S*** becomes ***I*** at ***t+1***

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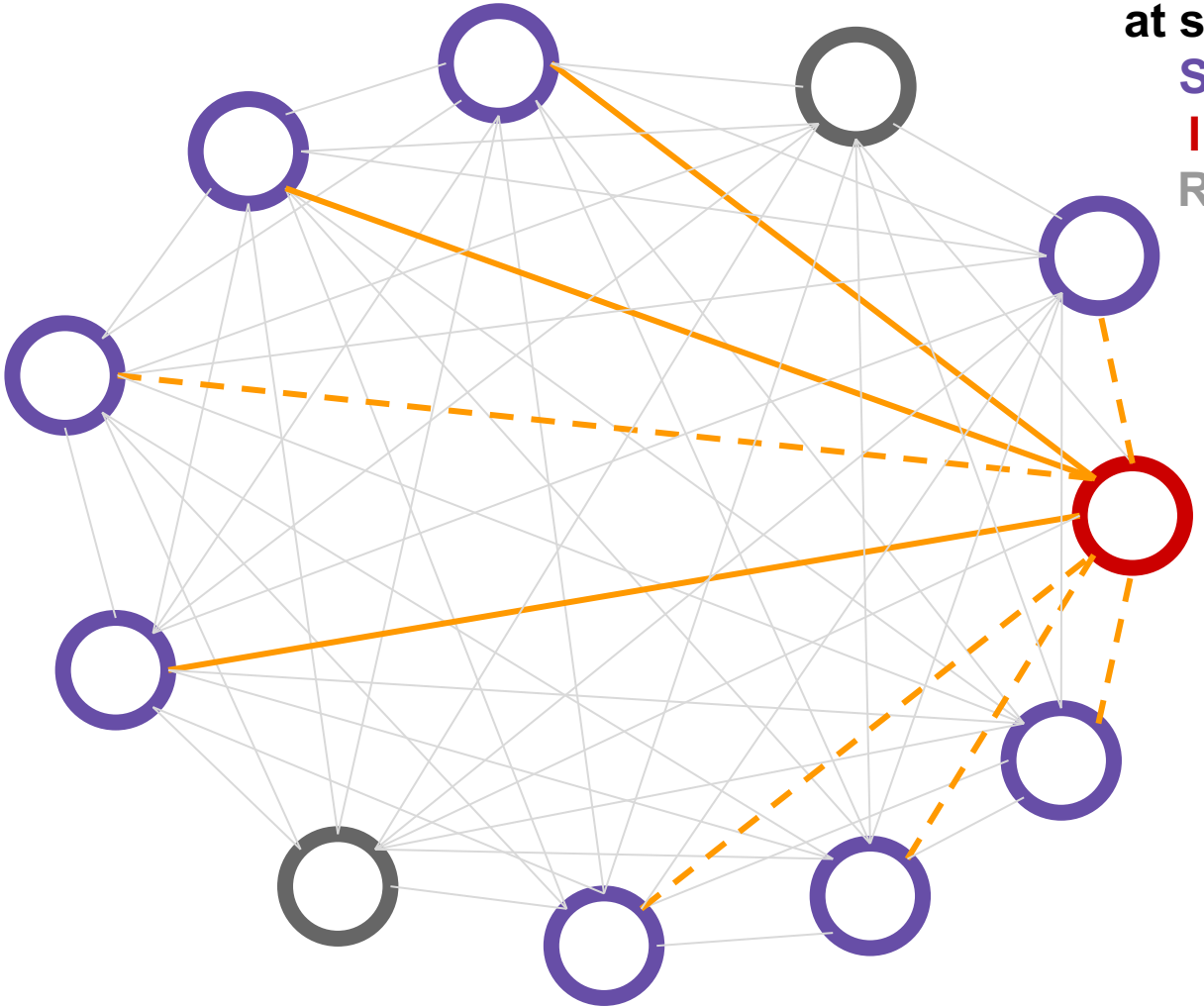

Population, ***N***, of hosts

"Time" in steps: ***t***, *t+1*, …

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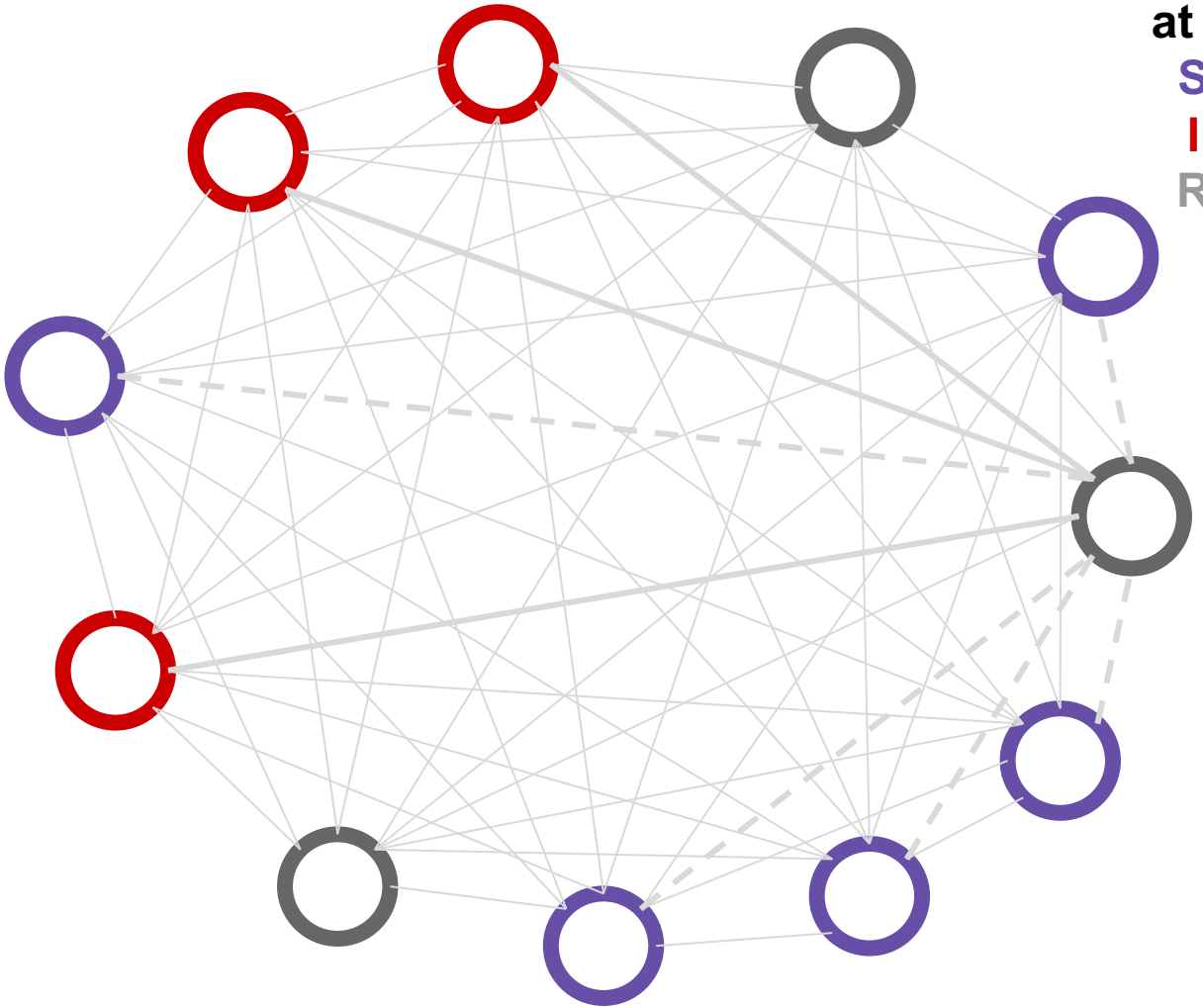
All ***I*** hosts at a time step ***t*** become ***R*** at ***t+1***



at *t + 1*,
S = 5
I = 3
R = 3

Mpox

Monkeypox virus, which causes mpox, spreads by close contact

Flu-like symptoms give way to rash especially on hands and feet, anogenital region, throat, trunk

Clade I and Clade II differ in transmission characteristics and severity

The median incubation period for the 2022 Clade IIb outbreak was 9 days (IQR: 5–13 days; McFarland et al., Euro Surveill.[1])

Transmission of Clade II has often been primarily among sexual networks of GBMSM due to close contact

[1] https://doi.org/10.2807/1560-7917.ES.2023.28.27.2200806

Practical 2

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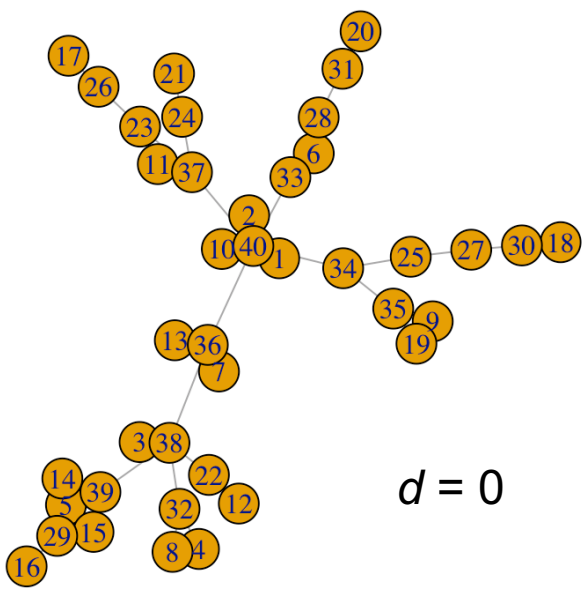
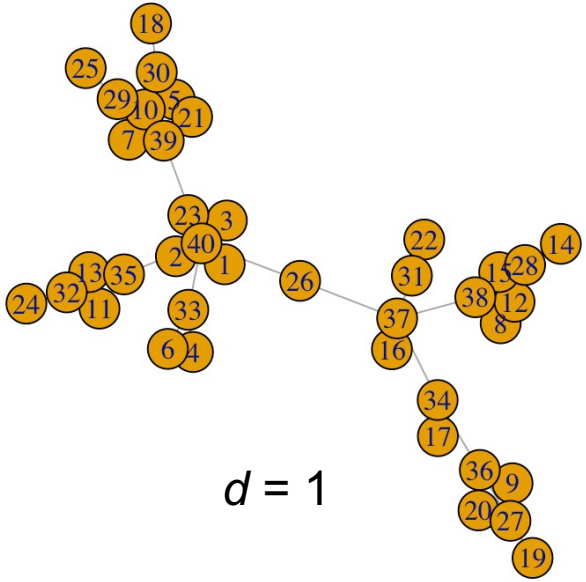
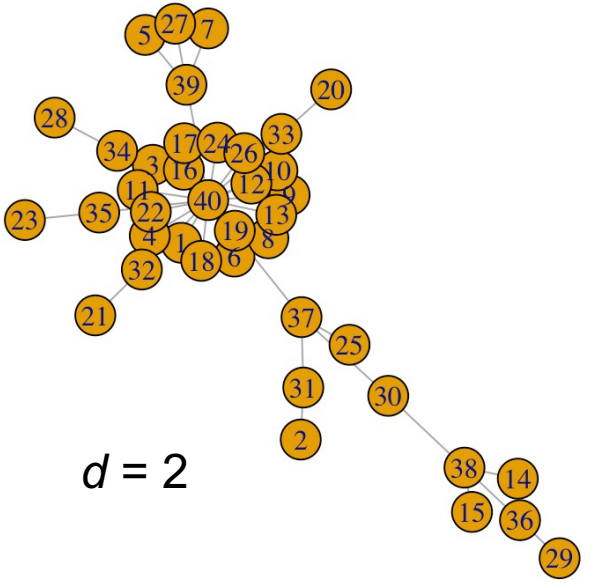
A network model of mpox transmission

Questions from the practical

1. Try varying the `d` parameter for `create_network()` between 0 and 2. What changes about the network?

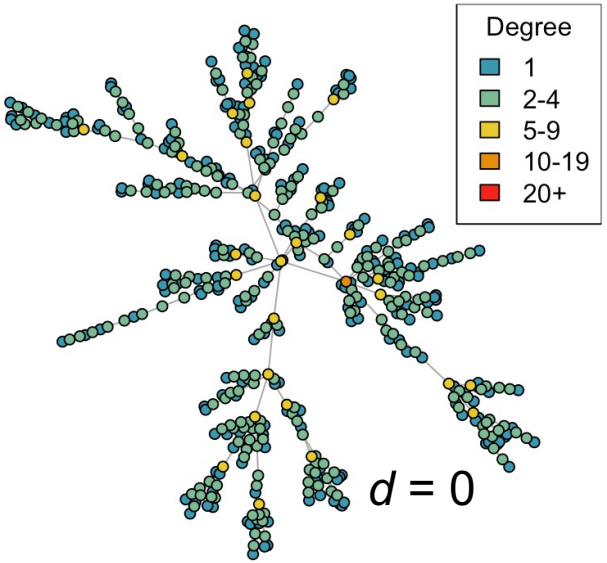


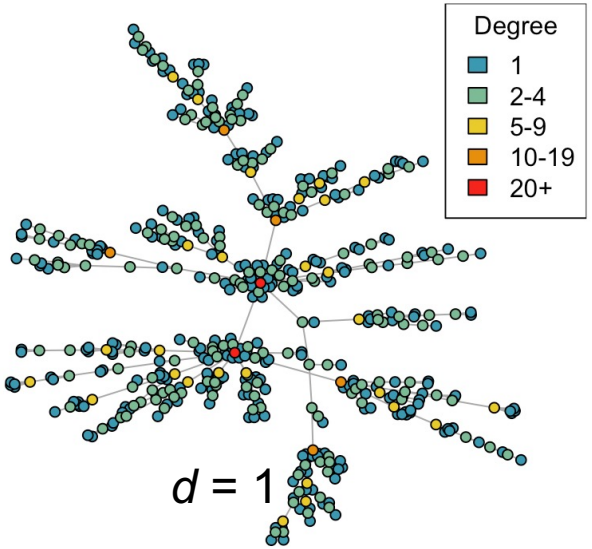


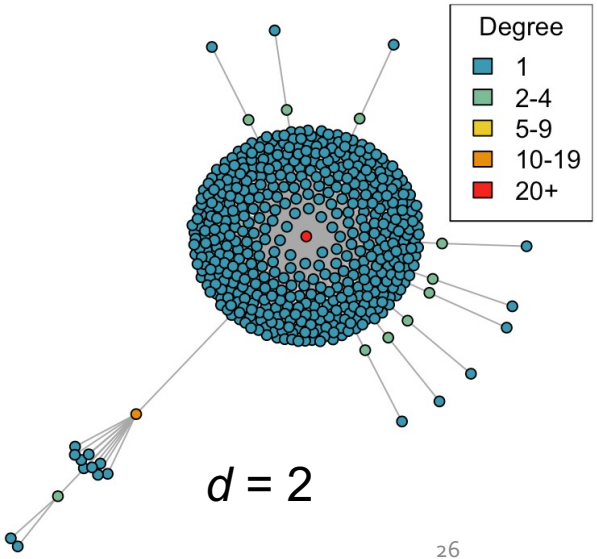


Questions from the practical

2. Plot using `plot_degree()` for 500 nodes…







Questions from the practical

```
net <- create_network(500, 1)

net <- network_step(net, p = 0.8)
plot_state(net)
```

3. After creating your network with the first line above, run the last two lines repeatedly to watch the network model evolve.

Questions from the practical

```
net <- create_network(500, 1)

net <- network_step(net, p = 0.8)
plot_state(net)
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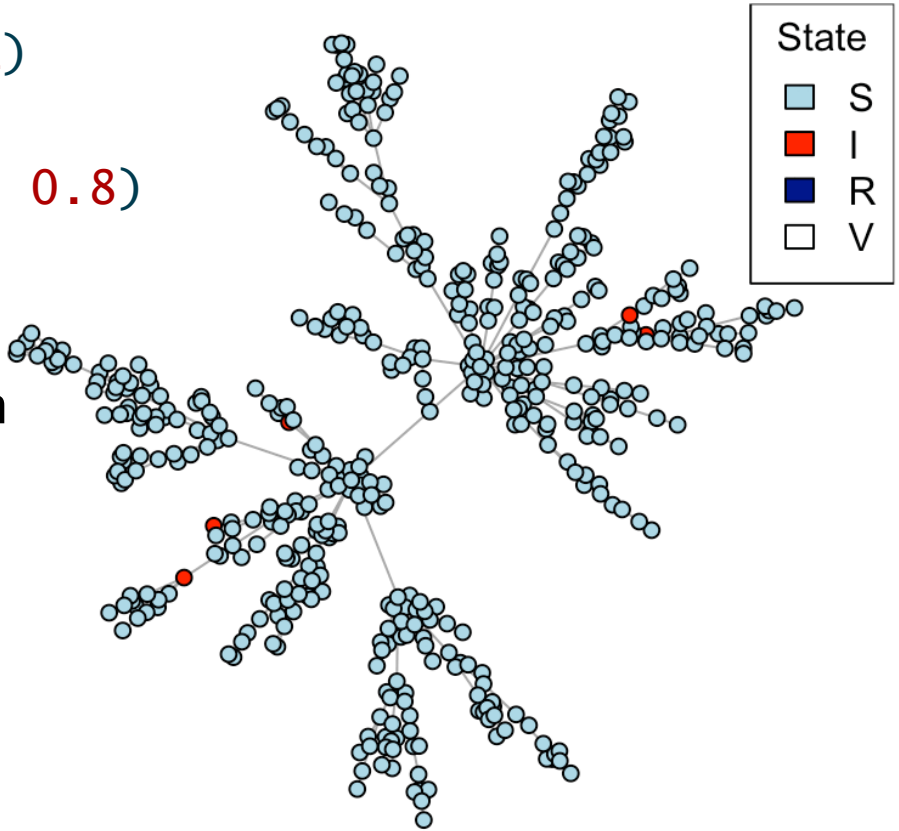

Questions from the practical

4. How does the preferential attachment parameter (`create_network` parameter `d`) affect the final outbreak size?

Summary of 100 runs

d	Final outbreak size Median (90% CI)
0.0	207 (84–308)
1.0	261 (131–335)
2.0	397 (379–415)

(Tip: quicker to run if you remove the plotting and pausing statements from `run_model`.)

Bonus material

Further “bonus” examples in the practical explore introducing vaccination to the model, and explores the impact of targeting vaccination to the least-connected or to the most-connected individuals.

Review

Introduced network modelling concepts

Discussed and implemented Reed-Frost ***SIR*** as a network model

Demonstrated strengths of network approach

Closing questions?

For early discussion of Reed-Frost Model, see e.g. *An examination of the Reed-Frost theory of epidemics. Abbey H. Hum Biol. 1952 Sep; 24(3):201-33.*