

# ITAO\_80870\_class\_10\_canvas

T. Zwiller

2024-04-17

## #1. Loading iGraph, GGraph, and NetDiffuse

```
#loading in the needed libraries
```

```
library(igraph)
library(ggraph)
library(netdiffuseR)
```

## #2. Loading in Egocentric Network Data

```
#loading in the edge and node data
```

```
edges <- read.csv('/Users/TomTheIntern/Desktop/Mendoza/Mod 4/Networks/Lab 2/edgelist.csv')
nodes <- read.csv('/Users/TomTheIntern/Desktop/Mendoza/Mod 4/Networks/Lab 2/nodelist.csv')
```

## #3. Making a directed iGraph Object

```
#making the iGraph
```

```
net <- graph_from_data_frame(edges, directed = F, vertices = nodes)
net
```

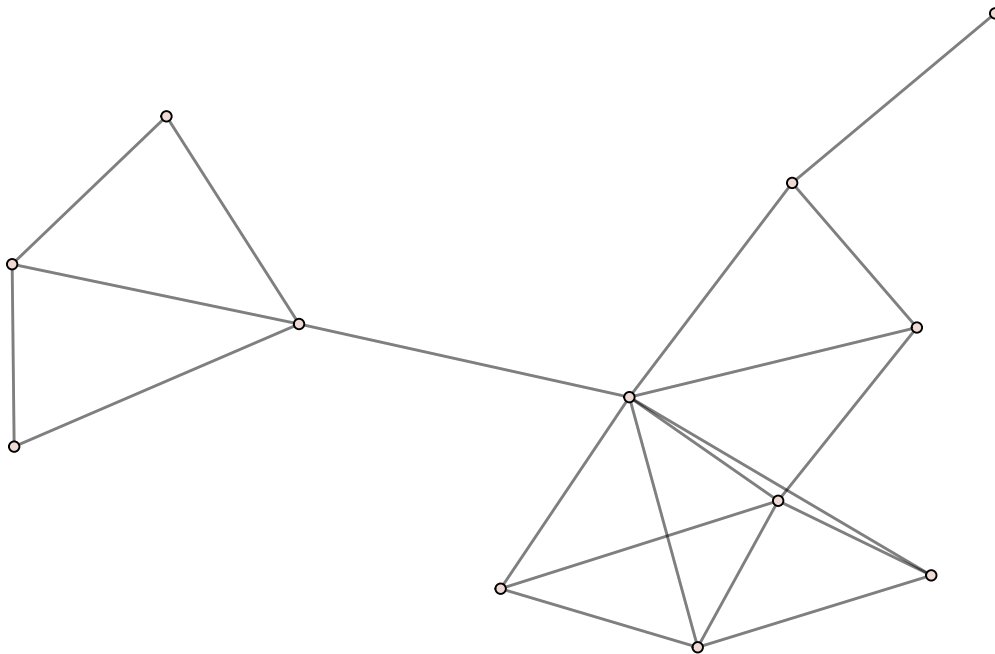
```
## IGRAPH 04c964a UN-- 12 40 --
## + attr: name (v/c), Name (v/c), Age (v/n), Gender (v/c), ego (e/c),
## | alter (e/c), type (e/c), strength (e/n)
## + edges from 04c964a (vertex names):
## [1] 1 --2 1 --2 1 --5 1 --5 1 --3 1 --3 1 --4 1 --4 1 --6 1 --6
## [11] 1 --7 1 --7 1 --10 1 --10 2 --4 2 --4 2 --3 2 --3 3 --4 3 --4
## [21] 4 --6 4 --6 4 --5 4 --5 3 --5 3 --5 9 --10 9 --10 10--11 10--11
## [31] 10--12 10--12 9 --12 9 --12 11--12 11--12 6 --7 6 --7 7 --8 7 --8
```

## #4. Visualize Your Network

```
#making the plot
```

```
ggraph(net) +
  geom_edge_link(color = "black", alpha = 0.3) +
  geom_node_point(color = "black", fill = "#efd9d3", shape = 21) +
  theme_graph()
```

```
## Using "stress" as default layout
```



#5. Add 4 Ties, 4 Nodes, Remove 3 Ties, 3 Nodes And Rewire Network

```
library(igraph)

set.seed(000027)

# 1. Add your new ties
net2 <- igraph::add_edges(net, c(1, 8, 2, 9, 3, 12, 7, 12))

# 2. Delete those edges by ID
net2 <- igraph::delete_edges(net2, c(1, 10, 3, 4, 10, 11))

# 3. Add 4 brand-new vertices (scalar count)
net2 <- igraph::add_vertices(net2, 4)

# 4. Remove vertices 12, 5, and 4 by position
net2 <- igraph::delete_vertices(net2, c(12, 5, 4))

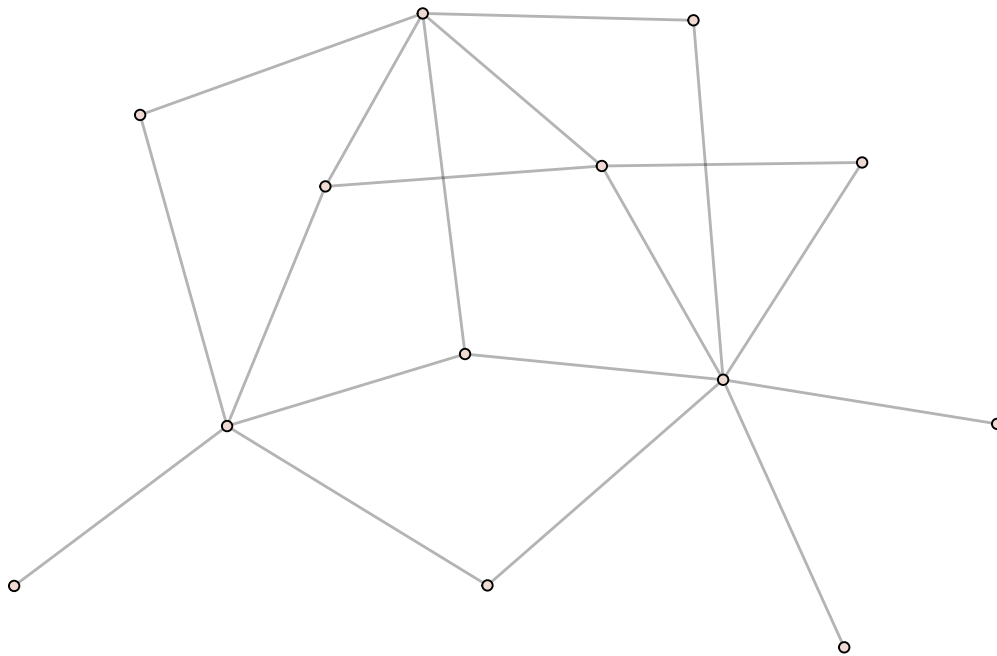
# 5. Re-name each node sequentially so name index stay in sync
V(net2)$name <- as.character(seq_len(vcount(net2)))

# 6. Randomly rewire 50% of edges, no loops
net2 <- igraph::rewire(net2, each_edge(p = 0.5, loops = FALSE))
```

#6. Plot the new network with GGraph

```
#plotting the new graph
ggraph(net2) +
  geom_edge_link(color = "black", alpha = 0.3) +
  geom_node_point(color = "black", fill = "#efd9d3", shape = 21) +
  theme_graph()
```

```
## Using "stress" as default layout
```



**#7. Run a threshold model over the original vs new graph**

```
#converting the og plot into a matrix
net_matrix <- as_adjacency_matrix(net)
n_nodes <- nrow(net_matrix)

#converting the new plot into a matrix
net2_matrix <- as_adjacency_matrix(net2)
n2_nodes <- nrow(net2_matrix)
```

Graphing Original Network

```
#setting the seed
set.seed(1)

#running the diffusion threshold model
diffnet_il <- rdiffrnet(
```

```

t = 10,
seed.graph = net_matrix,
seed.nodes = c(1, 7, 11), # chosen nodes
seed.p.adopt = 0.1,
rewire = F,
threshold.dist = function(i) 0.25,
exposure.args = list(normalized = T)
)

#getting the info and plots
diffnet_il

## Dynamic network of class -diffnet-
## Name      : A diffusion network
## Behavior   : Random contagion
## # of nodes : 12 (1, 2, 3, 4, 5, 6, 7, 8, ...)
## # of time periods : 10 (1 - 10)
## Type      : directed
## Final prevalence : 1.00
## Static attributes : real_threshold (1)
## Dynamic attributes : -

summary(diffnet_il)

## Diffusion network summary statistics
## Name      : A diffusion network
## Behavior   : Random contagion
## -----
## Period    Adopters    Cum Adopt. (%)    Hazard Rate    Density    Moran's I (sd)
## -----
##      1         3         3 (0.25)         -         0.30 -0.13 (0.05)
##      2         7        10 (0.83)        0.78         0.30 -0.13 (0.05)
##      3         2        12 (1.00)        1.00         0.30 -
##      4         0        12 (1.00)        0.00         0.30 -
##      5         0        12 (1.00)        0.00         0.30 -
##      6         0        12 (1.00)        0.00         0.30 -
##      7         0        12 (1.00)        0.00         0.30 -
##      8         0        12 (1.00)        0.00         0.30 -
##      9         0        12 (1.00)        0.00         0.30 -
##     10         0        12 (1.00)        0.00         0.30 -
## -----
## Left censoring : 0.25 (3)
## Right censoring : 0.00 (0)
## # of nodes      : 12
##
## Moran's I was computed on contemporaneous autocorrelation using 1/geodesic
## values. Significance levels *** <= .01, ** <= .05, * <= .1.

table(diffnet_il$toa) # time of adoption

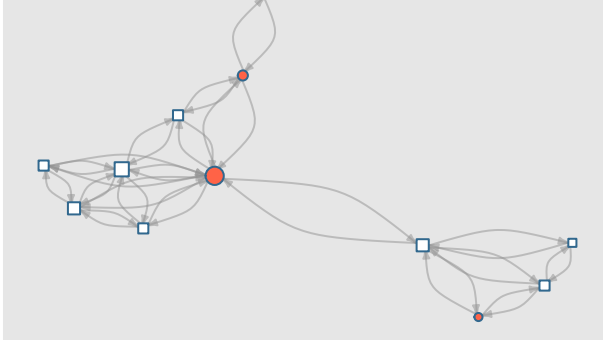
##
## 1 2 3
## 3 7 2

```

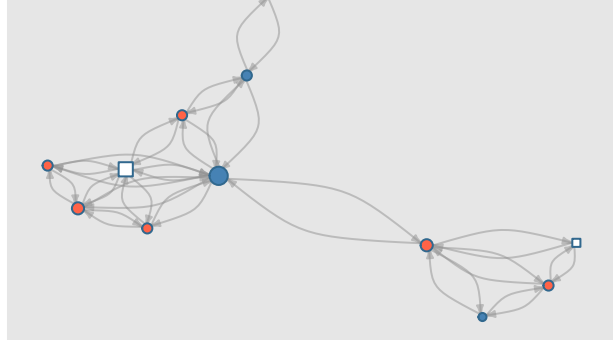
```
plot_diffnet(diffnet_il, slices = c(1, 2, 3, 4))
```

## Diffusion Network

Network in period 1



Network in period 2



Network in period 3



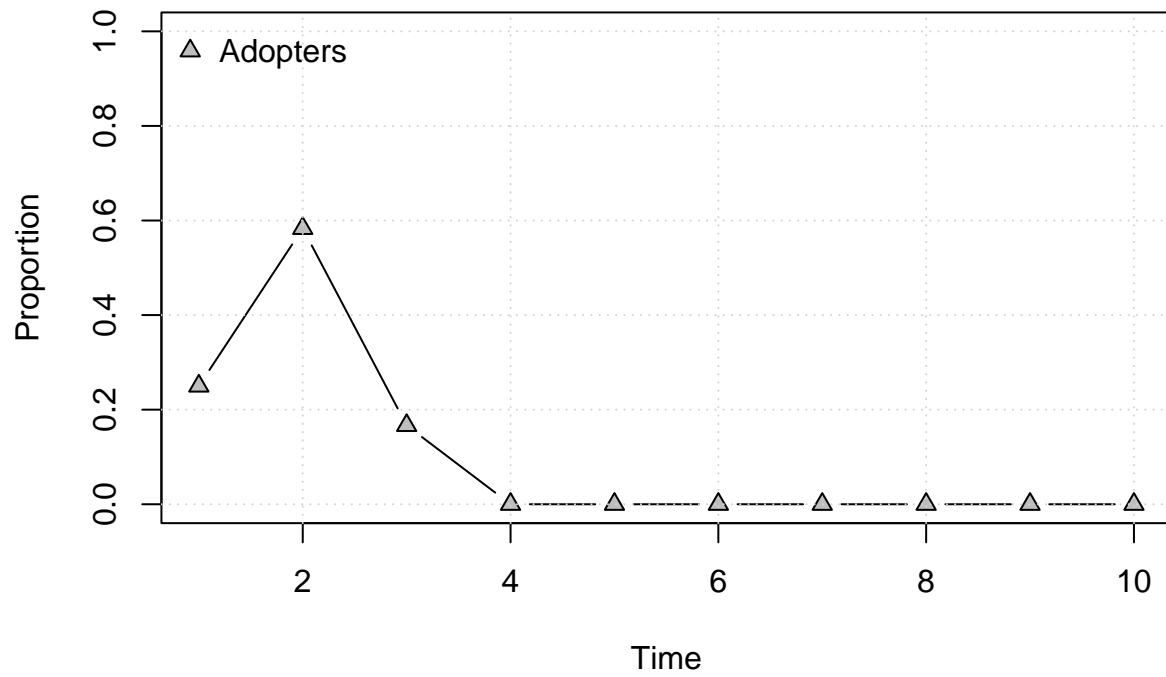
Network in period 4



□ Non adopters   ● New adopters   ● Adopters

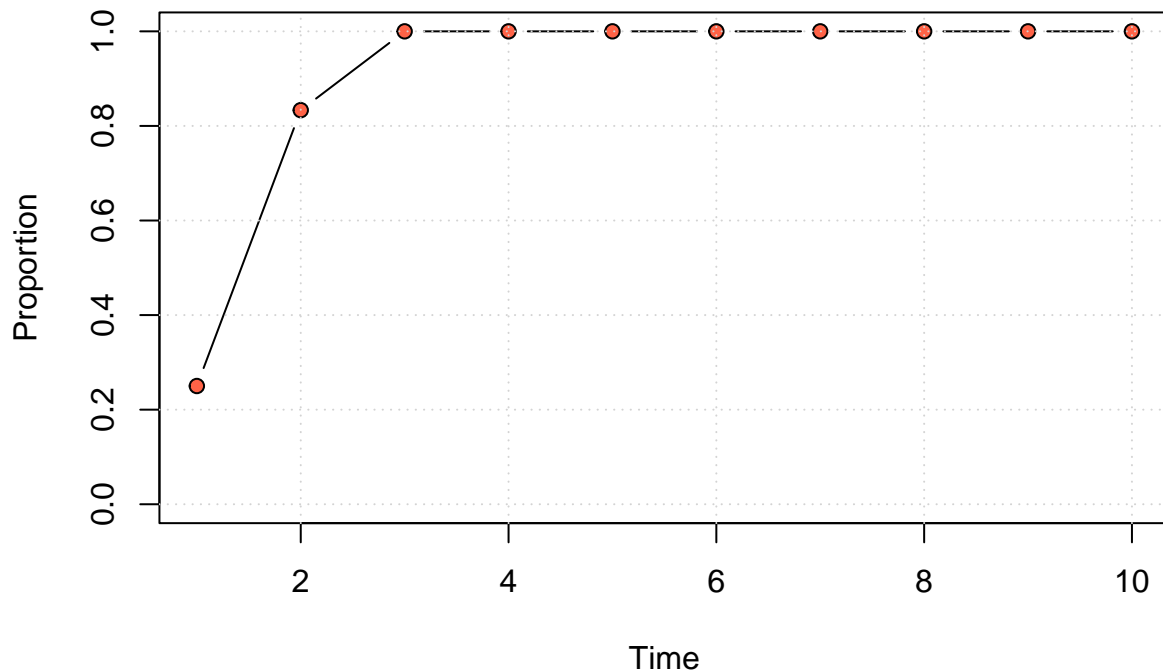
```
plot_adopters(diffnet_il, what = "adopt")
```

## Adopters and Cumulative Adopters



```
plot_adopters(diffnet_il, what = "cumadopt", include.legend = FALSE)
```

## Adopters and Cumulative Adopters



```
#setting the seed
set.seed(1)

#running the diffusion network
diffnet_il2 <- rdiffnet(
  t = 10,
  seed.graph = net2_matrix,
  seed.nodes = c(1, 7, 11), # chosen nodes
  seed.p.adopt = 0.1,
  rewire = F,
  threshold.dist = function(i) 0.25,
  exposure.args = list(normalized = T)
)

#plotting the graph
diffnet_il2
```

```
## Dynamic network of class -diffnet-
## Name : A diffusion network
## Behavior : Random contagion
## # of nodes : 13 (1, 2, 3, 4, 5, 6, 7, 8, ...)
## # of time periods : 10 (1 - 10)
## Type : directed
## Final prevalence : 1.00
## Static attributes : real_threshold (1)
## Dynamic attributes : -
```

```
summary(diffnet_il2)
```

```
## Diffusion network summary statistics
## Name      : A diffusion network
## Behavior  : Random contagion
## -----
## Period    Adopters    Cum Adopt. (%)    Hazard Rate    Density    Moran's I (sd)
## -----
##      1         3         3 (0.23)         -         0.24  0.03 (0.04) ***
##      2         3         6 (0.46)         0.30        0.24  0.08 (0.05) ***
##      3         3         9 (0.69)         0.43        0.24 -0.02 (0.04)
##      4         4        13 (1.00)         1.00        0.24
##      5         0        13 (1.00)         0.00        0.24
##      6         0        13 (1.00)         0.00        0.24
##      7         0        13 (1.00)         0.00        0.24
##      8         0        13 (1.00)         0.00        0.24
##      9         0        13 (1.00)         0.00        0.24
##     10         0        13 (1.00)         0.00        0.24
## -----
## Left censoring : 0.23 (3)
## Right censoring : 0.00 (0)
## # of nodes      : 13
##
## Moran's I was computed on contemporaneous autocorrelation using 1/geodesic
## values. Significance levels *** <= .01, ** <= .05, * <= .1.
```

```
table(diffnet_il$toa) # time of adoption
```

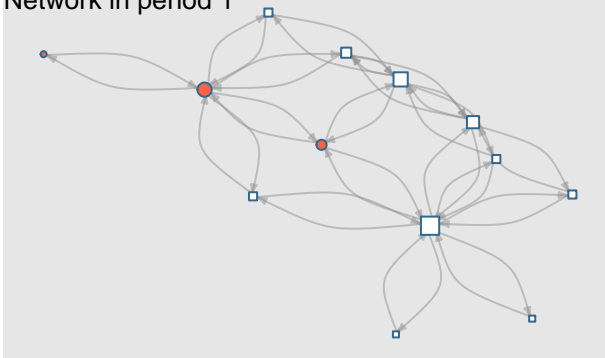
```
##
## 1 2 3
## 3 7 2
```

```
plot_diffnet(diffnet_il2, slices = c(1, 2, 3, 4))
```

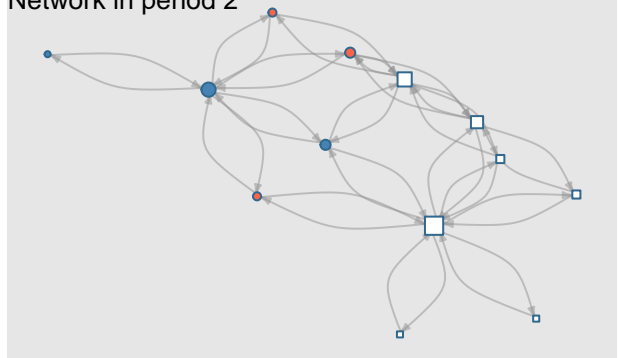


## Diffusion Network

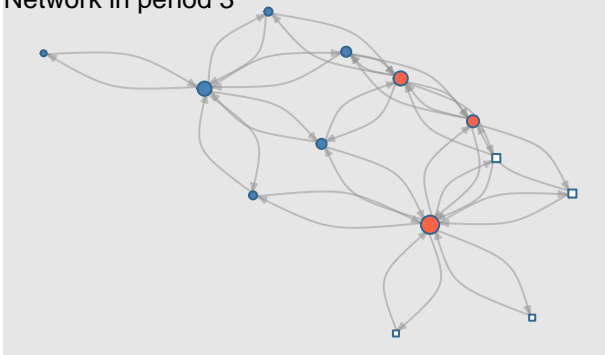
Network in period 1



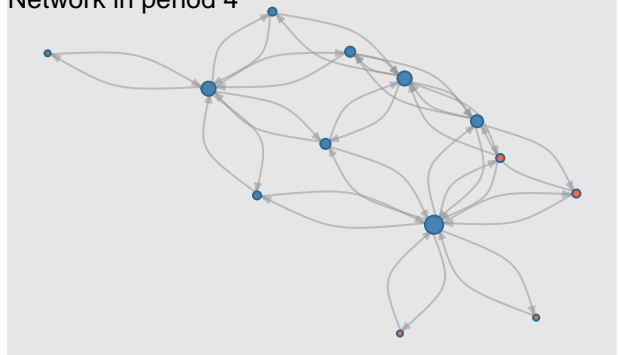
Network in period 2



Network in period 3



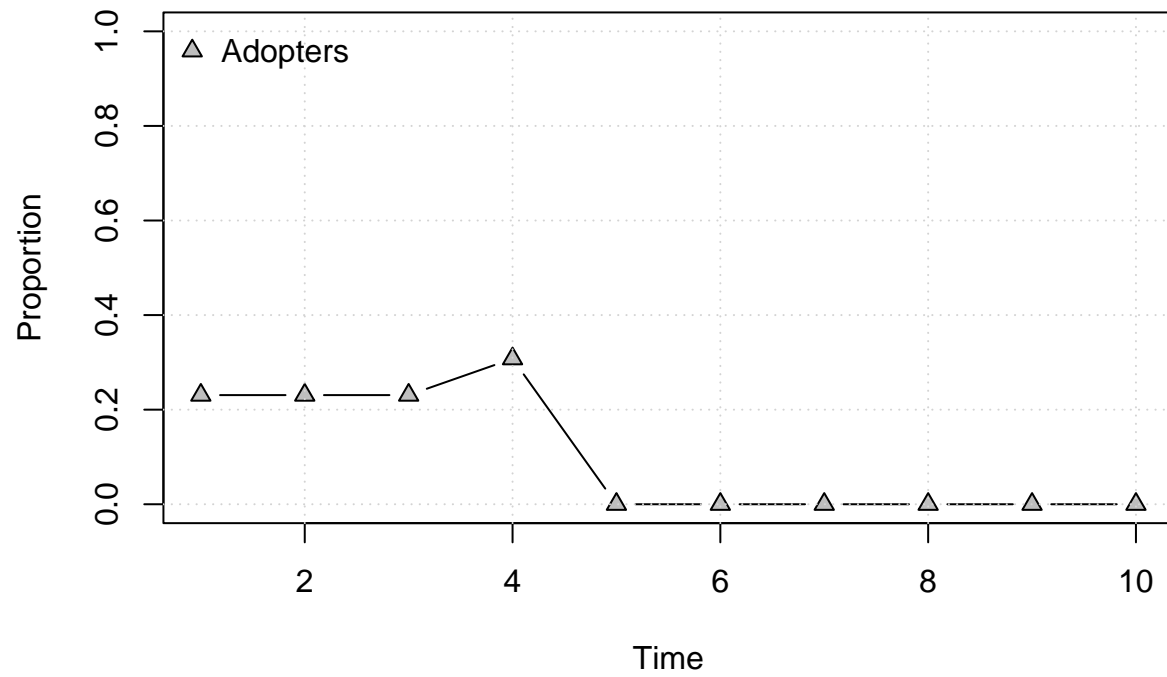
Network in period 4



□ Non adopters   ● New adopters   ● Adopters

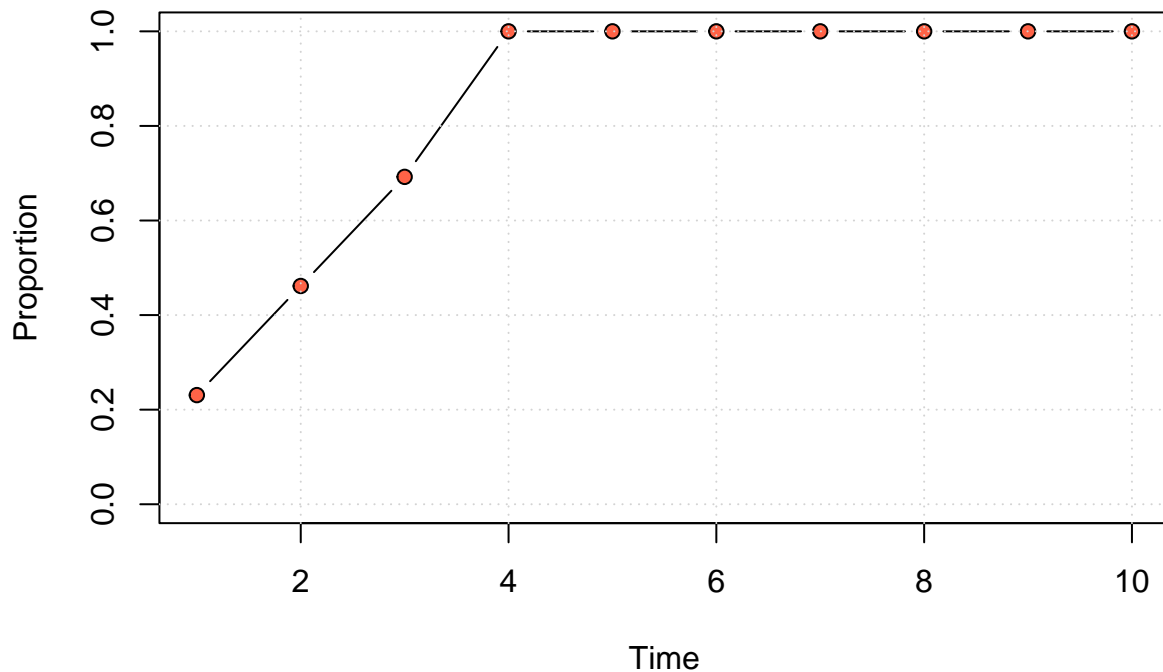
```
plot_adopters(diffnet_il2, what = "adopt")
```

## Adopters and Cumulative Adopters



```
plot_adopters(diffnet_il2, what = "cumadopt", include.legend = FALSE)
```

## Adopters and Cumulative Adopters



**#8. Changes in Network Structure on Diffusion** Looking at the adopters and cumulative adopters plot, the original network had a much earlier peak in adopters, with the peak hitting a proportion of 60% around time = 2. The newer network started off very slowly (as did the original plot!) but peaked at time = 4, around 30% before plateauing and staying at 0% for the rest of the plot.

This means that the original network had a much quicker rate of diffusion compared to the second network.

When I changed the slices on the diffusion plot (thank you for the help by the way!) I saw that the newer network had a more linear growth (hence it taking longer) whereas the original network was much exponential, which is why it maxed out at time = 3

My main takeaway is that the original plot (because it was highly structured by design) was a much more tightly connected plot compared to the new network (which had the random ties + random nodes)