

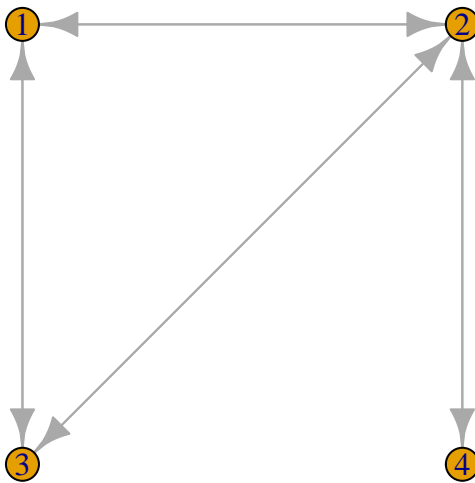
HW2_JeromeWong

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Contents

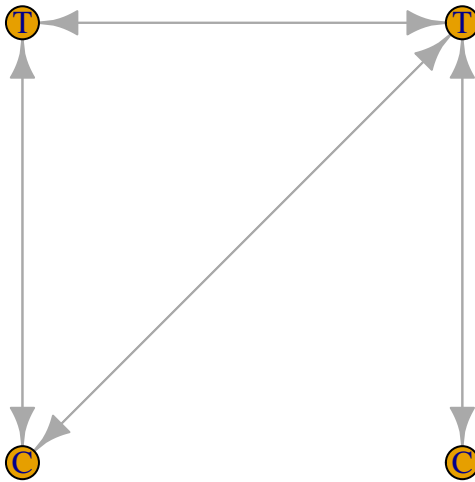
```
# Define our graph
dg <- graph.formula(1++2, 1++3, 2++3, 2++4)
# Plot; permute changes the orientation shown in the plot
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



Spillover

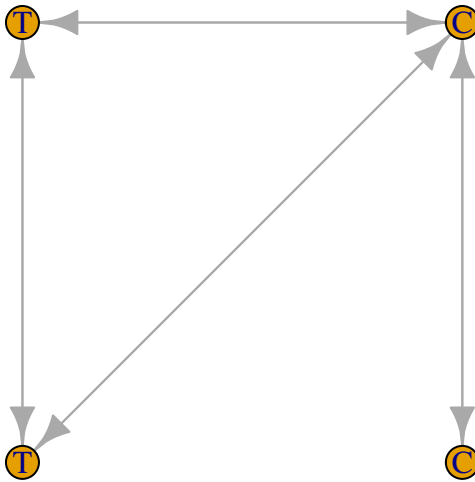
Qn1

```
# assign treatment labels T (treatment) or C (control)
# upper left, upper right, lower left, lower right
V(dg)$label <- c("T", "T", "C", "C")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



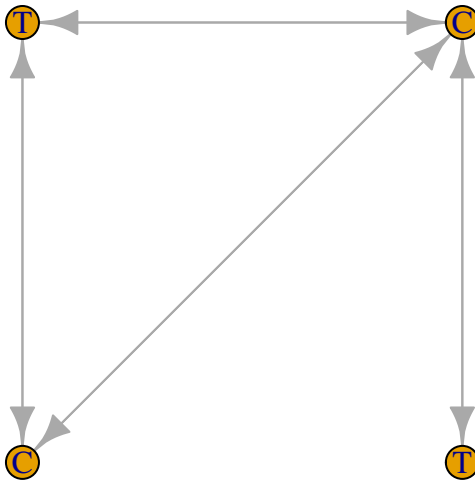
- (a) 0 no exposure
- (b) 0 direct exposure
- (c) 2 indirect exposure
- (d) 2 full exposure

```
V(dg)$label <- c("T", "C", "T", "C")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



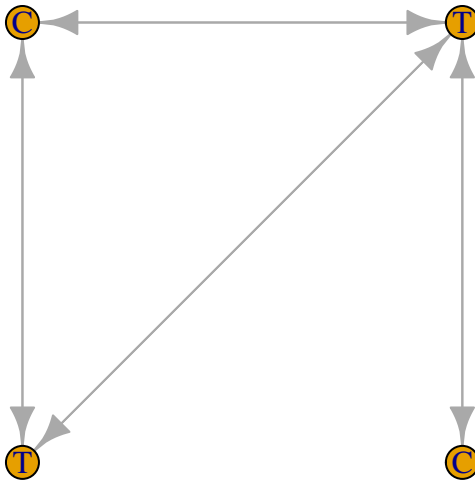
(a) 1 no exposure (b) 0 direct exposure (c) 1 indirect exposure (d) 2 full exposure

```
V(dg)$label <- c("T", "C", "C", "T")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



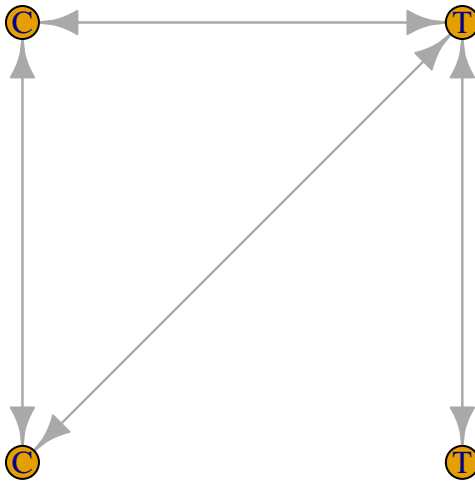
(a) 0 no exposure (b) 2 direct exposure (c) 2 indirect exposure (d) 0 full exposure

```
V(dg)$label <- c("C", "T", "T", "C")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



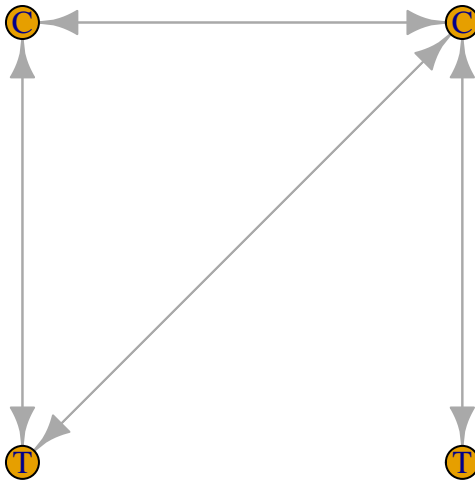
(a) 0 no exposure (b) 0 direct exposure (c) 2 indirect exposure (d) 2 full exposure

```
V(dg)$label <- c("C", "T", "C", "T")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



(a) 0 no exposure (b) 0 direct exposure (c) 2 indirect exposure (d) 2 full exposure

```
V(dg)$label <- c("C", "C", "T", "T")
plot(permute(dg, c(3,4,1,2)), layout=layout.grid(dg))
```



(a) 0 no exposure (b) 2 direct exposure (c) 2 indirect exposure (d) 0 full exposure

Qn2

This would violate the second assumption of the Horvitz-Thompson estimators. The observed in-degree of the network would be incorrect and since the in-degree is a function of the probabilities in the HT estimators, the probabilities obtained would be wrong. The inaccuracies in measuring the network introduces bias into the HT estimators.