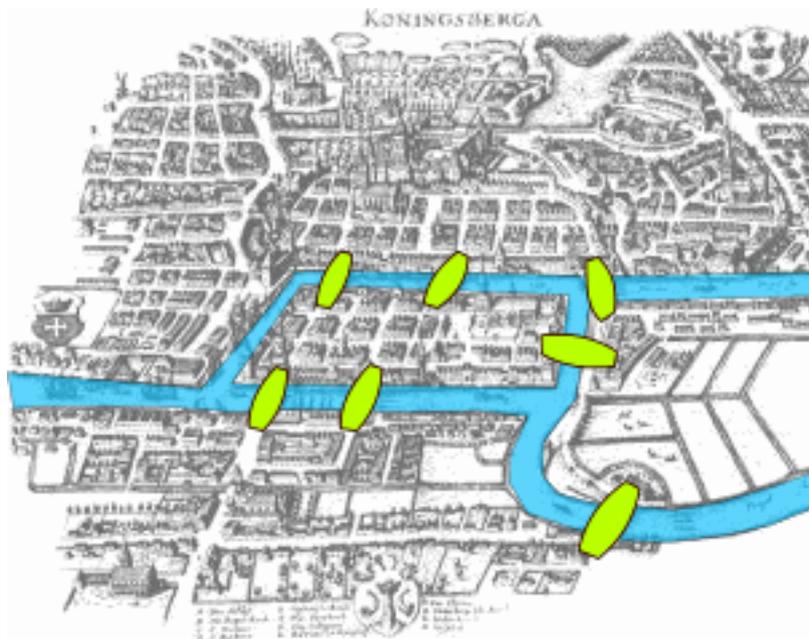


Day 1 exercises

Network Analysis

Exercise 1

Suppose we are allowed to build exactly two more bridges in 18th century Königsberg (now know as Kaliningrad). Can we place them in such a way that we can walk a path that crosses all bridges only once? Why? Suppose that afterwards one of the bridges in Königsberg is destroyed, can we still walk across all bridges in single path only once? Does it matter which bridge is destroyed? Why?



Exercise 2

a. Create the following matrix in R:

$$\begin{bmatrix} 1 & 2 & 0 \\ 0 & 0 & 3 \\ 0 & 0 & 0 \end{bmatrix}$$

b. This matrix represents a graph, how is this representation called?

c. Is this graph weighted or unweighted, directed or undirected and cyclic or acyclic?

Exercise 3

Create a *list* in R containing as first element the vector 1, 4, 7, 10, as second element the vector 2, 5, 8, 11 and as third element the vector 3, 6, 9, 12.

Exercise 4

On blackboard you can download the SPSS file `As1Q5.sav`. This dataset contains a subject id variable (`ppn`) and three variables called `A`, `B` and `C`. Use R to answer these questions.

- a. Read this file into R
- b. What are the mean scores of `A`, `B` and `C`?
- c. Compute the correlation matrix of `A`, `B` and `C`.

Exercise 5

Install the package `qgraph`, load it and look at the help page for the function `qgraph`. Go to the examples section, and copy the first 10 lines (including the example under `# Correlations:`) to your `.R` file you hand in with this assignment. Also copy these codes to your console, did it produce a plot? (You don't have to include the plot in the `.pdf` file).

Challenge Exercise

The R script <http://www.sachaepskamp.com/files/SymxDis.R> can be run to obtain a matrix called `SymxDis`. This matrix is the basis of the data used in the graph of the DSM shown in the lecture and described in Borsboom, Cramer, Schmittmann, Epskamp, and Waldorp (2011).

Each row of `SymxDis` indicates a unique symptom in the DSM, and each column of `SymxDis` indicates a disorder in the DSM.

Write R codes that do the following: First import the `SymxDis` matrix directly from the internet, next compute an *unweighted adjacency matrix* of a graph in which the symptoms are nodes and are connected with all other symptoms that are in the same disorder. Self loops should not be included in the adjacency matrix and should be removed.

For example, if symptom S_1 is only in disorders D_1 and D_2 , symptom S_2 is only in disorder D_1 and symptom S_3 is only in disorder D_2 , then S_1 will be connected with both S_2 and S_3 , and S_2 and S_3 will not be directly connected.

You will get one point if your script computes the correct adjacency matrix within 10 seconds and another bonus point if, after importing the data, the adjacency matrix is computed in a single line (without semi-colons) of R code within one second and without using a loop.

References

- Borsboom, D., Cramer, A., Schmittmann, V., Epskamp, S., & Waldorp, L. (2011). The small world of psychopathology. *PloS one*, *6*(11), e27407.