Inferring community-driven structure in complex networks

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Stellingen (Propositions)

behorende by het proefschrift (belonging to the thesis)

Inferring Community-driven Structure in Complex Networks

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1. Network science is a highly multidisciplinary field, with a strong potential to address crucial questions on the workings of cells and brains, the dynamics of social interaction, or the paths through which infectious diseases spread.

2. A graph is a mathematical abstraction employed to represent networks, subject to some conventions and simplifications. Often, a network can be represented by different graphs (Chapters 1, 3).

3. The specification of suitable and realistic null network models represents a crucial step in the study of community structure in networks (Chapters 2, 3, 4).

4. The analysis of genetic data often requires the preliminary screening of many hypotheses, whose verification can be computationally burdensome for large gene networks. Hence, the computational efficiency of methods for the analysis of biological networks is of primary importance (Chapter 2).

5. Penalized inference allows to perform consistent variable selection for stochastic blockmodels and to derive a sparse representation of relations between the blocks (Chapter 3).

6. Although latent space models do not exploit information on group membership of nodes, they yield a the latent space representation of Deputies in bill cosponsorship networks that displays the same pattern of collaborations between parties inferred with stochastic blockmodels (Chapter 4).

7. *Clustering* is rather common in network analysis - but, to network scientists, it typically means finding groups of nodes in a network. Thus, the idea of *clustering graphs* might sound a little awkward at first. However, it is a promising and powerful approach to the study of several network replicates (Chapter 5).