

## MASTER'S THESIS

### Inferring disease transmission networks

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# Abstract

To investigate how an infectious disease spreads, it is desirable to use the observed surveillance data to discover the underlying (often hidden) disease transmission networks. Previous studies have provided methods for inferring information diffusion networks in which each node corresponds to an individual person within the diffusion network. However, in the case of disease transmission, to effectively propose and implement intervention strategies, it is more realistic and reasonable for policy makers to study the diffusion patterns at a metapopulation level, that is, to consider disease transmission networks in which nodes represent subpopulations, and links indicate their interrelationships. Such networks can be useful in several ways: (i) to investigate hidden impact factors that influence epidemic dynamics, (ii) to reveal possible sources of epidemic outbreaks, and (iii) to practically develop and/or improve strategies for controlling the spread of infectious diseases. Therefore, this thesis addresses the problem of inferring disease transmission networks at a metapopulation level. A network inference method called NetEpi (Network Epidemic) is developed and evaluated using both synthetic and real-world datasets. The experimental results show that NetEpi can recover most of the ground-truth disease transmission networks using only surveillance data.

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# Table of Contents

<b>Declaration</b>	<b>i</b>
<b>Abstract</b>	<b>ii</b>
<b>Acknowledgements</b>	<b>iii</b>
<b>Table of Contents</b>	<b>iv</b>
<b>List of Tables</b>	<b>vii</b>
<b>List of Figures</b>	<b>viii</b>
<b>1 Introduction</b>	<b>1</b>
1.1 Overview and Objectives . . . . .	1
1.2 Contributions and Significance . . . . .	5
1.3 Outline of the Thesis . . . . .	7
<b>2 Related Work</b>	<b>9</b>
2.1 Information Diffusion Network Inference . . . . .	11
2.1.1 Information Diffusion Models . . . . .	11

2.1.2	Link Prediction Problem . . . . .	12
2.1.3	Diffusion Network Inference . . . . .	13
2.2	Disease Transmission Networks . . . . .	16
2.2.1	Disease Transmission Models . . . . .	16
2.2.2	Disease Transmission over Networks . . . . .	22
2.2.3	Inference Based on Surveillance Data . . . . .	28
2.3	Summary . . . . .	34
<b>3</b>	<b>Problem Statement</b>	<b>37</b>
3.1	Definitions . . . . .	38
3.2	Linear Transmission Model . . . . .	42
3.3	Network Inference Problem . . . . .	44
3.4	Summary . . . . .	45
<b>4</b>	<b>The Proposed Network Inference Method</b>	<b>46</b>
4.1	Basic Ideas . . . . .	47
4.2	Partial Correlation Network Construction . . . . .	47
4.2.1	Pearson Correlation Analysis . . . . .	50
4.2.2	First-Order Partial Correlation Analysis . . . . .	51
4.3	Back-Tracking Bayesian Learning . . . . .	53
4.3.1	Marginal Likelihood Function . . . . .	53
4.3.2	Expectation-Maximization Computation . . . . .	55
4.3.3	Back-Tracking Technique . . . . .	56
4.4	Discussions . . . . .	56

4.4.1	Stopping Criteria . . . . .	56
4.4.2	Computational Complexity of the Algorithm . . . . .	58
4.5	Summary . . . . .	59
<b>5</b>	<b>Experiments</b>	<b>60</b>
5.1	Experiments Based on Synthetic Data . . . . .	61
5.1.1	Experimental Setting . . . . .	61
5.1.2	Baseline Method . . . . .	65
5.1.3	Results . . . . .	66
5.1.4	Sensitivity Analysis . . . . .	76
5.2	Experiments Based on a Real-world Dataset . . . . .	93
5.2.1	Dataset Description . . . . .	93
5.2.2	Experimental Setting . . . . .	95
5.2.3	Results . . . . .	97
5.3	Summary . . . . .	112
<b>6</b>	<b>Conclusion and Future Work</b>	<b>114</b>
6.1	Main Contributions . . . . .	114
6.2	Future Work . . . . .	115
	<b>Curriculum Vitae</b>	<b>129</b>