

MASTER'S THESIS

Studies of metabolic network in E. coli using microarray data under diverse conditions

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**Studies of Metabolic Network in E. coli
Using Microarray Data under Diverse
Conditions**

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**A thesis submitted in partial fulfillment of the requirements
for the degree of
Master of Philosophy**

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Abstract

The prime challenge in research of metabolic network is to discover the design and organization principles. The increasing amount of microarray data in online databases makes the investigation of the functional metabolic network possible. By studying the enzyme pairs in strongly coherent metabolic subnets, it is found that internal-metabolite connected enzyme pairs exhibit higher coexpression level than those connected by external metabolites, and might have better reflected metabolic flow. Also observed is that a large portion of transcription units and regulons in *E. coli* encode enzymes catalyzing conversion of internal metabolites. The results suggest that the cell might have optimized utilization of resources by stringently coexpression enzymes performing conversion of specific compounds.

Table of Contents

Declaration	i
Abstract	ii
Acknowledgements	iii
Table of Contents.....	iv
List of Tables	v
List of Figures	vi
List of Abbreviations	vii
I. Introduction.....	1
I.1 Motivation.....	3
I.2 Goals	3
II. Related Work	4
II.1 Principles in Transcriptional Regulation Networks.....	4
II.2 Metabolic Network Topologies and Implications	5
II.3 Functional Analysis of Cellular Metabolism.....	7
III. My Approaches.....	8
III.1 Overview	8
III.2 Preparatory Work.....	9
III.3 Expression-profiling of Enzyme-enzyme Network	17
III.4 Identifying Strongly Coherent Blocks by Applying Thresholds Successively	18
III.5 Internal Metabolites and External Metabolites of Metabolic Subnets.....	21
III.6 Metabolic Blocks Defined by Genes in Transcription Units and Regulons.....	21
IV. Results and Discussion.....	22
IV.1 Internal- against External-metabolite Connected Enzymes.....	22
IV.2 Metabolic Enzymes Encoded in Transcription Units and Regulons.....	25
IV.3 Strongly Coherent Metabolic Blocks and KEGG Pathways.....	38
V. Conclusions and Future Work.....	44
V.1 Conclusions	44
V.2 Future Work	45
VI. Tools, Databases, etc	46
VI.1 Matlab® as a Platform in Exploratory Work.....	46
VI.2 Matlab® Sample Programs.....	47
VI.3 Online Databases	51
VI.4 Other Programs.....	51
VII. Reference List	52
VIII. Appendices	61
Curriculum Vitae	68