

CONTENT

<u>SUBJECT</u>	<u>PAGE NUMBER</u>
<u>ACKNOWLEDGEMENTS</u>	
<u>CERTIFICATES</u>	
<u>ABSTRACT</u>	
CHAPTER 1. INTRODUCTION	1-9
1.1 CENTRAL DOGMA OF BIOINFORMATICS	1
1.2 SIGNIFICANCE OF USING MICROARRAY TECHNIQUE	1
1.3 SIGNIFICANCE TO GENE SELECTION	1
1.4 THE IMPORTANCE OF GENE SELECTION	2
1.5 THE RELATION BETWEEN GENE FILTERING AND BIOLOGICAL RELEVANCY	2
1.6 COEXPRESSION OF GENES	3-4
1.7 COEXPRESSION NETWORK BETWEEN GENES	5
1.8 WEIGHTED CORRELATION NETWORK	6
1.9 CORRELATION BASED CLUSTERING OF GENES	6-7
1.10 PREDICTION FLOW BETWEEN THE CLUSTER NETWORK	7-8
1.11 OBJECTIVES OF THE PROJECT	8
1.12 THE ORGANISATION OF THE DISSERTATION	8-9
CHAPTER 2. RELATED WORK	10-13
CHAPTER 3: THEORITICAL BACKGROUND OF THE WORK	14-21
3.1 THE STRENGTH OF PREDICTION FLOW AND COSIDERABLE PREDICTION LENGTH	14-17
3.2 SIGNIFICANCE OF BASIS GENES AND BASIS CONDITIONS	18-20
3.3 DETERMINATION OF OPTIMAL LEVEL OF CORRELATION	20-21
CHAPTER 4. BACKGROUND OF THE PROPOSED METHOD	22-34
4.1 PREPROCESSING	22-23
A) NORMALIZATION OF DATASET	22
B) DISCRETIZATION OF THE DATASET	22-23
4.2 IMPLEMENTED ALGORITHM	24-32
i) SELECTION OF BASIS CONDITIONS AND BASIS GENES	24-25
ii) CONSTRUCTION OF GENE COEXPRESSION NETWORK THROUGHOUT ALL THE BICLUSTERS	26-29
iii) CONSTRUCTION OF GENE COEXPRESSION SUBNETWORK IN A	

PARTICULAR BICLUSTER	29-30
iv) EXPANSION OF THE SUBNETWORK	30-31
v) EXTRACTION OF CLOSELY RELATED CLUSTER	31-32
4.3 DETAILS OF THE DATASET USED IN THE PROPOSED METHOD	33
4.4 IMPORTANCE OF THE EFFECTIVENESS OF THE P-VALUE TO MEASURE THE INTEGRITY OF A GENE CLUSTER	34
CHAPTER 5: ILLUSTRATION OF THE IMPLEMENTED ALGORITHM ON SOME OF THE REPRESENTATIVE DATASET SPECIFIED IN EARLIER SECTION	35-60
5.1 ILLUSTRATION	35-59
5.2 COMPARATIVE TEST OF PROPOSED ALGORITHM WITH SOME STANDARD ALGORITHM	60
CHAPTER 6: CONCLUSION AND FUTURE WORK	61-63
6.1 QUALITATIVE DISCUSSION OF THE METHOD	61
6.2 SOME FUTURE PROPOSAL	61-62
BIBLIOGRAPHY	62
REFERENCES	62-63