# Contents

ENDLY: MODIFIED PROGRAMS IN THE CRACOR Preface

1 Introduction CHAPTER

.1	PIPELI	<b>INES TO</b>	ANALYZE	"OMICS"	DATA

- **RNA-Seq GENE EXPRESSION IN S2-DRSC CELLS** 1.2
- MICROARRAY GENE EXPRESSION IN YEAST CELLS 1.3 AND IN PROSTATE SAMPLES
- DNA METHYLATION IN NORMAL AND COLON/RECTAL 1.4 ADENOCARCINOMA SAMPLES

#### 2 Genome-scale gene expression data CHAPTER

#### **MICROARRAY GENE EXPRESSION DATA** 2.1

- Data generation 2.1.1
- Preprocessing and quality control of microarray 2.1.2

CHAPTER	3 = G	enome-scale epigenetic data	17
	2.2.2 Preprocessing and quality control of bulk RNA- Seq data		
	2.2.1	Data generation	14
2.2	DATA F	FROM NEXT GENERATION SEQUENCING	13
		data	7

|--|

17

XI

З

4

5

5

5

QUALITY CONTROL AND PREPROCESSING OF DNA 3.2 METHYLATION DATA 18

## viii Contents

4.1

4.2

	3.2.1	The control probe adjustment and reduction of global correlation pipeline (CPACOR)	18
	3.2.2	Quantile normalization with ComBat	21
3.3	CELL	TYPE COMPOSITION INFERENCES	22
	3.3.1	Reference-based methods	23
	3.3.2	Reference-free methods	27
3.4	APPE	NDIX – MODIFIED PROGRAMS IN THE CPACOR AN APPLICATION	31
APTER	4 = 5	Screening genome-scale genetic and epigenetic	

0	ata

- SCREENING VIA TRAINING AND TESTING SAMPLES SCREENING INCORPORATING SURROGATE VARI-ABLES
- 4.3 SURE INDEPENDENCE SCREENING4.3.1 Correlation learning
- 4.4 NON- AND SEMI-PARAMETRIC SCREENING TECH-NIQUES 50
  - 4.4.1 Random forest
  - 4.4.2 Support vector machine 53

CHAPTER 5 Cluster Analysis in Data mining

57

39

40

41

46

47

50

5.1	NON-P	PARAMETRIC CLUSTER ANALYSIS METHODS	S	57
	5.1.1	Distances		58
	5.1.2	Partitioning-based methods		59
	5.1.3	Hierarchical clustering		64
	5.1.4	Hybrids of partitioning-based and hierarchi clustering	cal	69
	5.1.5	Examples – clustering to detect gene expression patterns	ion	75
5.2	CLUST	FER ANALYSES IN LINEAR REGRESSIONS		85
5.3	BICLU	STER ANALYSES		91
5.4	JOINT	CLUSTER ANALYSIS		96

# Contents 🔳 ix

# CHAPTER 6 Methods to select genetic and epigenetic factors based on linear associations 101

1

A.I. Comparing undirected networks

6.1	FREQ	UENTIST APPROACHES	102
	6.1.1	Elastic net	102
	6.1.2	Adaptive LASSO	105
	6.1.3	Smoothly clipped absolute deviation (SCAD)	106
6.2	BAYES	SIAN APPROACHES	108
	6.2.1	Zellner's $g$ -prior	109
	6.2.2	Extension of Zellner's $g$ -prior to multi-component <b>G</b> -prior	s 111
	6.2.3	The spike-and-slab prior	113
6.3	EXAM	PLES – SELECTING IMPORTANT EPIGENETIC DRS	118
CHAPTER	7 = N	on- and semi-parametric methods to select	
	g	enetic and epigenetic factors	125
		These kills include builders hol limited to dollars	
7.1	VARIA	BLE SELECTION BASED ON SPLINES	126
7.2	OVER	VIEW OF THE ANOVA-BASED APPROACH	128
7.3	VARIA	BLE SELECTION BUILT UPON REPRODUCING ELS	129
7.4	EXAM	PLES	132
	7.4.1	Selecting important epigenetic factors	132
	7.4.2	Selecting variables with known underlying truth	139
CHAPTER	8 = N	etwork construction and analyses	145
8.1	UNDIF	RECTED NETWORKS	145
	8.1.1	The two-stage graphs selection method	146
	8.1.2	The GGMselect package and gene expression examples	147
8.2	CORR	ELATION NETWORKS	152

### x Contents

8.3	BAYES	SIAN NETWORKS	158
8.4	NETW	ORK COMPARISONS	161
	8.4.1	Comparing undirected networks	162
	8.4.2	Comparing Bayesian networks	163
Bibliog	graphy		165
Index			183

