

A Complex Systems Approach to Important Biological Problems

by

Matthew John Berryman

B.Sc. (Mathematical & Computer Sciences),
The University of Adelaide, Australia, 2001

B.E. (Computer Systems Engineering, First Class Honours),
The University of Adelaide, Australia, 2002

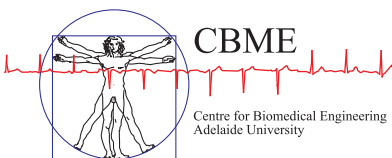
Thesis submitted for the degree of

Doctor of Philosophy

in

The School of Electrical and Electronic Engineering,
Faculty of Engineering, Computer and Mathematical Sciences
The University of Adelaide, Australia

3rd May, 2007



© 2007
Matthew John Berryman
All Rights Reserved



Abstract

Complex systems are those which exhibit one or more of the following inter-related behaviours:

1. Nonlinear behaviour: the component parts do not act in linear ways, that is the superposition of the actions of the parts is not the output of the system.
2. Emergent behaviour: the output of the system may be inexpressible in terms of the rules or equations of the component parts.
3. Self-organisation: order appears from the chaotic interactions of individuals and the rules they obey.
4. Layers of description: in which a rule may apply at some higher levels of description but not at lower layers.
5. Adaptation: in which the environment becomes encoded in the rules governing the structure and/or behaviour of the parts (in this case strictly agents) that undergo selection in which those that are by some measure better become more numerous than those that are not as “fit”.

A single cell is a complex system: we cannot explain all of its behaviour as simply the sum of its parts. Similarly, DNA structures, social networks, cancers, the brain, and living beings are intricate complex systems. This thesis tackles all of these topics from a complex systems approach. I have skirted some of the philosophical issues of complex systems and mainly focussed on appropriate tools to analyse these systems, addressing important questions such as:

- What is the best way to extract information from DNA?
- How can we model and analyse mutations in DNA?
- Can we determine the likely spread of both viruses and ideas in social networks?
- How can we model the growth of cancer?

- How can we model and analyse interactions between genes in such living systems as the fruit fly, cancers, and humans?
- Can complex systems techniques give us some insight into the human brain?

Contents

Heading	Page
Abstract	iii
Contents	v
Statement of Originality	xiii
Acknowledgments	xv
Thesis Conventions and Glossary	xvii
Publications	xix
List of Figures	xxi
List of Tables	xxv
Chapter 1. Introduction	1
1.1 Introduction	2
1.2 Analysis of DNA sequences	3
1.3 Mutations in DNA sequences	3
1.4 Viruses and memes	4
1.5 <i>Drosophila</i>	4
1.6 The <i>p53</i> gene	4
1.7 Cancer	5
1.8 The human brain during sleep	5
1.9 Metabolomics	5
Chapter 2. DNA analysis	7
2.1 Introduction	8
2.1.1 Novel contributions	8

2.2 Introduction to DNA analysis 8

2.3 Analysis of regions in DNA using spectrograms 11

2.4 Multifractal analysis 15

2.5 Phylogenetic trees 16

2.6 Exploring correlations and mutual information in DNA 20

 2.6.1 Mutual information functions 20

 2.6.2 Higuchi fractal measure 21

2.7 Conclusions 22

Chapter 3. Mutations **23**

3.1 Introduction 24

 3.1.1 Novel contributions 25

3.2 Sequences examined 25

 3.2.1 Real sequences 25

 3.2.2 Random sequences 26

 3.2.3 Virtual sequences 27

3.3 Results 29

 3.3.1 Short DNA sequences 29

 3.3.2 Whole chromosome sequences 33

3.4 Conclusions 33

Chapter 4. Viruses and memes **35**

4.1 Introduction 36

 4.1.1 SIRS model 36

 4.1.2 Memes 37

 4.1.3 Novel contributions 37

4.2 Model 38

 4.2.1 Viruses 38

 4.2.2 Memes 40

4.3 Methods 42

 4.3.1 SIRS model 42

4.3.2	Mememes	42
4.4	Results	42
4.4.1	SIRS model	42
4.4.2	Mememes	43
4.5	Conclusions and future work	52
4.5.1	SIRS model	52
4.5.2	Mememes	53
4.5.3	General conclusions and future work	53
 Chapter 5. <i>Drosophila</i>		 55
5.1	Introduction	56
5.1.1	Novel contributions	56
5.2	Gene expression in <i>Drosophila</i>	57
5.2.1	Overview	57
5.2.2	Bicoid	58
5.2.3	Nanos	58
5.2.4	Staufen	58
5.2.5	Hunchback	61
5.2.6	Krüppel	61
5.2.7	Knirps	62
5.2.8	Giant	62
5.2.9	Even-skipped	63
5.3	Cellular automaton modelling	64
5.3.1	Overview	64
5.3.2	Bicoid model	64
5.3.3	Nanos model	65
5.3.4	Staufen model	65
5.3.5	Hunchback model	66
5.3.6	Krüppel model	66
5.3.7	Knirps model	67
5.3.8	Giant model	67

5.3.9	Even-skipped model	67
5.4	Results	68
5.4.1	Gene expression in the <i>Drosophila</i> model	68
5.5	Conclusions	72
Chapter 6. The <i>p53</i> gene		73
6.1	Introduction	74
6.1.1	Novel contributions	77
6.2	Gene networks	78
6.2.1	Background	78
6.2.2	Switching networks	78
6.2.3	Methods	79
6.2.4	Results	86
6.3	Mutations in <i>p53</i>	89
6.3.1	Methods	89
6.3.2	Results	90
6.3.3	Discussion	96
6.4	Conclusions	97
6.4.1	Gene networks	97
6.4.2	Modeling <i>p53</i> mutations	97
6.4.3	General conclusions	98
Chapter 7. Cancer		99
7.1	Introduction	100
7.1.1	Novel contributions	100
7.2	Structure and parameters of the model	101
7.3	Construction of the ODE model	103
7.4	Calculation of cell division and cell death rates	107
7.5	Kinetics of various paths to cancer	108
7.6	Effect of inherited mutations on cancer development	111
7.7	Sensitivity analysis of variations in the parameters	113
7.8	Conclusions	115

Chapter 8. The human brain during sleep	119
8.1 Introduction	120
8.1.1 Novel contributions	121
8.2 Noise removal	121
8.2.1 Introduction	121
8.2.2 Methods	125
8.2.3 Gaussian smoothing	125
8.2.4 Data model for blind signal separation	127
8.2.5 Blind signal separation	127
8.2.6 SOBI algorithm	128
8.2.7 JADE algorithm	128
8.2.8 JCC algorithm	129
8.2.9 Wavelet noise removal	129
8.2.10 MI estimation algorithm	131
8.2.11 Results	131
8.3 Nonlinear analysis	133
8.3.1 Overview	133
8.3.2 Participants	134
8.3.3 Overnight polysomnography	134
8.3.4 EEG recordings	135
8.3.5 EEG data analysis	135
8.4 Time reversal results	137
8.4.1 Participants and PSG findings	137
8.4.2 Verifying time reversal test	138
8.4.3 Time reversal test results	141
8.4.4 Higuchi fractal results	141
8.4.5 Discussion	142
8.4.6 Conclusions	144
Chapter 9. Metabolomics	145
9.1 Introduction	146

9.1.1	Novel contributions	146
9.2	Autism study participants	147
9.2.1	Inclusion and exclusion criteria	147
9.2.2	Ethical clearance	148
9.2.3	Cancer cells used	148
9.3	Methods	149
9.3.1	Pre-processing and preliminary analysis	149
9.3.2	k-means clustering analysis	150
9.3.3	Principal components analysis	151
9.3.4	Support vector machines	151
9.4	Cancer cell results	153
9.4.1	Pre-processing and preliminary analysis	153
9.4.2	k-means clustering analysis	159
9.4.3	Principle components analysis	159
9.4.4	Support vector machines	159
9.5	Autism results	161
9.5.1	Pre-processing and preliminary analysis	161
9.5.2	k-means clustering analysis	164
9.5.3	Principal components analysis	164
9.5.4	Support vector machines	165
9.6	Conclusions	168
Chapter 10. Conclusions		171
10.1	Overview	172
10.2	Analysis of DNA sequences	172
10.3	Mutations in DNA sequences	172
10.4	Viruses and memes	173
10.5	<i>Drosophila</i>	173
10.6	<i>p53</i>	173
10.7	Cancer	174
10.8	The human brain during sleep	174
10.9	Metabolomics	174
10.10	Overall conclusions	175

Appendix A. Cell cycle	177
Appendix B. SVM mathematical description	181
B.1 Introduction	181
B.2 Constrained optimisation problems	181
B.3 Goal of SVMs	183
B.4 C-SVMs	184
B.5 ν -SVMs	184
B.6 Kernels	185
Bibliography	187
Biography	201
Disclaimer	203

Statement of Originality

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by any other person, except where due reference has been made in the text.

I give consent to this copy of my thesis, when deposited in the University Library, being made available in all forms of media, now or hereafter known.

3 May 2007

Signed

Date

Acknowledgments

Thanks to Yulan, my angel, for her love and ongoing support.

Lots of thanks to Trevor & Heather, Nan & Grumpy, and Monique, David & Phoenix for all your love and support. Thanks to Angus and Jake for all your love, and big wet slobbery dog kisses.

Thanks to all my friends, particularly Tamath and Justin, for all your support.

Rod Kenyon deserves a special mention for guiding my mathematical and computer skills, and Ann Howland for guiding my writing skills. The chapter on cancer is for both of you.

A big thanks to Cosma Shalizi, Anne-Marie Grisogono, Alex Ryan, Nicky Grigg, Aaron Clauset, and Neil Johnson for your guidance in my understanding of complex systems.

Thanks to my supervisors Derek Abbott and Andrew Allison. A special mention to Derek for being a good mentor, editor-in-chief, and for the opportunities that you provided for me. I am deeply grateful.

Thanks to Sabrina Spencer and Melissa Ryan for their very perceptive understanding of cancer, and for aiding my research with that understanding.

Thanks to Yea Cheat for his tireless work on the autism study, to Damien Abarno for supplying me with cancer cell growth media for metabolite analysis, and to Cobus Gerber for slaving away over the mass spectroscopy machine in both studies.

Thanks to Scott Coussens, Yvonne Pamula, and Sarah Blunden for the data associated with their sleep studies.

A big thanks to Mark McDonnell and Cosma Shalizi for taking the time to read through my thesis and giving feedback. Thanks also to Dave Tagg for his professional editing work on my use (and misuse) of the English language.

Thanks to the University of Adelaide, Santa Fe Institute, and International Society for Optical Engineering for their financial support.

Thanks to Wentian Li, David Krakauer, Trachette Jackson, Gilbert Omenn, John Holland, Andrew Allison, Samuel Mickan, David Findlay, Brendon Coventry, Setayesh

Acknowledgments

Behin-Ain, Roger Reddel, Sara Dempster, Ross McKinnon, Manya Anglely, Michael Sorich, Declan Kennedy, Alfred Martin, Pedro Carpena, Chris Wilkinson, Matthew Roughan, Lang White, David Saint, Kurt Lushington, and Sheila Messer for useful advice on areas of my research.

- Matthew John Berryman

Thesis Conventions and Glossary

Typesetting This thesis is typeset using the L^AT_EX₂e software. Processed plots and images were generated using Matlab 6.1 (Mathworks Inc.) and the Matplotlib module for the Python programming language. TeXShop was used as an effective interface to the TeTeX version of L^AT_EX.

Spelling Australian English spelling is adopted, as defined by the Macquarie English Dictionary (Delbridge 2005).

Referencing The Harvard style is used for referencing and citation in this thesis.

Genetics nomenclature The nomenclature for human genes follows the standard as published by Wain *et al.* (2002). That for bacterial genes follows the standards as published by Demerec *et al.* (1966). That for *Drosophila melanogaster* (fruit fly) follows the standards as published by Lindsley and Zimm (1992). I did make one slight alteration to the rules for nomenclature in that where they state *italics* should be used, I instead used *slanted text* in order to clarify the difference between gene names and other italicised words (for example foreign words).

Mathematical notation I have used standard mathematical notation for sets in \mathbb{R} , namely $x \in (a, b)$ means $a < x < b$, $x \in (a, b]$ means $a < x \leq b$, $x \in [a, b)$ means $a \leq x < b$ and $x \in [a, b]$ means $a \leq x \leq b$. I use * to denote a complex conjugate of a value, for example if $z = a + bi$, then $z^* = a - bi$. For more details, refer to Alberts *et al.* (2002).

Some definitions of key terms used in the cancer and genetics chapters:

Oncogenesis is the genetic progression to cancer.

Metastasis is the spread of tumour cells to other sites in the body.

Angiogenesis is the formation of blood vessels, which occurs naturally during growth and injury, but is a key component of tumour formation.

Apoptosis (from the Greek for "falling leaves", an example of apoptosis) is programmed cell death, whereby a genetic cascade causes the cell to kill itself quickly and cleanly, as opposed to other cell deaths, such as necrosis which occurs when cells are physically damaged.

Homozygotes are organisms that carry two identical copies of an allele (gene), whereas

Heterozygotes carry two different copies of an allele (gene) across the two homologous chromosomes.

Publications

Journal Publications

- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2003). Statistical techniques for text classification based on word recurrence intervals, *Fluctuations and Noise Letters*, **3**, pp. L1-L10.
- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2004). Mutual information for examining correlations in DNA *Fluctuations and Noise Letters*, **4**, pp. L237-246.
- SPENCER, S. L., BERRYMAN, M. J., GARCÍA, J. A. & ABBOTT, D. (2004). An ordinary differential equation model for the multistep transformation to cancer, *Journal of Theoretical Biology* **231**, pp. 515-524.
- BERRYMAN, M. J., ALLISON, A., WILKINSON, C. R. & ABBOTT, D. (2005). Review of signal processing in genetics, *Fluctuations and Noise Letters* **5**, pp. R13-R35.
- KORNISS, G., HASTINS, M. B., BASSLER, K. E., BERRYMAN, M. J., KOZMA, B. & ABBOTT, D. (2006). Scaling in small-world resistor networks, *Physics Letters A* **350**, pp. 324-330.

Conference Publications

- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2002). Signal processing and statistical methods in analysis of text and DNA, in Nicolau, D V. & Lee, A. P. (eds.), *Proc. SPIE: Biomedical Applications of Micro and Nanoengineering 4937* Melbourne, Australia, pp. 231-240.
- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2003). Stochastic evolution and multifractal classification of prokaryotes, in Bezrukov, S. M, Frauenfelder, H. & Moss, F. (eds.), *Proc. SPIE: Fluctuations and Noise in Biological, Biophysical, and Biomedical Systems 5110*, Santa Fe, USA, pp. 192-200.
- SPENCER, S. L., BERRYMAN, M. J., DEMPSTER, S. & GARCÍA, J. A. (2003). Two models for the multistep transformation to cancer, *Proceedings of the Santa Fe Institute Summer School*, Santa Fe, USA.
- BERRYMAN, M. J., KHOO, W.-L., NGUYEN, H., O'NEILL, E., ALLISON, A. & ABBOTT, D. (2003). Exploring tradeoffs in pleiotropy and redundancy using evolutionary computing in Nicolau, D. V., Muller, U. R. & Dell, J. M. (eds.), *Proc. SPIE: BioMEMS and Nanotechnology 5275*, Perth, Australia, pp. 49-58.
- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2003). Cellular automata for exploring gene regulation in *Drosophila* in Nicolau, D. V., Muller, U. R. & Dell, J. M. (eds.), *Proc. SPIE: BioMEMS and Nanotechnology 5275*, Perth, Australia, pp. 266-277.
- BERRYMAN, M. J., SPENCER, S. L., ALLISON, A. & ABBOTT, D. (2004). Fluctuations and noise in cancer development and treatment in Gingl, Z. *et al.* (eds.), *Proc. SPIE: Noise in Complex Systems and Stochastic Dynamics 5471*, Maspalomas, Spain, pp. 322-332.

- BERRYMAN, M. J., MESSER, S., ALLISON, A. & ABBOTT, D. (2004). Techniques for noise removal from EEG, EOG and air flow signals in sleep patients in Abbott, D. *et al.* (eds.), *Proc. SPIE: Fluctuations and Noise in Biological, Biophysical, and Biomedical Systems* **5467**, Maspalomas, Spain, pp. 89-97.
- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2004). Optimizing genetic algorithm strategies for evolving networks, in White, L. B. *et al.* (eds.), *Proc. SPIE: Noise in Communication* **5473**, Maspalomas, Spain, pp. 122-130.
- BERRYMAN, M. J., ALLISON, A. & ABBOTT, D. (2004). Gene network analysis and design in Nicolau, D. V. (ed.), *Proc. SPIE: Biomedical Applications of Micro- and Nanoengineering II* **5651**, Sydney, Australia, pp. 126-133.
- RYAN, M., BERRYMAN, M. J., & ABBOTT, D. (2004). Modeling the effect of p53 on tumor heterogeneity and the mutator phenotype in Nicolau, D. V. (ed.), *Proc. SPIE: Biomedical Applications of Micro- and Nanoengineering II* **5651**, Sydney, Australia, pp. 144-152.
- BAKER, T. J. A., BOTTING, M., BERRYMAN, M. J., RYAN, A. & GRISOGONO, A.-M. (2004). Adaptive battle agents: emergence in artificial life combat models, in Al-Sarawi, S. F. (ed.), *Proc. SPIE: Smart Structures, Devices, and Systems II* **5649**, Sydney, Australia, pp. 574-585.
- SABORDO, M., CHAI, S. Y., BERRYMAN, M. J. & ABBOTT, D. (2004). Who wrote the Letter to the Hebrews? Data mining for detection of text authorship in Al-Sarawi, S. F. (ed.), *Proc. SPIE: Smart Structures, Devices, and Systems II* **5649**, Sydney, Australia, pp. 513-524.
- BERRYMAN, M. J., COUSSENS, S. W., PAMULA, Y., KENNEDY, D., LUSHINGTON, K., SHALIZI, C., ALLISON, A., MARTIN, A. J., SAINT, D. & ABBOTT, D. (2005). Nonlinear aspects of the EEG during sleep in children in Stocks, N. G., Abbott, D. & Morse, R. P. (eds.), *Proc. SPIE: Fluctuations and Noise in Biological, Biophysical, and Biomedical Systems III* **5841**, Austin, USA, pp. 40-48.
- BERRYMAN, M. J., JOHNSON, N. F. & ABBOTT, D. (2005). Contagions across networks: colds and markets in Bender, A. (ed.), *Proc. SPIE: Complex Systems* **6039**, Brisbane, Australia, pp. 60390O-1-13.
- LIM, K. L., MANN, I., SANTOS, R., TOBIN, B., BERRYMAN, M. J., RYAN, A. & ABBOTT, D. (2005). Adaptive battle agents: complex adaptive combat models, in Bender, A. (ed.), *Proc. SPIE: Complex Systems* **6039**, Brisbane, Australia, pp. 603907-1-13.
- ONG, Z. LO, A. H.-W., BERRYMAN, M. J. & ABBOTT, D. (2005). Multi-objective evolutionary algorithm for investigating the trade-off between pleiotropy and redundancy in Bender, A. (ed.), *Proc. SPIE: Complex Systems* **6039**, Brisbane, Australia, pp. 60390Q-1-12.
- BARAGLIA, D. P., BERRYMAN, M. J., COUSSENS, S. W., PAMULA, Y., KENNEDY, D., MARTIN, A. J. & ABBOTT, D. (2005). Automated sleep scoring and sleep apnea detection in children in Bender, A. (ed.), *Proc. SPIE: Complex Systems* **6039**, Brisbane, Australia, pp. 60390T-1-12.
- PUTNINS, T. J., SIGNORIELLO, D. J., JAIN, S., BERRYMAN, M. J. & ABBOTT, D. (2005). Advanced text authorship detection methods and their application to biblical texts in Bender, A. (ed.), *Proc. SPIE: Complex Systems* **6039**, Brisbane, Australia, pp. 60390J-1-13.
- BERRYMAN, M. J. (2006) Marital infidelity and its effect on pathogen diversity, in Bender, A. (ed.), *Proc. SPIE: Complexity and Nonlinear Dynamics* **6417** Adelaide, Australia, pp. 64170D-1-12

List of Figures

Figure		Page
2.1	The central dogma of biology	9
2.2	Colour spectrograms of <i>S. aureus</i>	14
2.3	Multifractal plot	17
2.4	Phylogenetic trees of bacteria using the multifractal distance metric . . .	19
<hr/>		
3.1	Mutation operations	28
3.2	Plots of mutual information for real and virtual DNA sequences	31
<hr/>		
4.1	Neighbourhoods typically used in cellular automata	39
4.2	Networks of share exchange traders	41
4.3	Plot of infections for K4 kindergarten classes	44
4.4	Plot of infections for K5 kindergarten classes	45
4.5	Plot of infections for grade 7 classes	46
4.6	Plot of infections for grade 8 classes	47
4.7	Share market graphs showing inflation	48
4.8	Share market graphs for totally disconnected network	48
4.9	Share market graphs for partly connected network	49
4.10	Share market graphs for totally connected network	49
4.11	Share market graphs for a network with two subgroups of traders	50
4.12	Distribution graphs for a network with two subgroups of traders	51
<hr/>		
5.1	Network of <i>Drosophila</i> gene interactions	57
5.2	Wild-type expression of bicoid	59
5.3	Maternal expression of <i>nanos</i> mRNA	59
5.4	Wild-type expression of <i>staufer</i> protein	60

List of Figures

5.5	Expression of bicoid and hunchback proteins at different temperatures	61
5.6	Expression of Kruüppel	62
5.7	Time evolution of knirps expression	62
5.8	Expression of giant and even-skipped	63
5.9	Expression of even-skipped	63
5.10	Modelled expression of bicoid	68
5.11	Modelled expression of nanos	69
5.12	Modelled expression of staufer	69
5.13	Modelled expression of hunchback	69
5.14	Modelled expression of hunchback and bicoid	69
5.15	Modelled expression of Krüppel	70
5.16	Modelled expression of knirps	70
5.17	Modelled expression of giant	71
5.18	Modelled expression of even-skipped	71
<hr/>		
6.1	<i>p53</i> -Mdm2 feedback loop	81
6.2	Influences on <i>p53</i> -Mdm2 network	82
6.3	Diagram of protein expression values and regulatory domains	82
6.4	Graph of states for no external stress on the cell	86
6.5	Mean phenotype (number of mutations) of cells against generations	91
6.6	Rate of mutation acquisition per cell cycle	93
6.7	Plot of genomic activity	94
6.8	Mean phenotype (number of mutations) of cells against generations (cell cycles)	95
<hr/>		
7.1	State diagram of the cancer model	104
7.2	Fastest path to cancer	110
7.3	Inherited mutations in cancer-critical genes	113
7.4	Sensitivity of the cancer model to changes in parameters	116

8.1	Time and power spectra plots for eye and brain wave data	123
8.2	Time and power spectra plots for thoracic and abdominal breathing data	124
8.3	Flowchart of signal processing steps	126
8.4	Wavelet decomposition	132
8.5	Time plots of EEG data fitting the linear hypothesis	139
8.6	Time plots of EEG data fitting the nonlinear hypothesis	140

9.1	Sample SVM boundary	152
9.2	Mass spectral plot of Huh7 cell growth medium	155
9.3	Mass spectra plots of changes in growth media over time	156
9.4	Grouping of non-normalised cancer data using t-statistic and neighbour joining algorithm	157
9.5	Grouping of normalised cancer data using t-statistic and neighbour joining algorithm	158
9.6	Three-dimensional PCA plots for the cancer cell data	160
9.7	Dendogram of the non-normalised autism study data	162
9.8	Dendogram of the normalised study data	163
9.9	Three-dimensional PCA plots for the autism study data	166

A.1	Four main stages of the cell cycle	178
A.2	Mitotic phase of the cell cycle	179

B.1	Disclaimer	203
-----	----------------------	-----

List of Tables

Table		Page
3.1	Details of the real mRNA sequences used	26
3.2	Approximate distance in base pairs at which there is no significant mutual information	30
3.3	Estimate of fractal dimension of DNA sequences	32
3.4	Average Higuchi fractal dimension over whole chromosomes	33
4.1	Table of probabilities used for the simulation of school data	39
6.1	Effect of mutations on $p53$	76
6.2	Protein equilibrium positions	84
6.3	Lowered protein equilibrium positions	85
6.4	Initial regulatory domains	85
6.5	Final state for no external stress on the cell	87
6.6	Final state for UV stress on the cell	87
6.7	Final state for DNA damage	88
6.8	Final state for DNA damage and UV stress	88
6.9	Mean phenotype and its derivative for different repair rates	92
7.1	Cancer model parameters	103
7.2	Sensitivity of the cancer model to changes in changes in parameters . . .	115
8.1	Mutual information differences between estimates sources and original signals	132
8.2	Mutual information differences between JADE estimated sources and wavelet denoised estimated sources	132
8.3	Mean percent of time the EEG shows significant behaviour	141
8.4	T-statistic comparing nonlinearity between sleep stages	141
8.5	Higuchi fract measure applied to EEG data	142

List of Tables

8.6	T-statistic comparing Higuchi fractal measure between sleep states . . .	142
9.1	Mass/charge ratios at which differences are significant	154
9.2	Sample classification using k-means clustering algorithm.	164
9.3	Success of SVM at distinguishing non-autistic from autistic children based on urine samples	167