

MODELLING OF MACROPHAGES INTERACTIONS IN BREAST CANCER
BY PARTIAL DIFFERENTIAL EQUATIONS

MOHD RASHID BIN ADMON

UNIVERSITI TEKNOLOGI MALAYSIA

MODELLING OF MACROPHAGES INTERACTIONS IN BREAST CANCER
BY PARTIAL DIFFERENTIAL EQUATIONS

MOHD RASHID BIN ADMON

A thesis submitted in fulfilment of the
requirements for the award of the degree of
Master of Philosophy

Faculty of Science
Universiti Teknologi Malaysia

NOVEMBER 2018

*Especially to my beloved parents,
Admon bin Ahmad and Jaliah binti Sulkiman
and my family members,
Abg Long, Kak Long, Dila, Fasha, Zahin,
Abg Ali, Kak Zura, Amani,
Kak Mas,
Abang Andak,
Abg Arib, Kak Linda, Ariqq, Ahnaf and Husna*

ACKNOWLEDGEMENT

In the name of Allah and with regards to Prophet Muhammad S.A.W for His blessing for giving me strength and health to complete this research.

First and foremost, a thousand thanks to my supervisor, Assoc. Prof. Dr. Normah Maan for her encouragement, patience, enthusiasm and immense knowledge. Her guidance has helped me constantly in conducting this research and in writing this thesis.

I am thankful to my co-supervisor, Dr. Wan Faiziah Wan Abdul Rahman from USM for her absolute support and understanding of biological facts for my research.

In preparing this thesis, I share the credit of my work with my beloved family because they continuously gave me strength and support to finish this project.

Last but not least, thanks to all of my lecturers, friends and everyone, that have contributed directly and indirectly in the duration of conducting this research.

ABSTRACT

The signalling interaction between tumor cells and macrophages will form spontaneous aggregation that causes tumor spreading. Tumor cells and macrophages interchange their respective signals which results a paracrine and autocrine signalling loop. This interaction process can be represented by mathematical model in the form of chemotaxis and reaction diffusion equations. The existing models that consider paracrine signalling loop alone or with the inclusion of paracrine and autocrine signalling loop had been developed by assuming linear signals production. However, this assumption does not give a better representation on the signal dynamics where it is supposed to be in nonlinear form that saturate with increasing cell densities. Therefore, in this research, two existing interaction models are improved by considering the nonlinear form of signals production. Besides, another new interaction model is also developed based on the facts that tumor cells release enzyme during the signaling interaction to penetrate the surrounding tissues. The stability analysis is conducted on three separated models to investigate the condition for spontaneous aggregation. Each of these conditions then are validated using numerical simulations. Stability analysis shows that for all models, the formation of aggregation could be determined by the parameter that represents the secretion and degradation rates of signals together with chemotaxis rates towards signals. However, the inclusion of autocrine signalling loop in the second model increase the possibility of the aggregation. While in the third model, an additional parameter that represents the secretion and degradation rates of enzyme as well as chemotaxis rates towards them could also determine the formation of the aggregation. By numerical simulations, the results are in agreement with the stability analysis obtained for each of the interaction models. Besides, cell clusters that result from the aggregation will be merged to the other cells cluster due to the “effective attraction” between them. Reducing the production rates of signal or chemotaxis rates towards signals or increasing degradation rates of signal is required to prevent aggregation. The same changes towards enzymes will give the same result on preventing the aggregation. These valuable suggestions are crucial for medical experts during treatments.

ABSTRAK

Interaksi secara isyarat di antara sel tumor dan makrofaj akan membentuk agregasi secara spontan yang mengakibatkan tumor merebak. Sel tumor dan makrofaj saling bertukar isyarat yang kemudiannya menghasilkan gelung isyarat parakrin dan gelung isyarat autokrin. Model matematik bagi proses interaksi ini boleh dibentuk menggunakan kemotaksis dan persamaan reaksi serapan. Model sedia ada yang melibatkan gelung isyarat parakrin sahaja atau bersama gelung isyarat autokrin telah dibentuk dengan andaian bahawa penghasilan isyarat adalah secara linear. Walaubagaimanapun, andaian ini tidak menggambarkan dinamik isyarat yang baik kerana penghasilan isyarat seharusnya dalam bentuk tidak linear yang mana tepu apabila ketumpatan sel bertambah. Oleh itu, dalam kajian ini, kedua-dua model yang sedia ada diperbaiki dengan mempertimbangkan bentuk tidak linear untuk penghasilan isyarat. Selain itu, satu interaksi model baharu yang lain telah dibentuk juga berdasarkan fakta bahawa sel tumor merembeskan enzim ketika interaksi secara isyarat itu berlaku untuk menembus tisu sekeliling. Analisis kestabilan dijalankan pada ketiga-tiga model tersebut untuk mengkaji syarat pembentukan agregasi secara spontan. Setiap syarat tersebut kemudiannya disahkan menggunakan simulasi secara berangka. Analisis kestabilan untuk kesemua model menunjukkan bahawa pembentukan agregasi boleh ditentukan oleh parameter yang mewakili kadar penghasilan dan penguraian isyarat-isyarat bersama dengan kecenderungan sel terhadap isyarat-isyarat tersebut. Walaubagaimanapun, penglibatan gelung isyarat autokrin dalam model kedua meningkatkan kebarangkalian untuk agregasi berlaku. Manakala model ketiga menunjukkan pertambahan parameter yang mewakili kadar penghasilan dan penguraian enzim beserta kecenderungan sel terhadapnya juga boleh menentukan pembentukan agregasi. Simulasi secara berangka telah mengesahkan keputusan yang telah diperolehi daripada analisis kestabilan bagi setiap interaksi model. Selain itu, pembentukan sel kluster hasil daripada agregasi akan bergabung dengan sel kluster yang lain disebabkan “penarikan berkesan” di antara mereka. Mengurangkan kadar penghasilan atau kecenderungan terhadap isyarat-isyarat yang terlibat atau menambah kadar penguraiannya diperlukan dalam mencegah agregasi. Perubahan yang sama juga perlu dilakukan kepada enzim untuk mencegah agregasi. Cadangan yang sangat berguna ini penting kepada pakar perubatan semasa merancang perawatan.

TABLE OF CONTENTS

CHAPTER	TITLE	PAGE
	DECLARATION	ii
	DEDICATION	iii
	ACKNOWLEDGEMENT	iv
	ABSTRACT	v
	ABSTRAK	vi
	TABLE OF CONTENTS	vii
	LIST OF TABLES	x
	LIST OF FIGURES	xi
	LIST OF ABBREVIATIONS	xviii
	LIST OF SYMBOLS	xix
	LIST OF APPENDICES	xx
1	INTRODUCTION	1
	1.1 Introduction	1
	1.2 Background of the Study	2
	1.3 Statement of the Problem	5
	1.4 Objectives of the Study	6
	1.5 Scope of the Study	6
	1.6 Significance of the Study	7
	1.7 Outline of the Thesis	8
2	LITERATURE REVIEW	9
	2.1 Introduction	9
	2.2 The Breast and Its Diseases	9
	2.3 Mathematical Modelling of Breast Cancer	12
	2.4 The Macrophage	15
	2.5 Extracellular Matrix and Matrix Degrading Enzymes-Matrix Metalloproteinases	16

2.6	Experimental Studies on Macrophages and Tumor Cells in Breast Cancer	18
2.7	Experimental Studies on Tumor Cells with Extracellular Matrix and Matrix Metalloproteinases in Breast Cancer	21
2.8	Mathematical Modeling of Interactions in Breast Cancer	23
2.9	Summary	31
3	MATHEMATICAL MODELLING OF INTERACTION IN BREAST CANCER INVOLVING PARACRINE SIGNALLING LOOP	32
3.1	Introduction	32
3.2	Mathematical Modelling of Macrophage in Breast Cancer involving Paracrine Signalling Loop	32
3.2.1	Nondimensionalization	35
3.2.2	Homogeneous Steady State	39
3.2.3	Reduction to a system of two equations	40
3.3	Linear Stability Analysis	42
3.3.1	Linearization of Equation (3.53)	42
3.3.2	Linearization of Equation (3.54)	44
3.4	Numerical Simulations	51
3.5	Discussion and Conclusion	75
4	MATHEMATICAL MODELING OF INTERACTION IN BREAST CANCER INVOLVING PARACRINE AND AUTOCRINE SIGNALLING LOOP	77
4.1	Introduction	77
4.2	Mathematical Modeling of Macrophage in Breast Cancer Involving Paracrine and Autocrine Signalling Loop	77
4.2.1	Nondimensionalization	79
4.2.2	Homogeneous Steady State	81
4.2.3	Reduction to a System of Two Equations	81
4.3	Stability Analysis	82
4.4	Numerical Simulations	89
4.5	Discussion and Conclusion	105

5	MATHEMATICAL MODELING OF INTERACTION IN BREAST CANCER INVOLVING EXTRACELLULAR MATRIX AND MATRIX DEGRADING ENZYME	107
5.1	Introduction	107
5.2	Mathematical Modeling of Macrophage in Breast Cancer Involving Extracellular Matrix and Matrix Degrading Enzyme	107
5.2.1	Governing Equation for ECM	108
5.2.2	Governing Equation for MDE	109
5.3	The Model	109
5.3.1	Nondimensionalization	110
5.3.2	Homogeneous Steady State	114
5.3.3	Reduction to a System of Two Equations	114
5.4	Linear stability analysis	116
5.4.1	Linearization of Equation (5.50)	116
5.4.2	Linearization of Equation (5.51)	117
5.5	Numerical Simulations	125
5.6	Discussion and Conclusion	145
6	SUMMARY AND CONCLUSIONS	148
6.1	Introduction	148
6.2	Summary and Conclusions	148
6.3	Recommendations	149
	REFERENCES	151
	Appendices A – B	159 – 162

LIST OF TABLES

TABLE NO.	TITLE	PAGE
2.1	Rare types of breast cancer.	12
2.2	A summary of assumed forms for cell birth/death, $f(m, c)$, and chemical production/decay rates, $g(m, c)$ in chemotaxis models.	27
2.3	Summary of dimensional parameter estimates used in Knutsdottir <i>et al.</i> [36] model.	30
3.1	Summary of dimensional parameter of h_i and b_i , where $i = 1, 2$ and the corresponding references.	34
3.2	Summary of the default dimensionless parameter used in this simulations for paracrine signalling loop and the corresponding references.	53
4.1	Summary of the default dimensionless parameter used in the simulations for paracrine and autocrine signalling loop and the corresponding references.	90
5.1	Summary of the default dimensionless parameter used in the simulations for interactions model involving ECM and MDE with their corresponding references.	126

LIST OF FIGURES

FIGURE NO.	TITLE	PAGE
1.1	Signalling communication between macrophage and tumor cell.	3
1.2	Signalling communication between macrophage and tumor cell in extracellular environment.	4
2.1	The anatomy of breast [45].	10
2.2	Invasive Ductal Carcinoma [46].	11
2.3	Lobular Carcinoma in situ [46].	11
2.4	Macrophage under light microscope [19].	15
2.5	Experiments conducted on mice using collection needle and multiphoton microscope (to view the process) [67].	19
2.6	<i>In vivo</i> experiment on human cancer transplanted in mice [68].	20
3.1	The concentration profiles of CSF-1 from a cell located at $x = 0$.	41
3.2	The concentration profiles of EGF from a cell located at $x = 0$.	41
3.3	The comparison of the particular value of P_1 obtained from this model (represents by the red line) with particular value of P_1^* obtained from Knutsdottir <i>et al.</i> (represent by the green line).	51
3.4	The flowchart of numerical simulations for the system considering paracrine signalling loop.	57
3.5	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulation result obtained when $A_1 = 556$, $A_2 = 1111$ and $B^2 = 2$.	58
3.6	Numerical solutions for M , T , C and E when $t = 1$ days. The default of dimensionless parameter used as in Table 3.2.	59

3.7	Numerical solutions for M , T , C and E when $t = 3$ days. The default of dimensionless parameter used as in Table 3.2.	60
3.8	Numerical solutions for M , T , C and E when $t = 5$ days. The default of dimensionless parameter used as in Table 3.2.	60
3.9	Numerical solutions for M , T , C and E when $t = 7$ days. The default of dimensionless parameter used as in Table 3.2.	61
3.10	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulation results obtained when $A_1 = 10$, $A_2 = 10$ and $B^2 = 2$.	62
3.11	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 100$, $A_2 = 1111$ and $B^2 = 2$.	63
3.12	Numerical solutions for M , T , C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$ and $B^2 = 2$.	64
3.13	Numerical solutions for M , T , C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$ and $B^2 = 2$.	64
3.14	Numerical solutions for M , T , C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$ and $B^2 = 2$.	65
3.15	Numerical solutions for M , T , C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$ and $B^2 = 2$.	65
3.16	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 3000$, $A_2 = 1111$ and $B^2 = 2$.	66
3.17	Numerical solutions for M , T , C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 3000$, $A_2 = 1111$ and $B^2 = 2$.	67
3.18	Numerical solutions for M , T , C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 3000$, $A_2 = 1111$ and $B^2 = 2$.	67

- 3.19 Numerical solutions for M, T, C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 3000, A_2 = 1111$ and $B^2 = 2$. 68
- 3.20 Numerical solutions for M, T, C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 3000, A_2 = 1111$ and $B^2 = 2$. 68
- 3.21 The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 556, A_2 = 100$ and $B^2 = 2$. 69
- 3.22 Numerical solutions for M, T, C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 556, A_2 = 100$ and $B^2 = 2$. 70
- 3.23 Numerical solutions for M, T, C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 556, A_2 = 100$ and $B^2 = 2$. 70
- 3.24 Numerical solutions for M, T, C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 556, A_2 = 100$ and $B^2 = 2$. 71
- 3.25 Numerical solutions for M, T, C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 556, A_2 = 100$ and $B^2 = 2$. 71
- 3.26 The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 556, A_2 = 3000$ and $B^2 = 2$. 72
- 3.27 Numerical solutions for M, T, C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 556, A_2 = 3000$ and $B^2 = 2$. 73
- 3.28 Numerical solutions for M, T, C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 556, A_2 = 3000$ and $B^2 = 2$. 73
- 3.29 Numerical solutions for M, T, C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 556, A_2 = 3000$ and $B^2 = 2$. 74

3.30	Numerical solutions for M , T , C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 556$, $A_2 = 3000$ and $B^2 = 2$.	74
4.1	The comparison of curve obtained in this model (represents by black curve) and curve obtained in previous model (represents by blue curve).	88
4.2	The flowchart of numerical simulations for the system considering paracrine and autocrine signalling loop.	93
4.3	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 556$, $A_2 = 111$, $A_3 = 1000$ and $B^2 = 2$.	94
4.4	Numerical solutions for M , T , C and E when $t = 1$ day. The default of dimensionless parameter used as in Table 4.1.	95
4.5	Numerical solutions for M , T , C and E when $t = 3$ days. The default of dimensionless parameter used as in Table 4.1.	95
4.6	Numerical solutions for M , T , C and E when $t = 5$ days. The default of dimensionless parameter used as in Table 4.1.	96
4.7	Numerical solutions for M , T , C and E when $t = 7$ days. The default of dimensionless parameter used as in Table 4.1.	97
4.8	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulation results obtained when $A_1 = 10$, $A_2 = 10$, $A_3 = 1000$ and $B^2 = 2$.	98
4.9	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 556$, $A_2 = 1111$, $A_3 = 100$ and $B^2 = 2$.	99
4.10	Numerical solutions for M , T , C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 556$, $A_2 = 1111$, $A_3 = 100$ and $B^2 = 2$.	100
4.11	Numerical solutions for M , T , C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 556$, $A_2 = 1111$, $A_3 = 100$ and $B^2 = 2$.	100

4.12	Numerical solutions for M , T , C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 556$, $A_2 = 1111$, $A_3 = 100$ and $B^2 = 2$.	101
4.13	Numerical solutions for M , T , C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 556$, $A_2 = 1111$, $A_3 = 100$ and $B^2 = 2$.	101
4.14	The kymograph shows the density macrophages and tumor cells (the first row) and concentration of the signals CSF-1 and EGF (the second row) with respect to position and time. This simulations results obtained when $A_1 = 100$, $A_2 = 1111$, $A_3 = 5000$ and $B^2 = 2$.	102
4.15	Numerical solutions for M , T , C and E when $t = 1$ day. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$, $A_3 = 5000$ and $B^2 = 2$.	103
4.16	Numerical solutions for M , T , C and E when $t = 3$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$, $A_3 = 5000$ and $B^2 = 2$.	103
4.17	Numerical solutions for M , T , C and E when $t = 5$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$, $A_3 = 5000$ and $B^2 = 2$.	104
4.18	Numerical solutions for M , T , C and E when $t = 7$ days. The dimensionless parameter used are $A_1 = 100$, $A_2 = 1111$, $A_3 = 5000$ and $B^2 = 2$.	104
5.1	The concentration profiles of MDE from a cell located at $x = 0$ with $b = 0.56$.	115
5.2	The comparison of curve obtained in this model (represents by blue curve) and curve obtained in previous model (represents by green curve).	125
5.3	The flowchart of numerical simulations for the system considering the inclusion of ECM and MDE.	130
5.4	Numerical solutions for M and T , when $t = 1$ day. The default of dimensionless parameter used as in Table 5.1.	131
5.5	Numerical solutions for C , E , and U when $t = 1$ day. The default of dimensionless parameter used as in Table 5.1.	131
5.6	Numerical solutions for M and T , when $t = 3$ days. The default of dimensionless parameter used as in Table 5.1.	132
5.7	Numerical solutions for C , E , and U when $t = 3$ days. The default of dimensionless parameter used as in Table 5.1.	132

5.8	Numerical solutions for M and T , when $t = 5$ days. The default of dimensionless parameter used as in Table 5.1.	133
5.9	Numerical solutions for C , E , and U , when $t = 5$ days. The default of dimensionless parameter used as in Table 5.1.	133
5.10	Numerical solutions for M and T , when $t = 7$ days. The default of dimensionless parameter used as in Table 5.1.	134
5.11	Numerical solutions for C , E , and U when $t = 7$ days. The default of dimensionless parameter used as in Table 5.1	134
5.12	Numerical solutions for V when $t = 1$ day, 3 days, 5 days and 7 days. The default of dimensionless parameter used as in Table 5.1.	135
5.13	Numerical solutions for M and T , when $t = 1$ day. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	136
5.14	Numerical solutions for C , E , and U when $t = 1$ day. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	136
5.15	Numerical solutions for M and T , when $t = 3$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	137
5.16	Numerical solutions for C , E , and U when $t = 3$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	137
5.17	Numerical solutions for M and T , when $t = 5$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	138
5.18	The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	138
5.19	Numerical solutions for M and T , when $t = 7$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	139
5.20	Numerical solutions for C , E , and U when $t = 7$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	139
5.21	Numerical solutions for V when $t = 1$ day, 3 days, 5 days and 7 days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 50, G = 0.05, a^2 = 2$ and $b^2 = 0.56$.	140

- 5.22 Numerical solutions for M and T , when $t = 1$ day. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 141
- 5.23 Numerical solutions for C, E , and U when $t = 1$ day. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 141
- 5.24 Numerical solutions for M and T , when $t = 3$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 142
- 5.25 Numerical solutions for C, E , and U when $t = 3$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 142
- 5.26 Numerical solutions for M and T , when $t = 5$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 143
- 5.27 The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 143
- 5.28 Numerical solutions for M and T , when $t = 7$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 144
- 5.29 Numerical solutions for C, E , and U when $t = 7$ days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 144
- 5.30 Numerical solutions for V when $t = 1$ day, 3 days, 5 days and 7 days. The dimensionless parameter used are $H_1 = 26.7, H_2 = 383, H_3 = 3000, G = 0.05, a^2 = 2$ and $b^2 = 0.56$. 145

LIST OF ABBREVIATIONS

CSF-1	–	Colony stimulating factor-1
CSF-1R	–	Colony stimulating factor-1 receptor
EGF	–	Epidermal growth factor
EGFR	–	Epidermal growth factor receptor
ECM	–	Extracellular matrix
MDE	–	Matrix-degrading enzyme
MMP	–	Matrix metalloproteinase
KS	–	Keller and Segel
TAMs	–	Tumor associated macrophages
DLIT	–	Diffuse Luminescent Imaging Topography
cAMP	–	cyclic adenosine monophosphate
uPA	–	urokinase plasminogen-type activator
Targit	–	Targeted intraoperative radiotherapy
EBRT	–	External beam radiotherapy
DLIT	–	Diffuse Luminescent Imaging Tomography

LIST OF SYMBOLS

∇	–	Differential operator
M	–	Density of macrophages
T	–	Density of tumor cells
C	–	Concentration of CSF-1
E	–	Concentration of EGF
μ	–	Random motility of cells
s_1, s_2, b_1, b_2	–	Secretion of signals
h_1, h_2	–	Average density of cells
$\chi_1, \chi_2, \chi_3, \chi_u$	–	Chemotaxis coefficient
D	–	Diffusion of signals
$\gamma_1, \gamma_2, \gamma_3$	–	Degradation of signals
ξ	–	Small perturbation of macrophages
η	–	Small perturbation of tumor cells
M_0, T_0	–	Amplitude of perturbation
q	–	Wavenumber of perturbation
σ	–	Linear growth rate of perturbation
x_{rand}	–	Random number
U	–	Concentration of MDE
V	–	Density of ECM
β	–	Digestion rate of ECM
D_u	–	Diffusion of matrix degrading enzyme
s_3	–	Secretion of matrix degrading enzyme
γ_3	–	Degradation of matrix degrading enzyme

LIST OF APPENDICES

APPENDIX	TITLE	PAGE
A	NUMERICAL SIMULATIONS USING MATLAB	159
B	PAPERS PUBLISHED DURING THE AUTHOR'S CANDI- DATURE	162

CHAPTER 1

INTRODUCTION

1.1 Introduction

Cancer continues to be an enormous global health problem, accounting for an estimate of 8.9 million deaths worldwide in 2016. The number is expected to increase significantly over 10 years if there is lack of effort to improve existing treatments. This issue arises due to the challenges faced by experts to deal with the heterogeneity of cancer itself. Cancer shows distinct characteristics and profiles within a patient's tumor and among tumors from different patients which can complicate diagnosis and therapy. The best way to overcome this challenges is to understand the characteristic and behaviour of cancer.

In general, there are more than 100 types of cancer that affect human. Breast cancer is the most common diagnosed cancer types and a leading killer among women across the globe [1–3]. It is also possible to occur in men and children, however this is rare. Breast cancer can begin in many different areas of the breast such as ductal (passage for milk) and lobule (stores milk) which can be non-invasive, invasive and metastatic. Non-invasive cancer do not spread to nearby tissue while invasive cancer can move out and spread from nearby breast tissues. If the cancer cells break free from the primary site and migrate to other parts of the body, it is considered as metastatic and can lead to death. Most previous studies aim to prevent metastatic event to reduce the death risks of breast cancer patients.

For human survival, the immune system plays an imperative role against cancer [4–6]. Macrophage is one of its division, and it stands out as the most multifunctional among other types of innate immune system [7–12]. It can perform different functions depending on the environmental cues. Tumor cells taking this advantage, manipulate the macrophages to escape themselves from being detected as foreign cells by creating

a signalling interaction with macrophages. This will induce the motility of tumor cells that results a spontaneous aggregation with macrophages which results in a migration to nearby tissues and form cancer in new sites. This situation often relates with a poor prognosis in several types of cancer including breast cancer [7–12].

The existence of interaction between macrophages and tumor cells is considered the most crucial event [10–13]. Both tumor cells and macrophages can interact by interchange their respective signals that results spontaneous aggregation for migration [10, 13–15]. During migration, tumor cells also try to break down the extracellular matrix (ECM) using mediators called matrix degradative enzymes. This method of invasion by tumor cells are the hallmarks of metastasis which causes death among breast cancer patients. Thus, the main focus in this research is to model the interaction and invasion process between macrophages and tumor cells using mathematical knowledge, known as a system of partial differential equations.

1.2 Background of the Study

Macrophage is derived from circulating precursor called monocytes in the blood vessels which comprises an approximate 2-10% populations of white blood cells. Generally, macrophages are essential component for host defense mechanism against pathogens [16–19]. They are also responsible to stimulate the growth of tissues, secrete molecules for angiogenesis (formation of blood vessels), engulfment of the dead cells and matrix remodeling (tissues compartment that defines shape, characteristic and dimensions of organs) [10, 15, 20].

Based on the diverse role of macrophages, it may act as a promoting or suppressing role in their immunity behaviour during immune response depending on the environmental cues. This fact further suggests that they may undergo classical M1 activation or alternative M2 activation [21–27]. M1 macrophages are pro-inflammatory that have the ability to kill pathogens while M2 macrophages are anti-inflammatory that downregulate the inflammatory response, promote angiogenesis and remodelling of tissues. In tumor environment, M1 macrophage are tumoricidal compared to M2 macrophage which have a weak tumoricidal capability.

In tumor microenvironment, macrophages are often referred as tumor associated macrophages, TAMs [28]. These macrophages are closely related to M2

type macrophages which tends to perform trophic and immunosuppressive rather than immunity behavior. TAMs are recruited by tumor cells using variety of growth factors and cytokines such as monocyte/macrophage chemoattractant protein-1, MCP-1/CCL2 [29]. MCP-1 possess chemotaxic activity for monocytes and T lymphocytes via its receptor called CCR2. Several cancer including mammary, ovarian, pancreatic, prostate and renal cancer have been shown that there is correlation between the concentration of MCP-1 with the leukocytes [30].

In breast cancer, the infiltration of macrophages result in a poor prognosis of the disease [9, 10, 12, 28]. The infiltration trigger the interaction to exist between tumor cells and macrophages. Qian and Pollard [11] have reviewed several studies on interaction between tumor cells and macrophages. The interaction initiated by tumor cells which secrete colony stimulating factor-1, CSF-1 that received by CSF-1 receptor, CSF-1R on macrophages. This will trigger macrophages to secrete Epidermal Growth Factor, EGF that can be received by its receptor, EGFR on the tumor cells. Each cell type responds to the signal from the other type by chemotacting towards a higher concentration gradient. This interaction will create a paracrine signaling loop which will results a spontaneous aggregation and leads to cooperative migration for metastasis. Recent studies also reveal that tumor cells have their own receptor for their own signal which then create another loop called autocrine signaling loop.

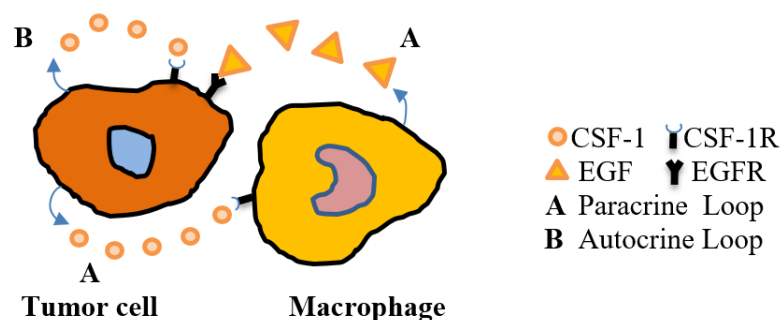


Figure 1.1: Signalling communication between macrophage and tumor cell.

During the interaction, there is another crucial event that need to be highlighted. As previously mentioned, tumor cells migrate in the sense of EGF released by macrophage. In order to move towards the concentration gradient, tumor cells need to pass through the surrounding tissue or extracellular matrix (ECM) [10, 14, 31]. This invasion process is facilitated by matrix degrading enzymes (MDEs), such as Matrix Metalloproteinases (MMPs) released by tumor cells. Since ECM components are made up of many macromolecules that have different physical and biochemical properties,

the MDEs are required to break down the component in order for tumor cells to invade the surrounding tissue.

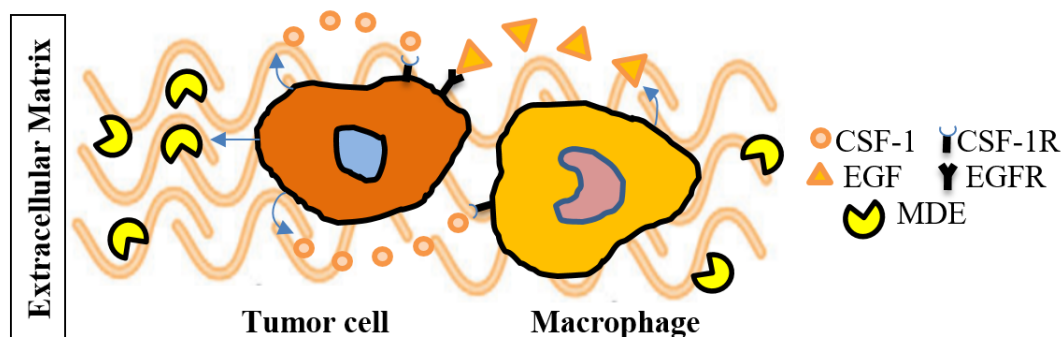


Figure 1.2: Signalling communication between macrophage and tumor cell in extracellular environment.

Based on the interaction, the movement of tumor cell and macrophages in response to chemical gradient can be referred as chemotaxis. It has great significant as proven in previous studies due to its critical role in a wide range of biological phenomena. Keller and Segel [32] first used partial differential equations to model the interactions of chemotactic cells (slime molds) and its secreted attractant (cAMP). Many researchers utilized their model since it is able to capture key phenomena, is easy to understand and analyzed analytically and numerically. For example, Lauffenburger and others [33, 34] motivated by the KS model to describe the inflammatory response of leukocytes to bacterial infection. Luca *et al.* [35] also investigated whether the chemotactic aggregation of microglia may contribute to senile plaques during development of Alzheimers diseases.

The earliest work that study the interaction between macrophages and tumor cells in breast cancer was done by Knutsdottir *et al.* [36]. They used a system of partial differential equations that consists of chemotaxis and reaction-diffusion equations to model the signalling interactions between both cells. Elitas and Zeinali [37] then, inspired by this work, developed another mathematical model in different sites. They developed a mathematical model of movement and binding between macrophage and glioma cells in the brain. Both models use the same type of signalling molecules, namely colony stimulating factor-1 (CSF-1) and epidermal growth factor (EGF).

In Knutsdottir *et al.* [36] works, they considered the secretion terms for both signals have linear relationship with the density of cells. In other words, the production

of both chemical signals are increases when the density of cells increases. However, this assumption is too simplistic and does not capture the true signal dynamics. Hillen and Painter [38] suggest that the production of chemical signals are supposed to saturate with increasing cells density which can be represented mathematically in the form of nonlinear functions. A number of chemotactic models also used this term that can be found in Maini *et al.* [39] and Myerscough *et al.* [40].

Besides, the model proposed by Knutsdottir and their co-workers does not consider the interaction involving ECM. In real situation, the interaction involved is not only between tumor cells and macrophage, but also ECM. This inclusion is motivated from pioneering work carried out by Anderson *et al.* [41]. They are among the earlier researchers who have developed a mathematical modelling using continuum and discrete model that describe the invasion of host tissue by tumor cells through ECM which is facilitated by MDEs. Afterwards, the model is improved by other researcher considering various assumptions to enhance understanding about the interaction involving tumor cell and ECM. Chaplain and Lolas [42] are one of them, focused on continuum model that consider chemotaxis and haptotaxis mechanism by tumor cells and remodelling of ECM after degrading process. Their work was then extended by Tao and Cui [43] where they assume nonlinear density-dependent term for chemotaxis and haptotaxis in tumor cells. Ramis-Conde *et al.* [44] take different approach by proposing a hybrid discrete-continuum two-scale model to study the early stage of tumor cell and its ability to invade the surrounding ECM.

1.3 Statement of the Problem

In breast cancer, the infiltration of macrophages lead to motility of tumor cells. Tumor cells and macrophages communicate by signalling to each other to form aggregation that results in migration. Previous researcher have proposed model using chemotaxis and reaction diffusion equations to illustrate the interaction between macrophages and tumor cells with their production of signalling molecules, EGF and CSF-1 respectively. The model assume each production of signals have linear relationship with the density of each cells. However, this assumption does not give a better representation about the true dynamics of signals. The production of chemical signals are supposed to saturate with increasing cells density. This term is in the form of nonlinear functions which have been widely used in a several number of chemotactic models.

Besides that, the existing model published does not consider the involvement of ECM and MDE during the interaction between macrophages and tumor cells. In real situation, tumor cells need to penetrate ECM for migration towards higher concentration gradients of EGF using MDE. This interaction also can be known as invasion process by tumor cells. Many mathematical models have been developed to illustrate this invasion process. Thus, this could help this research to develop new interaction model to study the effect of the inclusion of ECM and MDE in the interaction between tumor cells and macrophages.

1.4 Objectives of the Study

The objectives of this research are as follows:

1. To modify the mathematical model of interaction between macrophage and tumor cell by considering nonlinear functions for signals production in each cases:
 - Paracrine signalling loop.
 - Paracrine and autocrine signalling loop.
2. To modify the mathematical model of interactions between macrophages and tumor cells with the inclusion of extracellular matrix (ECM) and matrix degrading enzyme (MDE) by considering linear functions for signals production in paracrine signalling loop cases.
3. To determine the conditions for cell aggregation by performing stability analysis of the interaction models.
4. To validate the stability analysis of the interaction models and observe the behaviour of the aggregation by performing numerical simulations.

1.5 Scope of the Study

System of one dimensional partial differential equation that consists of chemotaxis and reaction-diffusion equation is used to develop a mathematical model for interaction between macrophage and tumor cells in breast cancer. In this research, the environmental cues involved in the interaction are epidermal growth factor, EGF, colony stimulating factor-1, CSF-1 and matrix degrading enzyme, MDE.

There are two methods to achieve the objectives which are stability analysis and numerical simulations. In stability analysis, the perturbation method is used to linearize the interaction models. In this research, small perturbation is introduced to the models which it is in the form of exponential type. While in numerical simulations, a built-in PDE solver called *pdepe* in MATLAB software is used to solve the interaction models to observe the aggregation behaviour. This solver is designed to solve parabolic and elliptic systems with the constraints that there must be at least one parabolic equation given.

There are limitations to validate the interaction models with the real data. Since the human breast cancer data are not possible to obtain in a local medical laboratory, the results obtained are only compared with the previous researcher. In previous research, the results obtained are validated with the experimental findings in the literature that conducted on mice. Although it compared with mice, their results are still relevant. This is because in clinical research, it is not suitable to experiment or test directly on human beings. Since mice is the most suitable animal that share almost the same biological characteristics with human, thus the findings are practical to be applied in human.

1.6 Significance of the Study

Macrophage is one of the earliest immune responses that reaches the tumor site to prevent tumor progression. However, the experimental studies reveal that macrophages are able to promote the progression of tumor in certain types of cancer. In the mathematics field, various mathematical models were developed based on the tumoricidal capability of the immune system. This research should inspire other mathematical researchers to keep updated about the new biological findings related to tumor immunology obtained from experimental studies. Thus, they can contribute either in developing a new mathematical model or improve the existing model.

Besides, this research highlights the interactions between macrophages and tumor cells, which results in spontaneous aggregation that leads to tumor spreading. Through a mathematical model, it is possible to determine the condition for aggregation so that several actions can be proposed to medical experts during drug treatments. This effort is aimed to prevent tumor progression, thus it can reduce the death risk among cancer patients.

REFERENCES

1. Wilking, N., Kasteng, F., Bergh, J., Jonsson, B., Kossler, I., Martin, M., Normand, C., Reed, L. and Widdershoven, G. A Review of Breast Cancer Care and Outcomes in 18 countries in Europe, Asia, and Latin America. 2009.
2. Mayer, M., Hunis, A., Oratz, R., Glennon, C., Spicer, P., Caplan, E. and Fallowfield, L. Living with metastatic breast cancer: a global patient survey. *Community Oncology*, 2010. 7: 406–412.
3. Althuis, M. D., Dozier, J. M., Anderson, W. F., Devesa, S. S. and Brinton, L. A. Global trends in breast cancer incidence and mortality 1973-1997. *Int J Epidemiol*, 2005. 34(2): 405–412.
4. Narendra, B. L., Reddy, K. E., Shantikumar, S. and Ramakrishna, S. Immune system: a double-edged sword in cancer. *Inflammation Research*, 2013. 62(9): 823–834.
5. T., I. Therapeutic uses of immune system: new possibilities, new hopes. *Pakistan Journal of Physiology*, 2015. 11(4).
6. O'Donnell-Tormey, J. and Tontonoz, M. Cancer and The Immune System the Vital Connection. *Cancer Research Institute*, 2016.
7. Elgert, K. D., Alleva, D. G. and Mullins, D. W. Tumor-induced immune dysfunction: the macrophage connection. *Journal of Leukocyte Biology*, 1998. 64(3): 275–290.
8. Leek, R. D. and Harris, A. L. Tumor-associated macrophages in breast cancer. *Journal of mammary gland biology and neoplasia*, 2002. 7(2): 177–189.
9. Lewis, C. E. and Pollard, J. W. Distinct role of macrophages in different tumor microenvironments. *Cancer Res*, 2006. 66(2): 605–612.
10. Condeelis, J. and Pollard, J. W. Macrophages: obligate partners for tumor cell migration, invasion, and metastasis. *Cell*, 2006. 124(2): 263–266.
11. Qian, B. Z. and Pollard, J. W. Macrophage diversity enhances tumor progression and metastasis. *Cell*, 2010. 141(1): 39–51.
12. Wynn, T. A., Chawla, A. and Pollard, J. W. Macrophage biology in

- development, homeostasis and disease. *Nature*, 2013. 496(7446): 445–455.
13. Goswami, S., Sahai, E., Wyckoff, J. B., Cammer, M., Cox, D., Pixley, F. J., Stanley, E. R., Segall, J. E. and Condeelis, J. S. Macrophages promote the invasion of breast carcinoma cells via a colony-stimulating factor-1/epidermal growth factor paracrine loop. *Cancer research*, 2005. 65(12): 5278–5283.
 14. Kim, Y., Stolarska, M. A. and Othmer, H. G. The role of the microenvironment in tumor growth and invasion. *Prog Biophys Mol Biol*, 2011. 106(2): 353–379.
 15. Lin, E. Y., Gouon-Evans, V., Nguyen, A. V. and Pollard, J. W. The macrophage growth factor CSF-1 in mammary gland development and tumor progression. *Journal of mammary gland biology and neoplasia*, 2002. 7(2): 147–162.
 16. MacPherson, G. and Austyn, J. *Exploring Immunology: Concepts and Evidence*. Wiley. 2012.
 17. Janeway, C. *Immunobiology Five*. Garland Pub. 2001.
 18. Raven, P., Johnson, G., Singer, S., Losos, J., Ober, W. and Garrison, C. *Biology*. McGraw-Hill Education. 2001.
 19. Parham, P. *The Immune System, Fourth Edition*. Taylor Francis Group. 2014.
 20. Cox, T. R. and Erler, J. T. Remodeling and homeostasis of the extracellular matrix: implications for fibrotic diseases and cancer. *Dis Model Mech*, 2011. 4(2): 165–78.
 21. van der Bij, G. J., Oosterling, S. J., Meijer, S., Beelen, R. H. J. and van Egmond, M. The Role of Macrophages in Tumor Development. *Cell Oncol*, 2005. 27(4): 203–213.
 22. Hao, N. B., Lu, M. H., Fan, Y. H., Cao, Y. L., Zhang, Z. R. and Yang, S. M. Macrophages in tumor microenvironments and the progression of tumors. *Clin Dev Immunol*, 2012. 2012: 1–11.
 23. Medrek, C., Pontn, F., Jirstm, K. and Leandersson, K. The presence of tumor associated macrophages in tumor stroma as a prognostic marker for breast cancer patients. *BMC Cancer*, 2012. 12: 306–315.
 24. Sousa, S., Brion, R., Lintunen, M., Kronqvist, P., Sandholm, J., Monkkonen, J., Kellokumpu-Lehtinen, P. L., Lauttia, S., Tynninen, O., Joensuu, H., Heymann, D. and Maatta, J. A. Human breast cancer cells educate macrophages toward the M2 activation status. *Breast Cancer Res*, 2015. 17: 101–115.
 25. Italiani, P. and Boraschi, D. New Insights Into Tissue Macrophages: From Their Origin to the Development of Memory. *Immune Netw*, 2015. 15(4):

- 167–176.
26. Bio-Rad. *Macrophage Polarization Mini Review*. Report. Bio-Rad Laboratories, Inc. 2016.
 27. Sica, A. and Mantovani, A. Macrophage plasticity and polarization: in vivo veritas. *J Clin Invest*, 2012. 122(3): 787–795.
 28. Goubran, H. A., Kotb, R. R., Stakiw, J., Emar, M. E. and Burnouf, T. Regulation of tumor growth and metastasis: the role of tumor microenvironment. *Cancer Growth Metastasis*, 2014. 7: 9–18.
 29. Ueno, T., Toi, M., Saji, H., Muta, M., Bando, H., Kuroi, K., Koike, M., Inadera, H. and Matsushima, K. Significance of macrophage chemoattractant protein-1 in macrophage recruitment, angiogenesis, and survival in human breast cancer. *Clin Cancer Res*, 2000. 6(8): 3282–9.
 30. Kper, C., Beck, F.-X. and Neuhofer, W. Autocrine MCP-1/CCR2 signaling stimulates proliferation and migration of renal carcinoma cells. *Oncology Letters*, 2016. 12(3): 2201–2209.
 31. Perumpanani, A. J., Simmons, D. L., Gearing, A. J. H., Miller, K. M., Ward, G., Norbury, J., Schneemann, M. and Sheratt, J. A. Extracellular matrix-mediated chemotaxis can impede cell migration. *Proc. R. Soc. Lond. B*, 1998. 265.
 32. Keller, E. F. and Segel, L. A. Model for chemotaxis. *Journal of theoretical biology*, 1971. 30(2): 225–234.
 33. Alt, W. and Lauffenburger, D. A. Transient behavior of a chemotaxis system modelling certain types of tissue inflammation. *Journal of Mathematical Biology*, 1987. 24(6): 691–722.
 34. Lauffenburger, D. A. and Kennedy, C. R. Localized bacterial infection in a distributed model for tissue inflammation. *Journal of Mathematical Biology*, 1983. 16(2): 141–163.
 35. Luca, M. Chemotactic Signaling, Microglia, and Alzheimer’s Disease Senile Plaques: Is There a Connection? *Bulletin of Mathematical Biology*, 2003. 65(4): 693–730.
 36. Knutsdottir, H., Palsson, E. and Edelstein-Keshet, L. Mathematical model of macrophage-facilitated breast cancer cells invasion. *J Theor Biol*, 2014. 357: 184–199.
 37. Elitas, M. and Zeinali, S. Modeling and Simulation of EGF-CSF-1 Pathway to Investigate Glioma Macrophage Interaction in Brain Tumors. *Int J Cancer*

- Stud Res*, 2016. S5(005): 1–8.
38. Hillen, T. and Painter, K. J. A user's guide to PDE models for chemotaxis. *J Math Biol*, 2009. 58(1-2): 183–217.
 39. Maini, P., Myerscough, M., Winters, K. and Murray, J. Bifurcating spatially heterogeneous solutions in a chemotaxis model for biological pattern generation. *Bulletin of mathematical biology*, 1991. 53(5): 701–719.
 40. Myerscough, M., Maini, P. and Painter, K. Pattern formation in a generalized chemotactic model. *Bulletin of mathematical biology*, 1998. 60(1): 1–26.
 41. Anderson, A. R. A., Chaplain, M. A. J., Newman, E. L., Steele, R. J. C. and Thompson, A. M. Mathematical modelling of tumor invasion and metastasis. *Journal of THEoretical Medicine*, 2000. 2: 129–154.
 42. Chaplain, M. A. J. and Lolas, G. Mathematical modelling of cancer invasion of tissue: dynamic heterogeneity. *Network and Heterogeneous Media*, 2006. 1(3): 399–439.
 43. Tao, Y. and Cui, C. A density dependent chemotaxis-hatotaxis system modeling cancer invasion. *J. Math. Anal. Appl.*, 2010. 367: 612–624.
 44. Ramis-Conde, I., Chaplain, M. A. J. and Anderson, A. R. A. Mathematical modelling of cancer cell invasion of tissue. *Mathematical and Computer Modelling*, 2008. 47: 533–545.
 45. Gunduz, M. and Gunduz, E. *Breast Cancer-Focusing Tumor Microenvironment, Stem cells and Metastasis*, InTech. 2011.
 46. Sharma, G. N., Dave, R., Sanadya, J., Sharma, P. and Sharma, K. Various types and management of breast cancer: An overview. *Journal of advanced pharmaceutical technology research*, 2010. 1(2): 109–126.
 47. Araujo, R. P. and McElwain, D. L. A history of the study of solid tumour growth: the contribution of mathematical modelling. *Bull Math Biol*, 2004. 66(5): 1039–1091.
 48. Ribba, B., Holford, N. H., Magni, P., Troconiz, I., Gueorguieva, I., Girard, P., Sarr, C., Elishmereni, M., Kloft, C. and Friberg, L. E. A review of mixed-effects models of tumor growth and effects of anticancer drug treatment used in population analysis. *CPT Pharmacometrics Syst Pharmacol*, 2014. 3: e113.
 49. Cameron, D. A. Mathematical Modelling of the Response of Breast Cancer to Drug Therapy. *Journal of Theoretical Medicine*, 1997. 1(2): 137–151.
 50. Enderling, H., Anderson, A. R., Chaplain, M. A., Munro, A. J. and Vaidya, J. S. Mathematical modelling of radiotherapy strategies for early breast cancer.

- J Theor Biol*, 2006. 241(1): 158–171.
51. Newbury, G. *A numerical study of a delay differential equation model for breast cancer*. Thesis. 2007.
 52. McDuffie, M. A hormone therapy model for breast cancer using linear cancer networks. *Rose-Hulman Undergraduate Mathematics Journal*, 2014. 15(1): 144–156.
 53. Kim, Y. and Othmer, H. G. A hybrid model of tumor-stromal interactions in breast cancer. *Bull Math Biol*, 2013. 75(8): 1304–1350.
 54. Brady, N. J., Chuntova, P. and Schwertfeger, K. L. Macrophages: Regulators of the Inflammatory Microenvironment during Mammary Gland Development and Breast Cancer. *Mediators Inflamm*, 2016. 2016: 1–13.
 55. Mills, C. D., Kincaid, K., Alt, J. M., Heilman, M. J. and Hill, A. M. M-1/M-2 Macrophages and the Th1/Th2 Paradigm. *The Journal of Immunology*, 2000. 164(12): 6166–6173.
 56. Daley, W. P., Peters, S. B. and Larsen, M. Extracellular matrix dynamics in development and regenerative medicine. *Journal of Cell Science*, 2008. 121: 3255–264.
 57. Lu, P., Takai, K., Weaver, V. M. and Werb, Z. *Extracellular Matrix Degradation and Remodeling in Development and Disease*, Cold Spring Harbor Laboratory Press. 2011.
 58. Xiong, G.-F. and Xu, R. Function of cancer cell-derived extracellular matrix in tumor progression. *J Cancer Metastasis*, 2016. 2: 357–364.
 59. Venning, F. A., Wullkopf, L. and Erler, J. T. Targeting ECM disrupts cancer progression. *Front. Oncol.*, 2015. 5: 1–15.
 60. Vakonakis, I. and Campbell, I. D. Extracellular matrix: From atomic resolution to ultrastructure. *Curr Opin Cell Biol*, 2007. 19: 578–583.
 61. Sternlicht, M. D. and Werb, Z. How matrix metalloproteinases regulate cell behaviour. *Annu Rev Cell Dev Biol*, 2001. 17: 463–516.
 62. Egeblad, M. and Werb, Z. New functions for the matrix metalloproteinases in cancer progression. *Nat Rev Cancer*, 2002. 2: 161–174.
 63. Cawston, T. E. and Young, D. A. Proteinases involved in matrix turnover during cartilage and bone breakdown. *Cell Tissue Res*, 2010. 339: 221–235.
 64. Jablonska-Trypuc, M., A. nd Matejczyk and S., R. Matrix metalloproteinases (MMPs), the main extracellular matrix (ECM) enzymes in collagen

- degradation, as a target for anticancer drugs. *J Enzyme Inhib Med Chem*, 2016. 31: 177–183.
65. Van Netten, J., Ashmead, B., Parker, R., Thornton, I., Fletcher, C., Cavers, D., Coy, P. and Brigden, M. Macrophage-tumor cell associations: a factor in metastasis of breast cancer? *Journal of leukocyte biology*, 1993. 54(4): 360–362.
 66. Lin, E. Y., Nguyen, A. V., Russell, R. G. and Pollard, J. W. Colony-Stimulating Factor 1 Promotes Progression of Mammary Tumors to Malignancy. *J Exp Med*, 2001. 193(6): 727–740.
 67. Wyckoff, J., Wang, W., Lin, E. Y., Wang, Y., Pixley, F., Stanley, E. R., Graf, T., Pollard, J. W., Segall, J. and Condeelis, J. A paracrine loop between tumor cells and macrophages is required for tumor cell migration in mammary tumors. *Cancer Res*, 2004. 64(19): 7022–7029.
 68. Patsialou, A., Wyckoff, J., Wang, Y., Goswami, S., Stanley, E. R. and Condeelis, J. S. Invasion of Human Breast Cancer Cells In vivo Requires Both Paracrine and Autocrine Loops Involving the Colony-Stimulating Factor-1 Receptor. *Cancer Research*, 2009. 69(24): 9498–9506.
 69. Wang, T. N., Albo, D. and Tyszynski, G. P. Fibroblasts promote breast cancer cell invasion by upregulating tumor matrix metalloproteinase-9 production. *Surgery*, 2000. 132: 220–225.
 70. Iwata, H., Kobayashi, S., Iwase, H., A., M., Fujimoto, N. and Okada, Y. Production of matrix metalloproteinases and tissue inhibitors of metalloproteinases in human breast carcinomas. *Jpn. J. Cancer Res.*, 1996. 87: 602–611.
 71. Garbett, E. A., Reed, M. W., Stephenson, T. J. and Brown, N. J. Proteolysis in human breast cancer. *Mol. Pathol.*, 2000. 53: 99–106.
 72. H., U., Sebens, S., Seidi, D., Lehnert, H. and Hass, R. Interaction of tumor cells with the microenvironment. *Cell Communication and Signaling*, 2011. 9: 1–8.
 73. Oskarsson, T. Extracellular matrix components in breast cancer progression and metastasis. *The Breast*, 2013. 22: 66–72.
 74. Liotta, L. A., Tryggvason, K., Garbisa, S., Hart, I., Foltz, C. M. and Shafie, S. Metastatic potential correlates with enzymatic degradation of basement membrane collagen. *Nature*, 1980. 284: 67–68.
 75. Cockett, M. I., Murphy, G. and Birch, M. L. Matrix metalloproteinases and

- metastatic cancer. *Biochem. Soc. Symp.*, 1998. 63: 295–313.
76. Kawamata, H., Kameyama, S. and Kawai, K. Marked acceleration of the metastatic phenotype of a rat bladder carcinoma cell line by the expression of human gelatinase A. *Int. J. Cancer*, 1995. 63: 568–575.
 77. Deryugina, E. L., Luo, G. X., Reisfeld, R. A., Bourdon, M. A. and Strongin, A. Tumor cell invasion through matrigel is regulated by activated matrix metalloproteinase-2. *Anticancer Res.*, 1997. 17: 3201–3210.
 78. Durko, M., Navab, R., Shibata, H. R. and Brodt, P. Suppression of basement membrane type IV collagen degradation and cell invasion in human melanoma cells expressing an antisense RNA for MMP-1. *Biochim. Biophys. Acta*, 1997. 1356: 271–280.
 79. Khokha, R. Suppression of the tumorigenic and metastatic abilities of murine B16-F10 melanoma cells in vivo by the overexpression of the tissue inhibitor of the metalloproteinases-1. *J. Natl Cancer Inst.*, 1994. 86: 299–304.
 80. Bartsch, J. E., Edgar, B. S., Staren, D. and Appert, H. E. Matrix Metalloproteinase Expression in Breast Cancer. *Journal o Surgical Research*, 2003. 110: 383–392.
 81. Kousidou, O. C. H., Roussidis, A. E., Theocharis, A. D. and Karamanos, N. K. Expression of MMPs and TIMPs Genes in Human Breast Cancer Epithelial Cells Depends on Cell Culture Conditions and is Associated with their Invasive Potential. *Anticancer Research*, 2004. 24: 4025–4030.
 82. Kohrmann, A., Kammerer, U., Kapp, M., Dietl, J. and Anacker, J. Expression of matrix metalloproteinases (MMPs) in primary human breast cancer and breast cancer cell lines: New findings and review of the literature. *BMC Cancer*, 2009. 9: 188–208.
 83. Figueira, R. C., Gomes, L. R., Neto, J. S., Silva, F. C., Silva, I. D. and Sogayar, M. C. Correlation between MMPs and their inhibitors in breast cancer tumor tissue specimens and in cell lines with different metastatic potential. *BMC Cancer*, 2009. 9: 20–31.
 84. Madsen, D. H. and Bugge, T. H. The source of matrix-degrading enzymes in human cancer: Problems of research reproducibility and possible solutions. *J. Cell Biol.*, 2015. 209: 195–198.
 85. Perumpanani, A. J., Sherratt, J. A., Norbury, J. and Byrne, H. M. Biological inferences from a mathematical model for malignant invasion. *Invasion Metastasis*, 1996. 16(4-5): 209–221.

86. Chaplain, M. A., McDougall, S. R. and Anderson, A. R. Mathematical modeling of tumor-induced angiogenesis. *Annu Rev Biomed Eng*, 2006. 8: 233–257.
87. Owen, M. R. and Sherratt, J. A. Pattern formation and spatiotemporal irregularity in a model for macrophage-tumour interactions. *J Theor Biol*, 1997. 189(1): 63–80.
88. Logan, J. D. *Reaction-Diffusion Systems*, John Wiley Sons, Inc. 2007, 267–344.
89. Grindrod, P. and Murray, J. D. Steady-state spatial patterns in a cell-chemotaxis model. *Journal of Mathematics Applied in Medicine Biology*, 1989. 6: 69–79.
90. Knutsdottir, H., Condeelis, J. S. and Palsson, E. 3-D individual cell based computational modeling of tumor cell-macrophage paracrine signaling mediated by EGF and CSF-1 gradients. *Integr Biol (Camb)*, 2016. 8(1): 104–119.
91. Langtangen, H. P. and Pedersen, G. K. *Scaling Differential equations*, Springer International Publishing. 2016, 125–126.
92. Edelstein-Keshet, L. *Mathematical Models in Biology*. Society for Industrial and Applied Mathematics. 1988.
93. Lee, C., Hoopes, M., Diehl, J., Gilliland, W., Huxel, G., Leaver, E., McCann, K., Umbanhowar, J. and Mogilner, A. Non-local concepts and models in biology. *J. Theor. Biol.*, 2001. 210: 201–219.
94. Smith, G. D. *Numerical Solution of Partial Differential Equations: Finite Difference Methods, 3rd. Edition*, Oxford University Press. 1985, 6–9.
95. Sankara Rao, K. *Introduction to Partial Differential Equations, 3rd. Edition*, PHI Learning Private Limited. 2015, 52–53.
96. Mathworks, I. *Matlab Math: For use with Matlab Version 7*, Mathworks, Inc. 2006, 95–110.
97. Mogilner, A., Edelstein-Keshet, L., Bent, L. and Spiros, A. Mutual interactions, potentials, and individual distance in a social aggregation. *J. Math. Biol.*, 2003. 47: 353–389.
98. Andasari, V., A., G., Lolas, G., South, A. P. and Chaplain, M. A. J. Mathematical modeling of cancer cell invasion of tissue: biological insight from mathematical analysis and computational simulation. *J. Math. Biol.*, 2011. 63: 141–171.