

Form 201 - Application for an NSERC Scholarship or Fellowship

Reference number:	456431445		
Applicant:	Tyler Cassidy	NSERC PIN:	439027
Program:	Postdoctoral Fellowships - PDF		
Application Title:	Developing evolutionarily inspired	treatment strategies to cont	rol and exploit tumor evolution

Tyler Cassidy

Form 201 - Application for a Postgraduate Scholarship or Postdoctoral Fellowship

Electronic Attachments:

Outline of Proposed Research - Cassidy_Proposed_Research Justification for Eligibility of Proposed Research - Cassidy_Research_Eligibility Contributions/Statements - Cassidy_Research_Contributions Transcripts - Direct - Cassidy_PhD_Transcripts



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Type of Awa	rd	l	(FORM 201)		C	TTEE
PDF	iid				D	ate 2020/10/19
Family name	e of applicar	t	Given name	Initial(s) of all given names	Personal	identification no. (PIN)
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ACADEMIC	BACKGR	OUND (include only	current and past degree programs)			T
Degree	Nar	ne of discipline	Department, institution and country	Month st	and year arted	Month and year awarded/expected
Bachelor's	Honors Ap	pplied Mathematics	Science, Faculty of Alberta, CANADA	9 / 2	2011	4 / 2015
Master's	Applied M	athematics	Mathematics and Statistics McGill, CANADA	9 / 2	2015	Transferred to Ph.D.
Doctorate	Applied M	athematics	Mathematics and Statistics McGill, CANADA	1 / 2	2017	10 / 2019



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Type of Award	Applic	ation for a Postgraduate Scholarship or Postdoctoral Fellowship		CTTEE
PDF		(FUKM 201)		Date 2020/10/19
Family name of applican	t	Given name	Initial(s) of all given names	Personal identification no. (PIN)
Cassidy		Tyler	TT	439027
ACADEMIC, RESEAR	CH AND OTHER RELEV	ANT WORK EXPERIENCE		·
Position held a (begin with current	and nature of work t) Full Time - Part Time	Organization and department	Supervisor	Period (mm/yyyy-mm/yyyy)
Postdoctoral research	associate - Full Time	Los Alamos National Laboratory	Dr. Alan S. Perelson	11/2019
Researcher in theoret	ical biology	Theoretical Biology and Biophysics		- 11/2021
Dynamical Systems M	Iodeller - Full Time	Pfizer Inc.	Dr. Cynthia J.	6/2017
Quantitative systems internal medicine rese	biology scientist in the earch unit.	Internal Medicine Research Unit	Musante	- 9/2017
Teaching Assistant - I	Part Time	McGill University	Dr. Sidney	9/2016
Teaching assistant for Management, Calcult	r Calculus for 1s II	Mathematics and Statistics	Trudeau	- 12/2017
Research Assistant - H	Full Time	University of Alberta	Dr. Hassan	5/2014
NSERC USRA resear	rch assistant	Mathematics and Statistics	Safouhi	- 9/2014
Research Assistant - I	Full Time	University of Alberta	Dr. Hassan	5/2014
NSERC USRA resear	rch assistant	Mathematics and Statistics	Safouhi	- 9/2015
Teaching Assistant - I	Part Time	University of Alberta	Dr. Sarah	1/2013
Teaching assistant for and linear algebra I co	r Statistics I, Calculus I, II ourses.	Campus Saint-Jean	Pelletier	- 4/2015
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		Personal identif	ication no. (PIN)	Family na	ame, given name and initial(s) of applicant
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AWARD APPLIED FOR		·			
Type of award Postdoctoral Fellowships	- PDF				Proposed starting date of award 2021/09
Proposed degree program	Proposed field of stud	y/research			Research subject code
(e.g. Masters, Doctorate)	APPLIED MATH	HEMATICS			2950
Title of proposed research Developing evolutionarily i	nspired treatment	strategies to	control and ex	ploit tu	mor evolution
List ten (10) key words that describe y Mathematical biology, Dyna Mathematical modelling,	your proposed research. Amical systems, Po	opulation dyr	namics, Mathe	matical	oncology, Numerical analysis,
PROPOSED LOCATION(S) OF TEN	JRE (in order of prefere	ence)	I		1
Institution/organization	Departm	ient	Program of s	study	Proposed supervisor
University of Oxford,	Mathematical In	istitute	Evolutionarily inspired thera cancer treatme	y pies in ent	Philip K. Maini
Are any of your proposed programs of Clinically-oriented?	f study:	int programs with	a professional deg	ıree (e.g., l	MD/PhD)? Yes X No
SECTION TO BE COMPLETED BY F	PGS APPLICANTS ONL	Y			
Indicate the total number of months o in the natural sciences and engineerin months of full-tir	f graduate studies (mast ng. ne studies	er's and doctoral) you have complete	ed as of De	ecember 31 of the year of application months of part-time studies
Indicate the number of months of stud	dies you have completed	l, as of Decembe	r 31 of the year of a	upplication,	, in the program for which you are
months of full-tir	ne studies			n	nonths of part-time studies
Indicate if you are attending university	at the time of application	on.			
Attending full time	Attending	g part time	Nc	ot attending	g
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Application for a Postgraduate Scholarship or Postdoctoral Fellowship (FORM 201)

Type of Award	Persona	al Identification no. ((PIN) F	amily	name, given name and initial(s) of app	licant
PDF	Valid	439027		Cassi	dy, Tyler TT	
SCHOLARSHIPS A	ND OTHER AWA	RDS OFFERED	(start with mo	st rec	ent and include NSERC awards)
Name of Award	Value (CDN\$)	Level Institutional, Provincial, National, International	Type Academi Researct Leadersh Communica	ic, h, iip, ation	Location of tenure	Period held (yyyy/mm - yyyy/mm)
FRQNT Bourse au doctorat	21,000	Provincial	Research		McGill University	Declined
Mittag-Leffler Fellowship	10,000	International	Research		Institut Mittag-Leffler	2018/10 - 2018/12
Murata Family Fellowship	3,300	Institutional	Research		McGill University	2018/09 - 2019/04
Trottier Science Fellowship	5,000	Institutional	Research		McGill University	2018/09 - 2019/04
NSERC PGS-D	21,000	National	Research		McGill University	2018/05 - 2019/09
James Lougheed Award of	20,000	Provincial	Research		McGill University	2017/09 - 2018/04
CRM Applied Math	10,000	Provincial	Research		McGill University	2016/09 - 2018/09
CAMBAM Fellowship	12,500	Provincial	Research		McGill University	2015/09 - 2017/04
James Lougheed Award of	15,000	Provincial	Research		McGill University	2015/09 - 2016/04
NSERC USRA	7,500	Institutional	Research		University of Alberta	2014/05 - 2014/09

Form 201 (2011 W)

Type of Award	Personal identific	ation no.(PIN)	Family name, given name and initial(s) of applicant
PDF	Valid	439027	Cassidy, Tyler TT
THESIS COMPLETED OR IN PROGRESS			
1. Degree Doctor of philosophy	Supervisor Antony R. Hum Craig	phries, Morga	n Date degree requirements completed 08/2019
Title of thesis On the development and application of	f distributed delay e	quations to ma	thematical physiology
2. Degree	Supervisor		Date degree requirements completed
Title of thesis			
SUMMARY OF THESIS MOST RECENTLY COMPL	ETED OR IN PROGRESS		
Human physiology is filled with examplement hematopoietic system, the time lag bet delay. In my dissertation, I derived a prinew techniques for analyzing physiolo tumour growth in the presence of imm	ples of time-delayed ween signal and res hysiologically realis gically structured ed une surveillance.	I feedback. In ponse is varial stic method of quations, and a	certain cases, such as the ble and distributed around a mean modelling these delays, developed applied these techniques to model
I began by deriving a general model of an age structured partial differential eq period and variable maturation rate. I t dependent distributed delay differentia dependent discrete DDE and generaliz concatenated ageing processes. To illu published models of hematopoiesis to resulting form.	f population renewal quation to model a p then reduced the age al equation (DDE). Thes the linear chain t distrate the utility of t their equivalent stat	I that includes opulation with structured par This general se echnique to inc he distributed the dependent di	an arbitrary maturation period. I used a randomly distributed maturation rtial differential equation to a state etting encompasses the common state clude variable transition rates and DDE framework, I simplified two istributed DDE and analysed their
Next, I developed and analyzed a math incorporates heterogeneity in tumour c analysis, I completely characterised the sufficient condition for disease remission of the mathematical model shows that through a transcritical bifurcation. By involvement is crucial in determining	nematical model of t cell cycle duration b e importance of tum ion. Consistent with decreasing tumour- incorporating a mod long-term treatment	umour-immun y using a distri our-immune in the immunoed immune intera lel of viral then outcomes.	the interaction that explicitly buted DDE. Through linear stability interaction by deriving a necessary and diting hypothesis, bifurcation analysis ction leads to tumour expansion rapy, I showed that immune
To understand the effects of genetic va viral therapy and immunotherapy. I qu simulating viral and immunostimulato genetic algorithm to create an optimal prognosis.	ariability in treatmen antified the synergis ry combination ther dosing regimen that	nt outcome, I p stic interaction apy. Finally, I t reduces treatr	erformed a virtual clinical trial of between these two treatments by exploited this synergy by using a nent burden and improves virtual
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Type of Award		Personal identific	ation no.(PIN)	Family name, given name and initial(s) of applicant
PDF		Valid	439027	Cassidy, Tyler TT
JUSTIFICATION FO	R LOCATION OF TENURE			

Provide a rationale for your choice(s) for location of tenure. See instructions for further details.

I intend to perform my postdoctoral research at the Wolfson Center for Mathematical Biology in the Mathematical Institute at the University of Oxford. I have already identified a mentor, Prof. Philip K. Maini, and received approval to join the Institute.

The Wolfson Center for Mathematical Biology provides a dynamic and collaborative atmosphere for my postdoctoral research. In particular, the Wolfson Center is home to a number of mathematical biologists studying cancer. Prof. Helen Byrne's research has illuminated the mechanisms underlying angiogenesis in tumour development, and Prof. Ruth Baker has focused on cellular migration and invasion which are critical to understanding tumour growth. The Center is also home to the Quantitative Biology Network which connects quantitative researchers with experimentalists and clinicians with the goal of driving interdisciplinary research into biology and medicine. The Center hosts weekly seminars with researchers from around the world.

At Oxford, I will work in close collaboration with Prof. Philip K. Maini. Prof. Maini is a world leader in mathematical biology and has a proven track record of productivity with over 80 published articles since 2016. He is a Fellow of the Royal Society, the Society of Industrial and Applied Mathematics, and the Society of Mathematical Biology. His ability to translate mathematical results into medical insight was recognized with his election to the Academy of Medical Sciences.

His research has focused on collective cell dynamics and has elucidated the mechanisms leading to cancer. In particular, he has proposed models that bridge scales between single cell and population-level dynamics. These techniques are particularly important in understanding non-genetic evolution in tumours, as recent experimental work has shown that epigenetic regulation is influenced by local behavior and the life history of the parent cell. Recently, his research in mathematical oncology has identified strategies for combination cancer therapies. Accordingly, he is an ideal supervisor and collaborator for my proposed research into the physiological mechanisms underlying epigenetic evolution and the development of evolutionarily inspired therapeutic strategies.

Prof. Maini has existing collaborations with experimentalists throughout Oxford and the world. In particular, he works closely with researchers and students at the Integrated Mathematical Oncology (IMO) group at the Moffitt Cancer Center in the USA. Moffitt Cancer Center is the host institution for a stage I adaptive therapy trial in prostate cancer. I will therefore be able to continue my collaboration with the IMO while having access to clinicians and experimentalists who are testing our mathematical predictions.

All told, collaborating with Prof. Philip Maini at the Wolfson Center for Mathematical Biology at the University of Oxford offers a exceptional atmosphere for my postdoctoral research.

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Application for a Postgraduate Scholarship or Postdoctoral Fellowship (FORM 201)

Type of Award		Persona	l identification no. (PIN)	Family name, given name and initial(s) of applicant						
PDF	,	Valid	439027	Cassidy, Tyler TT						
DIVERSITY CONSIDE	RATIONS IN RESEARCH DESIGN									
Are diversity cons design, methods, a	Are diversity considerations including, but not limited to, sex and gender taken into account in the research design, methods, analysis and interpretation, and/or dissemination of findings?									
Yes	X No									
NOTE			·							
If you answer "yes throughout your p their findings).	s" to the question above, pleas roposal (i.e. research design, r	se ensu method	re that diversity c ls, analysis and in	considerations are incorporated iterpretation, and/or dissemination of						
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My research concerepresent idealized models will be parcancer cell lines a mathematical modin cell culture seru influences will be	erns the development and ana d systems and their analysis for rametrized using in vitro data re expanded in vitro and form del. However, sex or race difforum, are not relevant to the dev critical when translating my v	lysis of orms a derived the in erences velopme work to	f mathematical ma significant propor d from genetically vitro systems that present in culture ent and analysis o the clinic, but th	odels. These mathematical models rtion of my work. The mathematical y engineered cancer cell lines. These t will be used to parametrize the e, possibly due to hormonal influence of the mathematical models. These at is not a goal of the current work.						

The development of new anti-cancer drugs can be expected to take over a decade and cost over \$1 billion USD. Despite advances in targeted and precision medicine, most patients with advanced cancer will experience drug resistance, treatment failure and, ultimately, disease recurrence [1, 2]. This resistance, long thought to result from genetic heterogeneity and evolution, is increasingly understood as the result of non-mutational evolutionary adaptations to therapy [3, 4]. Accordingly, my proposed research will develop mathematical models to understand the physiological mechanisms underlying this epigenetic resistance, and use these models to develop evolutionarily-inspired and clinically-actionable therapeutic strategies that mitigate the development of treatment resistance.

Typically, drug-resistant populations co-exist in a dynamic equilibrium with drug-sensitive populations [1], but therapeutic interventions upset this equilibrium by imposing evolutionary pressures that confer a fitness advantage to the drug-resistant populations. This treatment-induced selection of drug-resistant cells is a natural consequence of conventional maximally-tolerated cytotoxic therapy, which aims to kill as many drug-sensitive cells as possible, and therefore induces strong selection pressure against the drug-sensitive population [5]. Thus, the accepted standard of care may be leading to the competitive release of drug-tolerant populations and contributing to the inevitability of treatment failure and disease progression [4].

Therapeutic strategies have been proposed to exploit the competition between drug-sensitive and tolerant cells. These strategies aim to prolong the time to disease progression by inhibiting the emergence of drug-tolerant populations [5]. These adaptive strategies in cancer treatment make extensive use of the theoretical framework of evolutionary game theory. In these evolutionary games, the oncologist controls the environment through treatment while tumour sub-populations, or the players, strategize to maximize their reproductive ability by modulating their frequency inside the tumour. In the resulting game, drug-resistant cells exploit their treatment-induced fitness advantage to increase in frequency at the expense of drug-sensitive cells. This treatment-driven evolution is typically modelled as a multi-species replicator equation describing clonal dynamics on a fixed genetic landscape so the population dynamics are entirely determined by clonal frequency and pre-determined sensitivity to therapy. Thus, while the theoretical framework underlying adaptive therapy exploits both the competition between genetically distinct tumour sub-populations and the relatively slow timescales for genetic evolution [6], these evolutionary games do not consider the role of non-mutational factors in treatment resistance [3].

However, we are beginning to appreciate that genetic resistance may not be the principle driver of therapeutic resistance, and recent studies have identified the important role of non-mutational, or epigenetic, adaptations in treatment resistance [3, 4, 7]. For example, epigenetic regulation of genetically identical non-small cell lung cancer (NSCLC) cells induces a reversible drug-tolerant phenotype that expands during cytotoxic chemotherapy [7]. This non-mutational resistance, where genetically identical cells transiently adopt a drug-resistant phenotype to avoid the treatment imposed selection pressure, may thwart therapeutic strategies that rely on Darwinian evolution over a fixed genetic landscape. Consequently, it is presently unclear how to adapt evolutionarily inspired therapies to the address the difficulties posed by reversible non-genetic mechanisms that change on a faster timescale than Darwinian evolution.

To this end, recent experimental work suggests that this phenotypic heterogeneity can be modulated by a number of complex physiological factors, including the current state of the population, tumour microenvironment, and the life history of the parental cell [8, 9]. Accordingly, as systems-level experiments of these complex and non-linear interactions are currently intractable, standard experimental techniques are unable to probe the physiological determinants of non-genetic heterogeneity. *Therefore, mathematical modelling offers an unparalleled opportunity to identify the physiological mechanisms underlying non-mutational drug resistance and to use this understanding to extend adaptive therapies to non-genetic drug resistance.*

My research will address the systemic determinants of epigenetic resistance through the development of mechanistic mathematical models of tumour evolution in response to therapy. I will explicitly include the physiological mechanisms underlying phenotypic heterogeneity through the use of physiologically-structured population models. Unlike most game theoretical models, these mechanistic models take the form of partial

differential equations that are explicitly designed to study intra-clonal population heterogeneity. By using a combination of single cell RNA-sequencing and population level data arising from *in vitro* and *in vivo* experiments [8] in concert with sophisticated parameter estimation techniques and parameter identifiability analysis, I will calibrate and validate my mathematical models. After these steps, I will leverage these models to predict the epigenetic response to therapy, and to understand the mechanisms underlying treatment resistance and drug failure.

These models will serve as the basis of the development of evolutionarily inspired therapies that explicitly address non-mutational resistance. I have recently shown that it is possible to derive therapeutic strategies that exploit the epigenetic regulation of phenotypic resistance and drive extinction of a NSCLC population resistant to standard chemotherapies by combining techniques from infinite dimensional dynamical systems with physiologically based pharmacokinetic models. Effectively, my results show that oncologists can preserve a significant proportion of drug-sensitive cells while simultaneously driving tumour contraction by carefully choosing dose size and frequency to modulate selection pressure on drug-sensitive cells.

The theme of selectively applying treatment pressure to an evolving population underlies the main contribution of my proposal. I will use biologically-relevant and physiologically-structured mathematical models to understand how therapeutic selection shapes epigenetic evolution of malignant tumours. With this understanding in hand, I will use techniques from dynamical systems, pharmacometrics, and numerical analysis to develop rational and clinically-actionable treatment schedules to steer this epigenetic evolution towards desired clinical outcomes. This rational use of drug-interventions will be particularly important when considering large heterogeneous tumours where single drug therapies are unlikely to be successful. There, evolutionary steering may involve drug cycling to maintain a drug-sensitive population of cells and thus limit treatment failure, or strategies to induce collateral sensitivity wherein resistance to the first therapy increases sensitivity to subsequent therapeutics [10]. Finally, I will demonstrate the robustness of these clinically actionable strategies through the use of *in silico* clinical trials [11].

Most importantly, I will utilize my experience in the pharmaceutical industry and existing collaborations with experimentalists and clinicians to translate my mathematical results into new biological knowledge. Specifically, the mathematical models developed during this work will make predictions that will first be tested in *in vitro* experiments before being applied to patient-derived organoid models [12]. In this way, my research will inform a multi-disciplinary approach to rational personalized medicine and allow for these evolutionary steering techniques to be translated into clinically actionable strategies.

Despite significant progress in anti-cancer drug development, therapeutic success is often transient with treatment failure being driven by the emergence of resistant populations. These resistant populations then form the "minimal residual disease" that almost inevitably act as a reservoir of drug-resistant cells that drive refractory tumour growth. Therapeutic strategies have been developed to combat pre-existing genetic resistance and a recent pilot clinical trial in metastatic castrate-resistant prostate cancer has illustrated the possible clinical benefits of these so-called "adaptive therapies" [13]. My work is critical to extending these strategies to account for non-mutational evolutionary adaptations to therapy. My research will develop evolutionarily-inspired treatment strategies that will permit re-purposing of existing anti-cancer drugs, decrease treatment toxicity and burden, and ultimately support efforts towards improving clinical outcomes.

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- [2] McGranahan, N. and Swanton, C.(2017) Cell 168(4).
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- [4] Bell, C. C. and Gilan, O. (2020) Br. J. Cancer 122(4).
- [5] Gatenby, R. A. and Brown, J. S. (2020) Nat. Rev. Clin. Oncol.
- [6] Gluzman, M., Scott, J. G., and Vladimirsky, A. (2020) Proc. R. Soc. B Biol. Sci. 287(1925).
- [7] Sharma, S. V. et al. (2010) *Cell* **141(1)**.
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- [9] Yang, H. W., Chung, M., Kudo, T., and Meyer, T. (2017) Nature 549(7672).
- [10] Acar, A. et al., (2020) Nat. Commun.11(1).
- [11] Cassidy, T. and Craig, M. (2019) PLOS Comput. Biol. 15(11).
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The goal of the proposed research is to develop physiologically-structured and biologically relevant models of epigenetic resistance to anti-cancer therapies. While this work is translational and therefore interdisciplinary, my proposed research is entirely mathematical. In broad terms, my research aims to

develop(ing) new mathematical or statistical models, theories, methodologies, or analytical tools that may lead to potential future applications in human health ¹

Specifically, my work will involve

- The development of physiologically-structured mechanistic models of evolutionary selection in a heterogeneous population. These infinite dimensional models will either be systems of non-local partial differential equations or delay differential equations. The development, analysis, and simulation of these types of models is an active area of research in mathematics. For example, the extension of well-known linearisation techniques and bifurcation analysis from finite dimensional systems to these infinite dimensional dynamical systems is non-trivial and will require the development of new mathematical techniques.
- 2. The simulation of the mathematical models will require either the development of new numerical techniques or the derivation of mathematical equivalences with simpler models for which numerical techniques exist.
- 3. The parametrization and validation of these mathematical models will require the adaptation of existing statistical techniques to available data and model predictions. This will include the development of local sensitivity analysis techniques, optimization routines for parameter fitting, and practical identifiability analysis.

Accordingly, the proposed research will contribute to the advancement of knowledge in mathematical biology, dynamical systems, and numerical methods, all of which fall under the mandate of NSERC and its programmes.

¹Taken from: Addendum to the guidelines for the eligibility of applications related to health, https://www.nserc-crsng.gc.ca/nserc-crsng/policies-politiques/addendum-addenda_eng.asp, Accessed: 10/17/2020.

I Contributions to research and development

a) Articles published or accepted in peer-reviewed journals

1) **Cassidy, T.**, Humphries, A.R., Craig, M., and Mackey, M.C. (2020) Characterizing chemotherapyinduced neutropenia and monocytopenia through mathematical modelling, Bulletin of Mathematical Biology, **82**: 1-26. (Ph.D. Work)

2) **Cassidy, T.** and Craig, M., (2019) Determinants of combination GM-CSF immunotherapy and oncolytic virotherapy success identified through in silico treatment personalization, PLOS Computational Biology, **15**: 1-16. (Ph.D. Work)

3) **Cassidy, T.**, Craig, M. and Humphries, A.R. (2019) Equivalences Between Age Structured Models and State Dependent Distributed Delay Differential Equations, Mathematical Biosciences and Engineering, **16**: 5419-5450. (Ph.D. Work)

4) **Cassidy, T.** and Humphries, A.R., (2019) A Mathematical Model Of Viral Oncology As An Immuno-Oncology Instigator, Mathematical Medicine and Biology: A Journal of the IMA, **37**: 117-151. (Ph.D. Work)

5) De Souza, D.C, Craig, M., **Cassidy, T.**, Li, J., Nekka, F., Humphries, A.R. (2018) Transit and lifespan in neutrophil production: implications for drug intervention, Journal of Pharmacokinetics and Pharmacodynamics, **45**: 59-77. (Ph.D. Work)

6) **Cassidy, T.**, Gaudreau, P. and Safouhi, H. (2017) On the Computation of Eigenvalues of the Anharmonic Coulombic Potential, Journal of Mathematical Chemistry, **56**: 477-492. (B.Sc work)

b) Articles submitted to peer-reviewed journals

1) **Cassidy, T.**, Distributed Delay Differential Equation Representations of Cyclic Differential Equations, SIAM Journal on Applied Mathematics, Submitted: July 9th, 2020, Submission ID: M135160, 19 pp. (Postdoctoral Work)

2) Jenner, A.L., **Cassidy, T.**, Belaid, K., Bourgeois-Daigneault, M.C., and Craig, M. In silico trials predict that combination strategies for enhancing vesicular stomatisis oncolytic virus are determined by tumour aggressivity, Journal of ImmunoTherapy for Cancer, Submitted: July 7th, 2020, Submission ID: jitc-2020-001387, 33 pp. (Postdoctoral Work)

d) Non-peer-reviewed contributions

1) **Cassidy, T.,***, Transit compartmental representations of functional differential equations, Los Alamos National Laboratory Theoretical Biology and Biophysics Seminar, National institutional oral presentation, 2020 (Postdoctoral work)

2) **Cassidy, T.,***, Nichol, D., Robertson-Tessi, M., Craig, M. and Anderson, A.R.A., Insights from phenotype and age structured equations to avoid chemotherapeutic drug resistance, SIAM/CAIMS Joint Annual Meeting, International conference oral presentation, 2020, (Postdoctoral work)

3) **Cassidy, T.,***, Nichol, D., Robertson-Tessi, M., Craig, M. and Anderson, A.R.A., Using Structured Equations to Control Tumour Evolution and Avoid Chemotherapeutic Resistance, York University Laboratory of Industrial and Applied Mathematics Seminar, International institutional oral presentation, 2020, (Postdoctoral work)

4) **Cassidy, T**^{*}, Humphries, A.R., Craig, M. and Mackey, M.C., Innate Immune System Regulation in Health and Disease, Society for Mathematical Biology Annual Meeting, International conference oral presentation, 2019, (Ph.D. work)

5) **Cassidy, T***, Craig, M. and Humphries, A.R., The Linear Chain Trick in Modelling Drug Effects on Neutrophil Response, CAIMS Annual Meeting, International conference oral presentation, 2019, (Ph.D. work)

6) Cassidy, T*, Craig, M. and Humphries, A.R., A Recipe for State Dependent Distributed Delay Dif-

ferential Equations, SIAM Meeting on Dynamical Systems, International conference oral presentation, 2019, (Ph.D. work)

7) **Cassidy, T**^{*}, Craig, M. and Humphries, A.R., Understanding and Exploiting Immune Support of Cancer Virotherapy, Pfizer Inc. Quantitative Systems Pharmacology in Early Clinical Development Seminar, International institutional oral presentation, 2019, (Ph.D. work)

8) **Cassidy, T**^{*}, Craig, M. and Humphries, A.R., Modelling and Optimizing Immune Support of Cancer Virotherapy, Helmholtz Center for Infection Research Systems Immunology Seminar, International institutional oral presentation, 2019, (Ph.D. work)

9) **Cassidy, T**^{*} and Humphries, A.R., A Mathematical Model of Viral Oncology, 10th Swedish Meeting on Mathematics in Biology, International conference oral presentation, 2018, (Ph.D. work)

10) **Cassidy, T**^{*} and Humphries, A.R., Viruses as Instigators of Cancer Immunotherapy, SIAM Life Sciences Meeting, International conference oral presentation, 2018, (Ph.D. work)

11) **Cassidy, T.,***, Humphries, A.R. and Mackey, M.C, Mathematical Modelling of Cyclic Neutropenia, CAMBAM Seminar National institutional oral presentation, 2017 (M.Sc work)

12) **Cassidy, T.,***, Humphries, A.R. and Mackey, M.C, Understanding, Treating and Avoiding Hematological Disease: Better Medicine Through Mathematics, SIAM Life Sciences Meeting, International conference oral presentation, 2016 (Ph.D. Work)

f) Contributions resulting from your participation in industrially relevant RD activities

1) **Cassidy,T.,***, Rieger, T. and Baraldi, R., Modelling Lipoprotein Dynamics during PCSK-9 Inhibition, Pfizer Internal Medicine Research Unit Quantitative Research Group Seminar (Institutional oral presentation and technical report), 2017.

II Most significant contributions to research and development

1) A significant portion of my research has involved the development and analysis of mathematical models of hematopoiesis during immunosuppressive chemotherapy. In 2018, we compared three different mathematical models of granulopoiesis and showed that the "gold standard" Quartino model misspecifies the neutrophil precursor maturation stage as an additional proliferative stage¹ and published this work in the official journal of the International Society of Pharmacometrics. I showed that such misspecifications can be avoided by explicitly modelling the proliferative stage as a physiologically-structured partial differential equation. I established the equivalence between the common transit compartment ordinary differential equation models of hematopoiesis that include pharmacological interventions and a system of delay differential equations where the delay is both state dependent and distributed². This equivalence links the three major classes of physiologically based mathematical models of hematopoiesis and was published in a special issue dedicated to Advances in Mathematical Population Dynamics. I derived and validated a novel physiologically-structured model of monocytopoiesis to characterize the relationship between monocytopenia and neutropenia during chemotherapy. Our results suggest using monocyte concentrations as a early warning sign for chemotherapy induced neutropenia³. We published this work in the official journal of the Society of Mathematical Biology.

2) I developed a physiologically based mathematical model of tumour growth and oncolytic viral therapy⁴. Using a system of distributed delay differential equations, I explicitly incorporated intra-tumour heterogeneity in a model of tumour growth. I demonstrated that intra-tumour heterogeneity acts to destabilize the disease-free state and characterized the importance of immune recruitment in cancer

¹de Souza et al. *Journal of Pharmacokinetics and Pharmacodynamics* (2018)

²Cassidy, Craig, and Humphries, *Mathematical Biosciences and Engineering* (2019)

³Cassidy, Humphries, Craig, and Mackey, *Bulletin of Mathematical Biology* (2020)

⁴Cassidy and Humphries, *Mathematical Medicine and Biology: A Journal of the IMA* (2019)

progression. I extended the model to include oncolytic viral therapy and showed that the resulting immune involvement is critical for determining treatment outcome. By parametrizing the mathematical model to late stage melanoma and performing an in silico clinical trial, I showed the mathematical model can replicate the population-level results of the OPTIM clinical trial that led to FDA approval of the first oncolytic viral therapy⁵. I then investigated the synergy between standard immunotherapies and an oncolytic virus and thus tailored therapeutic strategies for our virtual population. I leveraged these individualized schedules to propose a clinically actionable combination therapy schedule that significantly improves virtual prognosis while minimizing treatment burden in a paper published in a special issue on Targeted Anticancer Therapies and Precision Medicine in Cancer. We recently extended this model to study combination oncolvtic virus treatment⁶. We worked closely with an experimental collaborator to identify optimal combination strategies that exploit the different immunological characteristics of candidate oncolytic viruses. This work illustrates the use of computational techniques in pre-clinical development and contains broad results that are of interest to clinical researchers. We therefore submitted this work to the official journal of the Society of Immunotherapy for Cancer where it is currently under review.

3) Structured population models allow for the explicit study of intra- and inter-patient heterogeneity. However, their implementation has been limited due to difficulties in analysis and simulation. I have addressed these difficulties by establishing the mathematical equivalence between these physiologically-structured models and simpler differential equation models. This work has broad implications in model development as researchers can use the model formulation best suited to their needs². It is common to use compartmental models to mimic time delays arising naturally in structured population models. I have recently formalized this relationship by establishing the equivalence between general compartmental models and functional differential equations. Using techniques from infinite dimensional dynamical systems and functional analysis, I developed new tools to simplify the study of these compartmental models⁷. Given the ubiquity of compartmental models throughout applied mathematics, I submitted this work to the founding journal of the Society of Industrial and Applied Mathematics where it is currently under review.

Part III Applicant's statement

Research experience: My academic career began with a NSERC-USRA funded summer research project at the University of Alberta. My undergraduate research involved the development of novel numerical techniques for Sturm-Liouville problems that arise in quantum mechanics. This work led to my first publication.

I then moved to McGill University for my doctoral training in applied mathematics. Broadly speaking, my research focused on using mathematics to address problems in medicine. My doctoral work, supported by a NSERC PGS-D award, was primarily centered on the development of physiologically-based structured population models to study the role of intra- and inter-patient heterogeneity in disease progression and therapeutic scheduling. This work led to five publications.

During my Ph.D., I spent 4 months working in the quantitative systems pharmacology group at Pfizer Inc. where I extended a mechanistic model of circulating lipoprotein dynamics to include the effects of a novel monoclonal antibody in monotherapy and in combination with statin treatment. We used the model to elucidate the mechanism leading to their synergistic function and impact on familial cholesteroalaemia. At Pfizer, I learned to effectively translate mathematical insights into actionable results through my collaboration with experimentalists and clinicians. This experience confirmed the importance of mathematical

⁵Cassidy and Craig, *PLOS Computational Biology* (2020)

⁶Jenner et al. Journal of ImmunoTherapy for Cancer, Submitted: July 7th, 2020

⁷Cassidy, SIAM Journal on Applied Mathematics, Submitted: July 9th, 2020

modelling for understanding disease progression and pre-clinical treatment development.

In the final year of my Ph.D., I was awarded a postdoctoral fellowship (now called junior fellowships) to attend the thematic semester in mathematical biology at the Institut Mittag-Leffler in Stockholm, Sweden. There, I began a collaboration with scientists from the Institute for Cancer Research in the UK and the Moffitt Cancer Center in the USA that has deepened my interest in non-genetic mechanisms of cancer drug resistance, and further entrenched my belief that mathematical modelling is critical in revealing important insights into disease progression and treatment resistance.

My postdoctoral work with Alan Perelson at the Los Alamos National Laboratory has involved the development of mathematical models to understand the evolution of treatment resistance in HIV. In particular, I have worked in close collaboration with clinical scientists to illuminate the dynamic pathways leading to HIV resistance against a broadly neutralizing antibody in a recently completed phase I clinical trial. I have also used mathematical modelling to identify the immunological mechanisms underlying post-treatment control of HIV infection. This work will submitted in the near future.

Relevant activities

Teaching: I was the teaching assistant for *Calcul élémentaire I* (2013), *Calcul élémentaire* (2013, 2014), *Calcul élémentaire* II (2013, 2014), *Algebre linéaire* I (2012, 2013, 2014) and *Statistiques* I (2012) at the University of Alberta–Campus Saint Jean. These tutorials were given in French. At McGill University, I was the teaching assistant for Calculus for Management (2016) and Calculus II (2017, 2018). I was awarded the departmental teaching assistant award in 2017 and 2018.

In 2020, I organized a day-long workshop titled *Problems and solutions in lifting individual behaviour to population level dynamics* during the Centre de Recherches Mathématiques-Center for Applied Mathematics in Biology and Medicine Workshop Series in Mathematical Biology. I developed the syllabus and lectured half of the workshop. The workshop had approximately 60 attendees and we covered the use of structured equations in the context of graduate-level mathematical biology.

Supervision and Mentorship:

Supervision: I supervised two undergraduate final projects at McGill, and the summer research of two undergraduate researchers. In all cases, I defined the research question, organized and guided their research and participated in writing manuscripts.

Mentorship: During my doctoral studies, I was an active mentor to the other graduate students in our research group by leading group discussions and student driven presentations. I was elected to the McGill mathematics graduate student government in 2017.

Activities Related to the Dissemination of Results:

Seminar organization: I organized a series of undergraduate research seminars at the University of Alberta– Campus Saint Jean. Undergraduate researchers presented their work to a multi-disciplinary audience during lunch. The seminar series included professional development presentations and social activities to promote interdisciplinary communication. I also organized a Montreal-wide student computational biology seminar during my time at McGill. The seminar involved presentations from student researchers in a variety of quantitative biology sub-fields.

Session organization: I organized a session titled *Quantitative approaches to unravel immune function and immunity* at the Society for Mathematical Biology's 2019 annual meeting.

<u>Peer review</u>: I am currently a reviewer for five journals.

<u>Awards</u>: I was awarded the best poster prize at the McGill Physiology Department Research Day in 2018 and at the 2019 Fields Institute Workshop on Mathematical Ecology. I received travel awards to attend the SIAM Life Sciences meeting (2018), SIAM Dynamical Systems meeting (2019), CAIMS Annual Meeting (2019), and the Fields Institute Workshop on Mathematical Ecology.



Application for a Postgraduate Scholarship or Postdoctoral Fellowship (FORM 201)

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TRANSCRIPT

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Page 3 Final Page

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DCS/DEC

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Graduation Honours – Effective September 2009

who have completed the required number of McGill credits for Distinction The notation of Distinction is awarded to students top 25%, but below the top 10%, of their Faculty's graduating graduation and whose cumulative grade point average is in the

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80 -	3.7	Ą	Ą	Ą
85 -	4.0	A	A	A
Échel numé des n	Notes pondérées	Notes de 1ª cycle	Notes de 2º/3º cycle	Médecine dentaire (depuis1987)

S = satisfaisant U = insatisfaisant Médecine (janvier 1970 à aujourd'hui)

Remarks – Prior to September 2002

degree program

excluded from the GPA and credit calculation included in the GPA and credit calculation excluded from the GPA and credit calculation included in the GPA calculation but not credits

normally at the time of a change in the student's

credit not normally allowed but permitted in this case

pass at undergraduate level

completion from earlier year

graphiques etaient indiquees pour certains cours. Avant septembre 2002, les notes numériques et les notes

le cas du programme de l'étudiant. est exigible pour d'autres cours ou si le cours est obligatoire dans « D » est une note de passage, mais qui ne suffit pas si le cours

avant 1987) à l'adresse avant 1980 (pour le droit, avant 1985 et la médecine dentaire, On trouvera des données sur les politiques de notation en vigueur

http://www.mcgill.ca/students/records/fr/transcripts/key.

Moyenne pondérée (MP)

subit un examen de reprise. auxquels l'etudiant a echoue et qu'il redouble ou pour lesquels il y compris les cours auxquels l'étudiant obtient un « D » ou les cours Toutes les unités visées servent au calcul de la moyenne ponderee

Autres notes

S

carries 3 credits. The number of credits completed is shown for

weight. Generally, a one-term course taught for 3 hours a week Since September 1971, most courses have carried a credit Credits

class average column.

most representative of the class performance, appears in the

Where appropriate, a class average expressed as the letter grade

Class Average

extra

course for non McGill DCS

ехпа

credit by exam only

course repeated to meet program time limit

course for McGill DCS

not for credit, not calculated in the GPA

most programs.

of courses not counted in the total credits earned

Non-Credit Courses

Prior to Fall 2002 an asterisk (*) appears next to the credit value

- Unité accordée en fonction de qualifications
- équivalentes
- 重 Э Q A suivre Echec, sans droit de passer un examen de reprise Dispense
- Absent En cours
- Incomplet
- KE ou K* Autre prolongation consentie
- Incomplet échec

겪

- Dispense d'achèvement
- 2 Reporté
- LE ou L* Reporté – prolongation accordée
- Abandon sans autorisation
- NA OU && Note pas encore disponible
- 出記の Sans évaluation Sans evaluation
- Aucune note déclarée par le chargé de cours (consignée par le registraire)
- Unité de cours Cours poursuivi au trimestre suivant
- Insatisfaisant Satisfaisant
- MAK C S R D P Abandoné
- Abandoné échec
- Autorisation de la faculté de ne pas subir un examen reporte
- W-ou Pas de note : l'étudiant a quitté l'Université

moyenne ponderee cumulative. devra être du nombre des étudiants de dernière année dans

July 2017

Adresse Université McGill Gestion de l'effectif étudiant 3415, rue McTavish Montréal (Québec) | H3A 0C8 | Canada | www.mcgill.ca/students/records/fr/transcripts

8 (applicables au tutoriel d'intégrité académique) Statuts administratifs Terminé

Incomplet

Remarques

- inclus dans le calcul de la MP, mais sans unités
- inclus dans la MP et le calcul des unités. . exclu de la MP et du calcul des unités
- ECC exciu de la MP et du calcul des unités, normalement de l'étudiant sanctionné par un grade au moment d'un changement dans le programme

Remarques – avant septembre 2002

- Unité normalement interdite, mais autorisée dans ce cas
- Réussite au niveau du 1^{er} cycle
- Cours redoublé pour respecter l'échéance du programme Terminé au préalable
- Unité accordée sur examen seulement
- Extra
- Cours valant pour un DEC hors McGill
- Extra

figure dans la colonne de la moyenne de la classe. note alphabétique la plus représentative des résultats de la classe,

exprime en unités. En général, un cours d'un trimestre enseigne trois heures par semaine vaut 3 unités. Le nombre d'unités Depuis septembre 1971, la plupart des cours ont un coefficient

Avant l'automne 2002, un astérisque (*) figure en regard du

dans le total des unités obtenues. coefficient d'unités des cours qui ne sont pas comptabilisés

Cours sans unités

Les cours dispensés par l'École d'éducation permanente pour lesquels l'étudiant n'a pas reçu d'unités donnent droit à des unités d'éducation permanente (UEC). Une UEC représente

Un cours echelonne sur plusieurs trimestres est indique par un \diamond suivi du numero du cours.

par un diplôme d'études collégiales (DEC/DCS) avant d'être Depuis 1969, les diplômés des écoles secondaires du Québec admis à l'Université. doivent suivre un programme collégial de deux ans sanctionné

Mentions d'honneur pour les diplômés –

depuis septembre 2009

chaque faculté, selon leur moyenne pondérée cumulative. (mais sous le seuil des 10 %) de l'affectit de dernière année dans 'obtention du diplôme et qui se classent parmi les meilleurs 25 % qui ont réussi le nombre exigé d'unités de McGill en vue de

chaque faculté se classant parmi les meilleurs 10 %, selon leur son diplôme et sélectionné en vue du Tableau d'honneur du doyen fableau d'honneur du doyen Un étudiant en passe d'obtenir

Juillet 2017

Sans unité, non calculé dans la MP

Cours valant pour le DEC de McGill

Moyenne de la classe

Lorsqu'il y a lieu, la moyenne de la classe, exprimée comme la

Unites

obtenues est indiqué pour la plupart des programmes.

10 heures de participation à un cours.

Cours échelonnés sur plusieurs trimestres

DCS/DEC

Distinction La mention de Distinction sera attribuée aux étudiants