

*This summer, 20 undergraduate students spent eight weeks at the Fields Institute carrying out research on applied mathematics projects. Topics ranged from placenta growth and dysfunction detection methods to high dimensional combinatorial games.*

# **FIELDS-MITACS UNDERGRADUATE SUMMER RESEARCH PROGRAM**

*Group supervisors came from the principle sponsoring universities and affiliates of the Fields Institute. The students found the program to be a unique experience, and many have developed new research interests as a result.*

*Compiled by Richard Cerezo*

## Thin Films Equations Group



Daniel Badali (Toronto), Alexandra Kulyk (National Technical University at Kharkiv Polytechnical Institute), Steven Pollock (McGill); Supervisors: Marina Chugunova (Toronto), Dmitry Pelinovsky (McMaster)

We wanted to look at the stability of the thin-film PDE

$$h_t - \frac{\partial}{\partial x} \left( h - \frac{1}{3} h^3 \cos(x) + \frac{1}{3} \epsilon h^3 (h_x + h_{xxx}) \right) = 0.$$

More specifically, we wanted to investigate what was going on with the steady-state solutions to the PDE. In other words, we were dealing with the equation

$$h - \frac{1}{3} h^3 \cos(x) + \frac{1}{3} \epsilon h^3 (h_x + h_{xxx}) = q.$$

The first week was spent getting us up to speed on a boat-load of linear algebra, ODEs, and Numerical Methods. For the first few weeks, a lot of the time was spent building the appropriate software to search for solutions to the above ODE, given varied  $\epsilon$ ,  $q$  and the mass,  $M$ , of the system.

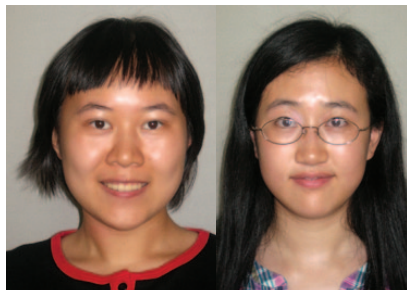
We had some challenges building plots for  $q$  vs.  $M$  for various  $\epsilon$ , since the curve was neither a legitimate function in  $q$  or  $M$ . We needed to build software that could intelligently overcome the multiple turning points and loops in the  $q$ - $M$  plane. The main goal behind this software suite was to automate the generation of these curves as we let  $\epsilon$  tend to 0. We quickly learned that no matter how intelligent our turning-point algorithm was,  $\epsilon \leq 10^{-4}$  created a graph which was too difficult for our software. Thus, we could build 3D plots of our  $q$  vs.  $M$  vs.  $\epsilon$  for  $\epsilon \in [10^{-4}, 10^{-2}]$  all with automation, but for  $\epsilon \leq 10^{-4}$ , we ended up having to guide the code by hand. Playing with the code and building these graphs dominated the first four weeks of our project.

At this point, the goal shifted from qualitatively investigating our ODE to performing bifurcation analysis. We realized we had some serious bifurcation as  $\epsilon$  became smaller, since our qualitative analysis would return more intricately knotted loops the smaller we pressed  $\epsilon$ . Since our ODE was non-linear, we spent a lot of time trying to gain some insight into the bifurcation process through linearization, and projection into "truncated Fourier spaces." That is, we assumed our ODE's solutions had the form  $h(x) = a_0 + a_1 \cos(x) + a_2 \cos(2x) + b_1 \sin(x) + b_2 \sin(2x)$ , and tried to see if we could recreate any form of bifurcation in this new, smaller, and more easily understandable space.

This is where our project came to an end. We're sitting on some qualitative information about  $h$ , when projected into this Fourier space, but we're not sure if we can see any bifurcation in this space, or in the space spanned by  $\{1, \cos(x), \sin(x)\}$ .

—Steven Pollock

## Combinatorial Games Group #1



Qiu Hua Tian (Toronto), Hera Yu (Toronto); Supervisors: Peter Danziger (Ryerson), Eric Mendelsohn (Toronto), Brett Stevens (Carleton)

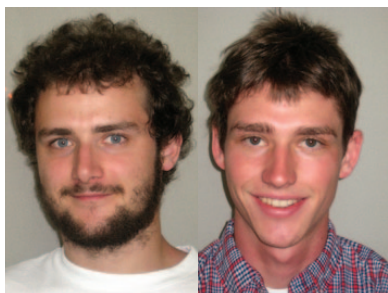
During the program, I worked on problems concerning combinatorial game theory under the supervision of Peter Danziger (Ryerson), Eric Mendelsohn (Toronto), and Brett Stevens (Carleton). While Brett guided us through the first week to give us some insight on the theory of combinatorics, Eric and Peter provided us with frequent and weekly help on technical questions and gave us great emotional support during the entire program.

My partner Yu He, an exchange student from Nanjing University, and I worked on proving that the tick-tack-toe game on an affine plane of order 5 always ends in second player draw. This problem has been previously tackled by stepwise analysis, which is extremely long and therefore impractical. We tried to find a simpler proof. We took two different approaches, one from proving the existence of a blocking set and one from finding an algorithm that suited the game. However, we were unable to find a valid proof through these approaches.

By definition, an affine plane of order 5 has 30 winning lines from 5 parallel classes.  $X$  is the first player and  $O$  the second. We first tried to prove that it is possible to form a blocking configuration that contains a line with 4  $O$ 's on it, and the minimal blocking set of each configuration always consists of 9  $O$ 's. Once the blocking configuration is formed,  $X$  cannot win. Nonetheless, we were not able to prove that the blocking configuration will always form before  $X$  wins. We spent the second month trying to find an algorithm for the game. The basic idea that guided our research was the weight function that assigns a value to each possible winning line. In the weight function defined by Erdős and Selfridge, the base of the weight function was defined to be 2. A weight function with base 2 proves that tick-tack-toe on an affine plane of order 6 or higher is second player draw, but it draws no conclusion on an affine plane of order 5. We first tried to modify the base, but it turns out that base 2 is the only valid base. We then tried to prove that the best move for  $X$  would be to follow the weight function step by step. Even so, he cannot win. We were unable to finish this proof because it is hard to predict the behaviour of the whole game.

—Qiu Hua Tian

## Combinatorial Games Group #2



Matthew Patrick Conlen (Michigan), Juraj Milcak (Toronto); Supervisor: Brett Stevens (Carleton)

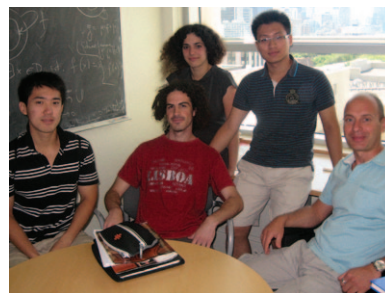
During the Fields-MITACS Undergraduate Research program, I was engaged in research in combinatorial game theory led by Brett Stevens

(Carleton). In the first week of the program we were lectured daily in this field. From then on we had meetings with our supervisors, who guided us throughout our research. Brett gave us a list of about 20 unsolved problems, all of which were accessible to undergraduates. From this long list, my colleague Matthew Conlen, from the University of Michigan, and I chose a problem concerning a winning strategy for the first player for a game of tick-tack-toe played on an affine plane of order four. We found no previous results regarding this problem. We only used properties of the affine plane and Latin squares, which describe the winning lines of the game board. A  $4 \times 4$  Latin square contains entries from  $\mathbb{Z}/4\mathbb{Z}$ , where equal numbers represent a line in the affine plane. We also considered two other non-Latin squares that represent the trivial horizontal and vertical winning lines. Altogether, this gave us a representation of the 5 parallel classes of our geometry. We used mappings  $\Psi_i$  that map a point of the game board to  $\mathbb{Z}/4\mathbb{Z}$ . We can use  $\Psi_i(A)$  to determine which line the point  $A$  belongs to in the  $i^{\text{th}}$  parallel class. We then considered sets of four points that have no three points on a line. We proved that creating such sets always allows the first player to win. We defined  $S_p$  to be a set as above also satisfying the following property: there exist two parallel classes  $i$  and  $j$  such that

$$\bigcup_{P \in S_p} \Psi_i(P) = \bigcup_{P \in S_p} \Psi_j(P) = \mathbb{Z}/4\mathbb{Z}$$

We found that  $S_p$  is the set the first player wishes to make the most often, depending on some other particulars. After proving that the first player can always create such a set with the first four moves, we carefully examined all possibilities, classified them up to isomorphisms, and proved that the first player can win by extending the lines generated by the set. —*Juraj Milcak*

## Placenta Modelling Group



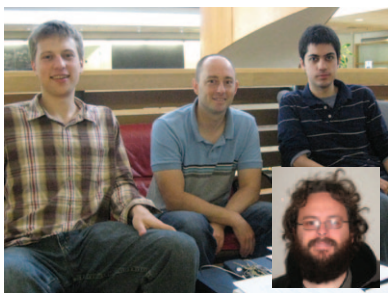
Gaole Chen (Rochester), Liudmyla Kadets (Kharkiv National V.N. Karazin University), Johnathan Wagner (Hebrew University of

Jerusalem), Zheng Wang (Toronto); Supervisor: Michael Yampolsky (Toronto)

Established on the assumption that evolution seeks to achieve energy minimization, Murray's law relates the radii of a parent vessel to that of the daughter vessels in a biological piping system. Over the years, new mathematical models for blood flow have been created to explain Murray's law. Large numbers of experiments have been conducted to verify this law in nature. Our objective was to determine if Murray's law is universal by reviewing current literature with experimental data, summarizing their findings and determining the validity of their results. In addition, we presented and discussed some of the prominent mathematical models that incorporate the physics of pulsatile flow and non-Newtonian fluids.

We also studied the human placenta to verify Murray's law in this organ. We studied pictures of the human placenta in which the blood vessels had been traced professionally. We wrote a program in C which processed these pictures and returned data such as vessel dimensions and the type of branching point. Finally, assuming Murray's law is correct, we constructed a "Murray's Grade," which is used to rank different branching points in a vascular system based on their deviation from optimality. This will enable us to investigate how deviation from Murray's law affects the performance of organs such as the placenta in future studies. —*Liudmyla Kadets*

## Pattern Avoiding Group

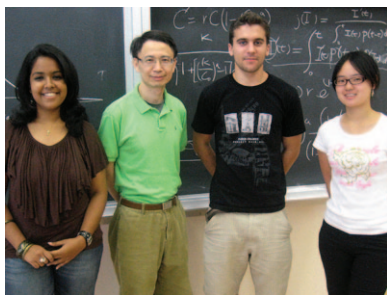


Chris Berg (York), Samer Doughan (Toronto), Steven Karp (Waterloo); Supervisor: Mike Zabrocki (York)

We started with the idea from combinatorics of enumerating permutations which avoid a pattern. A permutation 'contains' a pattern if there is a subsequence of the permutation which has the same relative order as the pattern and 'avoids' it otherwise. For example, 541632 contains the pattern 231 because, for instance, 462 is a subsequence of the permutation and has the same relative order as 231. However, this same permutation 541632 avoids the pattern 123.

With this idea in mind, we considered a different notion of pattern avoidance when the permutation is thought of as a minimal length word written in terms of the Coxeter group generators (elements  $s_i$  which exchanges  $i$  and  $i+1$ ). Every permutation can be written (non-uniquely) as a minimal length word in the generators  $s_i$ . We then considered the problem of enumerating permutations whose reduced words did not contain subsequences that had a relative order that matched a pattern. Along the way we found relationships with the Bruhat order, juggling sequences, and Hopf algebras. —*Mike Zabrocki*

## Infectious Disease Modelling Group



Cameron Davidson-Pilon (Wilfrid Laurier), Preeyantee Ghosh (Hyderabad), Yueh-Ning Lee (National Taiwan); Supervisor: Jianhong Wu (York)

After a disease outbreak, we can plot a curve for the cumulative number of infected individuals and fit it to a curve. Often, and with enough frequency to raise curiosity, the outbreak will follow the Richard's model, which is the solution to the differential equation

$$C'(t) = rC(t) \left( 1 - \left( \frac{C(t)}{K} \right)^a \right)$$

where  $C(t)$  is the cumulative number of infectives at time  $t$ . The model is very similar to the logistic model but possesses the parameter  $a$ , an index of the inhibitory effect of the deviation of growth from the exponential relationship.

The problem presented to us was to mathematically derive the Richard's model from first principles. In particular, we were to give epidemiological reasons for the characteristic growth of the accumulated infected. We started by reading the current literature on disease models. The most popular model is the deterministic, compartmental SIR model or a derivative of it. The most important feature of the standard SIR model is it gives relations between the number of infected and susceptibles and their rate of change in the form of differential equations. We started our task by abandoning this assumption and left the rate as an unknown and then assumed *a priori* that the cumulative total infected, followed the Richard's model. Using a very creative idea, Yueh-Ning derived a closed form expression for the incidence rate. An alternate novel approach to the problem, derived by Cameron, was to look at an outbreak as a branching process. Using a dynamic expected number of secondary infections per infection, Cameron could derive the expected number of accumulated total infected in terms of the mean duration of infection and a certain integration of the expected number of infectives up to the time of interest. Assuming the accumulated total follows the Richard's model, we could numerically examine how the disease spread.

Both methods show a defining characteristic of a disease following the Richard's model. Since the Richard's model often fits real life outbreaks, we decide with confidence that the outbreak will have a constant number of secondary infections, but then quite rapidly decrease to almost zero.

Preeyantee's work focused on the appearance of multiple strains or species of diseases in a single host, called a super-infection. She noticed that during treatment, it is possible to mistake resistance with super-infection, where the non-vanishing symptoms are caused by the other diseases and not the treated one. This idea led to a system of differential equations examining how resistance may evolve under such circumstances. This idea arose from discussions with several participants of the 2010 Summer Thematic Program on Mathematics for Drug Resistance of Infectious Disease that took place during our summer research program. We are trying to put everything together and submit it for possible publication.

—Cameron Davidson-Pilon

## Cancer Stem Cell Modelling Group



Abhishek Deshpande (IIIT Hyderabad), Joy Jing Liu (Ottawa), Philip Marx (Tulane), Tian An Wong (Vassar); Supervisors: Matthew Scott

(Waterloo) Mohammad Kohandel (Waterloo), Sivabal Sivaloganathan (Waterloo)

On the first day, we met with our advisers, who introduced us to two potential paths for research—modelling of hydrocephalus and stochastic simulations of brain tumour growth. As both were novel concepts to all of the group members, we spent the first few days reading papers to improve our understanding and decide which topic to pursue. After choosing the brain tumour problem, we read recent biology papers in the field, with the goal of formulating simple yet descriptive mathematical models, then testing them using MATLAB and C++.

Testing included setting parameters to fit the given data and, in the case that conclusions in the biology papers were inexplicable through the mathematical models, the addition and testing of additional assumptions about cell hierarchies and dynamics.

We ended up focusing on a specific paper, *A Hierarchy of Self-Renewing Tumor-Initiating Cell Types in Glioblastoma* by Chen et. al, which provided its own hypothesis on the still poorly understood tumour cell hierarchy. We focused on mathematically replicating the paper's data on neurosphere formation (through stochastic simulations) and CD133 percentages (using the system of deterministic equations). In order to explain the high CD133 percentages reported in the paper, we then inserted an element of dynamic de-differentiation, in which progenitor cells are able to "de-differentiate" to cells with stem-like properties, for example through the process of epithelial-mesenchymal transition (EMT). In a field where the cell hierarchy is still not well understood, this could yield interesting insight on current models and provide ideas for future biological experiments.

The dynamic evolution of the population can be described deterministically or stochastically. Stochastic models are appropriate for small cell populations during earlier stages of tumour growth. In later periods, when the cell number increases, stochastic fluctuations are minimized allowing a deterministic description of the dynamics. The great advantage of a deterministic framework is its analytic tractability allowing a larger perspective of the population growth and a facilitated estimate of parameter-sensitivity in the model.

—Philip Marx and Tian An Wong