10th Graduate Industrial Mathematical Modelling Camp

and

11th Industrial Problem Solving Workshop

June 6-15, 2007

Pacific Institute for the Mathematical Sciences

University of Alberta

Department of Mathematical and Statistical Sciences
University of Alberta
Edmonton

Alberta INNOVATION AND SCIENCE

AMI Applied Mathematics Institute

Program

Coffee Breaks:	10:30 AM and 3 PM	outside CAB 331 and 335
GIMMC:		
June 5, 07 7:00	Dinner for GIMMC mentors	Faculty Club
June 6, 07 9:00	GIMMC project presentation	in CAB 235
June 6, 07 18:30	Reception	in Lister Hall Prairie Room
June 6-8, 07	GIMMC project work	
	Computations	in CAB 331 and 335
	Piche (fluid carrying plate) Cobbold (Atherosclerosis) Hare (Health Service) Gumel (Epidemiology) Van Roessel (Coagulation) Hillen (Chemotactic Paradox)	colloquium room CAB 657 PIMS office CAB 449 conference room CAB 680 lecture room CAB 563 stat. meeting room CAB 415B faculty lounge CAB 649
June 9, 07, 9:00	GIMMC project presentations	in CAB 235
June 9, 07, 12:30	Pizza lunch	outside CAB
IPSW:		
June 10, 07 19:00	Dinner with industry and faculty participants	TBA
June 11, 07 9:00 14:00	Presentations of the industry projects Team formation and begin of project work	in CAB 235
	Computations	in CAB 331 and 335
	Project 1 (Cancer Drugs) Project 2 (Chinese Medicine) Project 3 (Energy Consumption) Project 4 (Foam Flows) Project 5 (Epidemiological Challenges) Project 6 (TV Demographics) Project 7 (Landscape Management)	colloquium room CAB 657 conference room CAB 680 lecture room CAB 563 stat. meeting room CAB 415B PIMS office CAB 449 faculty lounge CAB 649 math-bio room CAB 549
June 11, 07 18:30	Welcome reception	Faculty Club
June 12-14, 07	Project work in teams	

June 15, 07 9:00-14:00	Project presentations	in ED 158
June 15, 07 18:00	Farewell BBQ	in Emily Murphy Park
September 30, 07	Deadline for the written project reports.	published by CAMQ (Canadian Applied Mathematics Quarterly)

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Jack Macki (U Alberta and U Calgary)
John Stockie (Simon Fraser U)
Brian Wetton (UBC)
Jeff Williams (Simon Fraser U and MITACS)

GIMMC-Projects

	Project Name	Presenter
G1	A fluid carrying plate	Robert Piche, Tampere University of Technology, Finland
G2	Atherosclerosis	Christina Cobbold, University of Glasgow, UK
G3	Health Service	Warren L. Hare, Simon Fraser University
G4	Epidemiology	Abba Gumel, University of Manitoba
G5	Coagulation	Henry van Roessel, University of Alberta
G6	Chemotactic Paradox	Thomas Hillen, University of Alberta

IPSW-Projects

	Project Name	Sponsor	Presenter
I1	Cancer Drugs	Cross Cancer Institute	Jack A. Tuszynski, Cross Cancer Institute,
I2	Chinese Medicine	SinoVeda	Y.K. Tam, SinoVeda
I3	Energy Consumption	Urban Green Partnership	Mark Sciumeca, Urban Green Partnership
I4	Foam Flows	Syncrude	Mohammed Aziz Rahman, University of Alberta
I5	Epidemiological Challenges	US Smokeless Tobacco	Carl Phillips and Karyn Heavner, University of Alberta
I6	TV Demographics	Invidi	Dave Ballantyre, Invidi
I7	Landscape Management	Canadian Parks and Wilderness Society	Jack Teng, University of British Columbia

GIMMC Project Descriptions

G1: Natural Frequency of a fluid carrying plate
Robert Piche, Tampere University of Technology, Finland

Problem: Determination of the effect of the oil on the natural frequencies of a) a clamped rectangular plate carrying oil of different heights and b) a rectangular plate immersed in oil and clamped at three edges and free at the end in air.

Background: See Appendix A.

G2: The early stages of atherosclerosis and the 'Oxidative modification Hypothesis'.
Christina Cobbold, University of Glasgow, UK

Background: See Appendix B.

G3: Modeling Health Service Usage for Canada's Aging Population
Warren L. Hare, Simon Fraser University

The results of the 2006 national census have just been released, and have shown a continuation of the age trend predicted by the 1996 and 2001 censuses. In particular, Canada's population is getting older. Although the exact impact of this aging population is unknown, it is clear that it will results in an increased stress on the Home and Community Care branch of Canada's various health care systems. Predicting how this increased stress will impact the health care system is of high importance in developing policy and setting budgets for future years.

In the past, future demand and access to health care has been modeled through simple statistical predictions. Basically one takes the usage from previous years and multiplies by the predicted population for future years. These models are quick to produce, and easy to understand, but unfortunately not accurate and lack the ability to predict the result of interventions into the system. The goal of this project is to begin developing predictive models that can be used to help explore how Home and Community Care will be impacted over the next 10 to 20 years. Possible approaches include Markov Models, Queueing Theory Models, and System Dynamics models.

G4: Epidemiology
Abba Gumel, University of Manitoba

G5: Coagulation – Fragmentation Equations
Henry van Roessel, University of Alberta

A phenomenon that occurs frequently in nature in many guises is the coalescence or aggregation of one or more small particles to form larger particles. Examples of this phenomenon include:

- hail formation — the coalescence of smaller water droplets to form larger ones;
- blood clotting — the coalescence of blood cells to form blood clots;
- planet formation — the coalescence of interstellar gas particles, through the force of gravity, to form planets.

The reverse procedure, which involves the break-up of large particles into smaller ones, is called fragmentation. The goal of this study group is, first to derive equations which govern the evolution of particle concentrations, and then, if possible, to deduce the qualitative behaviour of the solutions of these equations. In addition to deriving equations for the particle concentrations, we would also like to derive equations that govern the evolution of the total number of particles in the system, as well as the total mass.

G6: The Chemotactic Paradox
Thomas Hillen, University of Alberta

Background: See Appendix C:

IPSW Project Descriptions

I1: Optimization of Drug Structure for Protein Targets Using Molecular Morphology Characterization

Jack A. Tuszynski, Cross Cancer Institute, Edmonton.

Description of the problem:

Rational drug design is becoming a very effective method of finding new chemical entities that may be tested and applied for therapeutic purposes such as new drugs for cancer. Huge databases have been produced that contain both the drug entities and molecular targets. Some of the most important targets involve functional proteins that may be misfolded due to mutations or epigenetic effects. The process of drug design and lead optimization can be accelerated and refined by the development of more effective mathematical algorithms that provided better matches between the drugs and their targets. The Molecular Biophysics group at the Cross Cancer Institute is involved in this program of investigations on a small scale and is hampered by its limited computational resources. We would like to overcome these difficulties by formulating a more exact mathematical problem, solving it and then moving on to the testing phase for the thus created novel drugs for cancer.

The starting point is the use of the Protein Bank Database (PDB) which contains some 30,000 3-D atomic-resolution structures of proteins. Its entries can be classified in terms of the corresponding boundary surfaces in 3-D space with special shapes (morphologies), their sizes (volumes in units of cubic Angstroms) and additional physical and chemical attributes such as maps of the electrostatic charge distribution and hydrophobicity maps. The main issue, however, from the point of view of drug binding is the presence of binding pockets (cavities) on the surface of a target protein. Hence the first task is that of finding all potential binding pockets and at least 1.5 million pockets are expected to exist for all known proteins in the PDB. Then the next task is to compute the volume of each pocket or cavity by removing (subtracting) the protein-occupied volume from the volume of the ellipsoid that encloses it followed by classifying all simply connected shapes as pockets.

The complementary aspect of this problem is to characterize all available chemical compounds regarding their volume and surface morphology. Thus we intend to catalogue all chemical compounds listed in chemical data bases (such as Merck, NCI, Maybridge, Pharmacopeia, Derwent World Patents Index, etc.) dividing them into groups by their 3-dimensional volumes in units of cubic Angstroms and surface boundary shapes (number of vertices).

Having accomplished the first two objectives of the problem, we then need to develop an optimization algorithm for a fit between a binding pocket and a chemical compound that is supposed to fill it. For each pocket, an optimal steric fit is created by maximizing the filling of each pocket (minimizing residual space), without intersection or overlap of vertices between each compound and its target protein. In addition to ranking the

goodness of fit for each case of the complementary protein/drug pair, one would like to quantify the results in terms of such properties as the percentage of pocket filled or the amount of water-accessible surface area occluded.

The procedure could start by keeping the pocket's surface fixed and rigid and matching its central point's radius of curvature with a point on the compound's surface that has the closest value of the radius of curvature to it but cannot exceed it to avoid overlap. To find the optimal docking of the compound, the compound's orientation with respect to the three Euler angles could be subjected to a volume minimization procedure. Note that the overlap between the surface of the compound and the pocket is disallowed in the calculation of the minimal residual space for a given compound. If an overlap occurs, the residual volume calculation should be repeated with the compound moved sufficiently away from the pocket's surface to allow at most a finite number of points in common with the pocket. The best compound is the one that fills most space.

After the results of the optimization procedure are obtained, there could be additional penalties/rewards given in each case for the occurrence of electrostatic conflicts or bonds due to repulsion/attraction, respectively. Likewise, chemical analysis of the surfaces of the protein and compounds in contact can reveal the various potentials for the hydrogen bond formation by finding corresponding pairs of hydrogen bond donors/acceptors facing each other when brought in contact (see the illustration below).

I2: Optimization of Multi-Drug Composition for the Most Efficacious Action,
Proposer:
Dr. Y.K. Tam of Sinoveda

Description of the problem:

Western medication acts on the principle of one drug for one target. However, traditional Chinese medication as well as herbal medicine in general operates differently by combining a large number of active ingredients together, each of which is given at a very low concentration. It is not only believed, but experimentally demonstrated, that these individual ingredients, when taken together, mutually reinforce each other synergistically. In a given herbal extract (e.g. Echinacea or ginko balboa), there could be several hundred chemical entities, dozen of which are active compounds. However, stringent standards of purity and quality control are generally not adhered to which makes scientific evaluation of these compounds very difficult. Furthermore, different regions of origin for a given plant produce significantly different product.

The mathematical problem that I'd like to propose, if solved, could move the field of traditional medicine forward towards a more generally accepted standard of quality

control and efficacy assessment. Suppose we have a number of samples of the same medicine coming from different origins and having different compositions. Suppose the samples are labeled by index "i" that runs from 1 to N. Suppose that each sample contains n active ingredients labeled by index "j" that runs from 1 to n. The concentration of each ingredient is known and denoted as c(i,j) such that summing c(i,j) from 1 to n over j gives 1 for all i's. Assume also that we know the activity of each sample to be A(i). We must also assume that activity A is an a priori unknown nonlinear function of the oncentrations c(i,j). The problem at hand is to determine the form of the function A(c(i,j)) using the limited data set available. We could assume A to be a linear combination of polynomials starting with linear functions of c. In this case, the first task is to determine the highest order of the polynomial in the expansion that will be consistent with the amount of data available. On the other hand, activity should show saturation effects more consistent with sigmoidal dependence and hence an exponential series. Once the function A(c(i,j)) is found, it will be necessary to find its maxima in the multi-dimensional space of concentrations to propose an optimal formulation of the medicinal extract. An additional layer of complexity can be added by putting error bars on the activity values since they come from multiple experimental assays. The final complication involves the pharmacokinetic properties of each individual ingredient. In other words each constituent compound show a different time course c(i,j; t) following drug administration. The question then arises how to compose the combination of ingredients to arrive at the optimal dose at the organ where the ingredients are supposed to be active at.

I3: How to model consumption of a populous at a per dwelling level based on inputs received from public sources and incentivised individual voluntary surveys?
Mark Sciumeca, Urban Green Partnership

Problem: how to model consumption of a populous at a per dwelling level based on inputs received from public sources and incentivised individual voluntary surveys?

Additional degree of toughness: take into account voluntary information provided by utility providers.

Givens: People live in dwellings. Some dwellings are occupied by more than one person. Appliances, heating and cooling, and plug in items are the sole causes of dwelling onsumption. Dwellings are used by humans and are abused by the elements and decrease in efficiency over time. Two types of consumption resources that are not consumed directly by human actions (Exe. water used for heating) resources that are consumed via direct actions, eating, bathing, watching, using.

Support information: Our organization is taking on educating the local consumers on how to become greener because it saves you money. We will need the ability to tack our progress within the Philadelphia region that is home to 5.5 million regionally. We have begun working with the commerce department to track trends in local disposable income

and business profits. This data does not have the fidelity needed to identify parts of the city that need help or types of education needed most by the community. We will eventually need to create a questionnaire that will be used to collect information on a per dwelling or per street address basis. We will need to create a formula for taking the dwelling's resource usage rates in water, gas, electric, and oil and relating them to the number and age of people that live in a dwelling, the number and types of appliances, the types of heating and cooling systems, the number of window and types etc, the size of the dwelling... This unitless number will be considered a score that puts all dwelling on an equal playing field with regards to how they use the resources they take from the system.

Possible uses: unitless number could be used in combination with GIS to create local maps of good bad and mediocre consumers http://www.environmenttimes.co.uk/cgi-local/newspro/viewnews.cgi?newsid1163085928,5989, trends could be used to measure effectiveness of local training trends could be used to identify areas that need to be concentrated on. We would be very interested in your findings and would try and give you support.

I4: 3-D Analytical Solution of Air/Water Two-Phase Bubbly Flows.
Mohammed Aziz Rahman, Syncrudeand University of Alberta

The main objective of this analytical analysis is to get a better insight of the basic phenomena associated with air/water two-phase bubbly flows through an industrial nozzle via mathematical formulation. Two-phase bubbly flows are quite complicated transport phenomena. There are still fundamental aspects of two-phase flows; whose physical descriptions are still unknown and modeling results are questionable. Experimental observations are difficult in this case, as the migration of dispersed bubbles towards the top of the pipe, due to buoyancy, causes a highly non-symmetric volume distribution in the pipe cross-section. Complicated interactions like break-up and coalescence among adjacent bubbles, interactions between bubbles and the pipe wall, and the deformation of the bubbles affect the local flow field conditions. Bubbles suspended in the liquid undergo various phenomena too complex for precise mathematical formulation. Hence we rely at present on empirical observations on macroscopic quantities.

Often existing theoretical solutions do not agree with experimental results. In the analytical analysis of mathematical formulation requires a system of non-linear differential equations. Because of the complex nature of the two-phase flow phenomena, a single-flow theory has not yet reached a mature stage. Instead, numerical solutions using computational fluid dynamics (CFD) code partially can treat two-phase flow problems. While the use of the CFD codes enables the solution of complex flow-fields, one loses much insight into the dominant parameters and fundamental physics that could be achieved through analytical treatments. Till to date much efforts have been devoted to one-dimensional or quasi-one-dimensional flows. Three-dimensional closed-form analytical solutions and expressions for bubbly flows including the effects of bubble size

distribution (BSD), bubble coalescence and break-up model, velocity distribution, volume fraction distribution, wall friction, and mass transfer would provide a better insight into the basic phenomena associated with two-phase bubbly flows.

The overall objective of this project is to optimize the operating range of the existing steam/bitumen nozzles used in the Syncrude coker. Knowledge obtained will contribute to the development of a new series of nozzles Syncrude is currently bringing to market. In fluid coking nozzles, the gas (steam) and liquid (bitumen) mix well in upstream of the pipe prior to feeding the mixture through the nozzles. One of the physical problems in the operation of fluid coking nozzles is the development of instabilities in the spray. This is caused by the two-phase flow pattern formed (slug/wavy annular flow) inside or upstream of the nozzle. Recent experiments conducted by the applicant show that if the air to liquid ratio by mass (ALR) increases to 1.50%, the spray becomes unstable (transition occurs from bubbly flow to intermittent flow).

The proposed analytical research program will contribute to the fundamental knowledge of two-phase flows and make concrete headway in the design of an industrial nozzle used in an extremely large-scale high impact operation. The outcome of this research will help in optimization of commercial process conditions in the recovery of light crude oil from heavy oil bitumen. It indeed will be of significant interest to the petroleum industries and helping the economy of the province of Alberta.

I5 The two core statistical/mathematical challenges in epidemiology.
Dr. Carl Phillips, Dr. Karyn Heavner, University of Alberta

Background: Epidemiology is a science whose reach far exceeds its grasp. That is, as the primary source of information for health policy and clinical decisions, epidemiology is extremely important and heavily relied upon. It is the most prolific science of the day, and has generated as many scientific papers in the last few years as physics and most other sciences have done in all previous human history. Yet epidemiology suffers from being an extremely *ad hoc* and underdeveloped science. It comes as a shock to experts in other fields that the methods that are used in this important field generate answers that are easily shown to be incorrect, and a literature that is often extremely misleading.

Definition: Epidemiology, the study of health with whole people and actual diseases as the unit of analysis. Sometimes it is interpreted overly narrowly to mean just observational population research, but clinical intervention studies also fall into the definition. Excluded are toxicology, biomarker studies, molecular research, and other health research that does not study whole people or actual diseases.

Quantifying uncertainty from study errors: Epidemiologic studies, particular observational studies of populations, are characterized by study errors that are widely discussed in intermediate and advanced classes and textbooks. These include measurement errors, confounding, non-comparability of compared groups, and non-generalizability of results to the whole population. But despite the attention to these

problems in the theory, the steps taken to minimize their impact are almost always (implicitly) assumed to be perfect, and results are calculated and reported as if there are no remaining study errors, even in the many cases where this is clearly not true. There have been efforts to develop methods to quantify the uncertainty resulting from the unknown (but almost certainly non-zero) levels of these various errors, many of them based on or inspired by my work on the subject that started in 1999. My approach was simply to show how probability distributions representing our beliefs about the values of key inputs (e.g., the sensitivity of a diagnostic test or the degree of bias in selection of a study control group) could be propagated through a series of calculations to generate a probability distribution for the final result. (The standard method can be seen as a special case of this, where all the input distributions have all the probability at the assumption "this is perfect".) Unfortunately, neither I nor anyone else has made much progress beyond this initial innovation. Probably the most promising current development comes from Paul Gustafson, a Bayesian statistician at UBC, who is working on how data can inform both the study result and the input distributions of errors. But there is a lot of room to develop methods that could – and this is not hyperbole – revolutionize this influential field.

Publication bias *in situ:*

A second fundamental problem that plagues epidemiology is that researchers often have a strong desire to produce particular results, and it is not very difficult for them to alter their analysis toward that end. Epidemiologic studies typically offer a wide variety of options for how to define key variables (e.g., how much second-hand smoke counts as exposed rather than unexposed), what covariates to include in models, what functional forms to use for variables, and which of the many possible results to report. Such decisions must be made, and the nature of the science is such that it is naive to try to specify analysis protocols before the data has been observed, so the choices are inevitably influenced by the data. There is often little reason to prefer a particular decision about these choices over the alternatives, creating the opportunity for the analysts to make the choices that produce the "best" results, however they might define that (often it means getting stronger associations, which make a paper more likely to be considered important, but it can also mean results that more closely resemble authors' previous claims or that support their policy advocacy position). Sometimes this is as grossly inappropriate as it sounds, though quite often innocent motives and beliefs about proper methods have the same effect ("I do not know what model best represents the world, so I will choose the one that shows the largest result because it must be doing the best job of teasing the true relationship out of the data"). The result is a kind of publication bias, not in the level of the literature due to some studies being published because of their results and others not, but at the level of the individual study report (thus, *in situ*). The entire literature is biased (away from the null, toward more popular conclusions) to an unknown, but probably quite substantial, degree. Researchers in other fields might find this phenomenon rather surprising, and figure that results that are biased in this way would not be replicated and would not stand up to scrutiny. But epidemiology is almost always characterized by a lack of replication, given the literally billions of combinations of diseases, exposures, and treatments that we are interested in, different populations, time trends, etc. What passes for replication in epidemiology is often a study of a similar (but not exactly the same)

exposure and disease in a different population; results are often declared to verify previous findings by virtue of having vaguely the same interpretation, even when the quantitative results are quite incompatible. Moreover, there are very limited resources to re-analyze previous study results (including when they are reviewed for publication), and when there is an interest it is often the case that the data is secret or the methods so poorly explained that it is not possible.

Thus, a solution is needed that does not depend on multiple studies of the same phenomenon or widespread re-analysis of data. A partial solution that I have proposed is that when new data is analyzed with respect to a certain question, the researchers should be expected to run the closest possible analogs to previously published models of similar studies (in addition to whatever *ad hoc* model they think is best, or that is most interesting given their data, which is all that is ever published now). But something more is needed, particularly because the incentives are for researchers to just keep doing what they are doing.

I6: Probabilistic Assessment of Television Viewer Demographics.
Dave Ballantyre, Invidi

What is the probability that various types of people watch various TV shows? More to the point, if a television has just been tuned to a particular channel that is playing a particular show, what are the probabilities that the person watching is in various demographic classes? The aim is to enable the construction of consumer electronics devices that act in ways that adapt automatically to who is using them. In this case, particularly for targeted advertising while respecting privacy.

Invidi has anonymized data of TV viewing behaviour for a sample collection of households. This data indicates when a TV is on in the household, who is watching it (up to a demographic class), and which channel it is tuned to. We also have incomplete schedule data indicating which programs are playing at which times for some channels. We are building software that will react differently depending on who it determines is watching the television, and have a system for inferring the demographic classes of the audience. However, for this system to work, we need to derive estimates for the probability that the viewer of a TV is in each of a set of demographic categories given that the television has just been tuned to a certain channel. There are immediate naive solutions that are overly certain in their estimates and don't account for the fact that the data is a sample of a larger universe of interest (among other problems). For example, suppose that we total the number of times that men and, separately, women tune to channel c from 8:30am to 9:00am on Saturdays. Suppose we find that, in total throughout our data, men tune in 70 times and women tune in 30 times. We could conclude that when a television is tuned to channel c on Saturday mornings at this time, P(man watching) = 0.7 and P(woman watching) = 0.3. But what if the sample contains 140 men and 100 women? There is an obvious normalization that could be done. But what if, instead, we found that men tuned in 4 times and women tuned in 0 times? It

would be incorrect to conclude that no women in the universe will ever watch channel c during this time period, using only statistics from the sample.

There are many additional quirks and complexities that can be considered. For example, there may be very sparse data for some times, channels, programs, and demographic groups, while at the same time there may be similarities between classes. So, females aged 65+ may act similarly to males 65+ and to females in the age range 55-64. Likewise, there may be similarities between programs, channels, and especially across time. In counterpoint, the usefulness of data may decay over time, as new programs begin to be displayed during a time period that replace old programs and encourage viewership by a new demographic. And, of course, there is the important issue that a television may be viewed by more than one person from the household at a time.

Invidi is interested in solutions that provide a plausible set of probabilities among demographic classes given a new channel tuning. We hope for solutions that incorporate and accommodate the maximum set of real problem complexities.

I7:, How does landscape management affect the infection risk to zoonotic diseases?.
Jack Teng, Canadian Parks and Wilderness Society and UBC

The South Okanagan valley is extensively being developed for vineyards, orchards, and ranching, and is also experiencing increased residential development pressure. In response, BC's Ministry of environment and NGOs, such as CPAWS have proposed the establishment of a National Park in the area, which comprises a series of existing provincial parks and environmental reserves, as well as privately managed land for agricultural and ranching purposes. As such, the region is an ideal case study to study how conservation and different land use practices can influence the infection risk to zoonotic diseases.

In particular, tick-borne zoonotic diseases (e.g., Lyme disease; *Ricketsia*) have been a growing public concern in the Okanagan area, where the presence or absence of the diseases have not been conclusively determined. This disease is transmitted by tick vectors (*Ixodes spp.*), carried in deer mice (*Peromyscus maniculatus*) hosts—two species which have higher population densities in landscapes that are fragmented by human development. Recent work, however, has shown that increased biodiversity can prevent outbreaks of disease carrying species by the presence of unsuitable disease hosts and vectors (i.e., dilution effect), and also by the presence of natural predators and competitors. Hence, the National Park could play a role in preventing the emergence and spread of tick-borne diseases. Creating a National Park could potentially lead to the following:
-a decrease in habitat suitability for ticks and deer mice
- an increase in the diversity (species number) and abundance of rodent species that compete with deer mice
-an increase in the diversity and abundance of rodent predators
- an increase in the diversity and abundance of tick predators, such as spiders and ants

We would like to know (1) how changes in the landscape and habitat suitability affect the population densities of disease hosts and vectors and their predators and competitors, (2) how different spatial configurations of conservation and land use affect biodiversity and the infection risk to zoonotic diseases. Understanding the potential infection risk to zoonotic tick-borne diseases in relation to human land use, and how the proposed National Park may play a role in mediating the infection risk are urgent concerns for both ecosystem and human health.

Participants

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