Program and Abstracts
### MIDWEST MATHEMATICAL BIOLOGY CONFERENCE
University of Wisconsin - La Crosse, May 21-22, 2016

**Saturday, May 21, 2016**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30-8:00</td>
<td>Registration and Continental Breakfast</td>
<td>HSC 2006</td>
</tr>
<tr>
<td></td>
<td>(2nd Floor Atrium Health Sciences Center (HSC) - See page 5 for map)</td>
<td>HSC Atrium</td>
</tr>
<tr>
<td>8:00-8:15</td>
<td>Welcome (2006 Health Sciences Center)</td>
<td>HSC 2006</td>
</tr>
<tr>
<td>8:15-9:15</td>
<td><strong>Plenary Speaker:</strong> &quot;Best&quot; in a Biological Context: Optimization,</td>
<td>HSC 2006</td>
</tr>
<tr>
<td></td>
<td>Space and Control, Dr. Louis Gross</td>
<td>HSC 2006</td>
</tr>
<tr>
<td>9:15-9:30</td>
<td>Break</td>
<td>HSC Atrium</td>
</tr>
</tbody>
</table>

**Session I**
All talks in the Health Science Center (HSC)

<table>
<thead>
<tr>
<th>Time</th>
<th>Talk</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:30-9:50</td>
<td>Modeling reproduction of whitetail deer, Amy Ekanayake</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td><em>Linking Cellular and Mechanical Processes in Articular Cartilage</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td></td>
<td>Lesion Formation: A Mathematical Model, Georgi Kapitanov</td>
<td>HSC 2066</td>
</tr>
<tr>
<td>9:55-10:15</td>
<td>Exploring the potential of energy budget models and body size in</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td>determining species' niches, Tanjona Ramiadantsoa</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td><em>Modeling and Analysis of Gene Regulatory Networks Using Finite</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td></td>
<td><em>Dynamical Systems, Eric Eager</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td>10:20-10:40</td>
<td>Management of species under phenotypic plasticity and stochasticity,</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td>Dinesh Ekanayake</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td><em>Probabilistic Models of Trypanosome RNA tails, Marshall Hampton</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td>10:45-11:05</td>
<td>Plasticity, competition, and the evolution of elevational ranges,</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td>Emma Goldberg</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td><em>Novel Methods for the Study of Human Metabolism Using Constraint</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td></td>
<td><em>Based Models, André Schultz</em></td>
<td>HSC 2066</td>
</tr>
<tr>
<td>11:10-11:30</td>
<td>Investigating the imperfect malaria vaccine, RTS,S using optimal</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td>control theory, Ruijun Zhao</td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td><em>Detecting seasonal trends in eDNA with occupancy modeling, Richard</em></td>
<td>HSC 2064</td>
</tr>
<tr>
<td></td>
<td>Erickson</td>
<td>HSC 2064</td>
</tr>
<tr>
<td>11:45-12:45</td>
<td>Lunch and Informal Poster Session</td>
<td>HSC Atrium</td>
</tr>
</tbody>
</table>
Plenary Speaker: *What can topology tell us about the neural code?*, Dr. Carina Curto, HSC 2006

1:45-2:00 Break, HSC Atrium

**Session II**

All talks in the Health Science Center (HSC)

2:00-2:20 *What makes a neural code convex?*, Katherine Morrison, HSC 2064

Computing Intensive Methods in ODE Modeling, Olcay Akman, HSC 2066

2:25-2:45 An Integrative Neural Model for Auditory Stream Segregation and Integration, Aarati Mahat, HSC 2064

Sensitivity Analysis and the Probability of Pest Eradication or Permanence in a Stochastic Model for Integrated Pest Management, Tim Comar, HSC 2066


On the Estimated Propensities from Stochastic Gene Regulatory Networks via Evolutionary Computing, Dan Hrozencik, HSC 2066

3:15-3:35 On the evolution of the parameter distributions in epidemiological models, Artem Novozhilov, HSC 2064

Outbreak of waterfowl disease in the Upper Mississippi River: Analysis of a stochastic temperature-driven model, James Peirce, HSC 2066

3:40-4:00 Recovery from infection as a selective pressure for the evolution of migration, Allison Shaw, HSC 2064

4:00-6:00 Reception and Poster Session, HSC Atrium

7:00-8:30 Mississippi River Pizza Cruise (North end of Riverside Park) (Tickets required for this event)
Sunday, May 22, 2016

7:30-8    Continental Breakfast

**Session III (all talks in HSC 2006)**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00-8:20</td>
<td>Microarray Cancer Data Analysis through the TDA Looking Glass, Namyong Lee</td>
</tr>
<tr>
<td>8:25-8:45</td>
<td>Assessing spatial patterns of plant communities at varying stages of succession, Kevin Aagaard</td>
</tr>
<tr>
<td>8:50-9:10</td>
<td>Modeling and Analysis of the 2014-2015 Measles Outbreak Subject to Sociological Dynamics, Robert Allen and Eric Eager</td>
</tr>
<tr>
<td>9:15-9:35</td>
<td>Intercollegiate Biomathematics Alliance (IBA), Olcay Akman</td>
</tr>
<tr>
<td>9:40-10:00</td>
<td>Feedback Control for Management of Uncertain Populations, Richard Rebarber</td>
</tr>
<tr>
<td>10:00-10:15</td>
<td>Break</td>
</tr>
<tr>
<td>10:15-11:15</td>
<td>Plenary Speaker: Inferring Host-Pathogen Interactions from Diverse Data Sources, Dr. Mark Craven</td>
</tr>
<tr>
<td>11:15-11:20</td>
<td>Closing Remarks</td>
</tr>
<tr>
<td>11:30-1:00</td>
<td>Lunch on your own</td>
</tr>
</tbody>
</table>

**Afternoon workshops**

<table>
<thead>
<tr>
<th>Time</th>
<th>Workshop</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:00-4:00</td>
<td>Workshop I: Biomath Curriculum Development: Tips/Tricks</td>
</tr>
<tr>
<td>1:00-4:00</td>
<td>Workshop 2 R-Bootcamp: An interactive introduction to R (U.S. Geological Survey - Upper Midwest Environmental Sciences Center)</td>
</tr>
</tbody>
</table>

**Wireless Internet Access**

**Select UWLOpen.** UWLOpen grants *free* internet access to anyone on campus. After connecting to UWLOpen you will need to open a web browser and accept the agreement before continuing to the internet.
Health Science Center (HSC)

The Health Science Center (building #21 on map below), which was built in 2000, is a project of the La Crosse Medical Health Science Consortium, Inc. Health Programs from University of Wisconsin-La Crosse and Western Wisconsin Technical College share classrooms, laboratories and equipment.

**From Downtown:** Follow La Crosse St. east (towards bluffs). Turn right on Oakland St. Park in lot adjacent to the HSC (#21).
ABSTRACTS

Oral Presentation

Aagaard, Kevin (USGS UMESC) Assessing spatial patterns of plant communities at varying stages of succession

Ackman, Olcay, D. Akman, and E. Schaefer (Illinios St. Univ.) Computing Intensive Methods in ODE Modeling

We introduce and implement Engineered Genetic Algorithm and Particle Swarm Optimization to select parameters for compartmental models. We examine the performances of both techniques and compare our results to those obtained with Engineered Genetic Algorithm (Akman and Schaefer, 2014).

Ackman, Olcay (Illinios St. Univ.) Intercollegiate Biomathematics Alliance (IBA)

The Intercollegiate Biomathematics Alliance (IBA) for Scholarship, Teaching, and Advanced Research (STAR) Development is a consortium of academic institutions as a platform for collaboration of researchers, educators, and scientists in order to provide a wide range of expertise and interests in biomathematics, ecology, and related areas to the future researchers, mathematics and biology educators, and currently active scholars.

Allen, Robert, E. Eager, and K. Healy (University of Wisconsin - La Crosse) Modeling and Analysis of the 2014-2015 Measles Outbreak Subject to Sociological Dynamics

Mathematical modeling of infectious diseases typically involves the use of some variant of the classic SIR model, which tracks susceptible, infected, and recovered population densities. Much has been learned about infection dynamics using this modeling paradigm. However, most studies ignore underlying sociological dynamics that can drive the spread of disease. We derive and analyze a model of the measles outbreak at Disneyland in 2014-2015, extending the basic SIR model to include pro- and anti-vaccination sentiment in the populations.

Comar, Timothy, O. Akman, and D. Hrozencik (Benedictine University) Sensitivity Analysis and the Probability of Pest Eradication or Permanence in a Stochastic Model for Integrated Pest Management

We explore deterministic and stochastic models for integrated pest management. The stochastic version incorporates competing stochastic elements in the prey birth rate. We prove the conditions under which solutions to the deterministic model are permanent, which correspond to economically viable solutions with minimal negative impacts. We then compute the probabilities of having either a pest eradication solution or a permanent solution when the birth rates are randomly chosen from particular probability distributions. We also perform sensitivity analysis for certain model parameters.

Craven, Mark (University of Wisconsin-Madison) Inferring Host-Pathogen Interactions from Diverse Data Sources

Insight into the mechanisms and context of host-pathogen interactions can be gained by applying computational methods to a broad range of experimental, observational, and secondary data sources. I will discuss our work in several studies that involve developing and applying predictive methods in order to characterize host-pathogen interactions. In the first study, we are focused on inferring host subnetworks that are involved in viral replication from genome-wide loss-of-function experiments. Although these experiments can identify the host factors that directly or indirectly facilitate or inhibit the replication of a virus in a host cell, they do not elucidate how these genes are organized into the biological pathways that mediate host-virus interactions. We are developing novel computational methods that use a wide array of secondary data sources, including the scientific literature, to transform the measurements from these assays into hypotheses that predict the pathways in the cell that relate implicated genes to viral replication. In the second study, we are applying machine-learning methods to understand how variation in the genome
of the HSV-1 virus influences multiple ocular disease phenotypes in a host. In the third study, we are investigating the extent to which risk for various infectious disease phenotypes can be predicted from electronic health records by using machine-learning methods.

Curto, Carina (Pennsylvania St. Univ.) *What can topology tells us about the neural code?*

Cracking the neural code is one of the central challenges of neuroscience. Neural codes allow the brain to represent, process, and store information about the outside world. Unlike other types of codes, they must also reflect relationships between stimuli, such as proximity between locations in an environment. In this talk, I will explain why algebraic topology provides natural tools for understanding the structure and function of neural codes.

Eager, Eric and A. Garza (University of Wisconsin - La Crosse) *Modeling and Analysis of Gene Regulatory Networks Using Finite Dynamical Systems*

In this talk we discuss the process of modeling the gene regulatory network responsible for germ layer formation in Xenopus laevis and axolotl using finite dynamical systems. We show that a simple Boolean network is not capable of reproducing established in vitro and in vivo network dynamics for both species, but that a model evolving in a higher-dimensional discrete space is. We show that this modeling difficulty is present in the process of modeling stem cell dynamics using finite dynamical systems as well.

Ekanayake, Amy and D. Ekanayake (Western Illinois University) *Modeling reproduction of whitetail deer*

Deer exhibit a high level of phenotypic plasticity by changing phenotypes in response to changes in resources. Many regional factors, such as climate and competition, affect resource availability from one region to another. For species exhibiting phenotypic plasticity, embedding phenotypes in a model of population dynamics is important, as the region itself plays a significant role when evaluating parameters values. We propose a representation for region-driven and trait-mediated reproduction rates for whitetail deer populations. We further discuss the usefulness for prediction and control.

Ekanayake, Dinesh and A. Ekanayake (Western Illinois University) *Management of species under phenotypic plasticity and stochasticity*

Many biological processes that influence demographic rates must be considered in developing a management plan. Estimating parameters is based on count statistics and can be costly with respect to the intended application. However, if the species change phenotypes, then changes in fitness components may be predicted using observable species characteristics. We discuss how management strategies can be derived under phenotypic plasticity and stochasticity, without explicitly needing count statistics. As an example, we demonstrate how the methods can be utilized for a deer harvesting strategy.

Erickson, Richard, C. Merkes, and J. Amberg (USGS UMESC) *Detecting seasonal trends in eDNA with occupancy modeling*

Environmental DNA (eDNA) can be used to detect the presence of a species at a location without directly observing an individual. Occupancy modeling can be used to estimate the probabilities of both detecting and observing a species. We applied occupancy modeling to estimate the probability that a sample contains eDNA and also the probability of detecting eDNA for two species of invasive bighead and silver carps. We found seasonal changes in detection probabilities for each species, with higher detection probabilities in the spring.

Goldberg, Emma (University of Minnesota, Twin Cities) *Phylogenetic inference of trait evolution during speciation*

Over macroevolutionary timescales, traits may evolve within single lineages, or they may change when one lineage splits into two. Traits that evolve by the latter mode are of particular interest because they may be involved in the process of speciation. These two modes of evolution can be separated by fitting a mathematical model of speciation, extinction, and trait change to data on the phylogenetic relationships
among species. Collaborative applications of this method in plants investigate whether flower color shifts are most common during speciation, and whether whole genome duplication is a common mechanism of speciation.

**Gross, Louis** (University of Tennessee, Knoxville) "Best" in a Biological Context: Optimization, Space and Control

Many central concepts in biology involve notions of what is "better" or "best" in the context of evolution, physiology, and behavior. Similarly, in many applied areas of the life sciences, we are concerned with developing a "best" method to carry out drug therapies, resource harvesting, pest management, and epidemic control. I will give a variety of examples of ecological projects that lie at the interface between theory and practice, providing some indication of the utility of quantitative methods to elucidate general patterns of natural system response to management actions. An emphasis will be on spatial control: what to do, where to do it, how to do it and how to assess success. This will include applications to wildlife management and disease ecology and examples using individual-based models. An objective of these approaches is to develop hypothetical "best" methods to manage a system, and use this as a template to compare and contrast management scenarios arising from the differing viewpoints of diverse stakeholders in a relative assessment framework.

**Hampton, Marshall and S. Zimmer** (University of Minnesota Duluth) Probabilistic Models of Trypanosome RNA tails

Trypanosomes several diseases including sleeping sickness and Chagas disease. Their mitochondrial genome has unusual properties, being essentially encrypted - requiring massive editing by their minicircle DNA. Mitochondrial RNA transcripts also have complicated 3’ tail additions incorporating uridine (U) as well as adenine (A); these unique features provide possible drug targets.

**Hrozencik, Dan, O Akman, and Tim Comar** (Chicago St. Univ.) On the Estimated Propensities from Stochastic Gene Regulatory Networks via Evolutionary Computing

Stochasticity in gene regulatory networks is crucial to understanding the variability in the network and its effect on genetic expression. Prior studies have used fixed parameters for the propensity of a gene activation or degradation to predict a network structure. While these studies have revealed some effects of stochasticity, they are often more idealistic than what is experimentally measurable. Experimental measurements often reveal the network, but not the propensities. Here we explore the feasibility of using the network to determine the propensities via evolutionary computing.

**Kapitanov, Georgi, X. Wang, B. Ayati, M. Brouillette, and J. Martin** (University of Iowa) Linking Cellular and Mechanical Processes in Articular Cartilage Lesion Formation: A Mathematical Model

An injurious impact applies a significant amount of physical stress on articular cartilage and can initiate a cascade of biochemical reactions that can lead to the development of osteoarthritis. In our effort to understand the underlying biochemical mechanisms of this debilitating disease, we have constructed a multiscale mathematical model of the process with three components: cellular, chemical, and mechanical. The model creates a platform for incorporating explicit mechanics, simulated by finite element analysis, into a theoretical biology framework.

**Lee, Namyoung** (Minnesota State University, Mankato) Microarray Cancer Data Analysis through the TDA Looking Glass

Clinical Big Data, such as Microarray and Next Generation Sequencing have many challenging features in analysis: noisy and contaminated data, missing values, data set shift and class imbalance, and very high dimensional features with relatively small number of sample sets. In this connection, we introduce basic idea of TDA (Topological Data Analysis) and its' advantage in visual analysis compare other methods. A few concrete examples will be given including microarray cancer data analysis.
Auditory stream integration and segregation is an important feature of auditory perception. An example of such a phenomenon is demonstrated when one is subjected to a sequence of alternating tones, ABAB, where tones “A” and “B” differ by frequency DeltaF. When the presentation rate is high or DeltaF is large, the sequence is perceived as parallel auditory streams. Studies have shown that such perceptual phenomenon have a cortical basis. We construct an integrative model of the primary auditory cortex (A1) for auditory streaming and show that it parallels dynamics of data from ECoG recordings.

The brain represents stimuli via patterns of neural activity. These activity patterns can be described by a neural code, i.e. a collection of indicator vectors showing which neurons co-fire in response to various stimuli. It is believed that the brain can infer many properties of the stimulus space purely from the intrinsic structure of the neural code, e.g. through the convex structure of receptive fields that give rise to convex neural codes. In this talk, we demonstrate combinatorial and algebraic techniques that enable us to determine if a given neural code is convex.

In heterogeneous epidemiological mathematical models two simultaneous processes occur: First, the ecological process that is responsible for the interactions of different populations and changes in the population numbers; second, the evolutionary process of the change of the population structure. Usually in simple mathematical models we follow only the former process. I will present a transparent mathematical framework to study the latter, evolutionary, process, and discuss several, not that obvious, implications of using such heterogeneous model.

I will present a mathematical model that focuses on understanding the relative importance of processes that shape the energy budget of income-breeding insects. I define performance as the net energy gain that is the difference between energetic gain and energetic cost and ask whether performance breadth as a function of temperature increases or decreases with body size. In short, the model exhibits numerous
scenarios of how niche differs among body sizes. Distinguishing these scenarios requires more specific information about where in the parameter space the species are located.


We present theoretical methods of population management using feedback control theory. For conservation, we give examples of how integral tracking can be used to determine how to replant or restock. For management of invasive species, we give an example of how high gain feedback can be used for eradication via biological control. The control methods are implemented with only access to specified, limited observations of the population, in a manner that is independent of the initial population distribution and robust to model uncertainty, measurement errors, and disturbances.

Schultz, André and A. Qutub (Rice University, Department of Bioengineering) Novel Methods for the Study of Human Metabolism Using Constraint Based Models

Many of the methods and assumptions used to study the metabolism of unicellular organisms using constraint based models cannot be directly applied to mammalian cells. This is due to the fact that (1) mammalian cells do not optimize their cellular objective, and (2) different subsets of the human metabolism take place in different tissues, making these models context specific. Here we present two novel algorithms: (1) corsoFBA aims to predict metabolic fluxes at sub-optimal objective levels, and (2) CORDA aims to construct context specific models of human metabolism based on experimental data.

Shaw, Allison and S. Binning (University of Minnesota) Recovery from infection as a selective pressure for the evolution of migration

Seasonal migration influences how animals acquire and transmit parasites. Past work shows that migration can reduce infection via escaping infected areas or culling infected individuals. Here I propose a third process: migratory recovery, where infected individuals lose their parasites (recover from infection) during migration. Although migratory recovery is likely widespread, it is challenging to empirically test it as a selective force promoting migration. I will present a model that couples continuous and discrete time dynamics to determine when migratory recovery can select for migration.

Zhao, Ruijun and D. Abdurakhimova (Minnesota State University, Mankato) Investigating the imperfect malaria vaccine, RTS,S using optimal control theory

Malaria is a serious and sometimes fatal disease caused by parasite Plasmodium through mosquito bites. Children under age 5 suffer malaria most and people in endemic region gradually gain partial immunity. RTS, S is the first malaria vaccine which has gone through human trials. However, the human trials indicate that the vaccine is not perfect and its efficacy also varies in different age groups. In this talk, we will formulate an optimal control problem to study the imperfect vaccine, in which state equations are described by an age-structured mathematical model.

Poster Presentations

Eberle, Megan, E.Eager and J. Peirce. (UW-La Crosse) How infectious was #Deflategate?.

On January 19, 2015 a story broke that the National Football League (NFL) started an investigation into whether the New England Patriots deliberately deflated the footballs they used during their AFC Championship win. Like an infectious disease, discussion regarding Deflategate grew rapidly on social media sites in the hours and days after the release of the story. We created and analyzed a standard SIR model for the spread of this news story on the social media site Twitter, and showed that the basic reproduction number of this story rivaled that of many famous disease outbreaks.
Methylation of DNA is a well understood epigenetic mechanism that influences gene expression and can trigger specific gene silencing in eukaryotes. Recent next-generation sequencing (NGS) techniques have allowed researchers to examine methylation rates across whole genomes and test for differential methylation across different biological conditions using newly developed analytical methods. To better understand the interaction of cytosine contexts and respective methylation rates in plants, an algorithm in R was used to develop realistic, simulated methylation datasets for plant species.

**Hanson, Danny and S. Wagenius** (Chicago Botanic Garden) *Effects of individual variation on mating synchrony*

Individuals often vary substantially in reproductive timing which means populations don’t mate in complete synchrony. We conducted a simulation study that explores effects of individual variation on synchrony. The standard deviations of mating initiation and duration and mean mating duration impacted synchrony the most. Mating synchrony affects population growth and evolutionary dynamics. Elucidating fundamental relationships between individual traits and synchrony will help us understand reproduction, inter- and intraspecific interactions, and other phenological life-history traits.

**Harkness, Alexander, E. Goldberg, and Y. Brandvain** (University of Minnesota) *Restoration of inbreeding depression through secondary contact*

Based on new circularized RNA deep sequencing data, we present different probabilistic approaches to modeling the structure of these RNA tails, and how the models can inform biological interpretation.

**Healy, Kaitlin, R. Allen, and E. Eager** (UW-La Crosse) *Modeling and Analysis of Disease Dynamics Subject to Unvaccinated Subpopulations*

In this poster we present a model for the dynamics of a population where there is a subgroup of adults that choose not to vaccinate their children. We fit this model, which is an SIS model for the propagation of anti-vaccination sentiment coupled with an SIR model for the dynamics of the disease, to CDC data from the 2014-15 Measles outbreak in Southern California. We show that this simple model fits the CDC data well, and our analysis demonstrates a critical value of anti-vaccine sentiment can cause an otherwise eradicated disease to experience substantial outbreaks.

**Sandland, Greg** (UW-La Crosse) *Modeling cooperation for fishery by catch avoidance*

We present a game-theoretic model to understand when cooperative by catch avoidance behavior can be attained under different management regimes. We identify the conditions when cooperative arrangements between fishers are vulnerable to cheating, and whether cheating completely takes over the system or can coexist with cooperative strategies in a fishery. We also make comparisons between globally optimal solutions, the arrangement of cooperative and selfish behaviors that maximize the whole fishing fleet's revenue, and non-cooperative equilibria where individuals optimize their revenue.

**Wang, Kun-Chieh** (University of Wisconsin-Madison) *Phylogenetic Network Reconstruction from Distorted Metrics*

We introduce a new phylogenetic network reconstruction algorithm which guaranteed to reconstruct all the splits in a weakly compatible network that are sufficient heavy from its distorted metric. Because of the fact that the algorithm does not rely on the distances between taxa which are too long, it has higher accuracy in successfully reconstructing the splits than the other two distance-based algorithms, Neighbor-Net and Split Decomposition Method, in some models in practice. The algorithm runs in polynomial time.
Additional Activities in La Crosse Area

In La Crosse
- Historic Trolley Tours of La Crosse
- Hixon House
- Riverside Park
- Riverside Museum
- Myrick-Hixon EcoPark
- Grandad Bluff
- Cycling the many areas in and around La Crosse.
  - Trail/road ride options
    - La Crosse River State Trail
    - Elroy-Sparta State Bike Trail
    - Great River State Trail
    - Root River Trail
    - Trempealeau County back roads
  - Bike rentals
    - Outdoor Connection
    - Blue Heron Bicycle Works
    - River Trail Cycles
- Breweries
  - Pearl Street Brewery
  - Turtle Stack Brewery

In the surrounding area
- Norskedalen Nature and Heritage Center (Coon Valley, WI)
- National Eagle Center (Wabasha, MN)
- Minnesota Marine Art Museum (Winona, MN)
- River View Vineyards (La Crescent, MN)
- Cave Tours
  - Forestville/Mystery Cave State Park
  - Niagara Cave
- State Parks within 1.5 hour drive
  - Wisconsin State Parks
    - Perrot State Park
    - Wyalusing State Park
    - Wildcat Mountain State Park
    - Merrick State Park
  - Minnesota State Parks
    - Great River Bluffs Minnesota State Park
    - Beaver Creek Valley Minnesota State Park
    - Forestville/Mystery Cave Minnesota State Park
    - Whitewater Minnesota State Park
    - John A Latsch Minnesota State Park
  - Iowa State Parks
    - Pikes Peak Iowa State Park
  - National Parks
    - Effigy Mounds National Monument
Special Thanks
University of Wisconsin-La Crosse College of Science and Health
The Mathematics and Biology Departments
UW-L Office of Continuing Education and Extension

Wisconsin Mathematical Modeling Challenge

Each October, the University of Wisconsin-La Crosse Department of Mathematics hosts an annual mathematics contest called the Wisconsin Mathematical Modeling Challenge (WMMC). This regional math contest gives undergraduate students the opportunity to apply their math skills to real world problems. The WMMC is currently one of three regional mathematical modeling contests.

In teams of three, students have 23 hours to develop and test a model and write a one-page summary of their findings; teams have one additional (24th) hour to finalize a 10-minute presentation explaining their results. Soon after preparing their presentations, teams present their findings to other student WMMC participants. The event concludes with an award ceremony that highlights the work of winning teams as determined by students and advisors. In the past, cash prizes have been awarded. Information can be found on the WMMC website

http://www2.uwlax.edu/Mathematics/Wisconsin-Mathematical-Modeling-Challenge-(WMMC)/

Letters in Biomathematics

Letters in Biomathematics seeks high quality manuscripts that describe mathematical and statistical techniques to solve problems in biological settings or that address the study of the teaching and learning at the intersection of mathematics and biology. Manuscripts that describe novel approaches in biomathematics or biomathematics pedagogy will be considered along with well-established approaches. Accepted papers show a strong level of interdisciplinary content and clear exposition. Articles must be of interest to and understandable by a wide spectrum of scientists from related fields. Manuscripts reporting preliminary results will be considered.

The Midwest Mathematical Biology Conference has partnered with Letters in Biomathematics to publish the proceedings of the conference as a special volume in their journal. We invite you to contribute a manuscript inspired by your presentation at this unique event. Further information on publication criteria, guidelines, and templates may be found on the Letters in Biomathematics website (http://lettersinbiomath.org/).