

Program

2010 SIAM Great Lakes conference:
Modeling and Numerical PDEs in Mathematical Biology

University of Michigan-Dearborn, Dearborn, MI, April 17, 2010



<http://groups.engin.umd.umich.edu/siam/spring10.htm>

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Organizers

Yangjin Kim, Michael Lachance, Joan Remski
Department of Mathematics & Statistics
University of Michigan-Dearborn

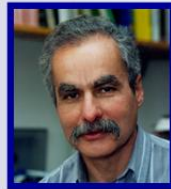


2010 SIAM Great Lakes Conference on Modeling and Numerical PDEs in Mathematical Biology

April 17, 2010

University of Michigan-Dearborn

Invited Speakers



Leonard Sander
Univ. of Michigan



Avner Friedman
MBI, Ohio State Univ.



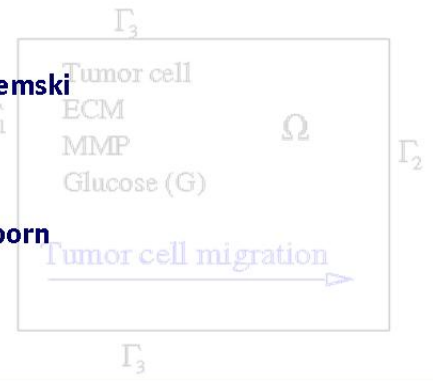
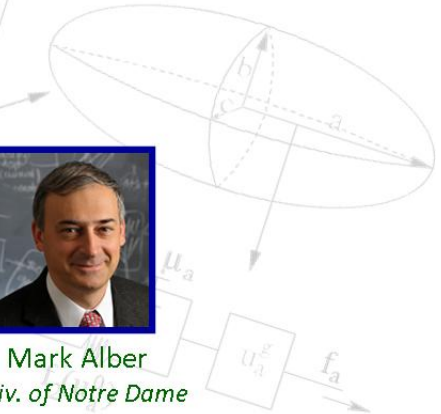
Mark Alber
Univ. of Notre Dame

Organizing Committee

Yangjin Kim, Michael Lachance, Joan Remski
University of Michigan-Dearborn

Sponsors

SIAM, University of Michigan-Dearborn



$$U_t = DAU + \lambda G + \lambda \int_{\Omega} f(x,y) dx$$



For more information, visit <http://www.engin.umd.umich.edu/glsiam/spring10.htm>

Conference

Website

<http://groups.engin.umd.umich.edu/siam/spring10.htm>

Conference Site

Fairlane Center South (University of Michigan-Dearborn)
19000 Hubbard Drive
Dearborn, MI 48126-2638, USA

Contact Information

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Assistant professor
Department of Mathematics & Statistics
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University of Michigan - Dearborn
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Email: yangjink at umd.umich.edu
<http://www-personal.umd.umich.edu/~yangjink/>

* Staff members Belinda Soliz and Sandra Lupfer in the Department of Mathematics and Statistics at the University of Michigan-Dearborn will be available to assist you for the detailed information.

Driving Directions

[1] Driving directions from Windsor (27.9 km; 22 mins)

- (0) Windsor, ON, Canada
- (1) Head northeast on Wyandotte St E toward Dufferin Ave (go 0.2 km)
- (2) Take the 1st left onto Goyeau St (About 1 min, go 74 m)
- (3) Take the 1st left onto Detroit-Windsor Tunnel (Toll road Entering United States (Michigan), About 2 mins, go 1.1 km)
- (4) Continue onto Unknown road (About 1 min, go 1.1 km)
- (5) Slight left at Randolph St (go 43 m)
- (6) Take the 1st right onto E Jefferson Ave (go 0.3 km)
- (7) Continue onto I-375 N (About 2 mins, go 2.1 km)
- (8) Continue onto I-75 N, go 1.2 km)
- (9) Take exit 53A toward Warren Ave (go 0.4 km)
- (10) Merge onto Chrysler Dr (About 1 min, go 0.5 km)
- (11) Take the ramp on the left onto I-94 W (About 6 mins, go 10.1 km)
- (12) Take exit 210A for US-12/Michigan Ave toward Dearborn (go 0.6 km)
- (13) Turn right at Michigan Ave/US-12 W, Continue to follow US-12 W (About 5 mins, go 4.2

km)

- (14) Take the exit toward MI-39 N/Southfield Fwy (go 0.4 km)
- (15) Merge onto Southfield Rd (About 1 min, go 0.9 km)
- (16) Turn left at Hubbard Dr. Destination will be on the right (About 2 mins, go 0.7 km) (total 23.8 km)
- (17) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)

[2] South (From Toledo, OH; 56 miles, 1 hour)

- (0) Toledo, OH
- (1) I-75 N (About 45 mins, go 48.5 mi)
- (2) Take exit 41 for MI-39/Southfield Rd (About 1 min, go 0.3 mi)
- (3) Turn left at MI-39 N/Southfield Rd (About 4 mins, go 1.4 mi)
- (4) Slight left to stay on MI-39 N/Southfield Rd, Continue to follow MI-39 N (About 4 mins, go 3.9 mi)
- (5) Take exit 6 toward Michigan Ave/US-12 (go 0.2 mi)
- (6) Merge onto Southfield Frwy Srv Rd (About 1 min, go 0.4 mi)
- (7) Continue onto Southfield Rd (About 1 min, go 0.6 mi)
- (8) Turn left at Hubbard Dr. Destination will be on the right (About 2 mins, go 0.4 mi, total 56.7 mi)
- (9) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)

[3] West (From Ann Arbor; 34 miles, 35 mins)

- (0) Ann Arbor (I-94)
- (1) I-94 E (About 22 mins, go 23.9 mi)
- (2) Take exit 204 to merge onto MI-39 N/Southfield Fwy (About 4 mins, go 4.0 mi)
- (3) Take exit 6 toward Michigan Ave/US-12 (go 0.2 mi)
- (4) Merge onto Southfield Frwy Srv Rd (About 1 min, go 0.4 mi)
- (5) Continue onto Southfield Rd (About 1 min, go 0.6 mi)
- (6) Turn left at Hubbard Dr. Destination will be on the right. (About 2 mins, go 0.4 mi)
- (7) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)

[4] North (From Lansing)

- (0) Lansing
- (1) I-96 E toward Detroit (About 1 hour 10 mins, go 75.8 mi, total 82.0 mi)
- (2) Take exit 183 for MI-39/Southfield Fwy (go 0.2 mi, total 82.3 mi)
- (3) Keep right at the fork to continue toward MI-39 S/Southfield Fwy and merge onto MI-39 S/Southfield Fwy (About 3 mins, go 3.0 mi, total 85.3 mi)
- (4) Take exit 7 toward MI-153/Ford Rd (go 0.2 mi, total 85.4 mi)
- (5) Merge onto Southfield Rd (About 1 min, go 0.8 mi, total 86.2 mi)
- (6) Turn right at Hubbard Dr. Destination will be on the right (About 1 min, go 0.4 mi, total 86.6 mi)
- (7) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)

Audio-Visual Policy

All meeting rooms (plenary, special sessions) are equipped with a computer, projector, and an overhead projector. To inquire about additional audio-visual equipment, please contact Yangjin Kim (yangjink@umd.umich.edu). Speakers may use their own computers, but SIAMGL is not responsible for the safety or security of speakers' personal computers.

Registration

SIAM Great Lakes section member: free

Non-member : \$5.00 at the door to attend

UM-Dearborn Student : free

<http://www-personal.engin.umd.umich.edu/~boss/siam/register.php>

Parking

Parking is available for free in the lot adjacent to Fairlane Center South. See the campus map (page 33) for more details. Note: Fairlane Center is located at the left upper corner on the map.

Internet/Email

An Internet cafe is available at the conference site (Fairlane Center) for attendees and free wireless service is available throughout the building. Please use the following account and password:

User Name: umd-guest

Password: 08A-D49-669

Log on to: UMROOT

Local Area

Visit www.detroit.world-guides.com for more information on Detroit and the surrounding area. The average temperature in Dearborn during April varies between 40 degree(F) and 62 degree(F).

Poster Presentations

Posters need to fit within a 48 inch (122cm) square. Please submit your poster when you arrive at the conference site and staff members will mount your poster in the presentation area. Contact local organizers, Yangjin Kim and Joan Remski, if you need any help.

Airport

(Detroit Metropolitan Wayne County Airport (DTW))

<http://www.metroairport.com/>

- Ground Transportation (<http://www.metroairport.com/transportation/>)

(Taxi: about \$41 to the conference site

Metro Cars (<http://www.metrocars.com/>, 800-456-1701)

Metro Cab (734-997-6500)

To the airport: Dearborn Cab: 313-582-6900, 734-942-6700)

- Driving directions (14.4 mi, 20 mins)

(0) Detroit Metropolitan Wayne County Airport, Detroit, MI 48242

(1) Head southwest (0.2 mi)

- (2) Slight right toward John D Dingell Dr (1.0 mi, about 3 mins)
- (3) Continue straight onto John D Dingell Dr (1.3 mi, about 3 mins)
- (4) Continue onto W G Rogell Dr (0.6 mi, about 1 min)
- (5) Slight right to merge onto I-94 E (5.7 mi, About 6 mins)
- (6) Take exit 204 to merge onto MI-39 N/Southfield Fwy (About 4 mins, go 4.0 mi)
- (7) Take exit 6 toward Michigan Ave/US-12 (go 0.2 mi)
- (8) Merge onto Southfield Frwy Srv Rd (About 1 min, go 0.4 mi)
- (9) Continue onto Southfield Rd (About 1 min, go 0.6 mi)
- (10) Turn left at Hubbard Dr: Destination will be on the right (About 2 mins, go 0.4 mi; total 14.4 mi)
- (11) Conference site (University of Michigan-Dearborn, Fairlane Center South, 19000 Hubbard Drive, Dearborn, MI 48126-2638)

Hotels

[1] Hyatt Regency Dearborn

600 Town Center Drive,
 Dearborn, Michigan, USA 48126-2793
 Tel: +1 313 593 1234 Fax: +1 313 593 3366
<http://dearborn.hyatt.com/hyatt/hotels/>

- To receive the special rate for the conference, call reservations and ask for the University of Michigan-Dearborn rate of \$85.00 or email Scott Bray scott.bray@hyatt.com with your name and credit card information.
 - Distance : a short walk (1.0 mile).
 - The Hyatt Regency Dearborn offers guests high speed wireless Internet access.
 - Driving directions (1.0 mile; 3 mins):
- (0) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)
 - (1) Head west on Hubbard Dr (go 289 ft)
 - (2) Make a U-turn (About 1 min, go 0.2 mi)
 - (3) Turn right at Northwood Dr (go 0.1 mi)
 - (4) Turn left at Town Center Dr (About 1 min, go 0.5 mi)
 - (5) Turn left at Hyatt Regency Dr (go 0.1 mi)
 - (6) Take the 1st right to stay on Hyatt Regency Dr (go 72 ft)
 - (7) Take the 1st left to stay on Hyatt Regency Dr, Destination will be on the left (go 233 ft)
 - (8) Hotel (600 Town Center Dr, Dearborn, MI 48126)

[2] Doubletree Hotel

5801 Southfield Expressway,
 Detroit, Michigan, United States 48228
 Tel: 1-313-336-3340 Fax: 1-313-336-7037
http://doubletree1.hilton.com/en_US/dt/hotel/DTTDBDT-Doubletree-Hotel-Detroit-Dearborn-Michigan/index.do

- University of Michigan-Dearborn Rate : \$82.00
- Distance : a short walk (1.8 mile).

- Directions :

- (0) Conference site (19000 Hubbard Dr, Dearborn, MI 48126)
- (1) Head west on Hubbard Dr (go 289 ft)
- (2) Make a U-turn (About 2 mins; go 0.5 mi)
- (3) Turn left at Southfield Rd (About 1 min; go 0.6 mi)
- (4) Take the ramp onto Ford Rd/MI-153 W (About 1 min; go 0.5 mi)
- (5) Turn right at Crossroad Center Dr (go 0.2 mi)
- (6) Turn right. Destination will be on the right (go 167 ft)
- (7) Hotel (Doubletree Hotel Detroit/Dearborn, 5801 Southfield Expressway, Detroit, MI 48228)

[3] The Dearborn Inn, A Marriott Hotel

20301 Oakwood Boulevard
Dearborn, Michigan 48124 USA
Phone: 1-313-271-2700
Fax: 1-313-271-7464
Sales: 1-313-271-3899
Sales fax: 1-313-271-6682

<http://www.marriott.com/hotels/travel/dtwdi-the-dearborn-inn-a-marriott-hotel/>

- Call in University of Michigan-Dearborn Rate : \$139.00

- Distance : 3.8 mile; 8 mins.

- Driving directions :

- (0) Hotel (20301 Oakwood Boulevard, Dearborn, Michigan 48124 USA)
- (1) Head northwest on Oakwood Blvd toward W Rd (About 2 mins; go 0.9 mi)
- (2) Turn right at Michigan Ave (About 3 mins; go 1.5 mi)
- (3) Take the Southfield Fwy exit toward MI-39 N (go 0.2 mi)
- (4) Merge onto Southfield Frwy Srv Rd (go 0.2 mi)
- (5) Continue onto Southfield Rd (About 1 min; go 0.6 mi)
- (6) Turn left at Hubbard Dr Destination will be on the right (About 2 mins)
- (7) Conference site (19000 Hubbard Drive, Dearborn, MI 48126-2638)

Speaker List

(P) = Plenary speaker, (I) = Industry

Ahmed, S. Ejaz (Mathematics & Statistics, University of Windsor)
Alber, Mark S. (P) (Center for the Study of Biocomplexity, University of Notre Dame)
Arciero, Julia C (Mathematics, University of Pittsburgh)
Bobeldyk, Denton (I) (Davenport University and DJB Consulting L.L.C.)
Chou, Ching-Shan (Mathematics, Ohio State University)
Eden, Gideon (CEO, Biolumix)
Friedman, Avner (P) (Mathematical Biosciences Institute, Ohio State University)
Gurarie, David (Mathematics, Case Western Res University)
Heng, Henry (I) (Center for Molecular Medicine and Genetics, and Karmanos Cancer Institute,
Wayne State University School of Medicine)
Jain, Harsh (Mathematical Biosciences Institute, Ohio State University)
Kang, Yeona (Applied Mathematics, SUNY at Stony Brook)
Kao, Chiu-Yen (Mathematics, Ohio State University)
Khain, Evgeniy (Physics, Oakland University)
Kim, Eunjung (Mathematics, University of Notre Dame)
Lee, Pilhwa (Courant Institute, New York University)
Lim, Sookkyung (Mathematics, University of Cincinnati)
Liu, Di (Richard) (Mathematics, Michigan State University)
Matzavinos, Anastasios (Mathematics, Iowa State University)
Mikhaylov, Jessica (Mathematics Sciences, United States Military Academy)
Rong, Libin (Los Alamos National Laboratory, Mathematics at Oakland University)
Sander, Leonard M. (P) (Physics, University of Michigan-Ann Arbor)
Sheng, Jim (I) (U.S. Army Tank Automotive Research and Development)
Spagnuolo, Anna (Mathematics, Oakland University)
Srinivasan, Parthasarathy (Mathematics, Cleveland State University)
Stolarska, Magdalena (Mathematics, University of St. Thomas)
Tian, Paul (Mathematics, College of William and Mary)
Thomas, Peter J. (Mathematics & Biology, Case Western Reserve University)
Umulis, David (Agricultural and Biological Engineering, Purdue University)
Wei, Guowei (Mathematics, Michigan State University)
Xue, Chuan (Mathematical Biosciences Institute, Ohio State University)
Yamada, Richard (Mathematics, University of Michigan-Ann Arbor)
Zheng, Xiaoming (Mathematics, Central Michigan University)

Poster presentation:

Baek, Seunghyeon (Mathematics, Korea University, Korea)
Byun, Jonghyuk (Mathematics, University of Cincinnati)
Chen, Duan (Mathematics, Michigan State University)
Du, Huijing (Mark Alber group, Mathematics, University of Notre Dame)
Gejji, Richard (Mark Alber group, Mathematics, University of Notre Dame)
Hengenius, James (Gribskov and Rundell Labs, Agricultural and Biological Engineering, Purdue University)
Holmes, William (Mathematics, Indiana University)

Im, Jeong Sook (Mathematics, Ohio State University)
Jordan, Benjamin (Organismic & Evolutionary Biology, Harvard University)
Karim, Mohammad Shahriar (Electrical and Computer Engineering, Purdue U)
Kim, Jae Kyoung (Mathematics, University of Michigan-Ann Arbor)
Lee, Sang-hun (Agricultural and Biological Engineering, Purdue University)
Lioi, Josh (Mark Alber group, Mathematics, University of Notre Dame)
Liu, Sijia (Mathematics, Iowa State University)
Liu, Yuan (Mathematics, University of Notre Dame)
Luterek, Adam (Brad Roth Group, Physics, Oakland University)
Pargett, Michael (Weldon School of Biomedical Engineering, Purdue University)
Srivastava, Prashant (IIT Kanpur, INDIA)
Stevens, Joshua B. (School of Medicine, Wayne State University)
Wang, Xiaoxia (Mathematics, Case Western Reserve University)
Xu, Dana (Brad Roth Group, Physics, Oakland University)

Time /Room	Program			
09:00 - 09:50 (Room D)	Registration and Coffee (Opening remarks (09:40): Chancellor, Daniel Little)			
09:50 - 10:35 (Room D)	Plenary talk (Avner Friedman) (What is mathematical biology and how useful is it?) [Chair: David Field]			
10:35 - 11:20 (Room D)	Plenary talk (Mark Alber) (Multiscale Modeling in Biology) [Chair: David Field]			
11:20 - 11:30 (Room D)	Coffee Break			
11:30 - 12:30 (Rooms 161, 163,172,173)	Session A-1 (Room 161) (Systems Biology I) [Chair: Kim]	Session A-2 (Room 163) (Spatial Pattern) [Chair: Stolarska]	Session A-3 (Room 172) (Modeling I) [Chair: Moylan]	Session A-4 (Room 173) (Modeling IV)
12:30 - 1:30 (Room D)	Lunch (Lunch Box)			
1:30 - 3:30 (Rooms 161, 163,172,173)	Session B-1 (Room 161) (Mechanics) [Chair: Srinivasan]	Session B-2 (Room 163) (Wound Healing) [Chair: Xue]	Session B-3 (Room 172) (Cancer I) [Chair: Yamada]	Session B-4 (Room 173) (Industry) [Chair: Remski]
3:30 - 3:45 (Room D)	Coffee Break			
3:45 - 4:45 (Rooms 161, 163,172,173)	Session C-1 (Room 161) (Systems Biology II) [Chair: Umulis]	Session C-2 (Room 163) (Cancer II) [Chair: Massey]	Session C-3 (Room 172) (Modeling II) [Chair: Lim]	Session C-4 (Room 173) (Modeling III) [Chair: Kim]
04:45 - 05:05 (Room D)	Poster Session			
05:05 - 05:15 (Room D)	Coffee Break			
5:15 - 6:00 (Room D)	Plenary talk (Leonard Sander) (Biomechanics of cell motility in <i>Dictyostelium</i>) [Chair: David Field]			
6:00	End			

Table 1: Schedule

Program

Plenary talks

- 09:50 - 10:35 **Avner Friedman** [APS2] (Ohio State University)
What is mathematical biology and how useful is it?
- 10:35 - 11:20 **Mark Alber** [APS1] (University of Notre Dame)
Multiscale Modeling in Biology
- 05:15 - 06:00 **Leonard Sander** [APS3] (University of Michigan-Ann Arbor)
Biomechanics of cell motility in Dictyostelium

Special session A [11:30 - 12:30]

- Session A-1 (Systems Biology I) [Session Chair: Yangjin Kim]
- 11:30 - 12:00 **Thomas, Peter J.** [AS23] (Case Western Reserve University)
Effects of Fluctuations in a 2D Model of Gradient Sensing
- 12:00 - 12:30 **Rong, Libin** [AS18] (Oakland University)
Rapid emergence of hepatitis C virus protease inhibitor resistance

- Session A-2 (Spatial Pattern) [Session Chair: Magda Stolarska]
- 11:30 - 12:00 **Chou, Ching-Shan** [AS4] (Ohio State University)
Spatial Dynamics of Stem Cells and Multi-Stage Cell Lineages in Tissue Stratification
- 12:00 - 12:30 **Umulis, David** [AS25] (Purdue University)
Systems biology of tissue patterning: insights from Drosophila embryos, Zebrafish embryos, and the Drosophila germarium

- Session A-3 (Modeling I) [Chair: Ed Moylan]
- 11:30 - 12:00 **Srinivasan, Parthasarathy** [AS21] (Cleveland State University)
Estimating Biophysical Properties of Nitric Oxide
- 12:00 - 12:30 **Kang, Yeona** [AS9] (SUNY at Stony Brook)
A structural basis for the Hodgkin and Huxley relation

Special session B [1:30 - 3:30]

- Session B-1 (Mechanics) [Chair: Partha Srinivasan]
- 1:30 - 2:00 **Lim, Sookkyung** [AS14] (University of Cincinnati)
Electrostatic effects on the supercoiling DNA
- 2:00 - 2:30 **Stolarska, Magdalena** (Mathematics, University of St. Thomas)
A model of cellular movement and its effect on substrate traction patterns
- 2:30 - 3:00 **Liu, Di (Richard)** [AS15] (Michigan State University)
Numerical methods for stochastic bio-chemical reacting networks with multiple time scales
- 3:00 - 3:30 **Kim, Eunjung** [AS12] (University of Notre Dame)
Contributions of branching points to fibrin network strength and stability

Session B-2 (Wound healing) [Chair: Chuan Xue]

1:30 - 2:00 **Xue, Chuan** [AS27] (Mathematical Biosciences Institute)

Modeling Ischemic Cutaneous Wounds

2:00 - 2:30 **Lee, Pihwa** (Cell Biology, University of Connecticut Health Center)

Toward wound healing of MDCK tissue : model and experiments

2:30 - 3:00 **Arciero, Julia** [AS2] (University of Pittsburgh)

Simulating wound healing with a two dimensional continuum mechanical model

3:00 - 3:30 **Kao, Chiu-Yen** [AS10] (Ohio State University)

Modeling oxygen transport in surgical tissue transfer

Session B-3 (Cancer I) [Chair: Richard Yamada]

1:30 - 2:00 **Khain, Evgeniy** [AS11] (Oakland University)

Clustering of brain tumor cells: theory and experiment

2:00 - 2:30 **Jain, Harsh** [AS8] (Mathematical Biosciences Institute)

A Biochemical Perspective to an Agent-based Model of VEGF-induced Capillary Formation

2:30 - 3:00 **Mikhaylov, Jessica** [AS17] (United States Military Academy)

Evaluating an improved two-compartment model to determine tumor angiogenesis

parameters using contrast-enhanced dynamic imaging data

3:00 - 3:30 **Zheng, Xiaoming** [AS29] (Central Michigan University)

A continuous model of angiogenesis: initiation, extension and maturation

Session B-4 (Industry Session) [Chair: Joan Remski]

1:30 - 2:00 **Eden, Gideon** [AS5] (CEO, Biolumix)

Practical Aspects of Bacterial Growth Model

2:00 - 2:30 **Heng, Henry** [AS7] (Wayne State University School of Medicine)

Can mathematics solve the mystery of biology?

2:30 - 3:00 **Sheng, Jim** [AS19] (U.S. Army Tank Automotive Research and Development)

Occupant Injury Risk Assessment Under Vertical Loading

3:00 - 3:30 **Bobeldyk, Denton** [AS3] (Davenport University and DJB Consulting L.L.C.)

Biometrics - Applications and Challenges

Special session C [3:45 - 4:45]

Session C-1 (Systems Biology II) [Chair: David Umulis]

3:45 - 4:15 **Gurarie, David** [AS6] (Case Western Res University)

Immune regulation of malaria infection: model calibration and Agent-Based

Communities

4:15 - 4:45 **Spagnuolo, Anna** [AS20] (Oakland University)

A Mathematical Model for Vibrio Cholera Colonization in the Human Intestine

Session C-2 (Cancer II) [Chair: Frank Massey]

3:45 - 4:15 **Ahmed, S. Ejaz** [AS1] (University of Windsor)

Improved Estimation Strategies for Tumor Growth Rate

4:15 - 4:45 **Tian, Jianjun Paul** (Mathematics, College of William and Mary)

A challenging problem in the competition between two stem cells

Session C-3 (Modeling II) [Chair: Sookkyung Lim]

3:45 - 4:15 **Wei, Guowei** [AS26] (Michigan State University)

Differential geometry based multiscale models for biomolecular systems

4:15 - 4:45 **Yamada, Richard** [AS28] (University of Michigan-Ann Arbor)

Molecular Noise Enhances Oscillations in the Supra-Chiasmatic Nuclei Network

Session C-4 (Modeling III) [Chair: Yangjin Kim]

3:45 - 4:15 **Matzavinos, Anastasios** [AS16] (Iowa State University)

Spectral clustering methods in data processing and image analysis

Poster Session [4:45 - 5:05]

Baek, Seunghyeon [AP1] (Korea University, South Korea)

Stationary pattern and stability in a tumor-immune interaction model with immunotherapy

Byun, Jonghyuk [AP2] (University of Cincinnati)

Fluid motion in an urban pipe with various surfaces

Chen, Duan [AP3] (Michigan State University)

Multiscale Modeling and Simulation for Proton Translocation in the Ion Channel

Du, Huijing [AP4] (Mathematics, University of Notre Dame)

Multiscale Models of Bacterial Swarming

Holmes, William [AP5] (Indiana University)

A 3D computational model of the Mammalian Cochlea with Asymptotics

Hengenius, James [AP6] (Purdue University)

*Effects of a realistic 3D domain on models of *Drosophila melanogaster* gap gene regulation*

Im, Jeong Sook [AP7] (Ohio State University)

Boundary integral method for shallow water and evaluation of the KdV equation in random wave field

Jordan, Benjamin [AP8] (Harvard University)

Coupling tissue growth and reaction kinetics to model chick limb development

Karim, Mohammad Shahriar [AP9] (Purdue University)

Secreted, receptor-associated BMP regulators reduce stochastic noise intrinsic to many extracellular morphogen distributions

Kim, Jae Kyoung [AP10] (University of Michigan-Ann Arbor)

Modeling the Interaction between Circadian and Metabolic Regulation

Lee, Sang-hun [AP11] (Purdue University)

*Dynamic simulation of Bone Morphogenetic Protein patterning in a 3D finite-element model of the *Danio rerio* embryo*

Lioi, Josh [AP12] (University of Notre Dame)

Study of the role of Factor VII in Venous Thrombus Formation Using a Combination of a Multi-scale Model and Experiment

Liu, Sijia [AP13] (Iowa State University)

Novel clustering methods for the analysis of biological data

Liu, Yuan [AP14] (University of Notre Dame)

A preliminary study of two models on angiogenesis

Luterek, Adam [AP15] (Oakland University)

Studying the Movement of Nerve Axons Under the Influence of Strong Magnetic Fields

Pargett, Michael [AP16] (Purdue University)

*Brat-mediated bi-stability and cell-competition autoregulate stem cell number in the *Drosophila ger-marium**

Srivastava, Prashant [AP17] (IIT Kanpur, INDIA)

Dynamical Model of HIV and CD4+ T cell with drug therapy

Stevens, Joshua B. [AP18] (Wayne State University School of Medicine)

Dynamics of Somatic Cell Evolution During Cancer Progression

Wang, Xiaoxia [AP19] (Case Western Reserve University)

A New Approach to Modeling Schistosomiasis Transmission Based on Stratified Worm Burden

Xu, Dan [AP20] (Oakland University)

The Magnetic Field Produced by the Heart and Its influence on MRI

Abstracts

(Alphabetical order)

1 Plenary Speakers

[APS1] **Alber, Mark S.** (Center for the Study of Biocomplexity, U of Notre Dame)

-Title: *Multiscale Modeling in Biology*

-Abstract:

A multiscale model of blood clot formation will be described which combines a detailed tissue factor pathway submodel of blood coagulation, a blood flow submodel and a stochastic discrete cell submodel [1,2]. It will be shown that low levels of FVII in blood result in a significant delay in thrombin production demonstrating that FVII plays an active role in promoting clot development at an early stage. We will also describe a new subcellular element method for simulating cellular blood components. In addition, multiscale models of chemotactic cell motion [3] and bacterial swarming will be discussed [4].

[1]. Xu, Z., J. Lioi, J. Mu, X. Liu, M.M. Kamocka, E.D. Rosen, D.Z. Chen and M.S. Alber, A Multiscale Model of Venous Thrombus Formation with Surface-Mediated Control of Blood Coagulation Cascade, *Biophysical Journal* (to appear).

[2]. Xu, Z., Chen, N., , Kamocka, M.M., Rosen, E.D., and M.S. Alber [2008], Multiscale Model of Thrombus Development, *Journal of the Royal Society Interface* 5 705-722.

[3]. Lushnikov, P.P., Chen, N., and M.S. Alber [2008], Macroscopic dynamics of biological cells interacting via chemotaxis and direct contact, *Phys. Rev. E.* 78, 061904

[4]. Wu, Y., Jiang, Y., Kaiser, D., and M. Alber [2009], Periodic reversal of direction allows Myxobacteria to swarm, *Proc. Natl. Acad. Sci. USA* 106 4 1222-1227 (featured in the Nature News, January 20th, 2009, doi:10.1038/news.2009.43).

[APS2] **Friedman, Avner** (Mathematical Biosciences Institute, Ohio State University)

-Title: *What is mathematical biology and how useful is it?*

-Abstract:

I shall define what is meant by 'mathematical biology', and then proceed to illustrate the degree of its usefulness by examples taken from projects developed at the Mathematical Biosciences Institute: chronic wound healing; modeling of the immune rheostat of macrophages in the lung in response to infection; neointimal hyperplasia occurring in dialysis, tuberculosis as a disease with prognosis which depends on the age of the patient, and viral treatment of glioblastoma. All these examples are modeled by systems of differential equations, and the challenges are: 1) Researching the biological literature in order to set up a mathematical model; 2) Determining the rate parameters; 3) Simulating the model. The final test is to show good fit with experimental results, after which the model can be used to suggest new biologically testable hypotheses.

[APS3] **Sander, Leonard M.** (Physics, University of Michigan-Ann Arbor)

-Title: *Biomechanics of cell motility in Dictyostelium*

-Abstract:

The mechanics of cell motility has a number of surprising features that need to be included in models of the process. Recent experiments on the motion of the ameba *Dictyostelium discoideum* in chemotaxis show that contractile forces on the substrate are two orders of magnitude larger than the force necessary to propel the cell forward against fluid friction. Most of the work done by the

cell goes towards peeling it from the substrate (breaking the adhesive bonds); viscoelastic effects and friction are completely negligible. We give a new mechanical model based on this idea, and show how it agrees with experimental results on the cell speed of wild-type and mutated dicty.

2 Special Sessions

[AS1] **Ahmed, S. Ejaz** (Mathematics & Statistics, University of Windsor)

-Title: *Improved Estimation Strategies for Tumor Growth Rate*

-Abstract:

From tumor to tumor, there is a great variation in the proportion of cancer cells growing and making daughter cells that ultimately metastasize. The differential growth within a single tumor, however, has not been studied extensively and this may be helpful in predicting the aggressiveness of a particular cancer type. The estimation problem of tumor growth rates from several populations is studied. The baseline growth rate estimator is based on a family of interacting particle system models which generalize the linear birth process as models of tumor growth. These interacting models incorporate the spatial structure of the tumor in such a way that growth slows down in a crowded system. Approximation-assisted estimation strategy is proposed when initial values of rates are known from the previous study. Some alternative estimation strategies are suggested and the relative dominance picture to the benchmark estimator is investigated. The analytical and numerical results demonstrate that our suggested estimator outperforms the classical estimator.

[AS2] **Arciero, Julia C** (Mathematics, University of Pittsburgh)

-Title: *Simulating wound healing with a two dimensional continuum mechanical model*

-Abstract:

Collective cell migration is an important mode of cell movement during wound healing. We have developed a two-dimensional continuum mechanical model that is used to simulate cell sheet migration and that captures the mechanical coupling between cells in the layer, the adhesion of cells to the substrate, the forces generated by lamellipodia at the cell edge and within the layer, and the proliferation and apoptosis of cells in the layer. The governing equations are solved numerically using a level set method. The model is calibrated by comparing the predicted density of the layer with experimentally observed cell density. Model results show good agreement with experimental observations of the dependence of the rate of wound closure on time.

[AS3] **Bobeldyk, Denton** (Davenport University and DJB Consulting L.L.C.)

-Title: *Biometrics - Applications and Challenges*

-Abstract:

Biometrics is the science of teaching machines (computers) to identify unique biological characteristics or traits in humans; these identifications are then used to authenticate people or pick out known terrorists in a crowd. Uniquely identifying people based on biological traits can be quite a challenge. Some modalities provide high accuracy such as iris or fingerprint, while other modalities provide the ability to identify from large distances such as gait (the way you walk). A brief overview of the algorithms currently being used for each of the modalities will be discussed as well as areas that require further mathematical research.

[AS4] **Chou, Ching-Shan** (Mathematics, Ohio State University)

-Title: *Spatial Dynamics of Stem Cells and Multi-Stage Cell Lineages in Tissue Stratification*

-Abstract:

In developing and self-renewing tissues, differentiated cell types are typically specified through the actions of multistage cell lineages. Such lineages commonly include a stem cell and multiple progenitor (transit amplifying; TA) cell stages, which ultimately give rise to terminally differentiated (TD) cells. Typically, as the tissue reaches a tightly controlled steady-state size, the cells at different lineage stages also assume distinct spatial locations within the tissue. Although significant genetic information are revealed on locations of different type of cells, the underlining mechanisms that cause the spatial heterogeneity are not yet completely understood. In this talk, I will present modeling and simulations to explore several plausible strategies that can be utilized to create stratification during development or regeneration of olfactory epithelium (OE) in mouse.

[AS5] **Eden, Gideon** (CEO, Biolumix Inc)

-Title: *Practical Aspects of Bacterial Growth Model*

-Abstract:

An automated optical instrument has been developed to rapidly detect the presence of bacteria in a sample. The instrument is based upon the analysis of bacterial growth patterns manifested by their metabolic processes in a mixture of growth media and optical indicators. A mathematical model is presented to predict the nature of the patterns detected by the instrument, and to derive intrinsic properties of bacterial growth. Correlation to the traditional "plate counts" performed in Petri dish is demonstrated.

[AS6] **Gurarie, David** (Mathematics, Case Western Res University)

-Title: *Immune regulation of malaria infection: model calibration and Agent-Based Communities*

-Abstract:

The talk will outline basic biology of malaria infection within host, and develop mathematical models that account for parasite growth and its immune regulation. We shall discuss how such models can be calibrated using malaria-therapy data, and present some recent results. Our calibrated in-host model can serve as a building block for Agent-based Communities (ABC). We shall demonstrate a few examples of such ABC, and look at the effect of transmission intensity on the resulting patterns of parasitemia. Our long-term goal is to apply 'agent-based' methodology to study parasite transmission and control in realistic environment, as an alternative to the standard population-based SIR approach (Ross-Macdonald).

[AS7] **Heng, Henry** (I) (Center for Molecular Medicine and Genetics, and Karmanos Cancer Institute, Wayne State University School of Medicine)

-Title: *Can mathematics solve the mystery of biology?*

-Abstract:

The interface between mathematics and biology presents both a challenge and an opportunity for biologists and mathematicians. Underscored by the explosion of biological data and the increasing usage of computational modeling, 21st-Century biology requires new mathematic tools to solve biological mysteries. In this presentation, I will briefly review some of the key features that are unique to biological systems, and some corresponding limitations of current mathematic tools. By asking a fundamental question, is mathematical theory required for the maturation of biological science, this presentation strives to call attention to this important issue and hopes to develop collaboration with mathematicians.

[AS8] **Jain, Harsh** (Mathematical Biosciences Institute, Ohio State University)

-Title: *A Biochemical Perspective to an Agent-based Model of VEGF-induced Capillary Formation*

-Abstract:

I present a hybrid model of VEGF-induced capillary network formation, based on the theory of reinforced random walks. A major component of such a model is endothelial cell (EC) chemotaxis. I therefore begin with simulating the motion of a single EC under the influence of a gradient of VEGF. In this model, the cell responds by polarizing itself in response to VEGF bound to cell-surface receptors. This is in contrast to the classical modeling approach that approximates motion as a function of free VEGF concentrations. A novel chemotactic sensitivity function is proposed for cellular motion, incorporating biological details hitherto ignored by the phenomenological sensitivity functions in current literature. Biologically observed phenomena such as the ability of endothelial cells to sense a chemical gradient as low as 1-2% across their lengths, and their resulting polarization and movement is captured by this model. Later, the model for the motion of a single cell is modified to simulate capillary network formation under the influence of VEGF. Empirically observed proliferative regions behind developing sprout tips match those in our simulations, thereby validating this model. To our knowledge, this is the first instance of the inclusion of this level of molecular detail in a spatial model of VEGF-induced angiogenesis. It provides a basic framework for the addition of further cellular and sub-cellular events in such models, in order to elucidate the mechanisms of chemokine mediated vasculogenesis.

[AS9] **Kang, Yeona** (Applied Mathematics, SUNY at Stony Brook)

-Authors: Yeona Kang* and C. M. Fortmann

-Title: *A structural basis for the Hodgkin and Huxley relation*

-Abstract:

Neural channel transport was analyzed using a previously reported relation for charged particle transport in two energy-type gradients: the electric field and here a water/structural deformation energy. Neural channels are lined with α -helix structures filled with water vapor and sequestered hydrophobic amino acids arranged to present minimum water vapor and water-hydrophobic interface. Cation point charges generate enormous electric fields on sub-nanometer distances. Electrostatic energy reduction is characterized by dielectric water being pulled toward the transporting ion deforming the neural channel. An ion-water-structure coupling energy is induced by changes in channel diameter width. The resultant two energy gradient relation for cation transport: reduces to the Hodgkin-Huxley relation [A. L. Hodgkin and A. F. Huxley, J. Physiol. (London) 116, 449 (1952)], explains channel selectivity and environmental sensitivity, predicts fast non-dispersive transport under a narrow range of conditions, and produces current-voltage characteristics consistent with observation.

[AS10] **Kao, Chiu-Yen** (Mathematics, Ohio State University)

-Authors: Anastasios Matzavinos, Chiu-Yen Kao, J. Edward F. Green, Alok Sutradhar, Michael Miller and Avner Friedman

-Title: *Modeling oxygen transport in surgical tissue transfer*

-Abstract:

Reconstructive microsurgery is a clinical technique used to transfer large amounts of a patient's tissue from one location used to another in order to restore physical deformities caused by trauma, tumors, or congenital abnormalities. The trend in this field is to transfer tissue using increasingly smaller blood vessels, which decreases problems associated with tissue harvest but increases the possibility that blood supply to the transferred tissue may not be adequate for healing. It would thus be helpful to surgeons to understand the relationship between the tissue volume and blood vessel diameter to ensure success in these operations. As a first step towards addressing this question, we present a simple mathematical model that might be used to predict successful tissue transfer

based on blood vessel diameter, tissue volume, and oxygen delivery.

[AS11] Khain, Evgeniy (Physics, Oakland University)

-Authors: E. Khain, C. M. Schneider-Mizell, M. O. Nowicki, E. A. Chiocca, S. E. Lawler and L. M. Sander

-Title: *Clustering of brain tumor cells: theory and experiment*

-Abstract:

We investigate clustering of malignant glioma cells [1]. In vitro experiments in collagen gels identified a cell line that formed clusters in a region of low cell density, whereas a very similar cell line (which lacks an important mutation) did not cluster significantly. We hypothesize that the mutation affects the strength of cell-cell adhesion. We investigate this effect in a new experiment, which follows the clustering dynamics of glioma cells on a surface. We interpret our results in terms of a stochastic model and identify two mechanisms of clustering. First, there is a critical value of the strength of adhesion; above the threshold, large clusters grow from a homogeneous suspension of cells; below it, the system remains homogeneous, similarly to the ordinary phase separation. Second, when cells form a cluster, we have evidence that they increase their proliferation rate. We have successfully reproduced the experimental findings and found that both mechanisms are crucial for cluster formation and growth.

Ref. E. Khain, C. M. Schneider-Mizell, M. O. Nowicki, E. A. Chiocca, S. E. Lawler and L. M. Sander, EPL (Europhysics Letters) 88, 28006 (2009).

[AS12] Kim, Eunjung (Mathematics, University of Notre Dame)

-Authors: Eunjung Kim, Zhiliang Xu, and Mark Alber

-Title: *Contributions of branching points to fibrin network strength and stability*

-Abstract:

Blood clots are primarily composed of a network of branched fibrin fibers. These fibrin networks stabilize the primary platelets and enable blood clots to withstand the blood flow during wound healing at sites of vascular injury. The structure of the network is believed to be an essential component to its function. In the present study, a three-dimensional mechanical model of a fibrin network was developed to determine the detailed relationship between the network structure and its mechanical properties. We compare the mechanical responses of the network for two distinct structures; high branching vs. low branching based on image analysis of in situ fibrin network data.

[AS13] Lee, Pilwha (Wolgemuth lab, Department of Cell Biology, University of Connecticut Health Center, Courant Institute, New York University)

-Title: *Toward wound healing of MDCK tissue : model and experiments*

-Abstract:

The migration of crawling cells is considered in their behavior of wound closure. The talk is focused on the mechanical contribution of crawling cells, i.e. dipole stress, and the stress dynamics derived from Lacker-Peskin model. In our model, actomyosin driven purse-strings or biochemical signaling of Rho family do not involve directly. In simplified one-dimensional formulations, velocity profiles for healing are explored in terms of turn-over rate and cell-to-cell viscosity mediated by Cadherin proteins. For the circular wound assay, we show a transition from closure to non-closure behavior with the dead cell zone in the epithelial layers, which supports the hypothesis that a crawling cell's dipole can close wounds without purse strings or signaling. In a rigorous two-dimensional model, we observe the healing speed is dependent on the assay width. There are long-range correlations in the scale of 100 micron from streaming and circulating cells. All of them are consistent with experimental data from MDCK assay. Interestingly, a bundle of tissue parameters applied

in the one-dimensional approximation is a good precursor for the parameter exploration on two-dimensional simulation.

[AS14] **Lim, Sookkyung** (Mathematics, University of Cincinnati)

-Title: *Electrostatic effects on the supercoiling DNA*

-Abstract:

We investigate the effects of electrostatic and steric repulsion on the dynamics of pre-twisted circular DNA in a viscous incompressible fluid. The DNA is modeled as a charged elastic rod represented by a three-dimensional closed axial curve and orthonormal triads embedded in each cross-section. Equations of motion of the rod, which include the fluid-structure interaction, are solved by the generalized immersed boundary method combined with the Cosserat theory of an elastic rod. We include a modified Debye-Hückel repulsive force in which the electrostatic force depends on the salt concentration and the distance between base pairs, and a close range steric repulsion force to prevent self-penetration. We find that after perturbation a pretwisted DNA circle collapses into a compact supercoiled configuration. The collapse proceeds along a complex trajectory that may pass near several equilibrium configurations of saddle type, before it settles in a locally stable equilibrium. The final configuration is sensitive to the initial excess link, ionic strength of the solvent, and the initial perturbation.

[AS15] **Liu, Di (Richard)** (Department of Mathematics, Michigan State University)

-Title: *Numerical methods for stochastic bio-chemical reacting networks with multiple time scales*

-Abstract:

Multiscale and stochastic approaches play a crucial role in faithfully capturing the dynamical features and making insightful predictions of cellular reacting systems involving gene expression. Despite their accuracy, the standard stochastic simulation algorithms are necessarily inefficient for most of the realistic problems with a multiscale nature characterized by multiple time scales induced by widely disparate reaction rates. In this talk, I will discuss some recent progress on using asymptotic techniques for probability theory to simplify the complex networks and help to design efficient numerical schemes.

[AS16] **Matzavinos, Anastasios** (Mathematics, Iowa State University)

-Title: *Spectral clustering methods in data processing and image analysis*

-Abstract:

The need to interpret and extract possible inferences from high-dimensional datasets has led over the past decades to the development of dimensionality reduction and data clustering techniques. Scientific and technological applications of clustering methodologies include among others computer imaging, data mining and bioinformatics. Current research in data clustering focuses on identifying and exploiting information on dataset geometry and on developing robust algorithms for noisy datasets. Recent approaches based on spectral graph theory have been devised to efficiently handle dataset geometries exhibiting a manifold structure, and fuzzy clustering methods have been developed that assign cluster membership probabilities to data that cannot be readily assigned to a specific cluster. In this talk, we develop a novel fuzzy spectral clustering algorithm that combines seamlessly the strengths of spectral approaches to clustering with various desirable properties of fuzzy methods. The developed methodology is applied to biomedical image segmentation and registration problems.

(Work in collaboration with Sunder Sethuraman of Iowa State University and Philip K. Maini, Radek Erban, and Ornella Cominetti of the University of Oxford.)

[AS17] **Mikhaylov, Jessica** (Mathematics Sciences, United States Military Academy)

-Title: *Evaluating an improved two-compartment model to determine tumor angiogenesis parameters using contrast-enhanced dynamic imaging data*

-Abstract:

The most common methods for determining the efficacy of cancer treatments against tumors involves a pair of pre/post-treatment contrast-enhanced medical image sequences, such as MRI or CT. Currently, this data is often analyzed using static images to do a visual size comparison. Unfortunately, the time between image sequences must be large, on the order of months, to see a meaningful potential change in tumor size. With the goal of reducing the time between tests to a time scale of weeks, radiologists and mathematicians have explored methods of using the dynamic data available from the tests to see if blood flow parameters (perfusion, permeability, volume compartment sizes for the plasma and the interstitial space) can be estimated and if these measurements can in turn provide insight about the efficacy of the treatment. In previous work, it was shown that a fundamental assumption regarding capillary re-uptake was flawed, and current work attempts to recover the parameters without this assumption. Using model data sets and sampled model data sets, two of the parameters can be recovered, however, in the presence of noise, these methods show weakness. This talk will give an overview of the background research and will show the current results using model data sets subjected to Gaussian noise (with and without smoothing) and a fixed bias.

[AS18] **Rong, Libin** (Dept of Mathematics, Oakland University)

-Title: *Rapid emergence of hepatitis C virus protease inhibitor resistance*

-Abstract:

Telaprevir, a novel hepatitis C virus (HCV) protease inhibitor, has demonstrated substantial antiviral activity in patients with chronic HCV infection. However, drug-resistant variants emerge at frequencies of 5-20% as early as day 2 after treatment initiation. Using probabilistic and viral dynamic models, we show that such rapid emergence of drug resistance is expected. We calculate that all possible single and double mutants preexist, and that one additional mutation is expected to arise during therapy. Examining the case of telaprevir therapy in detail, we show the model fits observed dynamics of both drug-sensitive and resistant viruses, and argue that combination therapy of direct antivirals will require drug combinations that have a genetic barrier of 4 or more mutations.

[AS19] **Sheng, Jim** (I) (U.S. Army Tank Automotive Research and Development)

- Title: *Occupant Injury Risk Assessment Under Vertical Loading*

- Abstract:

During the past five decades, tremendous efforts have been made in understanding human injury during automotive crashes, and in developing test devices for occupant protection studies. In most cases of an automotive crash, occupants experience lateral loadings. The occupant protection in vertical loading conditions originated from the work in the early years of ejection seat designs, where DRI is the main injury risk assessment index. During the last few years, blast threats such as landmines and improvised explosive devices (IED) posed a significant injury and fatality risk to occupants in military ground vehicles. The occupant injuries associated with severe vertical loading have drawn more and more attention of researchers, and engineers. While DRI is still a useful tool to assess occupant spinal injury associated with vertical loading, Effective G and the associated pulse duration is found to be a better index to be correlated to occupant injuries. This presentation will discuss DRI, Effective G and pulse duration and their correlation to occupant injury during vertical loadings.

[AS20] Spagnuolo, Anna (Mathematics, Oakland University)

-Title: *A Mathematical Model for Vibrio Cholera Colonization in the Human Intestine*

-Abstract:

Vibrio cholera is a strict human pathogen that causes pandemic cholera. It is an old-world pathogen that has re-emerged as a new threat since the early 1990s. *V. cholera* colonizes the upper, small intestine where it produces a toxin that leads to the watery diarrhea, characterizing the disease. Colonization dynamics of the bacteria are largely unknown. Although a large initial infectious dose is required for infection, data suggests that only a smaller sub-population colonizes a portion of the small bowel leading to the disease. There are many barriers to colonization in the intestines. In this talk, I will elaborate on the dynamics of *V. cholera* infection by describing a mathematical model that governs the colonization process for the bacterial dynamics.

[AS21] Srinivasan, Parthasarathy (Mathematics, Cleveland State University)

-Title: *Estimating Biophysical Properties of Nitric Oxide*

-Abstract:

Nitric oxide (NO) derived from the endothelium is a potent vasodilator, and plays a crucial role in maintaining vascular tone. Being a small diatomic molecule, it has so far been assumed that the diffusion rate of NO is the same as in solution. However, this hypothesis has not been tested experimentally. Recent methods have enabled us to measure the flux of NO across the aortic wall directly. We present a simple mathematical model from which we can obtain the diffusion and partition coefficients of NO across the aortic wall using these measurements. Our results show that the diffusion coefficient of NO in tissues is four times slower than in solution under normal physiological conditions, which indicates that the diffusion of NO (and hence its bioavailability) in the vascular wall is crucially dependent on the environment where the molecule diffuses. We also examine the role that oxygen plays in the bioavailability of NO in the vasculature. Our results suggest that the oxygen-dependent NO consumption could play an important role in dilating blood vessels during hypoxia by increasing the effective NO diffusion distance.

[AS22] Stolarska, Magda (Mathematics, University of St. Thomas)

- Authors: Magdalena A. Stolarska

- Title: *A model of cellular movement and its effect on substrate traction patterns*

- Abstract:

Mechanical interactions between a cell and the substrate are vital for cell migration and are involved in various cellular processes, such as wound healing, embryonic development, and metastasis of cancerous tumors. As a result, understanding the nature of force generation by single cells and the mechanical interaction of a cell with the substrate is extremely important, and mathematical models are being used in furthering this understanding. In this talk, we present a continuum model of the mechanics of single cell motility in which the stresses that result from the active deformation of the cell are transmitted to a deformable substrate via adhesion sites that are modeled as either fixed connections or frictional interaction between the cell and the substrate. A finite element implementation of this model is used to numerically examine the nature of the stresses generated by the cell and the resulting traction patterns that occur at the substrate. We use the model to better understand what are the local active deformation profiles and the adhesion types necessary to replicate experimentally observed motion and traction patterns of different cell types.

[AS23] Thomas, Peter J. (Mathematics & Biology, Case Western Reserve University)

-Authors: Suparat Chuechote¹, Harihara Baskaran^{2,3}, Peter Thomas^{1,4,5} (Case Western Reserve University, Departments of ¹ Mathematics, ²Chemical Engineering, ⁴ Biomedical Engineering, ⁴

Biology, ⁵Cognitive Science)

-Title: *Effects of Fluctuations in a 2D Model of Gradient Sensing*

-Abstract:

Chemotaxis is the directed migration of cells guided by chemical gradients. This process plays a role in embryogenesis, immune response, wound healing and tumor metastasis. During chemotaxis, a cell detects extracellular chemoattractants and translates these signals into a complex cellular response resulting in morphological reorganization and motility. The accuracy with which a cell can determine an external chemical gradient is limited by fluctuations arising from the discrete nature of second messenger release and diffusion processes within the small volume of a living cell. These sources of intrinsic noise have the potential to attenuate or disperse gradient information transduced by the membrane bound receptors. At the same time, models of the intracellular signaling network have been devised that use a combination of local excitation and global inhibition to sharpen the intracellular gradient signal. In this study, we implement a stochastic version one such model, the "balanced inactivation" model (Levine et. al. 2006), in a two dimensional geometry. We develop a fixed timestep approach in which the probabilities of individual molecules making spatial or chemical transitions is treated as a system of multinomial random variables. With this numerical framework we investigate the relationship between the amplification of the gradient signal, the propagation of noise in the signaling pathway, and fundamental limits on the accuracy of the gradient sensing mechanism.

[AS24] **Tian, Jianjun Paul** (Mathematics, College of William and Mary)

-Title: *A challenging problem in the competition between two stem cells*

-Abstract:

In this talk, I will briefly introduce a difficult problem arising from two germline stem cell competition process. In the female germline stem cell niche, there are 2 or 3 stem cells. Recent biological experiments showed that there is a competition for the niche space occupancy among stem cells. Stem cells compete by means of physical interaction. This is a new mechanism of cell interactions, and it is different from the well-understood cell interaction via sending and receiving chemical signals. The stem cell physical interaction involves a series of biochemical and biophysical processes. It is difficult to understand without considering these processes in molecular level. We propose a model that is a reaction-diffusion system over cell surfaces with two free boundaries. I will report the model and some research on simplified version of the model.

[AS25] **Umulis, David** (Agricultural and Biological Engineering, Purdue University)

-Title: *Systems biology of tissue patterning: insights from Drosophila embryos, Zebrafish embryos, and the Drosophila germarium*

-Abstract:

The spatiotemporal regulation of cell differentiation relies on numerous extracellular cues, intracellular responses, and feedback interactions between the intra- and extracellular environment. However, the classic view of morphogen-mediated patterning considers decoupled gradient formation and cell-interpretation events. To investigate the dynamic signaling landscape of cells embedded in a tissue we focused on models of stem cell regulation and early embryo development. For each unique patterning context, we developed 3D finite element models based on available image data and employed a common approach to address the following question: How does feedback between intra- and extracellular environments impact morphogen activity and patterning? To address this question in the context of stem-cell regulation by Bone Morphogenetic Proteins (BMPs), we developed a 3D model of the Drosophila germarium. We found that positive feedback that enhances ligand endocytosis leads to cell competition for limited amounts of BMP ligands and support for

only 2-3 stem cells per niche, consistent with experimental observations. We extended the study to embryonic patterning by BMPs and found that positive feedback that leads to increased endocytosis capacity leads to a similar cell-competition event and autoregulation of the number of high BMP-signaling cells. In the context of developing Zebrafish embryos, positive feedback on an extracellular regulator called Sizzled autoregulates the morphogen distribution shape, ensuring robust patterning of multiple target genes. In summary, the autoregulation of morphogens by feedback provides a mechanism to ensure robust delineation of cell populations through competition and modification of gradient shape.

[AS26] **Wei, Guowei** (Mathematics, Michigan State University)

-Title: *Differential geometry based multiscale models for biomolecular systems*

-Abstract:

This talk focuses on a new multiscale paradigm developed at MSU — the differential geometry based multiscale models of biomolecules. Under the physiological condition, most biological processes, such as signal transduction, ion channel transport and protein folding, occur in water, which consists of 65-90 percent human cell weight. Therefore, solvent and synergy of solvent-solute are important to the understanding of biomolecular structure, function, dynamics and transport. I will discuss the use of differential geometry theory of surfaces for coupling microscopic and macroscopic scales at an equal footing. The biomolecule of interest is described by discrete atomic and quantum mechanical variables. While the aquatic environment is described by continuum hydrodynamical variables. We derive the coupled geometric flow equation, Navier-Stokes equation, and generalized Poisson-Boltzmann equation (PBE) to describe the dynamics of the biomolecular systems. Applications will be discussed to protein folding, ion channels, micro/nanofluidics, and nano-bio sensors.

Acknowledgment: This work was supported by NSF and NIH grants.

[AS27] **Xue, Chuan** (Mathematical Biosciences Institute, Ohio State University)

-Title: *Modeling Ischemic Cutaneous Wounds*

-Abstract:

Chronic wounds represent a major public health problem affecting 6.5 million people in the United States. Ischemia, primarily caused by peripheral artery diseases, represents a major complicating factor in cutaneous wound healing. In this talk, we present a mathematical model of ischemic dermal wounds. The model consists of a coupled system of partial differential equations in the partially healed region, with the wound boundary as a free boundary. The extracellular matrix (ECM) is assumed to be viscoelastic, and the free boundary moves with the velocity of the ECM at the boundary. The model equations involve the concentration of oxygen, PDGF and VEGF, the densities of macrophages, fibroblasts, capillary tips and sprouts, and the density and velocity of the ECM. Simulations of the model demonstrate how ischemic conditions may limit macrophage recruitment to the wound-site and impair wound closure. The results are in general agreement with experimental findings.

[AS28] **Yamada, Richard** (Mathematics, University of Michigan-Ann Arbor)

-Title: *Molecular Noise Enhances Oscillations in the Supra-Chiasmatic Nuclei Network*

-Abstract:

In this talk, we will discuss a detailed mathematical model for circadian timekeeping within the SCN. Our proposed model consists of a large population of SCN neurons, with each neuron containing a network of biochemical reactions involving the core circadian components. Using mathematical modeling, our results show that both intracellular molecular noise and intercellular coupling (nonlinear in nature) are required to sustain stochastic oscillations in the SCN oscillator network.

Our work focuses on the problem of overcoming noise in oscillator systems, and our results highlight the importance of transcriptional noise in enhancing oscillations rather than dampening them. Surprisingly, our predictions from our model have been confirmed experimentally; we conclude with a short discussion of these results.

[AS29] **Zheng, Xiaoming** (Mathematics, Central Michigan University)

-Authors: Trachette Jackson (Mathematics, University of Michigan), Gou Young Koh (National Research Laboratory of Vascular Biology, Korea Advanced Institute of Science and Technology)

-Title: *A continuous model of angiogenesis: initiation, extension and maturation*

-Abstract:

Angiogenesis, formation of new blood vessels, is essential to many physiological and pathological processes, such as wound healing and tumor growth. Angiogenesis is one of the fastest growing biomedical research disciplines in the past 20 years. However, there are very few mathematical models of angiogenesis compared with the explosion in experimental data. In this talk, we will present a brand new mathematical model of angiogenesis, which covers three critical events: endothelial cell activation (or the new blood vessel initiation), sprout extension, and maturation of new blood vessels. We investigate the regulating mechanisms of three families of growth factors: Vascular Endothelial Growth Factor (VEGF), Angiopoietins (including Ang1 and Ang2), and Platelet-Derived Growth Factor (PDGF-B). The biochemical and biophysical properties of two types of cells, endothelial cells that line the inner wall of blood vessels and pericytes that coat the outer surface of blood vessels, will be examined. These growth factors and cells form a complex multiscale system composed of molecular reactions, cellular responses and tissue growth. The numerical simulations of the mathematical model will be presented along with the main results of the study, which include: demonstrating how the balance of the angiopoietin system serves as angiogenic switch; highlighting that a proper mechanical model is necessary to address the blood vessel extension; showing that pericytes and angiopoietins are central to the maturation process.

3 Poster presentation

[AP1] **Baek, Seunghyeon** (Mathematics, Korea University, Korea)

-Authors: Inkyung Ahn, Wonlyul Ko and Seunghyeon Baek (Korea University, South Korea)

-Title: *Stationary pattern and stability in a tumor-immune interaction model with immunotherapy*

-Abstract:

A diffusive tumor-immune system with immunotherapy is investigated under homogeneous Neumann boundary conditions. The large time behavior of nonnegative equilibria and the persistence of the solution in the time-dependent system are studied. Especially, a sufficient condition for the tumor-free states is provided. Furthermore, for this coupled reaction-diffusion system, we obtain the results for the existence of nonconstant positive steady state solutions in case that the parameter for immunotherapy effect is small.

[AP2] **Byun, Jonghyuk** (Mathematics, University of Cincinnati)

-Authors: Donald A. French, Jonghyuk Byun, M.Kupferle, Nick G. Cogan and Sookkyung Lim

-Title: *Fluid motion in an urban pipe with various surfaces*

-Abstract:

We investigate the motion of the fluid dynamics in an urban pipe system in which the geometry of the pipe surfaces varies. The fluid motion is compared in two different types of surfaces, cylindrical

surface and curved surfaces. We expect the shear force near the surface to be influenced by the fluid motion and hence the wall shear stress may affect on the thickness of the biofilm along the pipe surface.

[AP3] **Chen, Duan** (Mathematics, Michigan State University)

-Title: *Multiscale Modeling and Simulation for Proton Translocation in the Ion Channel*

-Abstract:

Aiming at the special properties of the proton and unique transport mechanism, a general multiscale partial differential equations model, containing classical and quantum mechanical theories, is proposed to simulate the translocation of protons in the ion channel with reasonable biological assumptions and approximations. Several associated numerical schemes are employed to solve the model numerically with high accuracy and efficiency. At last, the validity of this model is tested through a specific proton channel, the well-known Gramicidin A, by the channel electrostatic profile and conductance. With parameters taken in the physiological ranges, the simulation results agree with the experimental data well. The limitation of this model will be addressed in future work.

[AP4] **Du, Huijing** (Mark Alber group, Mathematics, University of Notre Dame)

-Authors: Huijing Du, Mark Alber, and Zhiliang Xu

-Title: *Multiscale Models of Bacterial Swarming*

-Abstract:

We present an off lattice stochastic model which incorporates the different motility engines and the reversing capability to examine the swarming of *M. Xanthus*. The model also accounts for the interactions of individual cells with the slime on the surface left by other cells. Simulations involving the variation of cell density, aspect ratio, and reversing period were made and we present some of the results including the optimization of *M. Xanthus* reversing period at eight minutes which was observed experimentally.

[AP5] **Holmes, William** (Mathematics, Indiana University)

-Title: *A 3D computational model of the Mammalian Cochlea with Asymptotics*

-Abstract:

We seek to build a computational model for the simplified Mammalian Cochlea with the standard coupled fluid-plate equations as our base. Physiological data shows a clear wave nature in the response of the basilar membrane to stimulus. We seek to explain the presence of this wave nature and use it as inspiration for a 3D numerical solver. The results of simulations along with asymptotic arguments suggest a relationship between the form and function of the cochlea which we compare to physiological data.

[AP6] **Hengeniuss, James** (Agricultural and Biological Engineering, Purdue University)

-Authors: James Hengeniuss*, Ann E. Rundell, Michael Gribskov, and David M. Umulis

-Title: *Effects of a realistic 3D domain on models of *Drosophila melanogaster* gap gene regulation*

-Abstract:

The fruit fly *Drosophila melanogaster* is a model organism for studying spatio-temporal dynamics of animal development. In the gap gene regulatory network, an initial non-uniform distribution of the transcription factor Bicoid controls downstream expression of additional interacting transcription factors. This leads to the formation of non-uniform protein distributions along the anterior-posterior axis of the embryo. Previous studies have considered gap gene regulation as a reaction-diffusion system in one dimension, fitting models to protein expression data from a limited lateral region of the embryo. While these models agree with data in the sampled lateral region, the embryo has a

complex three-dimensional geometry. Because poor agreement over the full embryo geometry would indicate incomplete understanding of gap gene regulation, we evaluated existing model structures over this domain. Additionally, we optimized model parameters on the 3D domain. We first implemented a full 3D model using the finite element method with a mesh derived embryonic nuclei positions. Model output was fit to expression data from the Quantitative Spatiotemporal Gene Atlas (Fowlkes et al., 2008) by minimizing a sum-of-squared-error function. Model outputs from the best parameter sets were compared to results using previously published 1D model parameters. While previously published parameter values recapitulated data in the lateral region, the model deviated from data over most of the 3D domain. Our parameter optimization recovered parameter sets that fit the full 3D model better than previously published parameters. Our findings indicate that the current models of gap gene regulation are incomplete and must be revised to account for geometric effects and possible genetic interactions occurring outside the lateral region.

[AP7] **Im, Jeong-sook** (Mathematics, Ohio State University)

-Title: *Boundary integral method for shallow water and evaluation of the KdV equation in random wave field*

-Abstract:

Consider the two-dimensional incompressible, inviscid and irrotational fluid flow of finite depth bounded above by a free interface. Ignoring viscous and surface tension effects, the fluid motion is governed by the Euler equations and suitable interface boundary conditions. A boundary integral technique (BIT) which has an advantage of reducing the dimension by one is used to solve the Euler equations. For convenience, the bottom boundary and interface are assumed to be 2π -periodic. The complex potential is composed of two integrals, one along the free surface and the other along the rigid bottom. When evaluated at the surface, the integral along the surface becomes weakly singular and must be taken in the principal-value sense. The other integral along the boundary is not singular but has a rapidly varying integrand, especially when the depth is very shallow. This rapid variation requires high resolution in the numerical integration. By removing the nearby pole, this difficulty is removed. In situations with long wavelengths and small amplitudes, one of the approximations for the Euler equations is the KdV equation. I compare the numerical solution of Euler equation and the solution of KdV equation and calculate the error in the asymptotic approximation. For larger amplitudes, there is significant disagreement. Indeed, the waves tend to break and the boundary integral technique still works well. The comparison is also done in random wave field. The strong nonlinearity has made a huge difference in the power spectrum between Euler equation and KdV equation.

[AP8] **Jordan, Benjamin** (Organismic & Evol Biol, Harvard University)

-Title: *Coupling tissue growth and reaction kinetics to model chick limb development*

-Abstract:

The limb of the chicken (*G. gallus*) is a model organism in developmental biology used to study the patterning of tissues, cell specification, and cell fates. The developing limb bud tissue responds to protein-gradients in a concentration-specific manner. Amongst the myriad cellular responses to these signals, division, differentiation, death, and changes to the extracellular matrix are crucial to our understanding. These responses feed back into both the chemical interactions and the material properties of the growing limb bud. To understand the interplay between growth and patterning, we have developed a model that couples the production, diffusion, reaction and advection of the relevant chemical species to the growing tissue domain. By assuming that growth is a plastic-process which occurs beyond some given yielding threshold, we model the tissue as a viscous free-boundary fluid with a volumetric source, which is in turn dependent on the concentration of specific growth

factors included in the kinetics network. In this poster, I describe the mathematical model, discuss the parametrization, and explain the algorithm for the numerical solution. Specifically, details on the remeshing, convection, and split-time stepping are discussed. Preliminary results suggest that both the shape and protein distribution can be described accurately by such a model, and the next steps of this work are discussed.

[AP9] **Karim, Mohammad Shahriar** (Electrical and Computer Engineering, Purdue University)

-Authors: Mohammad Shahriar Karim*, Gregory T. Buzzard, and David M. Umulis

-Title: *Secreted, receptor-associated BMP regulators reduce stochastic noise intrinsic to many extracellular morphogen distributions*

-Abstract:

Morphogens specify cell-fate in a concentration dependent manner. Intriguingly, recent measurements of ligand-receptor binding suggest that many morphogens saturate receptors at concentrations less than 1nM or less than 20 molecules/cell. Low molecule number, combined with slow binding kinetics leads to a noisy interpretation of extracellular concentration that fluctuates on the time-scale of hours, however many morphogen patterning networks are remarkably robust. To investigate mechanisms of biological robustness and signal interpretation we developed a stochastic model of the local ligand-receptor dynamics and extended this work to consider spatial patterning and measure the errors in positional information expected for each local regulatory mechanism. We find that if a secreted non-receptor such as Crossveinless-2 (Cv-2) partially regulates ligand-receptor interactions, the amplitude of ligand-receptor fluctuations can be reduced by about 2-folds depending on specific parameter values and non-receptor concentration. Receptor-ligand regulation by secreted factors can also modify the binding dynamics to increase the frequency of fluctuations, which can be buffered out immediately downstream by the intracellular network if the time-scale for intracellular dynamics are slow relative to ligand-receptor fluctuations. This phenomenon of non-receptor imitates performance of a simple low pass filter for the system. Together, these data indicate that one of the benefits of receptor-ligand regulation by secreted non-receptors may be greater reliability of morphogen patterning mechanisms and we are developing experiments to test these conclusions.

[AP10] **Kim, Jae Kyoung** (Mathematics, University of Michigan-Ann Arbor)

-Title: *Modeling the Interaction between Circadian and Metabolic Regulation*

-Abstract:

Recent experimental evidence has discovered strong links between circadian timekeeping and metabolic regulation. Because of the complexity of the biochemical networks that underlie these systems, mathematical modeling has the potential to help clarify experimental results and predict new phenomena. Here we review mathematical models that can be used to understand the links between circadian and metabolic regulation. We present a preliminary model for the role of SIRT1 in circadian rhythms. This model predicts experimental findings that can be used to understand the link between circadian regulation and metabolism. Further modeling can account for other links beyond these systems; one current interest is how circadian rhythm affect cancer through metabolism.

[AP11] **Lee, Sang-hun** (Agricultural and Biological Engineering, Purdue University)

-Authors: Sang-hun Lee*, and David M. Umulis

-Title: *Dynamic simulation of Bone Morphogenetic Protein patterning in a 3D finite-element model of the Danio rerio embryo*

-Abstract:

Zebrafish development relies on the spatiotemporal distribution of molecules called morphogens that pattern anterior/posterior (AP) and dorsal/ventral (DV) axes in a concentration-dependent manner. Numerous secreted regulators control the spatiotemporal distributions of BMP signaling along the DV axis, however, the mechanisms of dynamic regulation of BMP signaling remain unclear. To determine the relative contributions of the Alk8 receptors, Chordin, Tolloid-like molecules, and Sizzled, we developed and tested a full 3D mathematical model of a developing zebrafish embryo. We developed an image registration algorithm to assign point-cloud experimental data to a reference set and determine both the stage of development and the orientation of the embryo. Following development of the image registration methodology, we converted the point-cloud reference into 3D finite element meshes for each 1.5 minute time-point during growth from early blastula through gastrula stages (200-500 minutes post fertilization (MPF)). We then developed a seamless modeling strategy to test alternative hypotheses regarding the mechanism of BMP-mediated patterning on the dynamically evolving mesh and found that Sizzled-mediated regulation of Tld leads to robust mechanism to regulate gradient shape of BMP activity. We also investigated mechanisms of dynamic morphogen scale-invariance in zebrafish embryos and present a summary of these findings.

[AP12] Lioi, Josh (Mark Alber group, Mathematics, University of Notre Dame)

-Authors: Joshua Lioi¹, Zhiliang Xu¹, Malgorzata M. Kamocka³, Danny Z. Chen², Elliot D. Rosen³, and Mark Alber¹ (¹ Department of Mathematics, University of Notre Dame, ² Computer Science University of Notre Dame, ³ Medical and Molecular Genetics, Indiana University School of Medicine)

- Title: *Study of the role of Factor VII in Venous Thrombus Formation Using a Combination of a Multiscale Model and Experiment*

- Abstract:

We extend a two-dimensional multiscale model of thrombus formation by including surface-mediated control of the coagulation pathway. The model was used to simulate thrombus formation in normal or limited levels Factor VII (FVII). Simulation predictions were compared with experimental results involving thrombogenesis following laser-induced injury of venules in wild type and FVII deficient mice. It is shown that low levels of FVII in blood results in a significant delay in thrombin production demonstrating that FVII plays an active role in promoting thrombus development at an early stage.

[AP13] Liu, Sijia (Mathematics, Iowa State University)

- Title : *Novel clustering methods for the analysis of biological data*

- Abstract:

The need to interpret and extract possible inferences from high-dimensional datasets has led over the past decades to the development of dimensionality reduction and data clustering techniques. In this poster, we present a novel family of clustering algorithms that combine seamlessly the strengths of existing spectral approaches to clustering with various desirable properties of fuzzy methods. We discuss examples of gene expression datasets for which the developed methodology outperforms other frequently used algorithms.

[AP14] Liu, Yuan (Mathematics, University of Notre Dame)

- Title : *A preliminary study of two models on angiogenesis*

- Abstract:

We are studying two PDE models regarding to angiogenesis. One model is proposed by G. Serini et.al in [1], in which the cell population is described by a continuous distribution of density and velocity. The other one is a PDE system derived from a two-dimensional stochastic cellular Potts

model (CPM) describing cell moving in a medium and reacting to each other through direct contact, cell-cell adhesion, and long-range chemotaxis [2]. In the first system, we successfully solved the hyperbolic system in third order finite difference weno scheme and third order finite volume weno scheme on triangular mesh., in both way, we could observe the formation of blood vessel networks similar to those observed in the experiments. We also quantitatively studied the relationship between the endothelial cell number, the range of activity of chemo-attractant and the vascular network formation and size. However, the numerical simulation will blow up as is expected. In the model derived from CPM, the networks are also observed. And the numerical solutions of the model with/without the excluded volume indicate that the excluded volume interactions are important in the chosen range of values of parameters. Contrary to classical Keller-Segel model, solutions of this one do not collapse in finite time. [1] G. Serini, D. Ambrosi, E. Giraudo, A. Gamba, L. Preziosi and F. Bussolino, Modeling the early stages of vascular network assembly, *The EMBO Journal*, Vol.22, No.8, (2003), pp1771-1779. [2] P. Lushnikov, N. Chen and M. Alber, Macroscopic dynamics of biological cells interacting via chemotaxis and direct contact, *Phys. Rev. E*. 78, 061904.

[AP15] **Luterek, Adam** (Brad Roth Group, Physics, Oakland University)

- Authors : Adam Luterek and Bradley J. Roth

- Title : *Studying the Movement of Nerve Axons Under the Influence of Strong Magnetic Fields*

- Abstract:

We extend a model introduced by Roth and Bassar (*Magn. Reson. Med.*, 61:59-64, 2009) to study the movement of a nerve during magnetic resonance imaging. When exposed to a magnetic field, neural action currents are subjected to a Lorentz force that moves the nerve. Roth and Bassar considered action currents that were uniform along the length of the nerve. In our study, we examine the full three-dimensional distribution of current. We calculate the nerve displacement for the case of the nerve perpendicular to the magnetic field. Additionally, if the magnetic field is parallel to the nerve, it may be possible for the axon to twist due to the Lorentz force.

[AP16] **Pargett, Michael** (Weldon School of Biomedical Engineering, Purdue University)

- Authors: Michael Pargett, Robin Harris, Hillary Ashe, and David Umulis

- Title: *Bmp-mediated bi-stability and cell-competition autoregulate stem cell number in the Drosophila germarium*

- Abstract:

Complex organisms must maintain stable populations of stem cells to remain healthy and support somatic tissues. In the germline stem cells (GSC) of the *Drosophila* ovary, Bone Morphogenetic Protein (BMP) signaling regulates the decision between stem cell self renewal or differentiation. Our collaborators have elucidated key players in the intracellular network that regulates cell-receptivity to extracellular BMPs, however the interaction between the intra- and extracellular regulation of BMP distributions and interpretations remains unknown. To determine the relative contribution of intra- and extracellular control of BMP regulation we developed a local model for a single cell receiving an extracellular cue and a 3D extracellular model of the germarium. The proposed intracellular feedback mechanism exhibits bistability in response to levels of BMP signaling, making cells refractory to additional signal. By combining intracellular and extracellular regulation in the 3D multi-cell model, we find that cell-mediated competition for limiting amounts of ligand leads to autoregulation of stem cell number in the niche. Competition, combined with the bistable intracellular system supports the maintenance of the constrained stem cell population, causing differentiation of extraneous GSCs and repopulating if GSCs are lost.

[AP17] **Srivastava, Prashant** (IIT Kanpur, INDIA)

-Title: *Dynamical Model of HIV and CD4+ T cell with drug therapy*

-Abstract:

Here we shall propose and analyse a dynamical model of HIV and CD 4+ T cells under the influence of drugs Reverse transcriptase inhibitor and protease inhibitor. The infection develops as HIV infects CD4+ T cells. Infected cells are divided into two sub classes: infected cells before completion of reverse transcription and infected cells after reverse transcription. It is assumed that a fraction of infected cells revert back to uninfected class. We performed stability and also solved model numerically to analyse the analytical results.

[AP18] **Stevens, Joshua B.** (School of Medicine, Wayne State University)

-Authors: Joshua B. Stevens, Guo Liu, Steven Bremer, Christine J Ye, and Henry H. Heng

-Title: *Dynamics of Somatic Cell Evolution During Cancer Progression*

-Abstract:

For decades cancer progression has been believed to be a linear process that was driven by stepwise accumulation of a small number of common gene mutations. Identification of these gene mutations and subsequent drug targeting of their functions promised to cure cancer. However, recent large scale cancer genome sequencing projects have failed to detect these expected common gene mutations. Similarly we have show that on the chromosomal level, there is no recurrent pattern of change which has lead to the development of the genome theory of cancer which states that cancer progression is a stochastic process driven by system replacement manifested by chromosomal change. During cancer progression population diversity increases during periods of stress such as prior to immortalization and during chemotherapy. This diversity increases the probability that a cell (or number of cells) will survive the stress, promoting further progression. Despite the recent success of the genome theory, many questions still exist. These questions include: What level (gene, epigenetic, or genome) has the most utility in predicting cancer progression, and how can measurements at all levels be integrated? Are there more or less favorable types of diversity? How do responses of populations of cells react to differing circumstances if one population is largely genomically homogenous and one is heterogeneous, but both populations share a similar level of some molecular marker? Answering these important questions will require a bio-mathematic approach to integrate these new cancer progression findings into clinically applicable models and treatment designs.

[AP19] **Wang, Xiaoxia** (Mathematics, Case Western Reserve University)

-Title: *A NEW APPROACH TO MODELING SCHISTOSOMIASIS TRANSMISSION BASED ON STRATIFIED WORM BURDEN*

-Abstract:

Multiple factors affect schistosomiasis transmission in distributed meta-population systems including age, behavior, and environment. Traditional modeling approach to macroparasite transmission often exploits “mean worm burden formulation” (MWB) for human hosts. Such approach oversimplifies the system, and can give wrong predictions for control interventions. Typical worm distribution in humans is overdispersed, and classic models either ignore it or make ad-hoc assumptions about its pattern (e.g. ‘negative binomial’). We propose a new modeling approach to macro-parasite transmission by stratifying human populations according to burden, and replacing MWB dynamics with that of ‘population strata’. The Stratified Worm Burden (SWB) approach offers many advantages; it accounts naturally for overdispersion, and accommodates other important factors and measures of human infection and demographics. We developed the calibration procedure for such extended (multi-component) systems, and run it for a specific data set collected in the Msabweni region of Eastern Kenya. The calibrated model was validated against additional

data, and applied to study control interventions (drug treatment). In particular, we simulated several control strategies proposed by WHO and examined their long term outcomes. We believe our model can provide useful information and tools for future WHO policies on eradication of schistosomiasis.

[AP20] **Xu, Dan** (Brad Roth Group, Physics, Oakland University)

- Authors : Dan Xu and Bradley J Roth

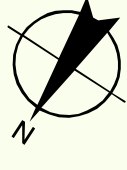
- Title: *The Magnetic Field Produced by the Heart and Its influence on MRI*

- Abstract:

Recently, much work has been done to detect neuronal activation by using the magnetic field produced by biocurrents. In general, these magnetic fields are too tiny to measure by magnetic resonance imaging. However, the heart is the source of the largest biocurrents in the body, so it may be easier to detect cardiac action currents using MRI compared to neural action currents. There are two sources that produce a magnetic field in cardiac tissue. One is the intracellular current in the tissue with the "return" current through an adjacent volume conductor; the other is the anisotropy of the tissue. In this study, we examine a simplified "spherical heart" model with a simple transmembrane potential distribution and calculate the resulting action currents and magnetic field, and estimate their impact on an MRI signal. This research was supported by the National Institutes of Health Grant R01EB008421.



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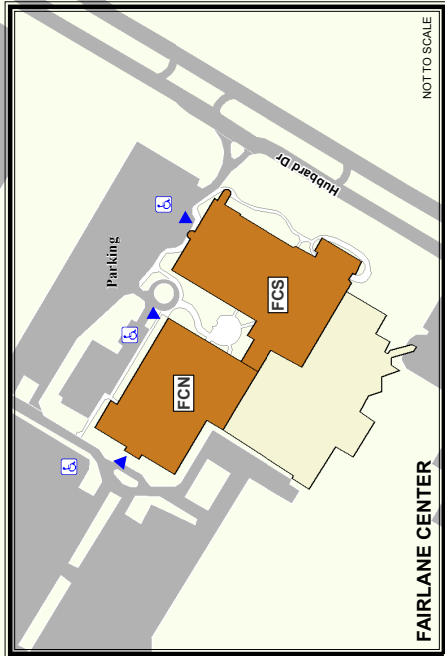


- Emergency Phones
- Handicap Parking
- Accessible Entry

UNIVERSITY OF MICHIGAN DEARBORN CAMPUS MAP

BUILDING	
AB	Administration Building
ASC	Academic Support Center
CSS	Campus Support Services
CB	College of Arts, Sciences, & Letters
CIS	Computer & Information Science
ELB	Engineering Lab Building
EIC	Environmental Interpretive Center
FCN	Fairlane Center-North
FCS	Fairlane Center-South
FLC	Fairlane Cottages
PLG	Fair Lane Greenhouse
FLPB	Fair Lane Pony Barn
FLPVC	Fair Lane Powerhouse / Visitor's Center
FHWC	Fieldhouse/Wellness Center
GRC	Gabriel Richard Center
GB	Grounds Building
HFE	Henry Ford Estate
HPEC	Heinz Prechter Engineering Complex
IAMS	Institute for Advanced Vehicle Systems
KM	Kindergarten Module
MSBL	Manufacturing Systems Engineering Lab
ML	Merdigian Library
MPS	Montleth Parking Structure
PEC	Professional Education Center
ROC	Recreational & Organization Center
SB	Science Building
SB/CW	Science Building / Computing Wing
SLRC	Social Learning & Research Center
SSB	Social Sciences Building
UC	University Center

Admissions / Visitor Parking



FAIRLANE CENTER

NOT TO SCALE

