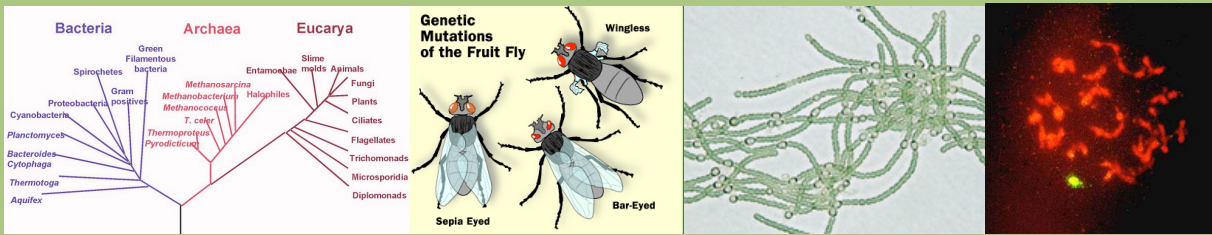# Symposium on Evolutionary Bioinformatics

Aura Soma Lava, Lava Hot Springs, Idaho, October 3-5, 2008

The 2008 Idaho State University Practical Bioinformatics Workshop

ISU's 4th Annual Workshop, "The Symposium on Evolutionary Bioinformatics," focuses on emerging applications and approaches for complex, data intensive evolutionary analyses. Join regional biologists to explore recent computational approaches for understanding the complex patterns and processes of evolution.

The **Research Symposium** will include talks by national & regional researchers using bioinformatics approaches to solve data-intensive problems. A **poster session** will provide an opportunity for researchers and grad students to highlight emerging research.

The **Training Workshops** will build expertise in commonly used bioinformatics methods for evolution.

Workshop I: Advance BLASTing for identifying distantly-related homologs
Workshop II: Models for phylogenetic analyses
Workshop III: Genome assembly & annotation

The **Breakout Sessions** will be organized but informal round-table discussions on integrating bioinformatics into the biology core curriculum.

Session I: Integrating bioinformatics into the core biology college curriculum
Session II: Creating bioinformatics research opportunities for undergraduate students
Session III: Tools at your fingertips: Choosing applications for successful undergrad educational experiences

The Symposium on Evolutionary Bioinformatics will be held at the **Aura Soma Lava Conference Center** in Lava Hot Springs, ID. The facility includes access to Lava's world-class hot springs. Registration and meals are provided by the generosity of our sponsors.

Speakers

Keynote speaker:
Dr. Sudhir Kumar — *Director, Center for Evolutionary Functional Genomics, Biodesign Institute, Arizona State University*

Other speakers:
- Dr. David Liberles, U. Wyo
- Dr. James Foster, U. Idaho
- ...and 8 other great talks

Schedule

- Friday, Oct. 3, 2008: Registration, Training Workshops I & II, Breakout Sessions I & II, poster session and reception.
- Saturday, Oct. 4, 2008: Research talks, banquet and keynote address.
- Sunday, Oct. 5, 2008: Training Workshop 3 and Breakout Session 3.

Information & Registration

Space is limited to 40 participants, so please register early!

Contact Mike Thomas (mthomas@isu.edu), visit egg.isu.edu (click "2008 Bioinformatics Workshop" under Quick Links) or go to pig.egg.isu.edu/workshop/ .

ISU Biomedical Research Institute · Idaho INBRE · INL · Fisher Scientific · MRCF · ISU Academic Affairs

Schedule

Thursday, October 2, 2008
7:00 p.m.: Checkin and V.P. debate-watching party.

Friday, October 3, 2008
8:30 a.m.—7:00 p.m.: **Check-in**, Conference Center

9:00 a.m.— Noon: Training Workshop I, *Advanced BLASTing*, Conference Center

10:00 a.m.—Noon: Breakout Session I, *Integrating bioinformatics into the core biology curriculum*, Riverside Inn

Noon—1:30 p.m.: Lunch & presentation, Fisher Scientific "**Western Blotting: Advanced Techniques and Troubleshooting**" (see info on last page)

1:30 p.m.—3:30 p.m.: Bioinformatics research poster session, Conference Center

3:30 p.m.—5:00 p.m.: Movie, *Flock of Dodos: The Evolution-Intelligent Design Circus* (or other activities — see list under "Activities in Lava")

5:00 p.m—6:30 p.m.: Reception and light dinner, catered by Grecian Key

7:00 p.m.—9:00 p.m.: Breakout Session II, *Creating bioinformatics research opportunities for undergraduate students*, Riverside Inn

7:00 p.m.—10:00 p.m.: Training Workshop II, *Models for phylogenetics*, Conference Center

Saturday, October 4, 2008
9:00 a.m.—Noon: Research Symposium 1 (see speaker list and schedule below)

Noon—2:00 p.m.: Lunch, on your own

2:00 p.m.—5:30 p.m.: Research Symposium 2 (see speaker list and schedule below)

6:00 p.m.: Banquet, catered by Riverwalk Thai

7:30 p.m.: Keynote presentation: Sudhir Kumar, Arizona State University, "***Software tools and Knowledge-bases for discoveries from genomes to phenotypes***"

Sunday, October 5, 2008
9:00 a.m.—Noon: Training Workshop III, *Small genome assembly & annotation*, Conf. Center

10:00 a.m.—Noon: Breakout Session III, *Tools at your fingertips*, Riverside Inn

Noon—1:30 p.m.: Lunch, on your own

Info

The conference was painstakingly organized by ISU's Evolutionary Genomics Group: Michael A. Thomas, Heath Ogden, Mitch Day, Luobin Yang, Scot Kelchner, Peter Hallock, Kelsey Metzger, Erin Naegle and Shannon Barry.

Dr. Sudhir Kumar
The Keynote presentation & banquet is sponsored by ISU's Biomedical Research Institute (IBRI) and Department of Biology.

Our Keynote speaker is **Dr. Sudhir Kumar**, Director of the Center for Evolutionary Functional Genomics at the Biodesign Institute & Professor of the School of Life Sciences at Arizona State University.

Dr. Kumar is a renowned expert in the field of evolutionary bioinformatics, who received an Innovation Award in Functional Genomics from the Burroughs Wellcome Fund in 2000. In 2004 he joined the elite ranks of most-cited researchers, being among the top ten in number of citations in computer science over the last decade. Among his more than 70 papers and books are three "Hot Papers," which were cited among the most of any in their fields. Dr. Kumar tackles long-standing problems in functional genomics and evolutionary biology. He has made pioneering efforts in developing bioinformatics tools and databases for analysis of gene expression patterns from early stages of fruit fly development. He has also conducted breakthrough work using protein molecular clocks to illuminate the Evolutionary Timescale of Life. He led development of Molecular Evolutionary Genetics Analysis (MEGA) software in order to make useful methods of comparative sequence analysis easily accessible to the scientific community for research and education.

Sponsorship
This year's ISU Bioinformatics Workshop is made possible by the ISU Office of Academic Affairs (bioinformatics-in-the-classroom Breakout Sessions), Idaho National Lab (Research Symposium), ISU Biomedical Research Institute and Department of Biological Sciences (speaker arrangements), ISU Molecular Research Core Facility (Training Workshops) and Fisher Scientific (Modern Western Blotting symposium). Critical funding for the ISU Bioinformatics Workshops comes from the NIH IN-BRE program and grant #P20 RR016454.

Symposium on Evolutionary Bioinformatics
This year's Research Symposium session is sponsored by the Idaho National Lab.

The Research Symposium is intended to take advantage of our very informal setting and extremely diverse group of researchers, becoming a forum for the exchange of ideas in a stimulating atmosphere. Talks will be 15-20 minutes followed by 10 minutes, or more, set aside for discussion. This is a slightly loose Symposium format, designed to facilitate discourse and debate by letting the discussion continue if the subject is of particular interest. To encourage this, speakers have been asked to end their talks with possible open questions, ideas for future research or other discussion stimulant.

Morning Speakers — Saturday, 9:00 a.m.
- Leonid Hanin, ISU: Periodic Patterns of Chromosomal Gene Expression
- James Foster, UI: Guide trees for multiple sequence alignment
- David Liberles, UWyo: Models for the retention of duplicate genes
- Scott Smith, BSU: RNA search with decision trees and partial covariance models
- Aaron Duffy, USU: Selection of matK following loss of its flanking intron

Afternoon Speakers — Saturday, 2:00 p.m.
- Michael Walter, UNI: Estimating the species richness of a *Bacillus anthracis* soil bacteriophage assemblage
- GongXin Yu, BSU: An exon-based approach to comparative variant analysis in human and chimpanzee
- Chris Feldman, UNev: Snakes, Salamanders and Sodium Channels: Convergence and Constraints in Snake-Amphibian Coevolution
- Vern Winston, ISU: Positive selection sites on IHNV G protein
- Frank Roberto, INL: Metagenomic analysis of Yellowstone hot springs microbial communities

Poster Session — Friday, 1:30 p.m.
- Pete Hallock, ISU: An Evolutionary Approach to the Network Biology of Alzheimer's Disease
- Erin Naegle, ISU: Student preconceptions of evolutionary relationships: A challenge to tree-thinking
- Kelsey Metzger, ISU: Molecular evolution of CCR5: HIV-1 co-receptor & West Nile Virus susceptibility
- Kristen Mitchell, BSU: Ah receptor activation suppresses liver regeneration through a p21Cip1-dependent pathway.
- Celeste Brown, UI: Models of evolution for disordered proteins
- Tuoen Liu, ISU: Investigation of the role of HSPa8 gene/HSC70 in regulating multidrug resistance in the L1210 murine leukemia cell lines.
- Caryn Evilia, ISU: Characterization of an Unusual tRNA synthetase from an extreme halophile
- Bryan Leatham, ISU: Characterization of an unusual Extreme Halophile tRNA synthetase

Keynote presentation — Saturday, 7:30 p.m., Dr. Sudhir Kumar
Software tools and Knowledge-bases for discoveries from genomes to phenotypes

Repositories containing primary sequences and patterns of gene expression, together with the scientific literature containing the inferences drawn from analyses of these data, have grown at an unprecedented rate in the last decade. With this growth, the need for tools that facilitate the mining and analysis of these data has also become more acute. We have responded to this need by developing a software for comparative analysis of molecular sequences (MEGA: www.megasoftware.net), a spatial expression pattern search tool for finding genes with overlapping patterns by image-matching (FlyExpress; www.flyexpress.net), and a literature-mining knowledge-base for information on the timescale of species divergence (TimeTree; www.timetree.org). In this presentation, I will discuss these biologist-centric tools and knowledge-bases to illustrate the basic principles that we have followed to design and implement these resources. I will focus on how MEGA is biologist-centric, rather than simply user-friendly, and how TimeTree and FlyExpress are knowledge-bases that go beyond classical data-mining and retrieval by providing answers to specific questions, and by breaking domain nomenclature barriers.

Beyond the Symposium
Still have a point to make? We've tried to include as much productive interaction time as possible. Please take the opportunity to join your colleagues at the Pub in the Riverside Inn (lower level) or in one of the famous Lava Hot Springs. Also, there are a number of pubs and restaurants within easy walking of the conference center (see page 6 for some suggestions).

Training Workshops: "Bioinformatics beyond default settings"

This year's training session is sponsored by the ISU Molecular Research Core Facility (MRCF).

The training workshops will include short lectures, demonstrations and round-table discussions regarding planning of bioinformatics projects and implementing bioinformatics into your research. Bring your laptop. Each session is led by experienced researchers.

I. Advance BLASTing for identifying distantly-related homologs

Led by Dr. Michael A. Thomas, Shannon Barry & Rich Beard. Mike is Associate Professor of Bioinformatics at ISU and director of the Evolutionary Genomics Group. He studies genome evolution. Shannon Barry is a third year M.S. student in Biology studying genome evolution. Rich Beard is a second year Ph.D. student in Biology studying physiological genomics.

Beyond BLAST default settings, we'll figure out how the alignment algorithms work and can be used to conduct fast, thorough searches of huge databases. We'll look at several advanced BLAST methods, including PHI-Blast and PSI-Blast, in addition to highly customized BLAST searches.

II. Use and importance of phylogenetic models

Led by Dr. Scot Kelchner, Ph.D. Scot is Assistant Professor of Systematics and Evolution at ISU. He is a phylogeneticist who studies organismal and molecular evolution in plants.

Selecting a model in most phylogenetic analyses is considered to be a critical step because model choice can have a strong impact on the estimation and interpretation of phylogenetic trees. This workshop describes the role of models in phylogenetic inference, discusses methods of model selection, and introduces tools that are available for exploring the fit and behavior of models in an analysis. Warning signs that might indicate model-related problems will also be discussed.

III. Small Genome Sequencing, Assembly & Annotation

Led by Dr. Mitch Day, Ph.D., a postdoctoral fellow at ISU working on a bacteriophage genome sequencing and annotation project. In December, Mitch will be an NSF Bioinformatics Postdoctoral Fellow at University of Idaho and the National Institute of Genetics, Center for Information Biology and DNA Data Bank of Japan.

We will discuss the practical, scientific and educational aspects of small genome sequencing, assembly and annotation. Small genomes of phage and viruses (<200Kb) present special economic challenges for sequencing, especially in academic labs. We will discuss these challenges as well as the opportunities for genuine scientific discovery and meaningful student projects.

Beyond the Training Workshops

Want more? Each spring, a graduate Bioinformatics course is offered at ISU by the Evolutionary Genomics Group (listed as BIOL 659: Adv. Topics in Genetics). In odd years, the course concentrates on bioinformatics applications and approaches for the study of **molecular evolution and phylogenetics**. In even year, the course concentrates on bioinformatics applications and approaches for **comparative and structural genomics**.

Breakout Sessions: Bioinformatics in undergrad education
This year's Breakout Sessions are sponsored by the ISU Office of Academic Affairs.

The Breakout Sessions are facilitated roundtable discussions designed to generate ideas and potential solutions for issues faced by educators wanting to integrate bioinformatics into the undergraduate curriculum. This integration is important for several reasons. First, bioinformatics approaches provide an excellent opportunity to illustrate key concepts in biology curriculum and experience with modern biology data analysis. Introducing bioinformatics as a legitimate aspect of biological inquiry and discovery helps prepare students for a changing job climate which continues to require proficiency in technology and newly developed approaches. Finally, including bioinformatics in the undergraduate curriculum helps attract talented students to this growing field.

Breakout Sessions are led by **Kelsey Metzger** and **Erin Naegle**. Kelsey Metzger is a third year Doctor of Arts student in the Thomas lab and member of the Evolutionary Genomics Group at ISU. She has conducted biological research in genetics and bioinformatics and has developed bioinformatics exercises aimed at undergraduate audiences. Erin Naegle is a fourth year Doctor of Arts student in the Evolutionary Genomics Group at ISU. Her dissertation research focuses on student misconceptions of phylogenetic trees.

I. Integrating bioinformatics into the biology curriculum: Success stories

Session led by Erin Naegle. The goal is to identify and discuss key themes in introductory biology that lend themselves well to bioinformatics instruction. After a general discussion of those concepts that are amenable to bioinformatics instruction, we will invite participants to share examples of utilizing bioinformatics: those endeavors that were/are successful and those that could be improved upon.

- What are the educational goals of these activities?
- How do we know when these goals have been achieved?
- What are the issues that make integrating bioinformatics into the core curriculum difficult?

II. Creating educationally successful broader impacts for grant proposals

Session led by Kelsey Metzger. This session will focus on how bioinformatics projects can successfully satisfy "Broader Impacts Criterion" as established by NSF, with special attention given to recruiting undergraduate students in bioinformatics research. We will first examine broader impacts criteria as outlined by NSF (or other relevant funding sources), and then discuss how these criteria apply to bioinformatics projects for undergraduate students.

- How does the activity advance discovery & understanding while promoting teaching & learning?
- What may be the benefits of the proposed activity to society?

III. Tools at your fingertips: Choosing applications for successful undergrad educational experiences

Session led by Kelsey Metzger and Erin Naegle. This session will provide participants with some examples of current bioinformatics tools that are readily accessible online. Resources to be discussed include the following:

- What considerations are important when choosing tools for the undergraduate classroom?
- What features make tools readily utilizable?

Beyond the Breakout Sessions

These Breakout Sessions are the kickoff of an ISU-sponsored bioinformatics-in-the-classroom project called "Bioinformatics: A Portal to 21st Century Biology Education." Portal-21 will consist of a set of innovative instructional exercises that target introductory biology students to (1) enhance understanding of the nature of science and research, (2) teach core biology concepts through the lens of genome data and methods, and (3) teach basic skills in bioinformatics and computational biology. The exercises will be widely field-tested with extensive outcomes assessment, revision and ultimate publication as a stand-alone CD and workbook. Portal-21 is being developed in conjunction with the Instructional Technology Resource Center (ITRC) at ISU in consultation with Colorado Springs-based Biological Sciences Curriculum Studies (BSCS). Contact Mike Thomas if you would like to get involved.

Activities in and around Lava Hot Spring

Lava Hot Springs is a year-round resort community located in a picturesque mountain setting, conveniently located between Salt Lake City, Utah and Yellowstone National Park. We think the intimate, resort-like setting suits the style of conference we host. There are a number of activities in Lava in which you can participate:

World famous hot springs: In addition to the hot spring pools associated with Aura Soma Lave Conference Center and the Riverside Inn (or your hotel), you can use the exceptional municipal facility located just east of the Conference Center: Bubbling out of natural underground springs and into the gravel-bottom pools, the hot water is laden with minerals but has no sulfur (and, therefore, no bad odor). Over 3 million gallons a day course through the springs and are diverted into the Portneuf River, keeping the pools ever-changing and clean. The spring's temperatures range from approximately 102˚ to 112˚ degrees. The facility is open until 11 p.m. and has a licensed massage therapist on staff. Passes are $6 (swimsuit & towel rental available).

Restaurants, bars:
- Blue Moon Bar and Grill, 100 S. 1st Ave.
- Riverside Restaurant, in Riverside Inn
- Johnny's Restaurant, 78 N. Main
- Chuckwagon Cafe, 211 E. Main
- Riverwalk Thai Restaurant, 695 E. Main
- Sweet Stuff, 34 E. Main

Other spots:
- Shawn's Market, Center & Main (groceries, sundries, beer)
- Idaho Outpost, 155 E. Main (clothing)
- Dempsey Creek Trading Company, 89 E. Main (gifts and souvenirs)
- Purple Moon and Merlin's Castle, 50 E. Main (gifts and souvenirs)

See www.lavahotsprings.org for information on tours, fishing, golfing, wagon and horseback riding.

About the ISU Bioinformatics Workshops

The Evolutionary Genomics Group at ISU has organized the annual ISU Bioinformatics Workshops to showcase bioinformatics approaches used by scientists in the region and to provide hands-on training for students and faculty interested in using these techniques. For each Workshop, we have arranged funding from a variety of academic and industry sources and hosted dozens of faculty and student participants. These interactions enhance regional collaborative interactions and research potential. **Critical funding for the ISU Bioinformatics Workshops comes from the NIH INBRE program and grant #P20 RR016454.**

2008 **Symposium on Evolutionary Bioinformatics**
Featuring research talks on evolutionary research approaches and applications. Held in Lava Hot Springs at the Aura Soma Lava conference center. Organized in collaboration with Drs. Heath Ogden.

2007 **Symposium on Biomedical Bioinformatics**
Featuring research talks on biomedical research approaches and applications with participants from five regional institutions. Held in Lava Hot Springs at the Aura Soma Lava conference center. Organized in collaboration with Dr. Heath Ogden. Over forty participants from six institutions participated in the Symposium.

2006 **Genome Annotation Jamboree**
Genome Annotation of *Acidophilium cryptum* using genome sequence generated by Dr. Tim Magnuson's lab). Held at ISU in the Plant Sciences Lecture Hall (on the ISU campus). Organized in collaboration with colleagues in the Magnuson lab.

2005 **Bioinformatics: Idahomics**
Training sessions for the use of standard bioinformatics approaches and highlighted research talks of users of those tools. Held at the ISU College of Pharmacy (on the ISU campus). Organized in collaboration with colleagues at the Aberdeen USDA-ARS.

What's next? While keeping the Workshop relatively small, we hope to continue the trend of increasing a substantial regional feel. Next is the **2009 Symposium on Disease Genomics**, featuring analyses of genes and systems involved in human diseases and disorders. To be held in Lava Hot Springs in October, 2009.

2008 ISU Bioinformatics Workshop Participants

There are over 50 participants this year, representing 14 different institutions.

First name	Last name	Institution
Shannon	Barry	Idaho State University
Richard	Beard	Idaho State University
Celeste	Brown	University of Idaho
Steve	Chiu	Idaho State University
Daniel	Conte de Leon	Lewis-Clark State College
Chris	Cretekos	Idaho State University
Chris	Daniels	Idaho State University
Mitch	Day	Idaho State University
Joshua	Der	Utah State University
Alex	Doetsch	College of Southern Idaho
Aaron	Duffy	Utah State University
John	Eley	Idaho State University
Jason	Evans	University of Idaho
Caryn	Evilia	Idaho State University
Chris	Feldman	University Nevada, Reno
Amanda	Fisher	Idaho State University
James	Foster	University of Idaho
Pete	Hallock	Idaho State University
Leonid	Hanin	Idaho State University
Rick	Holsten	Idaho State University
Merideth	Humphries	The College of Idaho
Marina	Kazakevich	Idaho State University
Scot	Kelchner	Idaho State University
Todd	Kelson	BYU-Idaho
Sudhir	Kumar	Arizona State University

First name	Last name	Institution
Bryan	Leatham	Idaho State University
David	Liberles	University of Wyoming
Tuoen	Liu	Idaho State University
Janet	Loxterman	Idaho State University
Mandira	Manandhar	Idaho State University
Kelsey	Metzger	Idaho State University
Kristen	Mitchell	Boise State University
Erin	Naegle	Idaho State University
Deborah	Newby	Idaho National Laboratory
Heath	Ogden	Idaho State University
Ryan	Patterson	Idaho State University
Frank	Roberto	Idaho National Laboratory
Heather	Silverman	Idaho National Laboratory
Elizabeth	Skendzic	Lewis-Clark State College
Wendy	Shuttleworth	Lewis-Clark State College
Scott	Smith	Boise State University
Rosemary	Smith	Idaho State University
Mike	Thomas	Idaho State University
John	Thorne	Idaho State University
Michael	Walter	University of Northern Iowa
Vern	Winston	Idaho State University
Paul	Wolf	Utah State University
Luobin	Yang	Idaho State University
Gongxin	Yu	Boise State University
Yan	Zheng	Idaho State University
Wenxiang	Zhu	Idaho State University

Western Blotting: Advanced Techniques and Troubleshooting

Presented by **Fisher Scientific Life Sciences**
Friday, October 3, 2008, Noon- 1:30 PM
Aura Soma Lava Conference Center

Topics:

- How to properly optimize your antibody concentrations for maximum performance
- How to select antibodies that work the first time
- How to systematically and methodically maximize sensitivity and specificity while minimizing background and promiscuous binding
- Tips for improving efficiency, reproducibility, and throughput

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