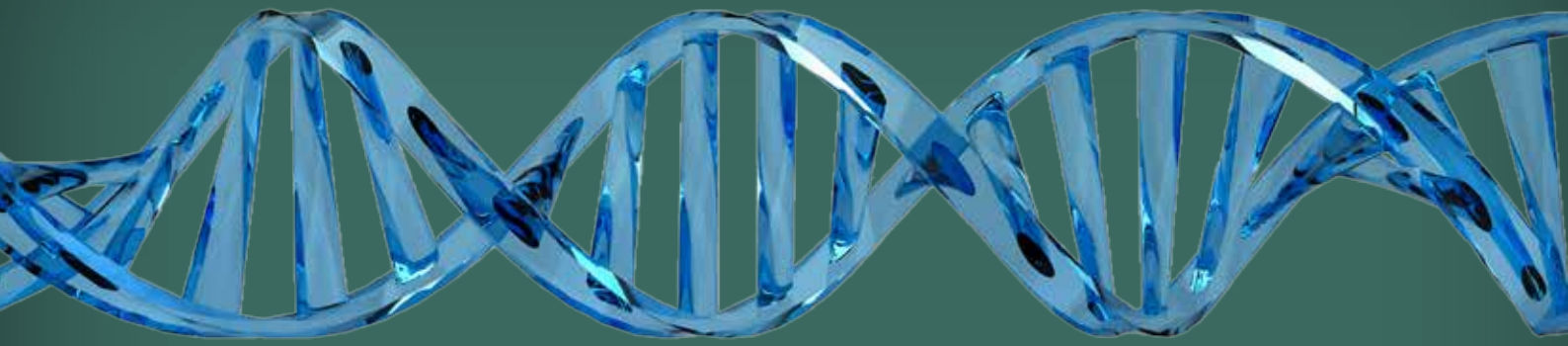
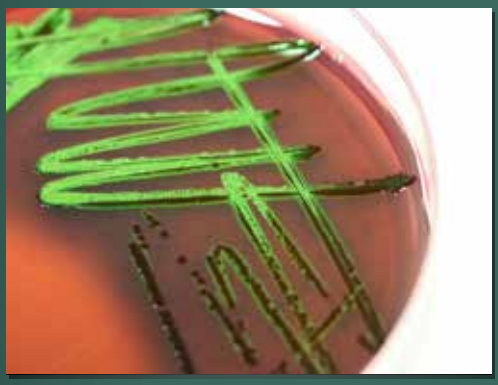
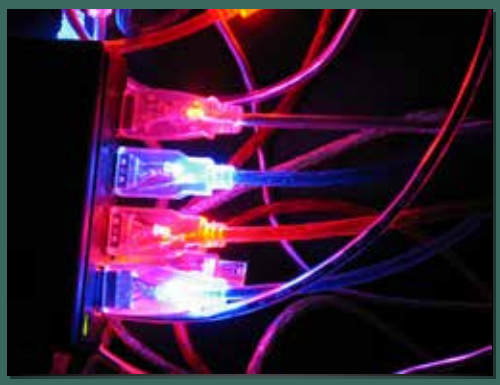


INSTITUTE FOR BIOINFORMATICS AND EVOLUTIONARY STUDIES

2012 ANNUAL REPORT





IBEST

PO Box 443051
Moscow, ID 83844
ibest@uidaho.edu
www.uidaho.edu/research/ibest

IBEST

THE INSTITUTE FOR BIOINFORMATICS AND EVOLUTIONARY STUDIES

Overview

The Institute for Bioinformatics and Evolutionary Studies (IBEST) is at the heart of a 'signature research area' at the University of Idaho: real-time evolution. The institute – one of only three at the University – was formed on July 1, 2011 following a competitive internal selection process. This prestigious designation is accompanied by significant institutional support in terms of funding, space and personnel that will provide for financial stability and a framework for IBEST longevity and the continued success of IBEST.

The institute was built on a financial foundation provided by Center of Biomedical Research Excellence (COBRE) awards from the NIH-IDeA Program. Ongoing COBRE funding will enable us to implement a plan to transition the IBEST Genomics and Computational Resource Cores and administrative support capabilities to a point where they can be sustained by a combination of grant support and university funds. As a research institute IBEST will receive a portion of the earned overhead from new grants from research related to the theme of 'real time evolution' as well as direct institutional support that will primarily be used to subsidize core facility operations and for the salaries of administrative staff. This financing will allow us to broaden our scope to include research unrelated to human health.

Participants in IBEST are nested within a vibrant community of scientists in which intellectual interactions and collaborations are many and varied. We encourage and foster interdisciplinary collaborations that blend the expertise of evolutionary biologists, ecologists, molecular biologists, biochemists, biophysicists, mathematicians, statisticians, and computer scientists to examine the underpinnings of evolutionary biology. This constitutes an important competitive edge to investigators because we can address research questions that are intractable to scientists from a single discipline. It is also an important element in the recruitment and retention of faculty, postdoctoral scientists and graduate students because comparable opportunities for cross-disciplinary training and research do not exist at many other institutions. In this way, IBEST is distinctive insofar as it is not a simple small set of individual investigators that work independently within a more or less well defined discipline. Instead, a network of collaborations has emerged that facilitates unselfish sharing of knowledge, expertise, and know how; all of which is made possible because of the collegial research climate within IBEST.

Director
Larry J. Forney PhD

Research Oversight Team
Holly Wichman PhD
James Foster PhD
Jack Sullivan PhD

Mission

The mission of IBEST is to:

Facilitate interdisciplinary research on evolutionary processes at different levels of biological complexity ranging from studies on the molecular processes of evolutionary change to the adaptation of organisms on a landscape level.

Establish and **nurture strategic collaborations or partnerships** with research groups across the United States and abroad.

Maintain and **enhance the capabilities of core facilities** for DNA sequence analysis, bioinformatics, and optical imaging and facilitate their use by investigators across campus.

Promote graduate and undergraduate education in bioinformatics and computational biology at the University of Idaho.

This mission is wholly consistent with Goal 2 of the University's Strategic Plan. This plan calls for expanded opportunities for ongoing interactions among faculty, increased financial support for graduate and undergraduate interdisciplinary research, increased national and international visibility of the University's contributions to interdisciplinary scholarship, partnerships with other educational institutions to expand resources and expertise, the submission of large, interdisciplinary research proposals, and sustaining successful projects that are already funded.

A VIBRANT COMMUNITY OF SCIENTISTS IN WHICH INTELLECTUAL INTERACTIONS AND COLLABORATIONS ARE MANY AND VARIED.

WE SEEK TO BUILD UPON PAST SUCCESSES

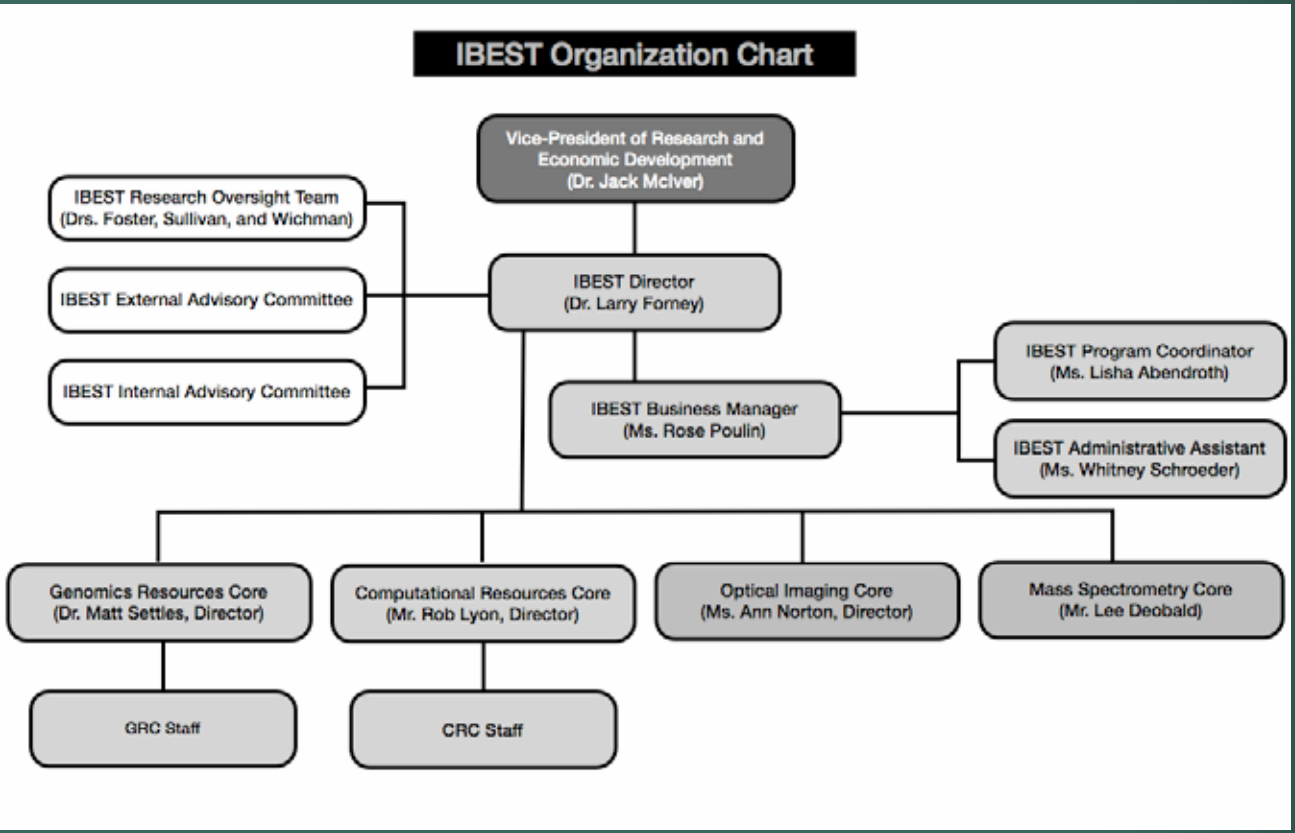
Interdisciplinary research on evolutionary processes

Evolution is the process by which the inherited traits of organisms change through successive generations. This encompasses changes in gene frequencies from one generation to the next in a population, the emergence of novel traits in organisms, and the descent of different species from a common ancestor. Studies of evolution provide insight to the history of life, patterns and the extent of biodiversity in different habitats, the mechanisms that underpin the emergence of disease, and much more. The extensive data sets collected by biologists in contemporary studies of natural and experimentally evolved populations enable mathematicians, statisticians, and computer scientists to quantify the probabilities of various evolutionary events and develop models that can subsequently be empirically evaluated and refined by biologists. Many of these studies are facilitated by recent advances in technologies for DNA sequencing and transcriptome analysis as well as the increased speed and capacity for data analysis. This allows investigators to explore evolutionary biology in ways that were never before possible.

We seek to build upon the past successes of the Initiative for Bioinformatics and Evolutionary Studies – the predecessor of the institute – that were made possible by teaming computational and empirical scientists to exploit technological advances in interdisciplinary research on evolutionary processes.

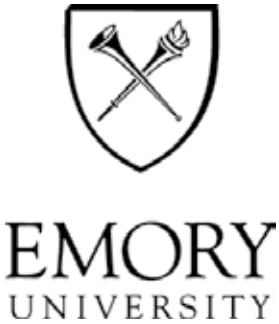
Administration

Dr. Larry Forney serves as the Director of IBEST and has overall responsibility for strategic planning, IBEST finances, oversight of IBEST Core facilities, supervision of administrative and core facility staff, coordination of research and education programs affiliated with IBEST, and responsibility for compliance with federal, state, and university policies and regulations (see Organization Chart on opposite page). The Research Oversight Team, the Intern Advisory Committee, and the External Advisory Committee advise him. Dr. Forney devotes 35% of his effort to being Director of IBEST and in this capacity he reports directly to the Vice-President for Research and Economic Development.



Research Oversight Team

The Research Oversight Team (ROT) serves as the executive board of IBEST and provides advice to the Director on the development of strategic plans and implementation of IBEST policies and procedures. In addition, ROT members work to ensure cross-communication among researchers, identify potential linkages between research projects, stimulate collaborations with investigators elsewhere, and mentor junior faculty in the development of their research programs. Drs. Foster, Sullivan and Wichman are currently members of the Research Oversight Team. These individuals devote 5% of their effort to service on ROT.



External Advisory Committee

We will continue to use our four-person External Advisory Committee (EAC) to suggest scientific direction and to identify potential opportunities that are consistent with our expertise. The Director and Research Oversight Team (the executive board of IBEST) will seek their advice on 'global' and 'local' issues. Global issues include potential strategic alliances with individuals and groups outside the University of Idaho and identifying important research opportunities. Local issues include plans for targeted recruitment of faculty with complementary expertise, how to maintain a well-balanced portfolio of research projects within IBEST, and one-on-one advice to IBEST investigators. In the past the last of these has occurred following oral or poster presentations by investigators or lab group members in which EAC members have shared their knowledge of emerging ideas and coached faculty regarding potential new lines of investigation. These exchanges often occur as part of in-depth one-on-one discussions during our annual meeting with the EAC and are highly valued because members of our EAC are exemplary scientists with decades of experience and broad understanding of science related to IBEST.

The EAC consists of distinguished faculty with expertise in research fields allied to those in IBEST, and experience in the administration of interdisciplinary academic research programs. The faculty and students of IBEST meet with the EAC each fall semester. A written committee report is provided to the Vice-President for Research and Economic Development and the leadership of IBEST, included in our annual COBRE report to NIH, and shared with key administrators at the University of Idaho. The following individuals are the current members of the EAC:

Dr. Warren Ewens
Christopher H. Browne
Distinguished Professor of Biology
University of Pennsylvania
Fellow of the Royal Society
Expertise: Theoretical population genetics

Dr. Bruce Levin
Samuel C. Dobbs Professor of Biology
Emory University
Member of the National Academy of Science
Expertise: Microbial population biology

Dr. John Roth, Chair
Distinguished Professor
University of California-Davis
Member of the National Academy of Science
Expertise: Microbial genetics and genome evolution

Dr. Michael Turelli, Vice-Chair
Distinguished Professor
University of California-Davis
Expertise: Evolutionary ecology

Internal Advisory Committee

The Internal Advisory Committee (IAC) consists of four Deans or their designees who are selected by the Vice-President for Research and Economic Development. The Internal Advisory Committee meets at least annually with the IBEST Director, Research Oversight Team, and others as appropriate to review accomplishments, programs and policies, and to provide strategic advice on future opportunities and directions. Recommendations approved by majority vote of the IAC are forwarded in writing to the Vice-President for Research and Economic Development for further consideration. The following individuals are the current members of the IAC:

Dean Paul Joyce, College of Science
Dean John Hammel, College of Agriculture and Life Sciences
Dean Kurt Pregitzer, College of Natural Resources
Dean Larry Stauffer, College of Engineering

Research grant administration

With the founding of the institute in July 2011 investigators could submit their research proposals to extramural agencies through the institute rather than a college if the research proposed was clearly related to the IBEST theme of 'real time evolution'. In short the administrative staff of IBEST does as much as possible to alleviate the administrative burden of proposal submission and grant award management faced by principal investigators. To do this they provide support to investigators in formulating budgets, completion of various proposal forms, and so forth, then shepherd the proposal through the pre-award division of the UI Office of Sponsored Programs (OSP). When a proposal is funded, the administrative staff works with the post-award division of OSP to set up project budgets, oversees purchasing and accounting of expenditures, assists in the recruitment and appointment of personnel, advises PIs on budgetary issues that arise, and if necessary assists in the preparation of annual reports.

An accounting of the grant proposals submitted, grants received, and grant expenditures is provided in the tables that follow (see pages 8-12.) More than $19,000,000 in research funding was requested in FY11-12, which illustrates the high level of activity by faculty to secure extramural funding. Grants totaling $6.8 million were awarded during the same time period. Actual grant expenditures totaled $3.9 million, which was accompanied by $946,300 in earned F&A (indirect costs) to the university.

IBEST ENCOURAGES AND FOSTERS INTERDISCIPLINARY COLLABORATIONS

PROPOSALS SUBMITTED THROUGH IBEST IN FISCAL YEAR 2011-2012

UI Proposal Number	PI	PI College	PI Dept.	Title	Sponsor	Submitted Date	Total Amount	Total Direct Cost	Total F&A
10674B	Forney, Larry J.	COS	Biological Sciences	Bacterial Biofilms	Proctor & Gamble	8/19/11			
12016	Tank, David C.	CNR	Forestry	Collaborative Research: Next-Generation Phylogeography of the Inland Temperate Rainforest Enables Community-Wide Tests of Dispersal Limitation	National Science Foundation	7/11/11			
12022	Harmon, Luke J.	COS	Biological Sciences	Detecting the signature of species interactions in the tree of life	National Science Foundation	7/9/11			
12040	Forney, Larry J.	COS	Biological Sciences	COBRE Phase III: Center for Research on Processes in Evolution	National Institutes of Health	7/20/11			
12049	Ytreberg, Frederick M.	COS	Physics	Dissecting the biophysical mechanisms for protein-protein interactions in viruses from an evolutionary perspective	National Science Foundation	7/25/11			
12111	Ytreberg, Frederick M.	COS	Physics	Crossing the Entropic Barrier to Coupled Folding and Binding	National Science Foundation	9/6/11			
12020	Settles, Matthew L.	ORED	IBEST	Genomic divergence in a ring species: Molecular processes underlying the evolution of reproductive isolation	Colorado State University	7/11/11			
12042	Settles, Matthew L.	ORED	IBEST	Source of heterogeneity in pathogen load: genes or environment?	Michigan State University	7/19/11			
12018	Krone, Stephen M.	COS	Mathematics	Spatial Structure and Adaptive Evolution of Viruses	National Science Foundation	7/9/11			
12514	Settles, Matthew L.	ORED	IBEST	Mechanisms of genome size differentiation between germline and soma	James Madison University	2/23/12			
12499	Hohenlohe, Paul	COS	Biological Sciences	Adaptation to life between two oceans: The role of dispersal in intertidal fishes along the southern African coast	National Science Foundation	2/15/12			
12167	Forney, Larry J.	COS	Biological Sciences	The Vaginal Microbiome During Puberty	Proctor & Gamble	10/5/11			
12274	Wichman, Holly A.	COS	Biological Sciences	Probing Retrotransposon Extinctions	National Science Foundation	11/10/11			
12707	Brown, Celeste J.	COS	Biological Sciences	Connecting Genotype, Phenotype and Fitness using Mathematical Modeling and Experimental Evolution	National Science Foundation	5/21/12			
10674C	Forney, Larry J.	COS	Biological Sciences	The development of microbicide resistance in bacterial biofilms	Proctor & Gamble	10/19/11			
12252	Harmon, Luke J.	COS	Biological Sciences	PhyloFlow: Comparative Analysis Workflows for the Tree of Life	National Science Foundation	11/4/11			
12159	Nuismer, Scott L.	COS	Biological Sciences	A Bayesian Approach to Inferring the Strength of Coevolution	National Science Foundation	10/3/11			
12202	Abdo, Zaid	COS	Math/Stats	Modeling the microbial community dynamics and ecology of the human microbiome: focus on the vaginal system	Keck Foundation	10/24/11			
12271	Tank, David C.	CNR	Forestry	Investigating the Accumulation of Evidence for Speciation: Species Delimitation in a Rapid and Recent Radiation	National Science Foundation	11/10/11			
12152	Settles, Matthew L.	ORED	IBEST	Systematic Genomics and Proteomics Analysis of HCV-associated HCC	Washington State University	10/1/11			
12154	Ytreberg, Frederick M.	COS	Physics	Crossing the Entropic Barrier to Coupled Folding and Binding	University of South Florida	10/5/11			
12262	Settles, Matthew L.	ORED	IBEST	Epigenetic Mapping of HCV-associated HCC	Washington State University	11/11/11			
12329	Top, Eva M.	COS	Biological Sciences	Persistence of Antibiotic Resistance Plasmids in Biofilms	Dept of Defense	12/7/11			
12404	Forney, Larry J.	COS	Biological Sciences	Modeling diversity and stability of vaginal microbial communities		1/13/12			
	# NEW SUBMISSIONS	**24**			**AMOUNT OF SUBMISSIONS**				

IBEST AWARDS RECEIVED IN FY 2012

Budget	Sponsor	PI	PI College	PI Department	CO-PI 1	CO-PI 2	Award Title	Award Amount	F&A Percentage
KGK001	National Science Foundation	Soule, Terence	COE	Computer Science	None	None	BEACON Yr2-Soule		
KGK001	National Science Foundation	Soule, Terence	COE	Computer Science	None	None	BEACON Yr2-Soule		
KGK002	National Science Foundation	Harmon, Luke J.	COS	Biological Sciences	None	None	BEACON Yr2-Harmon		
KGK002	National Science Foundation	Harmon, Luke J.	COS	Biological Sciences	None	None	BEACON Yr2-Harmon		
KGK003	National Science Foundation	Sullivan, Jack M.	COS	Biological Sciences	None	None	BEACON Yr2-Sullivan		
KGK004	National Science Foundation	Wichman, Holly A.	COS	Biological Sciences	None	None	BEACON Yr2-Wichman		
KGK005	National Science Foundation	Rosenblum, Erica B.	COS	Biological Sciences	None	None	BEACON Yr2-Rosenblum		
KGK005	National Science Foundation	Rosenblum, Erica B.	COS	Biological Sciences	None	None	BEACON Yr2-Rosenblum		
KGK006	National Science Foundation	McGowan, Craig P.	COS	Biological Sciences	None	None	BEACON Yr2-McGowan		
KGK007	National Science Foundation	Hohenlohe, Paul	COS	Biological Sciences	None	None	BEACON Yr2-Hohenlohe		
KGK008	National Science Foundation	Top, Eva M.	COS	Biological Sciences	None	None	BEACON Yr2-Top		
KGK009	National Science Foundation	Tank, David C.	CNR	Forestry	None	None	BEACON Yr2-Tank		
KGK010	National Science Foundation	Heckendorn, Robert B.	COE	Computer Science	None	None	BEACON Yr2-Heckendorn		
KGK011	National Science Foundation	Foster, James A.	COS	Biological Sciences	None	None	BEACON Yr2-Foster		
KGK012	National Science Foundation	Wichman, Holly A.	COS	Biological Sciences	Yang, Lei	None	Probing Retrotransposon		
KGK483	University of Idaho Foundation, Inc.	Foster, James A.	COS	Biological Sciences	None	None	Computational Support for Evolutionary Biology at UI		
KGK564	Michigan State University	Forney, Larry J.	COS	Biological Sciences	Abdo, Zaid	Zhou, Xia	Group B Streptococci		
KGK613	National Science Foundation	Tank, David C.	CNR	Forestry	Uribe Convers, Simon	None	Species Delimitation Radiation		
KGK692	National Science Foundation	Harmon, Luke J.	COS	Biological Sciences	None	None	Workflows for the Tree of Life		
KGK749	National Geographic Society	Harmon, Luke J.	COS	Biological Sciences	Hagey, Travis J.	None	How Geckos Stick		
ABK007	National Institutes of Health	Joyce, Paul	COS	Mathematics	Wichman, Holly A.	Miller, Craig R.	Patterns Adaptive Evolution		
ABK009	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	Eco-Pathogenomics III		
ABK010	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	Eco-Pathogenomics III		
ABK011	National Science Foundation	Nuismer, Scott L.	COS	Biological Sciences	None	None	Phenotypic Coevolution		
ABK213	The Procter & Gamble Company	Forney, Larry J.	COS	Biological Sciences	Zhou, Xia	None	Microbiota		
ABK907	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	Abdo, Zaid	None	Marmoset Project		
ABK908	National Institutes of Health	Top, Eva M.	COS	Biological Sciences	Abdo, Zaid	None	Plasmid Host-Range		
ABK909	The Procter & Gamble Company	Forney, Larry J.	COS	Biological Sciences	None	None	Bacterial Biofilms		
ABK918	National Science Foundation	Foster, James A.	COS	Biological Sciences	None	None	BEACON Yr2		
ABK918	National Science Foundation	Foster, James A.	COS	Biological Sciences	None	None	BEACON Yr2		
ABK919	National Science Foundation	Foster, James A.	COS	Biological Sciences	None	None	BEACON Heckendorn Support		
ABK919	National Science Foundation	Foster, James A.	COS	Biological Sciences	None	None	BEACON Heckendorn Support		
ABK920	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Admin Core-Yr 3		
ABK930	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Admin Core Yr 4		

IBEST AWARDS RECEIVED IN FY 2012 Continued

Budget	Sponsor	PI	PI College	PI Department	CO-PI 1	CO-PI 2	Award Title	Award Amount	F&A Percentage
ABK940	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Administrative Core Yr 5		
ABK943	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	Brown, Celeste J.	Wichman, Holly A.	COBRE Proj 3 Yr 5 - Brown		
ABK944	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	Hohenlohe, Paul	None	COBRE Proj 5, Yr 4 - Hohenlohe		
ABK945	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Computational Resources Core		
ABK946	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Genomics Resources Core		
ABK947	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Technology Access Grants		
ABK948	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	None	None	COBRE Pilot- McGuire3		
ABK986	National Institutes of Health	Forney, Larry J.	COS	Biological Sciences	Abdo, Zaid	None	Human Microbiome Project 2		
42 AWARDS RECEIVED							**TOTAL AMOUNT AWARDED**		

[Note that funds from the BEACON subcontract with Michigan State University were divided among the ultimate recipients of funding. The same was done for individuals the received funding from the COBRE grant.

FY2012 IBEST GRANT EXPENDITURES

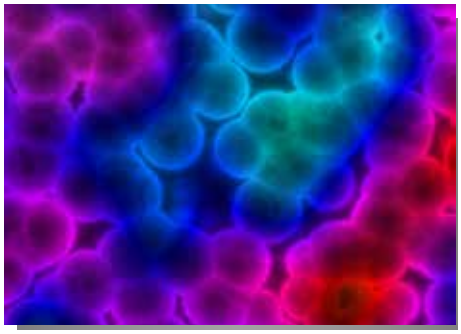
UI BUDGET	SPONSOR	PI	PI COLLEGE	PI DEPT	Award Title	Direct Expenditures	F&A Expenditures	Total Expenditures
ABK100	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	ARRA Processes in Evoluti			
ABK165	The Procter & Gamble Company	Forney Larry J.	COS	Biological Sciences	Vaginal & Vulvar Microbial Communities			
ABK213	The Procter & Gamble Company	Forney Larry J.	COS	Biological Sciences	Microbiota			
ABK319	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Genomic Tools for HVM			
ABK489	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Eco-Pathogenomics			
ABK678	National Science Foundation	Tank David C	CNR	Forestry	GRFP Marx			
ABK824	National Science Foundation	Robison Barrie Dennis	COS	Biological Sciences	UBM UI-WSU Math Bio			
ABK825	National Science Foundation	Robison Barrie Dennis	COS	Biological Sciences	UBM UI-WSU Par Sup			
ABK907	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Marmoset Project			
ABK908	National Institutes of Health	Top Eva M.	COS	Biological Sciences	Plasmid Host-Range			
ABK909	The Procter & Gamble Company	Forney Larry J.	COS	Biological Sciences	Bacterial Biofilms			
ABK917	National Science Foundation	Foster James A.	COS	Biological Sciences	BEACON YR 1			
ABK918	National Science Foundation	Foster James A.	COS	Biological Sciences	BEACON Yr2			
ABK919	National Science Foundation	Foster James A.	COS	Biological Sciences	Beacon Sabbatical			
ABK930	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Admin Core Yr 4			
ABK932	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Proj 2, Yr 4-Krone			
ABK933	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Proj 3, Yr 4-Brown			
ABK934	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Proj 5, Yr 4-Hohenlohe			
ABK935	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Bioinformatics Core Yr4			
ABK936	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE DNA Core Yr4			
ABK937	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Seq Pilots Yr4			
ABK938	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Pilot-McGuire2			
ABK939	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Pilot-Soule 2			
ABK940	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Admin Core Yr 5			
ABK943	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Proj 3 Yr 5- Brown			
ABK944	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Proj5 Yr 5- Hohenlohe			
ABK945	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE CRC Yr 5			
ABK946	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Seq GRC Yr 5			
ABK948	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	COBRE Pilot- McGuire3			
ABK988	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Human Microbiome Project 2			
AKK866	National Institutes of Health	Joyce Paul	COS	Mathematics	Patterns of Adaptive Evolution			

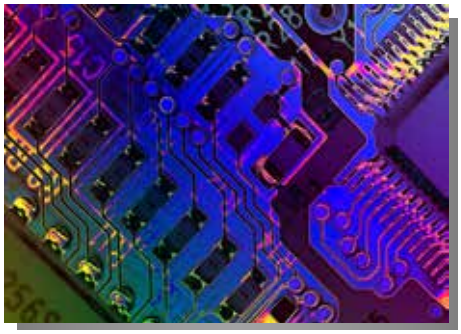
FY2012 IBEST GRANT EXPENDITURES Continued

UI BUDGET	SPONSOR	PI	PI COLLEGE	PI DEPT	Award Title	Direct Expenditures	F&A Expenditures	Total Expenditures
ABK003	National Institutes of Health	Abdo Zaid	COS	Mathematics/Statistics	Eco-Pathogenomics II			
ABK007	National Institutes of Health	Joyce Paul	COS	Mathematics	Patterns Adaptive Evolution			
ABK008	Cornell University	Forney Larry J.	COS	Biological Sciences	Vulvar Vestibulitis			
ABK009	National Institutes of Health	Abdo Zaid	COS	Mathematics/Statistics	Eco-Pathogenomics III			
ABK010	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Genomic Tools for HVM II			
ABK011	National Science Foundation	Nuismer Scott Landis	COS	Biological Sciences	Phenotypic Coevolution			
ABK097	National Institutes of Health	Forney Larry J.	COS	Biological Sciences	Process in Evolution			
KGK001	National Science Foundation	Soule Terence	COE	Computer Science	BEACON Yr-2			
KGK002	National Science Foundation	Harmon Luke J	COS	Biological Sciences	BEACON Yr-2			
KGK003	National Science Foundation	Sullivan Jack M.	COS	Biological Sciences	BEACON Yr-2			
KGK004	National Science Foundation	Wichman Holly A.	COS	Biological Sciences	BEACON Yr-2			
KGK005	National Science Foundation	Rosenblum Erica Bree	COS	Biological Sciences	BEACON Yr-2			
KGK006	National Science Foundation	McGowan Craig P	COS	Biological Sciences	BEACON Yr-2			
KGK007	National Science Foundation	Hohenlohe Paul	COS	Biological Sciences	BEACON Yr-2			
KGK008	National Science Foundation	Top Eva M.	COS	Biological Sciences	BEACON Yr-2			
KGK483	University of Idaho Foundation, Inc.	Foster James Arthur	COS	Biological Sciences	Murdock Computational Support			
KGK564	Michigan State University	Forney Larry J.	COS	Biological Sciences	Group B Streptococci			
KGK692	National Science Foundation	Harmon Luke J	COS	Biological Sciences	Workflows for the Tree of Life			
					TOTAL EXPENDITURES FOR FY20			

Future prospects

During the first year of the IBEST institute the faculty have aggressively pursued extramural funding, and they have been able to successfully compete for extramural funding. This is a testament to the quality of the faculty, students and research staff affiliated with IBEST. However, the competition for research funding continues to grow and the percentage of grants funded of those submitted continues to decrease, lingering between 5-10% (depending on the program) at NSF and NIH. To continue our success we will have to seek opportunities that well match the strengths of the interdisciplinary research done within IBEST and build on past successes. Among these successes are the individual grant awards mentioned above, the partnership established through the BEACON Science and Technology Center, the larger collaborative grants exemplified by the "Workflows for the Tree of Life" NSF grant, and the Cooperative Research Center on Sexually Transmitted Diseases focused on the ecogenomcis of chlamydia infections. In addition we continue to nurture the Bioinformatics and Computational Biology (BCB) graduate degree program, and the partnership with Washington State University for Undergraduate Biology and Mathematics research program. These programs are described in more detail elsewhere in this report.





IBEST IS DISTINCTIVE INSOFAR AS IT IS A NETWORK OF COLLABORATIONS THAT HAS EMERGED TO FACILITATE UNSELFISH SHARING OF KNOWLEDGE, EXPERTISE, AND KNOW HOW.

Strategic Reinvestments

Return of earned F&A to IBEST

In accordance with agreements that **pre-date** founding of the institute IBEST has received 25% of the F&A earned from expenditures from the COBRE grant, grants that were direct spin-offs from COBRE, and the BEACON grant. For FY10-11 this totaled $226,509. Of this, 30% was passed on to principal investigators, their co-investigators, and the home departments of principal investigators. Of this, the investigators and co-investigators received 20% of the earned F&A while the departments received 10%. These funds were intended to help offset the real costs of research incurred by departments and investigators that are not or cannot be expensed to grants. We anticipate that a comparable distribution formula will be used in the future, but under the institute charter it can be adjusted as appropriate.

Under the terms of the institute charter IBEST will receive 50% of the F&A earned on expenditures from grants awarded **after July 1, 2011** that are related to the theme of 'real time evolution'. The first fiscal year after founding of the institute (FY11-12) ended on June 30, 2012 and the UI is in the final stages of distributing earned F&A to administrative units. The amount of earned F&A to be returned to IBEST has not been finalized, but is expected to be more than $300,000.

Institutional support

The Office of Research and Economic Development provided $210,000 in direct support of IBEST in FY11-12. These funds have been primarily used to subsidize core facility operations and for the salaries of administrative staff.

Strategic reinvestments in FY11-12

During the past year a total of $350,729 in earned F&A funds have been strategically reinvested in research and research personnel related to the IBEST theme of 'real-time' evolution (see tables on pages 15-17). Based on the premise that human resources are the most critical our priorities have been placed on funding new faculty salary and research program start-up costs ($134,027) and the support of graduate students ($130,550). Other investments were made that provide broad benefit to IBEST affiliated faculty, their departments and colleges.

IBEST IS A TESTAMENT TO THE QUALITY OF THE FACULTY, STUDENTS AND RESEARCH STAFF AFFILIATED WITH IT.

STRATEGIC REINVESTMENTS CY2012						PAGE 1
DESCRIPTION	**AMOUNT 2012**	**AMOUNT 2013**	**AMOUNT 2014**	**AMOUNT 2015**	**IMPACT[a]**	**NOTES**
F&A RETURN TO DEPTS						
F&A to Biological Sciences	$20,380	ND[b]	ND	ND	COS/BIOL	
F&A to Mathematics	$1,609	ND	ND	ND	COS/MATH	
F&A to Statistics	$663	ND	ND	ND	COS/STATS	
TOTAL F&A	**$22,652**					
FACULTY SUPPORT						
Hohenlohe start-up funding	$89,027				COS/BIOL/STATS	
Buzba start-up funding	$35,000				COS/STATS	
McGowan start-up funding	$10,000	$10,000			COS/BIOL	
Wichman course buyout	$3,000				COS/BIOL	Leads COS Dean search
Evolutionary biology faculty start-up funding		$50,000	$50,000	$50,000	COS/BIOL	
TOTAL FACULTY	**$137,027**					
RESEARCH SUPPORT						
Technology Access grants	$46,000	ND	ND	ND	University	Recipients: Fortunato/COS/BIOL; Karasev & Brown/CALS/COS/BIOL/MATH; Miura & Miller/COS/BIOL/MATH; Waits/CNR/FISH&WILDLIFE
Idaho-INBRE support	$5,000				Statewide	Annual state-wide conference
MATLAB license	$1,500				University	
TOTAL RESEARCH	**$52,500**					

[a]Units benefited. College of Science, COS; College of Natural Resources, CNR; College of Engineering, COE; Department of Biological Sciences, BIOL; Department of Mathematics, MATH; Department of Statistics, STATS; Department of Fish and Wildlife, FISH&WILDLIFE; Bioinformatics and Computational Biology Graduate Program, BCB; NSF EPSCoR, NSF Experimental Program to Stimulate Competitive Research; and NSF Undergraduate Biology and Mathematics Program; UBM.

[b]Not yet determined. See text for details.

STRATEGIC REINVESTMENTS CY2012 (cont.)						PAGE 2
DESCRIPTION	**AMOUNT 2012**	**AMOUNT 2013**	**AMOUNT 2014**	**AMOUNT 2015**	**IMPACT[a]**	**NOTES**
STUDENT SUPPORT						
BCB Fellowships	$109,000				BCB	Five graduate students
BCB Gradaute student group	$1,000				BCB	Graduate student research collaboration
UBM Summer students	$1,000				COS/MATH	Food for program meetings
BEACON 101 students	$500				COS/BIOL	Food for program meetings
COGS Innovation showcase	$1,000				UNIVERSITY	Showcase undergradaute and graduate research
Women in Science Program	$2,000				STATEWIDE	Junior and senior high school students
Laptop computers for UBM students	$2,000				COS/MATH	Undergraduate researchers
Spangler undergraduate student fellowship		$500			UNIVERSITY	Undergraduate researcher
Graduate student bridge funding	$13,050				COS/MATH	Graduate student
BCB Graduate student office supplies	$500				COS/COE	BIOL/MMBB/BCB/NEUROSCI
TOTAL STUDENT	**$130,050**					
EQUIPMENT/IMPROVEMENTS						
1st & 2nd floor LSS conference rooms	$1,800				BIOL/COS	Videoconferencing
4th floor LSS conference room	$7,700				BIOL/COS	Electronic white board and videoconferencing
TOTAL EQUIP	**$9,500**					

[a]Units benefited. College of Science, COS; College of Natural Resources, CNR; College of Engineering, COE; Department of Biological Sciences, BIOL; Department of Mathematics, MATH; Department of Statistics, STATS; Department of Fish and Wildlife, FISH&WILDLIFE; Bioinformatics and Computational Biology Graduate Program, BCB; NSF EPSCoR, NSF Experimental Program to Stimulate Competitive Research; and Undergradaute Biology and Mathematics Program; UBM.

STRATEGIC REINVESTMENTS CY2012 (cont.)						PAGE 3
DESCRIPTION	**AMOUNT 2012**	**AMOUNT 2013**	**AMOUNT 2014**	**AMOUNT 2015**	**IMPACT[a]**	**NOTES**
OTHER/MISCELLANEOUS						
Donation of data storage equipment					COE	
Computer classroom usage					COS/BIOL	University Recruitment on Vandal Fridays
Computer classroom usage					UNIVERSITY	UI Courses: BIOL 102, BIOL 115, BIOL 116, BIOL 213, BCB 504, BIOL 456, MMBB 482/582, BIOL 489, FOR 540
Poster boards and easels					UNIVERSITY	EPSCOR, BIOL
Surplusing old equipment					COS/BIOL	
Administration of UBM Program					COS	Undergraduate Biology and Mathematics Research Program
GRAND TOTAL OF REINVESTMENTS	**$351,729**					

[a]Units benefited. College of Science, COS; College of Natural Resources, CNR; College of Engineering, COE; Department of Biological Sciences, BIOL; Department of Mathematics, MATH; Department of Statistics, STATS; Department of Fish and Wildlife, FISH&WILDLIFE; Bioinformatics and Computational Biology Graduate Program, BCB; NSF EPSCoR, NSF Experimental Program to Stimulate Competitive Research; and Undergradaute Biology and Mathematics Program; UBM.

Strategic collaborations

The extensive data sets that biologists collect in contemporary studies of natural and experimentally evolved populations enable mathematicians, statisticians, and computer scientists to quantify the probabilities of various evolutionary events and develop predictive models. These can be used to identify key variables that affect the outcome of evolutionary events and explore untested possibilities, which can subsequently be empirically evaluated and refined by biologists. This creates a continual feedback loop between empiricists, computational scientists, and theoreticians that tightly integrates research among multiple disciplines. *This integrative approach to evolutionary biology studies has become a hallmark of IBEST research programs that creates unique advantages in competition for extramural funding.* These teams can continue to exploit technological advances in genomics and computational sciences that allow exploration of genetic and functional diversity at multiple levels from individual cells to communities and across various spatial scales. Our research capacity in this area can be sustained and further grown because of the business plans we have developed for the continued operation, renewal and expansion of the genomics and computational resources core facilities that are critical for these studies.

Strategic Plan to Identify Scientific Opportunities

Communication in various forms—face to face and virtual meetings, conferences, email, vendor presentations, networking, and others—is required to stay abreast of new scientific opportunities, technologies, and methods that emerge in areas related to IBEST research programs. Over the course of the last ten years we have instituted additional successful mechanisms to increase awareness and to promote collegial interactions and support among IBEST researchers. These include the IBEST Lunch, the IBEST Annual Retreat, and an IBEST seminar program. We will continue these in the years ahead.

IBEST Lunch

The IBEST Lunch Series is the hidden key to our success. Each week at the same time and same place IBESTians – which include all individuals affiliated with IBEST including faculty, students, postdoctoral fellows and technicians – meet one hour for lunch. This occurs every week, all year long. These lunch meetings come in four basic flavors: (a) an IBEST investigator presents an informal "science update" on their work, (b) invited speakers present formal seminars; (c) core facility directors update IBESTians on new capabilities and changes to operating procedures; or (d) informal discussions occur at round tables of eight or more people. There is no doubt that this regular opportunity to meet fosters team-building and is highly effective as a means to communicate scientific advances, solve problems, and launch collaborations.

IBEST Annual Retreat

Each year we have an off-site annual weekend retreat that focuses on the development of strategic plans for IBEST and research proposals for teams of investigators. As part of this we decide which proposals for infrastructure and educational programs will be submitted, outline the elements of each, and assign specific tasks. We also schedule time for investigators to present their plans for research grant applications so that hypotheses and specific aims can be presented and critiqued. Through this retreat everyone gains a holistic understanding of IBEST plans, formal and informal peer mentoring, and a greater sense of community.

IBEST Seminar Program

The IBEST Seminar Series attracts top scientists from across the nation and world to the campus of the University of Idaho (see Appendix I for a listing of seminars in 2012). These seminars are used as a core element of a graduate seminar course (BCB 501), and are open to the public; often more than 50 people attend them. The persons invited typically spend two days on campus meeting one-on-one with faculty members or small groups of students and postdocs. These formal seminars and informal interactions expose IBEST personnel to the research interests, ideas, and expertise of leaders in the field. Over the years we have realized an indirect benefit of our seminar series in that invited speakers return to their home institutions and spread the word about the impressive work we are doing and the collegial and collaborative atmosphere within IBEST. This has bolstered our reputation in the scientific community and helped us recruit students. Often these seminar topics relate to a common theme. Past themes have included studies of adaptive evolution in natural populations, mathematical modeling of evolutionary processes, next-generation DNA sequencing technology and tools for the analysis of genomics datasets.

Affiliation with IBEST

There is no roster of faculty, students and staff affiliated with IBEST and we have deliberately avoided creating one. To do so would require that we set some sort of criteria and a more or less arbitrary threshold for 'membership'. This exclusionary maneuver would do nothing to achieve our goal of facilitating research and education in the intentionally broad realm of 'real-time evolution'. The closest we have come to a membership is an email list-serve that is used to disseminate announcements of seminars, IBEST Lunch topics, student thesis defense dates, and the like.

Instead we espouse an open organizational structure where people can self select and 'vote with their feet'. We extend offers to join us for IBEST Lunch with colleagues for free-ranging discussions that have often led to new collaborations, access to mentoring and advice, increased awareness of research programs related to their own, and the services and infrastructure available through IBEST Core Facilities. From there they can become 'regulars' and attend every week, choose to come occasionally, or decide that it is not worth their while. Ultimately, engaging with others and the programs of IBEST is by personal choice.

AN INTEGRATIVE APPROACH TO EVOLUTIONARY BIOLOGY STUDIES HAS BECOME A HALLMARK OF IBEST

Program for Advanced Study of Evolution and Computational Biology

A specific objective of the University's 2011-2015 Strategic Plan is to enable faculty, student, and staff engagement in interdisciplinary scholarship and creative activity. The strategies to accomplish this include expanding opportunities for ongoing interactions among faculty, students, and staff to identify areas of common interest, and increasing support for graduate and undergraduate interdisciplinary research and creative activity.[1] IBEST can significantly contribute to achieving this objective. To do so we must overcome the challenges we face by virtue of being at a small university with a limited number of faculty members that conduct research in areas pertinent to 'real-time evolution'. We propose to launch the **Program for Advanced Study of Evolution and Computational Biology**. This program will be designed to expand the intellectual capital of IBEST and opportunities for collaboration by increasing interactions with faculty at other institutions. The details of this program are being developed, and two proposals (that are not mutually exclusive) are under consideration. One strategy is to invite leading investigators in the field of evolutionary biology, computational biology, and bioinformatics to campus for extended visits of 1-4 weeks. This will permit them enough time to more deeply explore areas of common interest. Some individuals might be repeatedly invited. A second strategy would be to invite 4-6 individuals for an extended workshop in the summer (possibly 1-2 weeks in length) for brainstorming approaches to investigating key unanswered questions. The benefits of these strategies include the infusion of new ideas and expertise, lasting collaborations that generate funded research programs, new opportunities for the placement of undergraduate and graduate students, and a pipeline for the recruitment of the best graduate students and postdoctoral students from leading programs world-wide.

We envision that over time the Program for Advanced Study of Evolution and Computational Biology will create a 'virtual institute' with members located in various academic institutions and national laboratories throughout the U.S. and other countries by creating a web of collaborative partnerships. Technological advances in telecommunications have reduced geographic barriers to intensive and highly interactive research collaborations, and the University of Idaho is well-equipped with broadband Internet and the physical infrastructure (web-casting, video conferencing, etc.) to take advantage of opportunities for collaborations with leading scientists no matter where they are physically located. Importantly, the 'virtual institute' created by the Program for Advanced Study of Evolution and Computational Biology will grow the research expertise at the University of Idaho without actually having to recruit and hire faculty at the institution, overcoming a significant challenge.

Conference Travel

In 2013 we will set aside travel funds to send two faculty members each year to scientific conferences that focus on topics outside of their area of research; this will add breadth to their expertise. For example, an evolutionary ecologist might attend a conference on bioinformatics, or a statistician might attend a conference on infectious diseases. The intent is to expose individuals to new fields of investigation in order to identify new opportunities and potential collaborators. The individuals who wish to avail themselves of this opportunity can request these funds in a brief letter to the Director that explains why the proposed travel would be beneficial. Following the conference the attendee will be required to make an oral presentation as a "science update" at an IBEST Lunch.

[1] http://www.uidaho.edu/president/leadingidaho/goal2

Strategic Analysis

An abbreviated analysis of IBEST strengths, weaknesses, opportunities and threats is presented below.

Strengths

- Strong financial underpinning from university support and NIH-COBRE funding
- Nationally competitive faculty research programs
- Strong alliances and collaborations with leading scientists at other institutions
- Exceptional research core facilities

Weaknesses

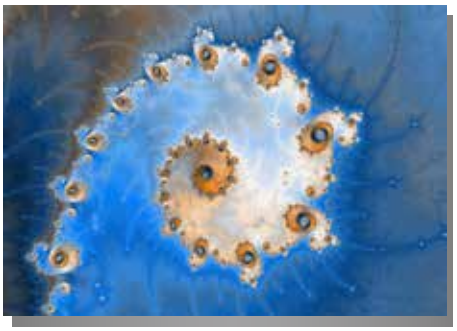
- Low targets for recruitment of IBEST-related faculty at the University of Idaho over the next five years
- Lack of start-up funding for newly hired faculty
- Inability to match the staffing of core facilities with increasing demand for services

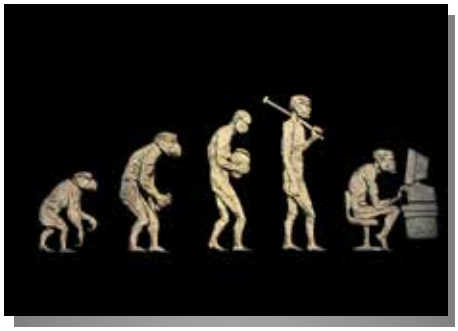
Opportunities

- Expand the intellectual capital of IBEST and opportunities for collaboration by increasing interactions with faculty at other institutions
- Addition of a grant/technical writer to the IBEST staff might facilitate efforts to submit shared instrumentation grants, training grants, and other multi-investigator proposals for program project grants and the like

Threats

- Ever increasing competitiveness for extramural funding
- Increasing administrative responsibilities that reduce involvement of senior faculty in IBEST research
- Ponderous hiring policies and procedures that are exceptionally burdensome for faculty and staff
- Policies and procedures that do not permit adequate compensation or classification of key employees
- Growth in the numbers of faculty may not balance targeted undergraduate enrollment growth
    * This is already a problem in departments of the College of Science that are responsible for a considerable amount of service courses required by students in a wide range of academic majors
    * The University seeks to grow undergraduate enrollment to 16,000 undergraduate students by 2020 – a 33% increase
- Intramural competition for program funding and the persistence of academic silos





Some programs under the IBEST umbrella.

NIH Center of Biomedical Research Excellence (COBRE)

The Center of Biomedical Research Excellence (COBRE) for Research on Processes in Evolution at the University of Idaho has received $21,649,028 in funding over 10 years from the NIH IDeA program. This funding has been critical to the growth and success of IBEST and enabled us to conduct leading-edge interdisciplinary research in computational and evolutionary biology and to mentor early career faculty to develop nationally competitive, independently-funded research programs. Under COBRE, we also established and expanded the Computational Resources and Genomics Resources Core facilities at the University. These facilities provide a diverse array of advanced instrumentation and computational resources as well as technical support to investigators that are well beyond what could be supported by single investigators or small groups. The capabilities and services of the cores have come to be integral parts and essential resources for on-going and proposed research programs.

Having established sustainable research programs, we sought a third phase of COBRE funding to further strengthen our two research cores and transition them to sustainability in a way that will continue to support the research of IBEST in the future. This proposal was submitted in July 2011 and following peer-review we have been informed that the proposal will be funded beginning in February 2013 for a five-year period and bring an additional $5,096,846 in funding to the university.

The funding will support the Computational Resources Core through purchases of previously leased equipment, upgrades to networking infrastructure, expansion and improvement of data storage and backup capabilities, and hiring of an Assistant Systems Administrator and a Systems Programmer. Support to the Genomics Resources Core will be used to purchase instruments for short-read DNA sequencing, real-time PCR, and automation of emulsion PCR (emPCR). In addition, the funds will be used to hire bioinformatics analysts, pay portions of equipment service and maintenance agreements, and purchase materials needed for protocol development and evaluation. The business plans for each of these cores are described below in their respective sections of this report. COBRE transition funding will also support three pilot grant programs for biomedical researchers: a Research Pilot Project Program, IBEST-INBRE Technology Access Grants, and Travel and Collaboration Grants. The first two programs will enable faculty to generate preliminary data that will make them more competitive for external funding, and the third will enable them to develop collaborations that support research.

COBRE Operations Budget 2012

Expense		Amount[a]
Director's salary	0.25 FTE	
Research Oversight Team	0.15 FTE	
Faculty salaries		
Administrative salaries		
Core facility staff salaries		
Postdoc salaries		
Scientific staff salaries		
Graduate student support		
Undergraduate support		
Research support		
Total COBRE support		

[a]Salary amounts include fringe benefits.

This final phase of COBRE funding, along with institutional investments in IBEST as a strategic institute, will ensure that the core facilities become self-sustaining and that we maintain the momentum of the highly competitive research programs built during the first ten years of COBRE funding.

Achievements

The COBRE has fundamentally changed the way biomedical research is done at the University of Idaho. This shift in culture is exemplified by the explosive increase in the use of next-generation sequencing and microarray technologies to explore biological diversity and evolutionary processes, and the ever-increasing demand for computational resources for biophysical studies, comparative genomics, phylogenetics, mathematical modeling, and statistical analyses. This expansion of activity has been driven by the coalescence of investigators around the scientific theme of the COBRE and ready access to the sophisticated technologies available through COBRE-supported core facilities. The uses and applications of the core resources are becoming increasingly intertwined as sophisticated computer modeling informs empirical research, and data-rich genomic analyses and population genetics studies demand advanced computational capabilities for analyses. These interdisciplinary research projects are at the forefront of understanding fundamentals of host-pathogen interactions, adaptive evolution of organisms, and several other areas. Since its inception the COBRE has mentored early career faculty to research independence, attracted new faculty into biomedical research, awarded pilot and technology access grants, developed undergraduate and graduate education programs, and formed important partnerships with investigators at other institutions throughout the nation.

Among the more notable accomplishments are the following:

- Became a founding partner in BEACON, an NSF Science and Technology Center for the Study of Evolution in Action whose investigators approach evolution in an innovative way to bring biologists, computer scientists, and engineers together to study evolution as it happens and apply this knowledge to solve real-world problems. BEACON is headquartered at Michigan State University with partners at University of Idaho, North Carolina A&T State University, University of Texas at Austin, and University of Washington
- Teamed with investigators from the University of Maryland and other institutions as part of an NIH funded STD-Cooperative Research Center on the EcoPathogenomics of Chlamydial Reproductive Tract infection (EPCRTI). The objective is to discover essential correlates of chlamydial infection of the human reproductive tract, conduct fundamental studies aimed at vaccine development, and characterize pathogenic mechanisms at play in the complex, natural environment of the female genital tract to identify targets for chemotherapeutic interventions.
- Developed a unique interdisciplinary graduate program in Bioinformatics and Computational Biology that provides students a strong intellectual foundation in three focus areas: Computer Sciences, Biological Sciences, and Mathematical Sciences, and an opportunity for truly interdisciplinary research experience.

Current and pending research funding

IBEST investigators have teamed to receive more than $30 million in research funding from the NIH-COBRE program, other NIH programs, NSF, and other sources. Since many of these projects are interdisciplinary collaborations between biologists and mathematicians, statisticians or computer scientists, many projects require the resources of both COBRE-supported core facilities. This funding has led to a rapidly increasing number of interdisciplinary publications (see Appendix 2), the recruitment of exceptional graduate students and postdoctoral scientists, and expansion of research infrastructure. This has been strengthened by incorporation of the interdisciplinary Bioinformatics and Computational Biology (BCB) graduate program under the IBEST umbrella.

We believe that the research programs of IBEST are becoming “autocatalytic” because faculty find themselves immersed in a supportive research environment that has both the intellectual and physical resources needed to conduct competitive biomedical research that is competitive for extramural funding.

Strategic Analysis

An abbreviated analysis of COBRE strengths, weaknesses, opportunities and threats is presented below.

Strengths

- Exceptional core facilities

Weakness

- There were only 7 awards from NIH state-wide in 2012 and these account for only 0.03% of the total funding awarded by NIH. All were awarded to the University of Idaho.[1]
  - This compares to 65 awards made to Washington State University, 447 awards to the University of California-Davis, 611 awards to Emory University, and 1,109 awards to the University of Pennsylvania.
- Inability to stem the tide of losing faculty who are competitive for NIH funding

Opportunities

- Sustaining momentum in biomedical research through the programs and administrative support made available through the institute

Threats

- Loss of faculty competitive with NIH grant awards
- Increasing administrative responsibilities that reduce involvement of senior faculty in IBEST research

[1] http://report.nih.gov/award/organizations.cfm

THE COBRE HAS FUNDAMENTALLY CHANGED THE WAY BIOMEDICAL RESEARCH IS DONE AT THE UNIVERSITY OF IDAHO.

BEACON

Overview of Mission and Goals

The BEACON Center for the Study of Evolution in Action is an NSF Science and Technology Center founded in 2010 with the mission of illuminating and harnessing the power of evolution in action to advance science and technology and benefit society. BEACON is a consortium of universities led by Michigan State University, with member institutions North Carolina A&T State University, the University of Idaho, the University of Texas at Austin, and the University of Washington. BEACON unites biologists, computer scientists and engineers in joint study of natural and artificial evolutionary processes and in harnessing them to solve real-world problems. Developers of evolutionary algorithms have long borrowed high-level concepts from biology to improve problem-solving methods, but have not captured the nuances of evolutionary theory. Likewise, studying the evolution of artificial systems can provide biologists with insight into the dynamics of the evolutionary process and the critical factors underlying emergent properties and behaviors. BEACON promotes the transfer of discoveries from biology into computer science and engineering design, while using novel computational methods and artificial evolutionary systems to address complex biological questions that are difficult or impossible to study with natural organisms.

As Dobzhansky famously noted[1], "Nothing in biology makes sense except in the light of evolution" BEACON's vision focuses that light, revealing fundamental biological concepts and illuminating the path toward computational applications. The key insight underlying the Center is that transformative discoveries in both computing and biology are possible through studying evolution as it happens, in both natural and digital domains. The philosopher Dennett[2] has pointed out the algorithmic nature of evolution as a process that will occur in any system with "replication, variation (mutation) and differential fitness (competition)." BEACON aims to understand evolution in this universal framework.

The overarching goal for BEACON is to unite biologists with computational researchers and other scientists and engineers in an effort to expand our understanding of fundamental evolutionary dynamics through a combination of theory and experiments on actively evolving systems, whether they are biological or computational systems. The Center helps researchers overcome the typical disciplinary biases and realize the sophistication and universality of evolution. Studies using a wide range of natural organisms (from simple bacteria like E. coli, to complex vertebrates, such as spotted hyena) are paired with novel evolutionary computation systems that allow both experimental and applied research. As a bridge between these domains, we also use digital organisms, which are self-replicating computer programs that undergo open-ended evolution. Such digital evolution systems are powerful research tools that make transparent the evolutionary process while giving researchers unparalleled control over their experiments.

The range of study systems and our focus on evolution in action allow us to explore fundamental issues in evolutionary theory. While science has come a long way in understanding evolutionary patterns and the history of life on earth, many important questions remain about the causal processes: How do complexity, diversity, and robustness arise in evolving systems? What conditions lead to the evolution of intelligent behaviors? How do ecological communities form? Why do multicellularity and other forms of cooperation evolve? How much do these processes vary between species or across biological, computational and robotic systems? Answering

[1] Theodosius Dobzhansky, "Biology, Molecular and Organismic", American Zoologist, volume 4 (1964), pp 443-452

[2] Dennett, Daniel C. (1995). Darwin's Dangerous Idea: Evolution and the Meanings of Life. New York: Simon and Schuster.

these and related questions will allow our understanding of evolution to better inform other areas of biological investigation and augment the practical utility of evolutionary design in engineering and industry. A guiding precept of this Center is that we must perform controlled experiments on evolution as it happens to fully understand, predict, and control evolutionary dynamics. These concepts demand exploration by interdisciplinary teams, joining biologists with computer scientists and engineers to solve increasingly difficult real-world design and optimization problems.

We share the deep understanding afforded by this transformative research with the broader public, encouraging exposure to and intuition about evolution through first-hand experience. Although evolutionary science is the fundamental explanatory principle in biology, it continues to be widely misunderstood and even rejected by a majority of Americans. Being able to observe and perform experiments on actively evolving systems will help people appreciate not only the creative power of evolutionary mechanisms, but also the nature of scientific reasoning itself. Digital evolution, in particular, provides a revolutionary educational tool that can bring evolution to the classroom, to a museum, and even to a web browser. The previous successes, such as the Avida-ED digital evolution educational software, have demonstrated the promise of this innovative approach, but the sustained infrastructure of an NSF Center allows us to bring it to fruition. We combine these techniques with new evolution-in-action experiments on natural organisms to advance internal training of students and post-docs as well as external education and outreach efforts (including development of curricula and educational tools). Faculty and students at all partner institutions participate fully in these educational activities, as developers and users. As part of the Center's large-scale effort, North Carolina A&T incorporates these techniques to teach about evolution in their core curriculum, a significant step for any school, and especially for an HBCU where religious pressures often cause such topics to be avoided.
For more information see: http://beacon-center.org/

BEACON Operations Budget 2012

Expense		Amount[a]
Director's salary	0.25 FTE	
Faculty salaries		
Postdoc salaries		
Graduate Student support		
Undergraduate support		
Other Research support		
Total BEACON support		

[a]Salary amount includes fringes.

BEACON research funding

BEACON promotes research on "Evolution in Action" that crosses academic areas (biological, artificial, engineering) and thematic boundaries (networks, communities, and behavior). Ideally the projects funded transcend geographic boundaries and engage investigators from multiple participating institutions. IBEST recipients of BEACON findings are described above.

BEACON administrative staff

Dr. James Foster is the Partner Lead and represents the University of Idaho on the BEACON leadership team, and also serves as a member of the BEACON Executive Committee. BEACON funds support 10% of the IBEST Business Manager's salary, who implements student hires, purchases, and oversees local finances and reporting. These funds have also provided salary support for Dr. James Foster, Program Coordinator at the University of Idaho.

In addition to Dr. Foster two other faculty members and one staff member also serve on the BEACON management team. Dr. Robert Heckendorn is represents the UI on the Diversity and Human Resource Development committee, Dr. Terrence Soule serves on the Education and Outreach committee, and Ms. Rose Poulin serves on the Financial committee.

Strategic Analysis

An abbreviated analysis of BEACON strengths, weaknesses, opportunities and threats is presented below.

Strengths

- The research foci of BEACON and IBEST, “evolution in action” and “real time evolution” respectively, are closely aligned
- Foster serves on both the BEACON Executive Committee and the IBEST Research Oversight Team. This provides IBEST a voice in BEACON decisions-making
- BCB provides a pool of talented graduate students that can work on BEACON projects
- IBEST has an international reputation for excellence in evolutionary biology

Weaknesses

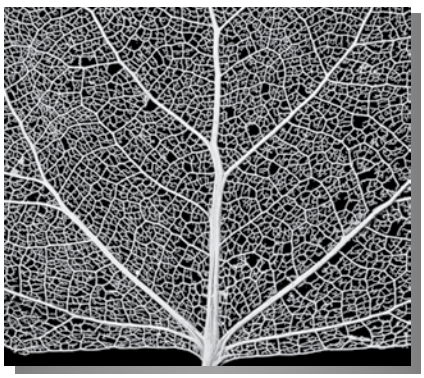
- Too few UI researchers that apply evolution in their research are engaged in BEACON
  - This is especially true for the application of evolution principles to engineering problems
  - The position descriptions of key faculty in the College of Engineering preclude significant research effort
- UI BEACON does a poor job of recruiting and engaging underrepresented groups and minorities who are also U.S. citizens
- UI BEACON does a poor job with community and industry outreach, particularly regarding educating the public and K-12 about evolution

Opportunities

- More UI faculty with interests in applied evolution (e.g., conservation genetics and evolutionary engineering) could engage in BEACON
  - There is untapped talent in the College of Engineering
- Participation in BEACON provides the experience and credibility that might increase competitiveness for other inter-institutional program project grants
- By engaging the UI STEM coordinator and the UI diversity coordinator we might develop strategies to recruit more under-represented minorities to BEACON
  - Growing Hispanic populations in Idaho represents an opportunity for increasing diversity recruitment

Threats

- Competition for BEACON funding will increase if the University of Washington and the University of Texas involve more of their faculty in BEACON
- BEACON funding to UI will decrease unless participants broaden their research collaborations to include faculty members from the other partner institutions of BEACON



NSF Interdisciplinary Training for Undergraduates in Biological and Mathematical Sciences

The goal of the Undergraduate Biology and Mathematics (UBM) program is to enhance undergraduate education and training at the intersection of the biological and mathematical sciences and to better prepare undergraduate biology or mathematics students to pursue graduate study and careers in fields that integrate the mathematical and biological sciences. The central activity is mentoring teams of undergraduate students (usually two individuals) in long-term interdisciplinary research projects that expose students to contemporary mathematics and biology and address research questions using with modern research tools and methods. That is, projects must be genuine research experiences rather than rehearsals of research methods. Projects must involve students from mathematical and biological sciences and include joint mentorship by faculty in both fields. It is expected that projects will strengthen the research and education capacity, infrastructure, and culture of the partner institutions, the University of Idaho and Washington State University. To this end, projects should create models for education in the mathematical and biological sciences and influence the direction of academic programs for a broad range of students.

Progress in 2012

The UBM program funded 24 undergraduate interns in Mathematical Biology across the UI and WSU campuses. The interns were placed in a diverse array of laboratories, ranging from very applied contexts (such as food science and agriculture) to basic research. Scientific disciplines in which students are actively engaged include evolutionary biology, biomedical research, microbiology, neuroscience, behavioral biology, genomics, and physiology. The interns engage in intensive research experiences during the summer, and attend monthly meetings where they present their research findings. In addition, many interns have presented their work at scientific meetings, and two students from the UI have received awards for their work. Two papers have been published with UBM interns as authors, and several more are in preparation. We have also begun institutionalizing curricular aspects of the UBM program at the UI through the creation of a new degree track (option) in “Mathematical Biology” within the mathematics department.

UBM Operations Budget

Expense		Amount[a]
Director's salary	0.08 FTE	
Other salaries		
Undergraduate support		
Other Research support		
Total NSF UBM support		

[a]Salary amounts includes fringe.

Bioinformatics and Computational Biology (BCB)

BCB Vision Goals and Impact

Technological advances in the last two decades have created an avalanche of biological data, and this challenge will only increase in the immediate future. The manipulation, analysis and interpretation of large, complex datasets are thus central to much of biology. To address this challenge investigators commonly resort to a division of labor between data generation and data analysis. For example, biologists generate massive genomic datasets and bioinformaticians develop programs to organize, analyze and display data. However, it has become increasingly clear that success in science requires an integrative approach that unites experimental design, data collection, analysis and interpretation in a common framework. To meet this need the University of Idaho launched the Bioinformatics and Computational Biology (BCB) interdisciplinary graduate program in 2003. This program includes faculty with expertise in the biological sciences, mathematics, statistics, and computer science.

Instead of training students to be skilled in one specific area, we equip students with a set of quantitative tools and conceptual skills that prepare them to integrate theoretical and empirical research endeavors. Our approach focuses on critical thinking and problem solving that can be applied across the spectrum of challenges in biological research: from developing mathematical models, to organizing and analyzing data, to understanding issues of biological complexity. In addition, the BCB program requires research rotations and core courses that facilitate both “breadth” and “depth”. The technology of the day is fleeting, but mastering the timeless principles that underlie solutions to biological problems enables scientists to tackle new questions and incorporate new technologies without reinvention.

With the advent of next generation sequencing and next generation bioinformatics approaches, we now require “next generation” scientists. Our vision is to bring together computational and empirical approaches in a unified, interdisciplinary graduate training program focused on evolutionary processes. Our primary goal is to train a new generation of scientists with the quantitative skills to merge empirical and theoretical approaches and have a profound impact on STEM (Science, Technology, Engineering and Mathematics) graduate training. The BCB approach to graduate education is a three-step process: building a strong foundation, gaining interdisciplinary breadth and depth, and conducting cutting edge research. A detailed description of our unique program can be found on our newly revamped webpage http://www.uidaho.edu/cogs/bcb.

Our performance demonstrates that we have delivered on the promise of a highly marketable transformative graduate education. The 19 PhD students who graduated between 2006-2011 have gone on to postdoctoral positions at prestigious institutions, including the University of Chicago, Yale University, and University of Michigan, and from there many have secured tenure track faculty positions at institutions with higher national profiles than the University of Idaho (see table on page 33).

BCB Alignment with the University Strategic Plan and UI Priorities

The mission of BCB directly mirrors Goal 1 of the University of Idaho Strategic plan. We have created an adaptable, integrative curriculum at the graduate level to prepare scientists for continued success in a rapidly changing world. We have developed co-curricular activities that are tightly integrated with our current program. This BCB program is also wholly consistent with Goal 2 of the Strategic Plan of the University in that it expands opportunities for ongoing interactions among students and faculty, increases financial support for graduate and undergraduate interdisciplinary research, enhances national and international visibility of the University’s contributions to interdisciplinary scholarship, and builds partnerships with other educational institutions. It also is catalyst for the submission of other large, interdisciplinary research proposals and sustaining successful projects that are already funded. As part of BCB training, students partner with faculty to experience the rewards of outreach and engagement (Goal 3) and become members of a well-established research community that is vibrant and open, and that teaches and fosters ethical conduct in science (Goal 4).

Current Status of BCB Program and Budget Summary

We currently have eighteen students in the program (see table on page 33). This year alone we have admitted six students into the BCB program, a record in the last four years. Only two of the eighteen students have been enrolled longer than four years. We expect several students to graduate in this academic year.

BCB is a very cost-effective program with a small operations budget. This is possible because it partners with other departments for course delivery. For example, Mathematical Genetics (Math 563) is a course required of all BCB students and is offered by the Mathematics Department and cross-listed with Washington State University. Similarly, the BEACON program provides opportunities for online course delivery from Michigan State University and is available to our students without cost.

Since BCB has no teaching assistantships it relies heavily on grant dollars to support its students. The small amount of fellowship funds provided by the University ($33,000) is strategically used to supplement existing funding, thus enabling faculty to support more students. Because the fellowship dollars are complimented by grant dollars it yields a much greater return on the small investment. IBEST currently provides $91,500 of the $453,900 used to support BCB students, while $137,500 is from NIH grant funds, and $58,000 is from NSF grant funds. The remainder of the student support consists of university funds, the USDA and various other funding sources, including industry. Last year and this year, only one student was supported on a teaching assistantship. Through strategic use of these funds we are able to provide students with attractive financial support that includes payment of a stipends, medical insurance, tuition, and fees.

BCB Graduate Program Operations Budget 2012 (UI portion only)

Expense		Amount[a]
Director's salary	0.25 FTE	
Administrative staff salary	0.20 FTE	
Graduate student fellowships		
Total UI BCB support		

[a]Salary amounts include fringe benefits.

Strategic Analysis

An abbreviated analysis of BCB program strengths, weaknesses, opportunities and threats is presented below.

Strengths

- Unique program
  - The BCB program at the University if Idaho is different from many other Bioinformatics programs as it does not just covers genomics but many other aspects of computational and mathematical biology and statistical genetics. It is uniquely positioned to address evolutionary questions.
- High quality students
- Nesting of program within IBEST
- Course offerings also benefit graduate students in other university programs
- Critical mass of faculty

Weaknesses

- Extraordinarily low institutional support in terms of graduate student fellowships
  - The UI currently only provides $33,000 for graduate student support – slightly more than the amount needed to fund one student.
- Low targets for recruitment of BCB-related faculty at the University of Idaho over the next five years
- Complex and changing administrative oversight requirements imposed by University administration
  - Oversight by a council of four deans weakens advocacy for the program
- Too few faculty members in computer science, mathematics and statistics with research programs allied with BCB
- Due to the interdisciplinary nature of the program some students find certain core courses challenging

Opportunities

- Growing awareness of program nationwide
  - Can improve caliber of student applicants
- Improve efforts to recruit students

Threats

- Nearly complete reliance on grant funding for students in a climate of increase competitiveness for extramural funding
- Faculty retention

WE EQUIP STUDENTS WITH A SET OF SKILLS THAT PREPARE THEM TO INTEGRATE THEORETICAL AND EMPIRICAL RESEARCH ENDEAVORS.

Bioinformatics and Computational Biology Program

Student	Degree	Advisor	Advisor Dept/College	Year Admitted	Research Topic	Annual Funding	Funding Source(s)
Daniel Beck	PhD	James Foster	Biological Sciences/COS	Fall 2009	Using classification models to detect microbial interactions.		NIH INBRE
Maia Benner	PhD	Barrie Robison	Biological Sciences/COS	Summer 2010	Nutritional Genomics: Selenium Status and Behavior		BCB/IBEST
KC Cho	MS	Zaid Abdo	Mathematics-Statistics, COS	Spring 2010	Utilize Bayesian networks for identifying the relationships between diseases, bacterial species, and metadata		NIH
Kelsie Evans	MS	Alex Karasev	Plant, Soil, & Environmental Sciences, CALS**	Fall 2011	Potato Virus Y Evolution and Recombination		USDA
Hua Feng	PhD	Paul Joyce	Mathematics-Statistics, COS	Fall 2005	Optimal Design and Computational Algorithm in Clinical Studies from Molecular and Clinical Perspectives		-
Michael France	PhD	Larry Forney	Biological Sciences/COS	Fall 2012	Evolutionary patterns of spatially structured bacterial populations		BCB/IBEST P&G
Tyler Hether	PhD	Paul Hohenlohe	Biological Sciences-Statistics/COS	Fall 2010	Identifying population level processes that generate genomic differentiation during ecological speciation		NSF BEACON
Roxana Hickey	PhD	Larry Forney	Biological Sciences/COS	Summer 2010	Ecological networks in the vaginal microbiome		NSF STEM/NIH
Samuel Hunter	PhD	Zaid Abdo	Mathematics-Statistics, COS	Spring 2006	Applications of next generation sequencing technologies for addressing a variety of biological problems and questions		-
Vandhana Krishnan	MS	Larry Forney	Biological Sciences/COS	Summer 2010	Unraveling the ecological functional diversity of prominent vaginal bacteria through comparative genomics		NIH
Hannah Marx	PhD	Dave Tank	Forestry/CNR	Summer 2012	Phylogenic community assembly at different scales and over time		BCB/IBEST
Genevieve Metzger	PhD	Jack Sullivan	Biological Sciences/COS	Spring 2012	Phylogenetic and population genetic research		BCB/IBEST/BioI
Matthew Pennell	PhD	Luke Harmon	Biological Sciences/COS	Spring 2012	Developing statistical models to test macroevolutionary hypotheses using phylogenetic trees		BCB/IBEST BEACON NESCent (NSF)
Pavitra Roychoudhury	PhD	Steve Krone	Mathematics-Statistics, COS	Spring 2009	Spatial structure and adaptive evolution in bacteriophages		NIH COBRE
Daniel Silva	PhD	Luke Harmon	Biological Sciences/COS	Fall 2012	Statistical comparative methods and macroevolution in ecology and behaviour		CAPES Foundation (Brazil)
Allison Tucker	MS	Zaid Abdo	Mathematics-Statistics, COS	Fall 2011	Creating a stimulation to gain information about plasmid host range shifts		NIH
Janet Williams	PhD	Mark McGuire	Animal Veterinary Science/CALS	Summer 2012	Exploring the milk microbiome and its relationships to health and disease (Genomics in Health and Disease)		Abbott Laboratories
Lei Yang	PhD	Holly Wichman	Biological Sciences/COS	Spring 2011	Probing the extinction of LINE and SINE transposons in the mammalian genomes		BCB/IBEST

Total AY 12-13 IBEST Support:

*College of Science

**College of Agriculture and Live Sciences

List of BCB graduates with their most recent employment information.

Former BCB Students	Current Position
Faculty	
Abdo, Zaid	Associate Professor of Mathematics and Statistics, University of Idaho
Bankhead, Armand R.	Assistant Professor of Medical informatics and Clinical Epidemiology, Oregon Health Science University, Portland Oregon
Beisel, Craig Jason	Computational Statistician, Information Project Manager at Unum Corporation, Portland Maine.
Bent, Stephen James	Assistant professor of Biological Sciences, University of Adelaide, Australia,
Buzbas, Erkan Ozge	Assistant Professor of Statistics, University of Idaho
Evans, Jason Owen	Computer Software Engineer, Facebook
Feng, Hua	Statistical Research Coordinator, University of Florida, Department of Epidemiology, College of Medicine
Guan, Yongtao	Assistant Professor, Baylor College of Medicine, Houston Texas, since fall 2010.
Hu, Xiaojun	Postdoctoral Fellow, Laboratory of Immunopathogenesis and Bioinformatics (LIB),Clinical Services Program (CSP) SAIC-Frederick, Inc. NIAID, NIH Contractor
Johnson, Audra KK	Bioinformatics Software Engineer, University of Washington, Seattle WA
Oswald, Benjamin	Postdoctoral Fellow, Department of Biological Sciences, Notre Dame University
Pierson, Jacob D.	Law school graduate, Business entrepreneur, Boise, ID
Ponciano, Jose Miguel Castellanos	Assistant Professor, Department of Biology, University of Florida
Rokyta, Darin Rene	Assistant Professor of Biological Sciences, Florida State University
Settles, Matt	Bioinformatics Scientist, University of Idaho
Shyu, Tse-Ming (Conrad)	Research Scientist, Department of Microbiology and Immunology, Virginia Commonwealth University
Wei, Wei	Assistant Professor of Biomedical Informatics and Computational Biology, University of Minnesota, Rochester
Zhong, Xue	Research Fellow, Vanderbilt Center for Quantitative Sciences

Core Facilities

Overview

We have seen that the core facilities can serve as "intellectual hubs" to stimulate cooperative research, solve common problems, and develop approaches that are widely applicable within IBEST. This occurs because IBEST cores provide research services and technical expertise to multiple IBEST investigators that have common needs although their research programs address quite different questions. In meeting the needs of investigators our research cores provide the facilities, services, and training needed for IBEST investigators to conduct their research more efficiently and effectively. Importantly the core personnel are aware of advances made in different research groups and serve as a community resource by sharing information among COBRE investigators. This collaborative approach avoids duplication of effort, increases cost effectiveness, and speeds progress.

Over the past decade significant funding from the NIH-COBRE, Idaho-INBRE, and the University of Idaho has been invested to build and operate impressive core facilities on campus for computation and genomics that are essential for scientists engaged in contemporary research on evolutionary and computational biology. However, not only are these facilities expensive to operate (e.g., personnel) and maintain (e.g., service contracts), they must also be 'renewed' through the replacement of obsolete instruments, networked computers, data storage, and software. These are formidable logistic and financial challenges that must be overcome to maintain the competitiveness of our research programs. We have taken critical steps to address this challenge. The Computational Resources Core (CRC), Genomics Resources Core (GRC), and the Optical Imaging Core (OIC) have been established as "service centers" in the university so they can charge fees to users and use the income to offset expenses. If use of the cores is sufficiently high they will become financially self-sustaining. Since usage has grown dramatically in recent years we are optimistic that this goal can be achieved by the Computational Resources Core and Genomics Resources Core. We are in the early stages of launching the Optical Imaging Core and the Mass Spectrometry Core as fee-for-service facilities so it is too early to make such projections. In the event that we fall short of this target, we must be in a position to assess their importance to research programs at the University, and if necessary substantially subsidize their operations using institutional funds.

Increasing Awareness and Use of Core Facility Resources

Increasing the number of core facility users is key to sustaining the cores. We have undertaken a series of steps to increase awareness of the capabilities and services offered by the core facilities in an effort to grow the user base. These have included:

- Updated the IBEST Core website to include descriptions of the core facilities, the capabilities of each, and fees for the services available. See: http://cores.ibest.uidaho.edu/
- Developed eye-catching flyers and posters for all IBEST Cores. The posters will be prominently posted in high traffic areas, and the flyers will be mailed to departmental email list-serves.
- The Core Directors have periodically made presentations as part of the IBEST Lunch Program to provide researchers of with information on the capabilities of each core, changes and updates in the services provided, and future plans.
- The Core Directors have arranged for vendors to make presentations as part of the IBEST Lunch Program to explain the technologies used by their instruments and products and how they can be applied in various research applications.
- The OIC Director has arranged for demonstrations of instruments
- Core Directors and staff have participated in regional and national core facility user groups and used these as opportunities to promote the capabilities and services of IBEST Core facilities.

Technology Access Grant Program

IBEST has partnered with the Idaho-INBRE to administer and fund the Technology Access Grant Program. This is essentially a pilot grant program that provides funding to investigators so they can conduct exploratory studies using the technologies and technical support of the IBEST Genomics Resources Core, Computational Resources Core, and Optical Imaging Core. These grants are intended to help investigators produce preliminary or proof-of-concept data needed for competitive external proposals. The reasoning behind the program is that the high costs of using the technologies available in the core facilities may often constitute a 'barrier to entry' that preclude such studies. This is often compounded by the fact that many PIs are not familiar with the technologies available and may be reluctant to invest precious research dollars to evaluate new or alternative approaches that could nonetheless provide significant benefit to their research. This program is also seen as a way to stimulate interest in use of the core facilities over the longer term. Armed with preliminary data some fraction of the PIs awarded will go on to submit research proposals that (if funded) will exploit the fee-for-services of the cores and become a revenue source. Finally, these Technology Access Grants essentially subsidize the operations of the core facilities, since the grants are used to purchase services, and revenues generated flow into the service centers and a portion is used to pay staff salaries and instrument service contracts.

Proposals are accepted at anytime during the year and the review process is simplified and expedited. The amount of each award depends on the analyses done, but typically range from $5,000 to $10,000. Amounts up to $15,000 may be awarded if the need is justified based on project requirements. Applicants consult with the appropriate IBEST Core facility director prior to submitting their proposals to obtain advice on experimental design, sample preparation (when appropriate), specific information on the cost of analytical or computational services, and data analysis services. With advice from the core director the investigator determines the services required, but the core director alone determines the costs of these services in compliance with University of Idaho policy.

Application and Proposal Review Procedures

The application procedure is uncomplicated and the expedited review process typically requires 7-10 days. Applications consist of a cover letter that briefly states how the proposed research is related to human health or consistent with the real time evolution theme of IBEST or cell signaling, the scientific theme of INBRE. It must also include a specific plan for preparing research proposal(s) to secure extramural funding from NIH or other federal agencies and related to the Technology Access Grant request; and explain how the investigator will comply with the necessary university and NIH regulations concerning research on Human Subjects, Animal Care and Use, or recombinant or infectious biological agents (if appropriate). The proposal itself is no more than two pages in length, and includes descriptions of the background and significance of the proposed research, experimental design, analytical or computational services, and data analysis services that are needed. Finally the proposal must contain a budget limited to $15,000 that includes a description of the specific services to be obtained. Budgets must include official quotes generated by the core facility director. Only costs incurred by the Core Facilities may be included. All other costs (i.e., sample collection and DNA or RNA extraction and purification) are borne by the investigator.

IBEST and INBRE require all recipients of a Technology Access Grant to cite this support in publications that emanate from this funding. For reporting purposes, IBEST and INBRE will also require information about all publications, presentations, and grant submissions that result from this funding.

The IBEST Research Oversight Team and an external reviewer (arranged by Idaho-INBRE) evaluate each proposal in terms of scientific merit and the potential to form the basis of a competitive proposal for extramural funding. Ranking will be based on (in descending order of importance): (i) potential to lead to new extramural funding from NIH or federal agencies or foundations, (ii) scientific merit, (iii) likelihood of publication, and (iv) the likelihood of future core facility usage. Preference is given to junior investigators who are developing their research program and established individuals who wish to extend their research program into a new area.

Four Technology Access Grant Awards have been made so far in 2012 (see page 15)

Strategic Analysis

An abbreviated analysis of the strengths, weaknesses, opportunities and threats from a programmatic perspective is presented below.

Strengths

- Impressive capabilities for a small research university
- Strong financial underpinning from university support and NIH-COBRE funding

Weaknesses

- Limited staffing
- Few research programs are now 'heavy users' of core facilities
  - Over the next five years few faculty that require core facility services will be recruited to the University of Idaho

Opportunities

- Increase numbers of off-campus users to provide revenues to pay the balance of staff salaries
- Ever advancing technology imposes pressure to 'keep pace' with the leading edge

Threats

- Increasing competitiveness for extramural funding – the primary source of user fees and financial support for staff
- Inadequate compensation for key personnel

The capabilities of the IBEST core facilities, the details of core facility sustainability plans, and the specific strengths, weaknesses, opportunities and threats of each core are provided below.

TECHNOLOGY ACCESS GRANTS HELP INVESTIGATORS PRODUCE PRELIMINARY DATA NEEDED FOR COMPETITIVE EXTERNAL PROPOSALS.

IBEST Computational Resources Core (CRC)

Overview

The IBEST Computational Resources Core (CRC) serves as the computational backbone of evolutionary and computational biology research at the University of Idaho. It provides investigators with state of the art high performance computing and large data storage capacity for use in analyzing and managing large volumes of research data. Users of the core run jobs that may use hundreds of processors in parallel or large memory allocations and may run require weeks to complete. The CRC is explicitly designed to manage the complex computational and storage requirements for the IBEST researchers and core facilities with very high data reliability and availability. The core contains an advanced mix of high performance computing clusters, powerful servers and reliable data storage components as well as the knowledge and technical skills required to compress years of analysis into days.

The CRC currently enables several computationally intensive research projects, including molecular modeling, statistical simulations, computer algorithm development, and machine learning and data mining. Our aim is to gradually wean the CRC from COBRE dependence by implementing a business model for fiscal autonomy, without sacrificing flexibility or innovation. The keystone of our plan is to implement a Feedback Lifecycle Model, with two mutually reinforcing pieces: one with purchased equipment for Research Program Development System and a Customer Supported System built with leased high-end equipment to support users with independent funding. Our objective is to recruit researchers to develop ideas and preliminary data for future projects on the Research Program Development System, and transition them to perform those projects on the Customer Supported System once funding for the research is secured. A key element of the plan is to purchase post-lease equipment for the Research Program Development System while using user fees to maintain the leased systems. In the near term COBRE funds will support operation of the Research Program Development System and “prime the pump” by moving the first round of leased equipment from the fee-for-service system to the development system, once the first round of leases expire. Over the longer term this strategy will make the data transport hardware and software of the two systems compatible.

Core Facility Resources

The CRC data center is a 1400 square foot facility in Room 124 in McClure Hall on the University of Idaho campus that has been specifically designed and renovated for the core. This room has a dedicated UPS with three-phase power and four-forced air handlers attached to redundant university chilled water systems. Optical fiber and copper interconnects provide high-speed data transfer for server and storage intercommunication and communication to the university backbone that is connected to the high-speed Internet 2 network. Our primary systems include the following:

Computing Clusters

The CRC has two distinct computer clusters for research and the genomic data analyses. The main cluster provides 512 processor cores and over 2 terabytes of system memory, with 40Gb/s QDR Infiniband connections providing a fast, low latency data transmission. The second cluster, comprised of older equipment, accommodates processing during peak demand times.

Analysis Systems

The CRC maintains six servers for jobs that require large amounts of shared memory for analyses such as distance-based phylogenetic analyses and molecular simulations. The most powerful server in this group contains over 48 times the system memory of a standard desktop (192 GB) and is used heavily for hybrid sequence assembly of next-generation sequencing data.

Support Systems

The CRC maintains its own support infrastructure because this scale of core operations falls well outside that of the University of Idaho Information Technology and Computing services. These include several servers for data storage and authentication of user accounts, domain name resolution, Internet address assignment, and secure connections to our private networks. The core also provides web and database services for online documentation and data sharing.

Cloud Systems

The CRC has recently implemented services that allow us to leverage the flexibility of cloud computing. These fee-based services are customized to meet the specialized needs of investigators working in the rapidly expanding fields of bioinformatics and next-generation DNA sequence data analysis. Our cloud environment is based on standard virtualization practices and open source management tools that mimic the well-known companies such as Rackspace and Amazon. This specialized group of systems comprises components designed for commodity and high performance data processing.

Data storage systems

The CRC maintains two kinds of data storage. The first of these include computational storage (198 TB gross) comprised of fast but more expensive disk arrays, and commodity storage on several control systems that are linked together through a special type of file system. The second is for long-term data archiving and backup storage (284 TB gross). This storage group comprises fast disk arrays for quick access to shared data, as well as commodity storage and tape robots for offsite storage of important data. In addition the core provides solutions to maintain data integrity and restoration.

Systems for education and training

To support educational programs and inter-institutional collaborations we maintain several teleconferencing enabled conference rooms and a state of the art technology classroom. The classroom is used extensively by instructors from the College of Science and the College of Natural Resources, and has the only high definition projector and screen on the UI campus. The classroom also has teleconferencing system, which allows us to offer workshops and classes from and to collaborating institutions such as Michigan State University, University of Texas at Austin, University of Washington, and North Carolina Ag and Tech.

Staff

Two full-time staff members manage the CRC infrastructure. They report to the Director and are advised by Dr. James Foster who serves as the Scientific Advisor. The core staff members are:

Acting Core Director

Mr. Robert Lyon serves as and is responsible for overseeing all core systems and personnel; management of the high-performance computing and cloud computing systems, several supporting and data storage systems; network management for the data center; developing custom management tools and facility web sites; programming and scripting; consultation; core facility grant reporting, and strategic planning to meet the future needs of the facility and researchers.

Assistant Computer Scientist

Mr. Trent Nelson is responsible for management of our account systems; management of several analysis systems; management of the database systems; liaisons with the Genomic Resources Core; system reporting; management of classroom and teleconferencing systems; classroom scheduling; system monitoring; and technology/networking support for researchers and labs.

Faculty Scientific Advisor

Dr. James Foster contributes to strategic planning efforts and provides technical advice on the hardware, software, and techniques that are most appropriate for the research done within IBEST. Dr. Foster was Director of the core from 1990, when he established it, until 2011 when he transferred administrative responsibility to Mr. Lyon.

CRC Clientele

The CRC has supported the efforts of researchers in the following departments at the University of Idaho: Animal and Veterinary Sciences; Bioinformatics and Computational Biology; Biological Sciences;; Computer Science; Electrical and Computer Engineering; School of Food Sciences; Fish and Wildlife; Forest, Rangeland, and Fire Sciences; Mathematics; Physics; and Statistics. In addition, researchers from the following universities currently hold system accounts: Stanford University; Syracuse University; University of Southern California, University of California-Berkley; Michigan State University; Washington State University; University of South Florida; University of Massachusetts; Willamette University; and Boise State University.

Financial Statement

The table below summarizes the reoccurring expenses and income for the CRC. One-time purchases of equipment and other items using grant funds are not included.

2012 Financial Summary : Computational Resources Core Operating Budget[a]

	Category	Amount	Amount	BALANCE
Expenses	Personnel			
	Equipment contracts			
	Other operating expenses			
Income	Users fees			
	Grant support			
	University support			
BALANCE				$0

[a]Purchases of equipment are not represented in this budget summary.

Major Accomplishments

This year has brought significant changes to the CRC, which has also reached impressive milestones. Our primary cluster, which has now been operating for 3 years, recently hit one of those milestones. Over one million jobs have been run on this cluster with a total compute time that would have taken nearly a millennium to complete on a standard desktop system. These jobs have allowed funded projects to be successful and the results have been incorporated into numerous peer-reviewed publications. To support the growing need for computational equipment and the storage of next-generation DNA sequencing data, we have begun a significant expansion of services and infrastructure. These have been funded by the COBRE and a newly awarded Murdoch Foundation grant, and leveraged the new equipment leasing policies of the university. In total we have purchased close to $900,000 of new equipment including high-speed networking, new large memory servers and close to 350 TB of new storage. These purchases have positioned us to meet the computational needs of our clientele and built the foundation for future advancement into large-scale data access, storage, and archiving.

Until last year the UI had a strict 'no leasing' policy for equipment. We facilitated discussions with the UI Departments of Finance and Administration, Office of General Counsel, and Dell Financial Services and these resulted in the first master lease agreement for equipment. This agreement increases operational flexibility and opens the way to obtain equipment with the lease payments paid by users while at the same time maintaining compliance with guidelines for federal grants.

Near-term Goals

The rapid addition of new services and equipment has stretched the CRC to its limits and negatively affected the usefulness and stability of the systems as a whole. Although the new equipment is operational, we have not been able to effectively integrate the equipment into the core. Our objectives for the coming year will be to:

- Perform a comprehensive audit of systems and services to determine focus areas for time and effort. The audit will include core staff, select customers, and IBEST administrators. This audit will be completed by May 2013 at which time we will use the findings to enhance services that will be sustainable and beneficial, and eliminate those which will not
- Stabilize equipment of the Customer Supported System (leased) and Research Program Development System (purchased with grant funds) to provide the best possible services for our core users. We will accomplish this by:
  - Hiring a programmer and a new lead system administrator to begin the process of effectively managing the influx of new equipment and services
  - Continue training the next generation of programmers and system administrators by focusing on our student helpers
- To transition core users to our Customer Supported Systems we will need to do the following in the coming year:
  - Create fee structures for the personnel time and effort expended to maintain high performance computing system
  - Simplify the pricing structure for the service center

Addressing these issues will allow us to meet our goal to provide researchers with an exceptional user experience and increase the visibility of the University through quality research.

In addition to the goals listed in the previous section, we are working to refine our strategies to increase revenue and promote sustainability, while maintaining the openness that has brought us success in the past. We will begin a target marketing campaign through the use of campus-wide workshops and seminars to give researchers and students hands on experience with these impressive systems, while at the same time increasing our visibility. This increased visibility and knowledge should translate into increased revenue as we demonstrate the capabilities and resources that principal investigators can bring to bear in their research programs.

There are also potential revenue sources separate from research. As funding at the UI becomes tighter and budgets shrink, there has been an effort by many departments to consolidate IT efforts. To help meet the need of the campus community and bring in funding through our service center, we have recently piloted an effort to provide data storage services to other departments and colleges. Our initial tests with IT staff in the College of Engineering have been promising. Once the tests have been completed, we will review the feasibility and sustainability of these services and make the decision whether or not to continue.

Summary

Over the past year the CRC has experienced significant increases in the size and types of services we can provide. Without the addition of additional staff we will not be able to sustain the levels of activity, much less expand to meet increasing user demand. We are also wary of becoming entrapped in a cycle of constant expansion to meet the needs of current and new clientele, especially to provide services to non-IBEST programs as a means to raise revenue. In the coming months we intend to refocus our efforts and add new talent to maintain the successful record of operation we have had for many years.

Strategic Analysis

An abbreviated analysis of CRC strengths, weaknesses, opportunities and threats is presented below.

Strengths

- The CRC has impressive capabilities
  - The systems for computation and data storage rival that of many larger universities
- Strong financial underpinning from university and funding agencies
  - A significant fraction of the earned overhead is returned to the institute
  - IBEST has a strong track record of grant funding from NIH, NSF, and the Murdock Trust
- Exceptionally qualified and dedicated core director
  - Single-handedly designed and implemented most of systems now in place
- Flexibility of core configuration through the use leased equipment:
  - UI adjusted policies on leased equipment and the lease costs can be recovered on grant proposals
  - New equipment can be purchased after the lease at a reduced cost and redeployed to replace aging equipment purchased with grant funding

Weaknesses

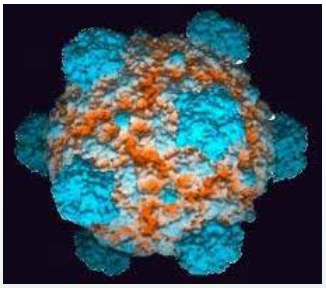
- Thin staffing
  - There is a pressing need to hire individuals that possess the specialized skills required to effectively care for our clientele and equipment
  - Staff members are unable to keep up with current demands for services

Opportunities

- Increasing the number of off-campus customers to raise revenue that can be used to pay the balance of staff salaries
- There are opportunities to expand our services to members of the campus community
  - UI departments and colleges are looking to outsource IT services created by consolidation and budget deficiencies; the CRC has the technology available to fill some of these gaps
- Expand the service center to bill personnel costs associated with maintaining the high performance computing clusters of the Research Program Development System
- Expansion of computational capabilities through use of cloud computing
  - Through the addition of our cloud computing equipment we can position ourselves for expanded usage during peak times. Known as cloud-bursting, this feature will allow us to push jobs to external cloud systems (at a cost) instead of purchasing equipment to satisfy short term demand.

Threats

- Few research programs are now 'heavy users' of the CRC
- Heavy users face high fees for use of Customer Supported Systems
- High equipment replacement costs
  - We have almost 2 million dollars of equipment in the core and it has a target life-span of 3 years. This estimate is twice as long as the industry standard (1.5 years) and reasonable given that the systems experience high load most of the time. The increased wear and tear from this heavy use translates directly to shorter lifespan and higher than average failure rates.
- Difficulty in recruiting and retaining qualified staff
  - UI Human Resources requires us to fit the specialized skills required to run these facilities into job descriptions and minimum requirements that do not correspond or translate to the needed skill sets.
  - Significantly lower than market salaries hinder the ability to recruit and retain experienced personnel in the areas of high performance research computing and data management.



CRC Research Highlight

The core facility has been an essential tool to many projects and collaborative partnerships. One such collaboration between Zaid Abdo, Matthew G. Stein, Andrzej Wojtowicz, Kim M. Pepin, and Eva M. Top is consists of statistical modeling techniques used to simulate and predict evolutionary processes of bacteria and phage, a type of virus that infects bacteria. Each year more than 2.4 million people are infected by drug resistant pathogens acquired at healthcare centers. Effective modeling techniques can significantly advance our understanding of how these pathogens evolve. Future use of these models has the potential for saving thousands of lives through the discovery of evolutionary mechanisms that can become targets for novel treatment therapies.

The complexity and the parameter rich nature of these models can limit the feasibility for statistical inference and their overall usefulness. To overcome this barrier, a new approach called Approximate Bayesian Computation (ABC) is being used together with a mechanistic model of experimental evolution. ABC is a fast and simple method for fitting complex models to data by comparing simulated data to observed data and using that to approximate the posterior distribution of the parameters of interest. .ABC requires: 1) designing a simulation based on the proposed model, 2) performing large number of simulations based on a set of proposed parameter values, and 3) comparing each of the resulting data sets to the observed. Comparisons are made using a distance measure. If the simulated data are equivalent to, or close enough, to the real data then the parameter values that were used to simulate these data are kept. This results in a set of candidate values that are used to construct the approximate posterior distributions for the parameters of interest. It avoids the direct evaluation of a likelihood function, which is computationally expensive.

Validating this method requires vast amounts of computational resources and the current project involves 250,000 'runs' of the proposed model, which could take up to 15 years on a standard desktop computer. The IBEST Computational Resources Core has the technology and expertise available that will compress this validation process to several weeks instead of several years.

Threats continued

- Ever advancing technology imposes pressure to keep pace with the leading edge in order to maintain relevancy in the research community
- A danger of “scope creep”
  - We should not to grow beyond what we can efficiently maintain and support or else we run the risk of poor system stability and performance
- Increased personnel and equipment costs cause pricing to be noncompetitive in respect to other commercial and academic facilities

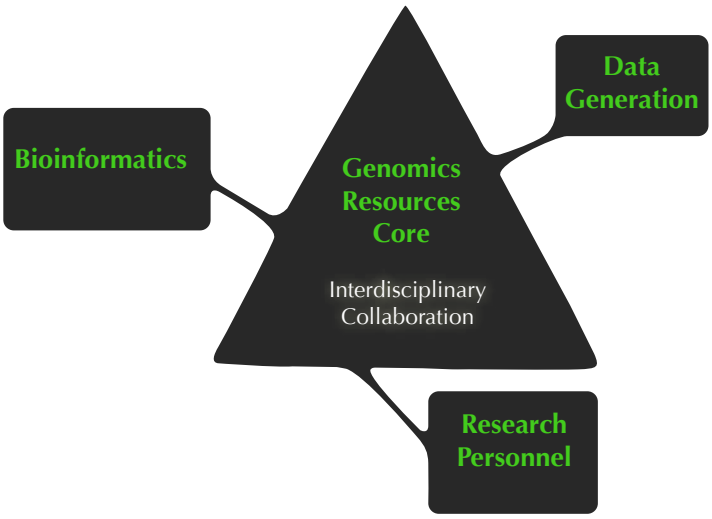
IBEST Genomics Resources Core (GRC)

Overview

The IBEST Genomics Resources Core (GRC) provides researchers at the University of Idaho access to the technology, experience, and expertise in molecular biology methods and bioinformatics needed to acquire, analyze, and visualize data generated from the high throughput technologies used in genomics research. For the first seven years, the GRC had only about $200,000 in capital equipment and no full time employees, but 2009 marked a period of explosive growth that is on-going. We have since acquired over $1.8 million of new instrumentation and this has led to a dramatic expansion of the capabilities and services offered by the GRC. Now investigators can exploit next-generation Roche 454 pyrosequencing, Illumina MiSeq sequencing, NimbleGen microarray services, single nucleotide polymorphism (SNP) analysis for genotyping, high-throughput sample preparation, and targeted re-sequencing of genes to assess allelic diversity.

Early on we recognized that most researchers lacked the training and specialized expertise needed to exploit these technologies. The size of "knowledge gaps" varied between research groups. Some lacked expertise in molecular biological methods used for sample preparation, while other lacked savvy in the use of bioinformatic tools and statistical methods for the analysis of genome sequence data or microarray data. Allowing investigators to stumble through knowledge gaps seemed treacherous and inefficient. To seamlessly bridge that gap, we devised and implemented an innovative approach to Core Facility management: the *Interdisciplinary Triangle of Collaboration*. This uncommon and innovative approach to core facility management allows the GRC to become an extension of an investigator's laboratory, providing specialized knowledge, technical know-how, and equipment that most single investigators do not have, nor could afford or sustain on their own.

The key to success of the *Interdisciplinary Triangle of Collaboration* is its holistic approach. Communication between all key personnel occurs from study planning and design, through data generation, to data interpretation, visualization, and manuscript preparation. This approach leads to three significant outcomes: (1) *Research Productivity*: Investigators with interesting research questions overcome the "barriers to entry" posed by their own lack of expertise in genomics and bioinformatics, enabling them to formulate and pursue research questions as they never could working in isolation. (2) *Intellectual Capacity*: GRC staff work in a more intellectually stimulating environment, one in which they share knowledge with and learn from researchers, and can place their work in larger context. (3) *Core sustainability*: This approach attracts more researchers to use the facility, which increases revenue from service fees. These three outcomes are mutually beneficial and create a positive feedback loop that has fundamentally altered the course of research programs – and we're still at the beginning of the revolution.



The equipment in the main laboratory is only used by highly trained GRC staff members. However, we also maintain equipment in the GRC Common Use Core (Gibb 116) that can be used by students and research staff for high-throughput sample preparation, sample quality assurance and others. Once trained, investigators can use Google calendar to reserve time to use the equipment. Users must provide all the consumables needed for their protocols, and for equipment there is a small fee to offset maintenance agreement costs. When needed, core laboratory staff is available to help troubleshoot problems that arise during equipment use.

Core Facility Resources

The Genomics Resources Core facility offers services to investigators in next-generation sequencing and targeted re-sequencing, microarray services, genotyping services, and high-throughput sample preparation, quantitation and quality assurance. Core facility staff has expertise in both molecular biology and bioinformatics.

Equipment

The capabilities of some of major equipment items in the GRC are described below.

DNA Sequencing

DNA sequencing has become an indispensible tool for basic biological research, biomedical research, diagnostics and biological systematics. Current applications using DNA sequencing include whole genome shotgun sequencing (including *de novo* sequencing of previously unknown genomes), transcriptome sequencing, targeted re-sequencing, single nucleotide polymorphism (SNP) discovery, amplicon sequencing for studies on microbial community composition, and many other applications. Equipment for DNA sequence analysis include the Roche 454 Genome Sequencer FLX+ Instrument, that produces long sequence reads (up to 1,000bp read) with exceptional accuracy (consensus accuracy 99.997% at 15x coverage. In addition the GRC has an Illumina MiSeq, requiring less than 36 hours to yield 6.0-7.0 Gb of DNA sequence per run. If greater depth of coverage is needed the GRC can prepare Illumina libraries that can be sent to other core facilities across the nation for sequencing using Illiumina HiSeq instruments, with data being sent back to the GRC for analysis. In this way the GRC can provide access to advanced sequencing technologies while maintaining control over sample quality and the processing of raw data and analysis of dataDNA sequences in a manner that is seamless for the investigators.

The Fluidigm Access Array System is the first high-throughput, target-enrichment system designed to work with all of the major next-generation sequencing instruments. The instrument performs 2,304 simultaneous PCR reactions across 48 primer pairs and 48 samples in a micro-fluidics device. The resulting product is a DNA library ready for sequencing by either the Roche 454 Genome Sequencer FLX+, or Illumina MiSeq. The Fluidigm workflow allows investigators to obtain quality results while minimizing the time, cost, and labor required for sequencing multiple loci in population-level studies, or sequencing small genomes in studies of evolutionary dynamics by designing primers to completely cover the genome.

The Apollo 324 Library Preparation System automates next-generation sequence library preparation workflows by using bead technology to execute high-performance isolation and purification of nucleic acids (DNA, RNA, plasmid and so on) and proteins. The system automates end-repair, A-tail addition, adapter ligation and final double-bead-based cleanup and size selection. The Apollo 324 enables simultaneous processing of one to eight samples, with batch processing for 32 samples at a time. Up to eight samples can be prepared in approximately four hours, yielding products ready for amplification or direct sequencing, and a batch of 32 libraries can be created in less than eight hours. By using this instrument high quality, consistent libraries are prepared in less time with fewer manual tasks, reduced errors and lower labor costs.

DNA Microarrays

Roche Nimblegen microarray instrumentation support a wide range of experimental applications including genome-wide gene expression studies, comparative genomic hybridization (CGH) to test copy number differences between genomes, exploration of regulatory protein-DNA interactions, and investigation of DNA methylation in studies of epigenetics. The GRC has two 4-Bay Maui hybridization systems, a 12-bay Maui wash station and a Roche Nimblegen MS200 microarray slide scanner. The latter instrument allows investigators to develop microarray chips with more than 4 million probes.

SNP Genotyping

Genotyping based on single nucleotide polymorphisms (SNP) is a means to measure the genetic variation within and between populations of a species. SNP profiles can be used for various purposes including the characterization of genetic differences within and between populations, and to dissect the genetics of complex characters quantitative trait locus (QTL) analysis wherein genetic characters are associated to phenotypic traits of interest. For these analyses the GRC has an Illumina BeadXpress that supports the development of both single- and two-color assays for genotyping, methylation analyses, and protein-based assays. The GoldenGate Genotyping Assay can assay 48-384 SNPs using multiplex kits for the VeraCode platform.

GRC Common Use Core Equipment

The GRC Common Use Core gives investigators access to equipment for high throughput sample preparation while simultaneously reducing sample-to-sample variability, and high-end equipment for assessment of sample quality. Equipment in the GRC Common Use Core includes the following:

- Qiagen QIASymphony SP: Processes 1-96 samples robotically in batches of 24 for purification of DNA, RNA, and protein from a wide range of sample types.
- Qiagen QIAgility: A compact bench top instrument that enables automated PCR setup in a wide range of formats in a rapid and reliable way eliminating manual pipetting steps that can be prone to human error.
- Qiagen QIAcube: Processes QIAGEN spin columns for nucleic acid and protein purification, enabling seamless integration of automated, low-throughput sample preparation.
- Qiagen QIAxcel: The QIAxcel system is a multi-capillary electrophoresis system for the rapid and precise analysis of DNA fragments and RNA in as many as 96 samples at a time.
- Molecular Devices SpectraMax Paradigm: A multimode microplate reader equipped with for absorbance (ABS) detection and tunable wavelength (TUNE) detection cartridges.
- Agilent 2100 Bioanalyzer: A microfluidics-based platform for sizing, quantification and quality control of DNA, RNA, proteins and cells.
- Diagenode Biorupter Plus (UCD-300): A sonication device idea for DNA and chromatin shearing as well as for cell and tissue disruption.

Bioinformatic Analysis Resources

The GRC offers bioinformatics support and can perform a full range of analytical tasks to address biological questions in areas such as population genetics, genomics, microbial community dynamics, functional genomics and systems biology. GRC bioinformaticians begin with raw data output from the equipment and proceed through quality assurance, data processing and analysis, to data interpretation and visualization. Analyses are done using pipelines for genome assembly, transcriptome analysis, population genetics, SNP/INDEL detection, RNA-seq analysis, gene set enrichment analysis of microarray data, and for processing Nimblegen differential gene expression data. These pipelines are found in the public domain or developed by GRC staff. As needed the GRC staff provides investigators with detailed protocols and bioinformatic methods so they can be included in reports and publications as needed.

Staff

Acting Core Director

Dr. Matt Settles manages all operations in the GRC. Dr. Settles has experience in engineering, computer science, bioinformatics, biology, and consultating. He is responsible for strategic planning for the GRC, and works with the IBEST Business Manager to determine the fee structure and is responsible for executing a plan for sustainability over the long-term. In addition Dr. Settles participates as a collaborator on grants that use GRC services.

Genomics Scientist

Dr. Suresh Iyer is the GRC genomics scientist that oversees the data-to-day operations of the GRC laboratory and supervises the Genomics Analyst. He is responsible for the operation and maintenance of all GRC laboratory equipment. In addition to contributing to sample analysis efforts, Dr. Iyer is responsible for the development of standard operating procedures, training of individuals who wish to use the GRC Common Use Core, and tracking the progress of samples submitted to the core for analysis. Lastly, he serves as the primary consultant on molecular biology techniques, and for liaisons with GRC laboratory clientele.

Genomics Analyst

Mr. Daniel New is a genomics analyst in the GRC and works under the direction of Dr. Iyer. He is primarily responsible for sample analysis and transfer of data to the GRC bioinformatics group. Mr. New also participates in the overall operation of the laboratory, including ordering supplies, maintenance of equipment, personnel training, and compliance with regulations.

Bioinformatics Analyst

Mr. Sam Hunter is a bioinformatics analyst that works under the direct supervision of Dr. Matt Settles. Primarily, he is responsible for the analysis of DNA sequence data gathered by staff in the GRC laboratory. Mr. Hunter also monitors the quality of data from the GRC laboratory and provides information, training, and support to GRC users as needed.

Bioinformatics Research Assistant

Mr. Ilya Zhbannikov is a PhD student in the Bioinformatics and Computational Biology program at the University of Idaho. Mr. Zhbannikov, working under the direction of Dr. Settles, is building new algorithms and applications for the analysis of next-generation DNA sequence data.

GRC Clientele

Over the past twelve months the GRC has performed contracted work, or provided letters of support for grant proposals to 48 investigators at 20 institutions in four countries and three continents (see map).

Location of IBEST GRC Clientele

Financial Statement

In FY 2011-12 GRC personnel costs totaled $201,400 and this accounts for 72% of the GRC operating budget. Revenues from user fees almost completely offset personnel costs, and the remainder of GRC operations were subsidized with funds from COBRE and funds provided by the Office of Research and Economic Development. Revenues fell short of projections primarily for two reasons: (1) the Roche 454 Genome Sequencer FLX+ was down while upgrades were installed and made operational, and (2) a significant amount of work occurred at the end of the fiscal year but was not billed until afterwards.

We project that over the next five years the GRC will become financially self-sustaining solely on the basis of revenue generated from the services provided with the exception of personnel costs. As noted above, the Core began a period of explosive growth in 2009 that has not abated, and the gross income of the GRC as increased accordingly. Because the equipment and instruments in the GRC were purchased with COBRE funds, our expenses are limited to personnel, service contracts, miscellaneous consumables and small equipment. There are three sound reasons to expect that Core facility usage and income will continue to increase rapidly in the coming years and balance our expenses: our strategy of forming collaborative partnerships with users, the stimulus for Core facility use provided by IBEST-INBRE Technology Access Grants, and the expansion of the analytical services offered by the GRC. By 2017 when financial support from the COBRE grant ends we expect most personnel and service contract costs to be recovered through user fees. Along the way we will seek shared instrumentation grant funding if useful new technologies emerge or demand for specific instruments outstrips our capabilities.

2012 Financial Summary : Genomics Resources Core Operating Budget[a]

	Category	Amount	Amount	BALANCE
Expenses	Personnel			
	Equipment contracts			
	Other operating expenses			
Income	Users fees			
	Grant support			
	University support			
BALANCE				$0

[a]Purchases of equipment are not represented in this budget summary.

We expect that IBEST investigators and other University of Idaho researchers will account for a large fraction of the increased usage of core resources, but a significant number of investigators from other institutions will also contract with the GRC for services. The latter has already occurred and is expected to increase in the future. Our record of growth (albeit short) is impressive, and based on the funded and pending research grant proposals it seems likely to continue for the foreseeable future.

Major Accomplishments

New Equipment

In 2012, the GRC added the Illumina MiSeq and the IntegenX Apollo 324 Library Preparation system for DNA sequencing and the Qiagen QIAxcel and Molecular Devices SpectraMax Paradigm for sample quality assurance.

New Personnel

A Bioinformatics Analyst and a Bioinformatics Research Assistant were hired to assist in data analysis and decrease the time required to obtain interpretable data.

New BCB Applied Bioinformatics Course

Dr. Matt Settles taught a new course in Applied Bioinformatics that is part of the Bioinformatics and Computational Biology graduate program. The course provides students with skills in computational and statistical sciences needed to analyze data using contemporary bioinformatic tools. In total 12 students from five departments enrolled in the course.

Near-term Goals

The GRC offers a wide spectrum of sample analysis services in addition to tailored data analysis using bioinformatic tools. This places extraordinary demands on GRC staff to become near experts in a wide range of research topics, model systems, analytical techniques, and methods for data analysis in order to support the research of faculty on topics across the expanse of biology. This plus the increased demand for use of GRC resources has stretched staff to the limit. The result is that sample analysis protocols have occasionally failed for unknown reasons, and there is inadequate oversight of GRC workflow. This leads us to propose the following objectives for the coming year:

- Minimize sample analysis protocol failure rate
  - Develop a system to document events surrounding protocol failures by the end of November 2012
  - Conduct in-depth reviews of protocol failures to identify possible causes and modify standard operating procedures and adjust workflows as needed.
- Perform a comprehensive audit of systems and services to determine high-priority areas for staff time and effort
  - Consider eliminating certain services based on their complexity, alternative analytical approaches, and hidden costs of time invested by staff
  - Identify which bioinformatics tasks can be automated to improve efficiencies.
  - Audit bioinformatic analysis services to determine the true time and effort required and adjust fee structure accordingly

Equipment

Recently both Roche Nimblegen and Illumina announced they are ending product lines that are used in the Core, Roche Nimblegen DNA Microarrays and the Illumina BeadXpress. These business decisions have been driven by the fact that decreasing sequencing costs have provided a more comprehensive and cost effective means to obtain the types of data obtained by these older technologies. Next year the GRC will follow suit and begin transitioning from both DNA Microarrays (specifically gene expression analysis) and Illumina BeadXpress genotyping to high throughput sequencing with the Illumina MiSeq.

Sample quantity, quality, and purity are critically important in high-throughput genomics. Therefore, we are currently evaluating the Aurora Nucleic Acid Extraction System by Boreal Genomics with an eye toward purchasing this instrument. This electrophoretic DNA purification technology is especially useful for samples with low amounts of DNA, samples contaminated with materials form the sample matrix (e.g., tissue or soil humic acids), or in cases where high molecular weight DNA is needed (e.g., PacBio DNA sequencing). Further, the Aurora Nucleic Acid Extraction System is expected to improve high-throughput sequencing results by purifying sample libraries with the result being cleaner sequence data with fewer short sequence reads and a narrow fragment size distribution.

Personnel

DNA sequencing costs continue to decrease, which allows more researchers to use high-throughput sequencing in their research. One outcome is that the quantity of high-throughput sequence data generated by the GRC has increased dramatically with 100–200 times more data being generated this year as compared to the previous year. Not surprisingly, data analysis (bioinformatics) has become the current bottleneck to completing projects in a timely manner. To meet this increase in demand for bioinformatic services we are in the process of hiring a second full time Bioinformatics Data Scientist; we have reviewed the initial applicant list and are at the stage of interviewing the top applicants.

Core visibility

The faculty in certain departments (e.g., Biological Sciences) and groups (e.g., IBEST) on campus are familiar with the capabilities and services of the GRC, but others are less familiar with the resources and services of the GRC that might benefit their research programs. To increase awareness of the GRC as a campus-wide resource we will take steps to increase awareness of the core to individuals on and off campus. In addition, the GRC will host the first annual "Regional Next Generation Genomics Research Symposium" in the Summer of 2013 that will provide researchers in the region an opportunity to learn about newly introduced technologies and methods for data analysis, as well as obtain an awareness of leading edge research projects done locally.

Strategic Analysis

An abbreviated analysis of GRC strengths, weaknesses, opportunities and threats is presented below.

Strengths

- The GRC has impressive capabilities
  - The GRC is an extremely comprehensive genomics facility, covering a wide swath of genomic capabilities and equipment on a fee for service basis, including: sample preparation and QA, DNA microarray, genotyping, next-generation sequencing, and targeted next-generation sequencing
  - Faculty profit from our knowledge and capabilities to obtain extramural funding
- Bioinformatics is integrated with genomics
  - Very uncommon combination in genomics core facilities
- Exceptionally qualified and dedicated core director
- Attractive to prospective faculty, research staff and graduate students
- Strong financial underpinnings from university support and funding agencies

Weaknesses

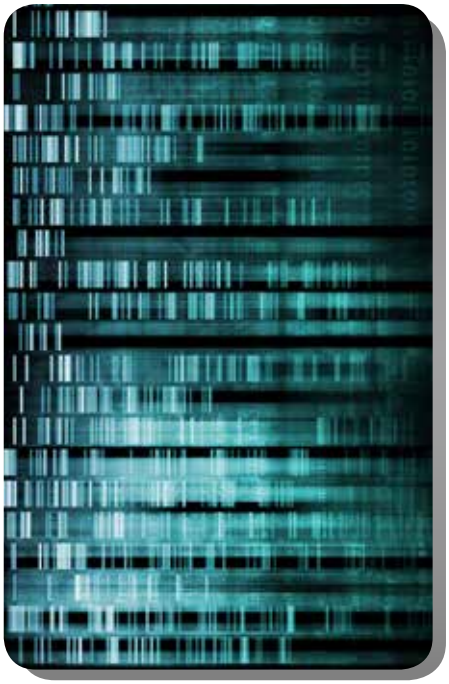
- Complex core facility
  - Staff must have expertise in a wide range of technologies and methodologies and risk becoming "Jack of all trades, master of none"
  - Significant amount of time is invested in user education
- Need to balance capabilities for data generation with those of data analysis
  - Thin staffing
  - Difficult to estimate the time required for data analysis on some projects

Opportunities

- Increase revenues to pay the balance of staff salaries by increasing the number of off-campus users
  - Market GRC capabilities to off-campus users when attending regional and national core facility conferences, and list the GRC in core facility directories

Threats

- Costs for data generation and analysis can be prohibitive
  - Size of grant awards from certain funding agencies will not support significant levels of genomics research
  - Principal investigators tend to underestimate (and under budget) for bioinformatic analysis
  - Personnel and equipment costs may lead to fees becoming noncompetitive with other academic and commercial facilities
  - Inability to recover actual costs through service center fees
- Difficulty in recruiting and retaining qualified staff
  - UI Human Resources requires us to fit the specialized skills required to run these facilities into job descriptions and minimum requirements that do not correspond to the needed skill sets
- Ever advancing technology imposes pressure to 'keep pace' with the leading edge
  - Significantly lower than market salaries hinder the ability to recruit and retain experienced personnel in the areas of high performance research computing and data management



GRC Research Highlight

While antibiotics have saved many lives, the rapid rise of bacterial pathogens that are resistant to multiple antibiotics is a growing threat to human health and well-being. Infections caused by these multi-drug resistant pathogens are increasingly difficult to treat. Many of the antibiotic resistance genes reside on plasmids, DNA molecules that replicate separately from the chromosome and can transfer between bacteria, thus spreading ten or more resistance traits in a couple of minutes. Alarmingly, little is known about the mechanisms by which multi-drug resistance plasmids can become more persistent in bacterial populations even in the absence of antibiotics.

IBEST investigator Dr. Eva Top's research has shown that genetic interactions between a plasmid and its novel host can lead to improved plasmid maintenance over time, suggesting a co-evolutionary process. In close collaboration with the Genomics Resources Core, Dr. Top has identified changes in the genome that may be responsible for these improvements in plasmid stability. As a model system, *Pseudomonas koreensis* R28 was used, a strain isolated from the local wastewater treatment based on its ability to receive but rapidly lose a model drug resistance plasmid. This organism is closely related to *Pseudomonas aeruginosa*, a bacterium that causes complications in patients with cystic fibrosis and other immune system deficiencies.

Dr. Top evolved five populations of *Pseudomonas koreensis* R28 bearing a newly introduced and initially unstable drug resistance plasmid under antibiotic selection for 1000 generations. From each evolved population the complete genomes of two clones were sequenced and compared to the common ancestor, and mutations and genomic re-arrangements common among many isolates were identified in both plasmid and chromosome. One striking finding was that a transposon with a putative toxin-antitoxin (TA) system from the host's indigenous plasmid hopped into the drug resistance plasmid, thereby increasing its persistence in the evolved host. These TA systems are well known to improve plasmid stability by killing plasmid-free cells. Second, stability patterns of evolved and ancestral plasmids in evolved and ancestral hosts suggest coevolution between one ore more candidate chromosomal mutations and the plasmid. To determine which of these mutations interact with the plasmid, mutation reconstruction experiments are in progress. This study thus indicates that coevolution between plasmid and chromosomal changes can contribute to increased persistence of antibiotic resistance in real time.

IBEST Optical Imaging Core (OIC)

Overview

High quality optical imaging and cytometry equipment is generally very expensive and difficult for faculty to justify or sustain for their individual laboratories. A core facility provides a way to share the costs of instrument repair and maintenance among more users, and eliminates the need for individual laboratories to retain technically skilled personnel to operate these sophisticated instruments. In addition, the OIC staff member can help coordinate the acquisition of new shared-use instruments using funds from instrumentation grant programs and foundations.

History of the OIC

The history of the OIC is complex. It originated nearly 20 years ago when Dr. Mike Laskowski was Director of the WWAMI Program and a Professor in the Department of Biological Sciences. It morphed once when Dr. Laskowski became PI of the BRIN Program (the predecessor of the Idaho INBRE), and again as Dr. Laskowski wound down his research program. At that time his technician (Ms. Ann Norton) came to be partly supported by the microbial pathogenesis COBRE led by Dr. Greg Bohach. This COBRE purchased several instruments for optical imaging and cell sorting. Ann was hired to oversee their operation and maintenance in addition to the pre-existing equipment. Once Dr. Bohach left the University, Ann worked more or less independently to maintain the "composite" imaging core that by then included instruments acquired by various means over the years.

In the fall of 2010, it was proposed that the OIC be merged into IBEST as a core facility. This idea was incorporated into the written proposal that IBEST submitted to become a research institute. We have been working to develop an operational plan for the OIC since launching the Institute in the fall of 2011. Progress has been slow for several reasons. One being that university funds to support operation of the OIC were available from the microbial pathogenesis COBRE through FY11-12, and that relieved a sense of urgency. More importantly, early efforts to consolidate 'critical' instruments in a single location (LSS 450) have been been complicated as we need to balance user needs and location with formulation of the OIC.

Core Facility Resources

Target capabilities

Instruments previously considered part of the OIC came via a variety of sources. Some were purchased with funds from NIH-shared instrument grants, the M.J. Murdock Charitable Trust, the NIH-COBRE-Pathogenesis grant, the Idaho INBRE program, and others. Individual departments donated some instruments when they were found to be underutilized or too expensive to maintain. We propose to divest the OIC of all except a small subset of these instruments. The ultimate fate of unwanted instruments will be decided in consultation with the Office of Research and Economic Development and other administrators. The instruments and data analysis systems we propose to retain in the core are listed in the table.

Equipment proposed to be part of OIC.

Equipment Description	Current location
Olympus Confocal Multiphoton Microscope	Life Sciences South 450
BD Biosciences FACSAria Flow Cytometer	Ag Biotech 221
Zeiss PASCAL Confocal Microscope	Ag Biotech 331
Nikon Eclipse 1000 Fluorescent Microscope	Life Sciences South 450
Leica Fluorescent Stereoscope	Life Sciences South 450
Image Data Analysis Station	Life Sciences South 450
FACS Data Analysis Station	Life Sciences South 450
Acquisitions planned FY2013	
Live Imaging Microscope	Life Sciences South 450

The instruments we wish to maintain in the OIC are limited in number, but represent the services most used by University of Idaho investigators and include:

- Confocal and multiphoton microscopy imaging
- Flow cytometry and cell sorting
- Fluorescence and transmitted light microscopy imaging
- Live cell microscopy
- Image processing and quantitative image analysis

High-resolution imaging and flow cytometry data provide information about populations of cells, as well as individual cells and tissues. High-resolution images using specific fluorescent labels clarify which cells or subcellular components are important in a particular metabolic pathway and how they change under different experimental conditions. Confocal microscopy increases the depth and resolution in observations of cells tissues. Fluorescence activated cell sorting identify specific subpopulation of cells that can be explored further via protein, RNA and DNA analyses.

An extensive suite of image analysis software is available to OIC users that permit simple image processing and annotations, automated cell counting, measuring and classifying, as well as, sophisticated modules for reconstruction of 3-D images.

Staff

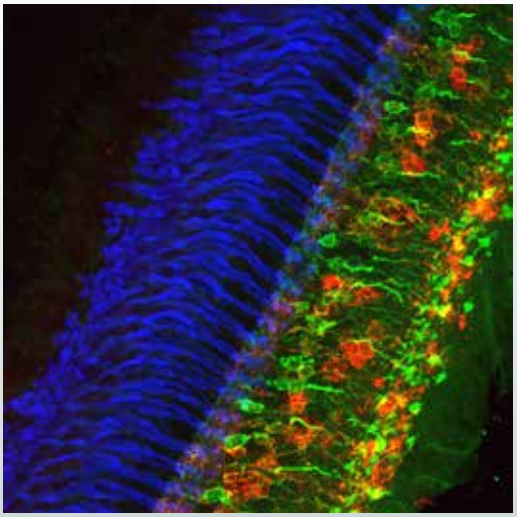
Acting Core Director

Ms. Ann Norton has worked in core facilities and individual research laboratories for 33 years. She provides guidance in experimental design, preparation techniques, biomarker and instrumentation choice, acquisition parameters, and analysis and image processing options. She trains the independent users individually on each instrument and presents campus workshops on the basics of fluorescence microscopy and flow cytometry.

Core facility management and oversight

The OIC Director will directly report to the IBEST Director. On a monthly basis and as needed the OIC Director will meet with the IBEST Director and Business manager to discuss issues related to the day-to-day operation of the OIC, revenues and expenditures, and progress toward achieving goals of the business plan. In addition the OIC Director will meet with other IBEST Core Facility Directors on a monthly basis to share 'best practices', coordinate activities, and participate in team problem solving and plan development.

Annually the Director of the OIC will convene a user group meeting to discuss capabilities within the core, future needs, and to solicit advice on how services could be improved. Changes made to OIC procedures and policies, OIC services and equipment, and proposed equipment acquisitions will be reported and reviewed annually by the IBEST External Advisory Committee and the IBEST Internal Advisory Committee.



OIC Research Highlight

The retina is the light-sensing tissue of the eye. In humans, if there is damage to the retina it cannot regenerate, resulting in loss of visual function. Zebrafish are very useful as an animal model, because unlike humans, they are able to regenerate retinal tissue following retinal damage. There is evidence that this process results in some restoration of visual function. Tim McGinn, Graduate student in Dr. Deborah Stenkamp's lab in the College of Science, is investigating the regenerative process, specifically the extent to which new (regenerated) neurons establish appropriate synaptic connections. The IBEST Optical Imaging Center is essential to his research objectives because it offers the resolution needed to detect the presence of specific synaptic connections in retinal tissues. In pursuing this project Tim has also mentored an undergraduate researcher supported by the UBM program. Together they are quantifying specific neuronal cell populations and characteristics of their synaptic connections in regenerated retina. They are optimistic this research will inform the development of cell replacement therapies for human disorders that cause blindness, such as age-related macular degeneration, retinitis pigmentosa, and traumatic injury.

OIC Clientele

The OIC clientele included 27 different principal investigators (77 individuals in total) that were mainly from various academic departments and colleges on the UI campus, with a handful from Washington State University and University of California-Davis.

Financial Statement

The table below summarizes the reoccurring expenses and income for the CRC. One-time purchases of equipment and other items using grant funds are not included.

Strategies to reduce OIC operating expenses

There are two major costs associated with OIC operations: personnel and instrument service contracts. While neither is entirely dispensable, the latter can be minimized by: (a) focus on a narrowed set of capabilities (b) judiciously choose which instruments will be fully supported with service contracts, and (c) have the OIC Director perform routine maintenance on some instruments in combination with 'self-insurance' against major problems that may occur in the future. We propose to implement all three strategies.

2012 Financial Summary : Optical Imaging Core Operating Budget[a]

	Category	Amount	Amount	BALANCE
Expenses	Personnel			
	Equipment contracts			
	Other operating expenses			
Income	Users fees			
	Grant support			
	University support			
BALANCE				$0

[a]Purchases of equipment are not represented in this budget summary.

Strategies to increase OIC revenues

Revenue from users fees represents the sole source of income to the OIC in the near term and we propose that the steps outlined below be taken to develop this revenue stream.

The OIC began operation as a fee-for-service center on October 1, 2012. Two different fee-for-services models are being implemented and promoted. The first is referred to as the "Self-Service Model" in which the principal investigator or a member of their research group acquire their own data. In this case only usage of instruments will be billed to the investigator. The OIC Director will provide training on instrument use to all investigators, and the time required for this instruction will be billed to the investigator. The second is referred to as the "Full-Service Model" in which the OIC Director consults with investigators from experimental design through to publication of the study findings. Under this model, the OIC Director will be personally responsible for sample processing, as well as data acquisition and analysis. Her time for consulting, sample preparation, and usage of instruments will be billed to the investigator.

We are aware that while OIC revenues must be collected from user fees in the future, we must also maintain an affordable service fee structure. If the latter is not achieved then users may be reluctant or financially unable to use the resources of the OIC, seek alternatives, or change their research plans. We have undertaken a study of the fees charged by other University service centers around the country and already proposed a fee structure to the university service center committee that we think is highly competitive and affordable to investigators.

Increase user base

We propose to take a tiered approach to promoting awareness of the OIC capabilities and the fee-for-service models described above. Initially, we will focus on on-campus users, secondly on potential users across the state, and finally a broader focus on the intermountain west. Already we have engaged with the Idaho INBRE to make biomedical researchers throughout the state aware of IBEST core facilities.

To increase awareness on-campus, we have updated the OIC website, and developed a poster that can be prominently displayed in key locations on campus, seek opportunities to make presentations to potential user groups and academic departments, and offer trial experiments to demonstrate capabilities at no charge to investigators. In our opinion, researchers in the plant sciences underutilize the facility and we will make special effort to reach out to this community.

The NIH-COBRE and Idaho INBRE programs are partnering to fund the Technology Access Grant program that provides funds to investigators so they can use IBEST Core Facility resources to obtain preliminary data that will be used in support of an extramural grant application related to human health. This will be an especially attractive opportunity for investigators to explore the capabilities of the OIC and generate revenue for the core when the pilot studies lead to extramural funding. We envision it as a particularly effective way to 'prime the pump'.

Add *capabilities*

We propose to acquire a system dynamic imaging system that allows researchers to work with live cells, tissues, and small organisms to observe and document changes over time. The imaging system will be able to capture events that occur in live cells, tissues and small organisms in milliseconds, keep samples stable and in focus for hours to days, and integrate the hardware and software needed to provide these conditions. Once the kinetic features are captured, mathematical analysis can provide molecular and cellular dynamic models, which can then be tested experimentally using the live imaging instrument. There is no substitute for being able to directly visualize experimental subjects. Efforts to acquire this instrumentation are being led by Dr. Deborah Stenkamp who submitted a concept paper to the Office of Research and Economic Development that was favorably reviewed and she was asked to prepare and submit a full proposal to the Murdoch Foundation later in 2012.

If efforts to secure funding for this acquisition are successful we propose to cease support of the laser used for multiphoton confocal microscopy because it requires a very expensive ($15,000) annual service contract and has historically been underutilized. Should an investigator require the depth of imaging required from a multiphoton confocal microscopy they will be referred to Washington State University where two such instruments are maintained.

Revenue Forecast

In FY2011-12 the Optical Imaging Core was fully supported by the Office of Research and Economic Development. We estimate that approximately 30% of the OIC expenses can be paid from user fees in FY12-13. This is a very rough estimate that could be significantly influenced by new grant awards (in which case the fee income might increase) and whether investigators balk at paying fees for OIC use when it had previously been available to them at no charge. The income from user fees is expected to increase with addition of the Dynamic Imaging System in 2014, and eventually grow to 47% ($77,250) by 2015. At this stage the user fees would approximate the amount of funds needed for the salary and fringe benefits of the OIC Director, leaving the University to subsidize the OIC to cover the costs of service contracts and maintenance, consumables, and professional development (see table below).

Estimated expenses and income to OIC for 2013-2016.

	Category	2013	2014	2015	2016
Total Expenses	See Table 2				
Total Income	User fees				
	University subsidy				

Major Accomplishments

- Developed a business plan for the OIC that was reviewed and approved by the Vice-President of Research and Economic Development
- Created a consolidated core of instruments to better meet the needs of our researchers while retiring aging and underutilized instruments

Near-term Goals

- Launch the OIC fee for service center
  - Work to make clientele familiar and comfortable with the "Self-Service Model" and "Full Service Model" of OIC operations
- Identify and nurture collaborations that might lead to the OIC Director's salary being partly funded on a handful of research grants
- Increase visibility of the OIC by continuing to provide basic microscopy and flow cytometry workshops to potential users
- Make the OIC facility compliant with BSL 2 safety guidelines by providing lab coats, restricting food and drink, providing appropriate safety glasses, posting specific safety concerns related to microscopy and flow cytometry in the lab

Strategic Analysis

An abbreviated analysis of OIC strengths, weaknesses, opportunities and threats is presented below.

Strengths

- The OIC has impressive capabilities
  - Off-campus users seek out our facility for quality results and flexibility of applications
- Strong financial underpinning from university support
- Exceptionally qualified and dedicated core director
- Consolidation of instrumentation in one location

Weaknesses

- Few high-use research programs
- High equipment maintenance and service contract costs
- Thin staffing
  - With only one staff member, there is no backup

Opportuntiies

- Increase numbers of off-campus users to provide revenues to pay the balance of staff salaries
  - Stimulated by addition of new capability for live imaging system
- The "full-service option" exploits the expertise of the core director is a unique service that reduces the barriers to the use OIC of instruments

Threats

- Income from all potential users may be insufficient to sustain core without substantial on-going financial support from the University
- Ability to offset OIC costs with user fees paid from extramural grant funds is inherently limited
  - Comparatively low number of research active faculty on the Moscow campus that require the capabilities of the OIC
  - User fees charged may be non-competitive in comparison to those of core facilities at Washington State University and elsewhere
- Advancing technology imposes pressure to 'keep pace' with the leading edge

IBEST Mass Spectrometry Core (MSC)

Overview

Effective in August 2012 the Mass Spectrometry Core was added to the suite of IBEST core facilities. The MSC will be built around the mass spectrometry and chromatography instruments purchased and operated as part of the former Environmental Biotechnology Institute (EBI). Dr. Andrzej Paszczynski, who was formerly affiliated with the EBI and has decades of experience in mass spectroscopy, has agreed to serve as the faculty scientific advisor to the MSC and assist in the development of strategic plans for building a sustainable facility.

We are in the early stages of this transition and our immediate objective is to identify precisely which capabilities should be retained in the MSC. In many ways this process parallels what has been done with the OIC as described above. First we must decide what services can and should be offered by the MSC to support a range of faculty research programs on campus. This will dictate which instruments and small equipment should be retained for sample preparation and analysis. We will divest ourselves of the remaining unneeded instruments and small equipment. The ultimate fate of unwanted instruments will be decided in consultation with the Office of Research and Economic Development and other administrators. We propose to begin operation as a fee-for-service center in January 2013.

Core Facility Resources

The MSC is currently operating in a portion of the laboratory space previously occupied by EBI in the Food Research Center building. The space includes an instrumentation lab and a wet lab for sample preparation. The major instruments we propose to retain in the MSC include

- A Waters Q ToF Premier MALDI/ESI Tandem Mass Spectrometer equipped with a nanoACQUITY ultra performance liquid chromatograph (UPLC) system to separate analytes in samples prior to delivery to the mass spectrometer. This is a sensitive, high-resolution mass spectrometer ideally suited to acquiring proteomic data via MS or MS/MS, and accurate mass spectra. In addition to instrument operation software, the core also owns software for processing raw proteomic LC-MS data for protein identification and relative quantitation.
- A Waters Xevo TQ mass spectrometer with an electrospray ion source and tandem quadrupole mass spectromter that is well suited to quantitation of peptides and low molecular weight organic compounds by multiple reaction monitoring (MRM).

Besides LC-MS instrumentation, the core also has a Hewlett-Packard 6890 gas chromatograph coupled to a 5973 mass selective detector for analysis of mixtures of volatile analytes; a gas chromatograph with a flame ionization and electron capture detectors; and a liquid chromatograph equipped with a diode array detector, as well as other resources for sample preparation.

Staff

The Acting Director of the MSC is Lee Deobald who holds a B.S. in Chemistry and a PhD in Microbiology, Molecular Biology, and Biochemistry. He has more than 25 years of experience operating gas and liquid chromatographs and more than 6 years experience operating and maintaining mass spectrometers.

MSC Clientele

Investigators that submit samples to the MSC for analysis fall into four categories. The first and largest includes those people interested in identifying proteins from 1-D or 2-D electrophoresis gel bands or spots. These analyses are done by LC-MS using UPLC and the Waters Q ToF Premier followed by data processing with proteomic data processing software. Customers seeking this service come from the UI, Washington State University, and occasionally from other universities like Oregon State and Idaho State. The second category of users includes synthetic organic chemists from the UI Department of Chemistry. These users are primarily interested in acquiring accurate mass determinations from samples of synthetic organic compounds and synthetic oligonucleotides to confirm the masses of synthesis products. These analyses are done also with the Q-Tof Premier mass spec using either the MALDI source or electrospray ionization (**ESI**) source with sample introduction by infusion of solutions from a syringe. The third category of users submit samples for quantitative analysis by LC-MS using the Waters Xevo TQ MS with a nanoAquity UPLC. Water soluble analytes with a fixed charge are suited for analysis by this method. Researchers from both UI and WSU are the primary customers for this service. The fourth category includes investigators that require various types of analyses including liquid chromatography with UV-VIS detection, GC-MS for sample characterization, and relative protein quantitation by LC-MS.

Financial Statement

The MSC has a variety of state of the art, sophisticated mass spectrometers interfaced with liquid chromatographs that provide the core with outstanding analytical capabilities. However, these capabilities are expensive to acquire and maintain. Most UI investigators only occasional need the kinds of analyses done by the MSC, and so it make little sense for them to invest the money needed to purchase and operate instruments like these in their own labs. Moreover, the complex nature of these instruments and their operation argues for a shared resource facility that is largely supported by user fees, but subsidized by the university. For the MSC to be viable over the longer term we must develop a critical mass of researchers that use the facility and pay a fair share of the operational costs (see table below). To date the MSC has been wholly supported by the Office of Research and Economic Development. This support will continue through FY2012-13. We have not yet projected the present or potential user base, or developed a forecast of the revenues from users fees

2012 Financial Summary : Mass Spectrometry Core Operating Budget[a]

	Category	Amount	Amount	BALANCE
Expenses	Personnel			
	Equipment contracts			
	Other operating expenses			
Income	Users fees			
	Grant support			
	University support			
BALANCE				$0

[a]Purchases of equipment are not represented in this budget summary.

Near term goals

As a new core within IBEST, the MSC is being transitioned from EBI to IBEST. The most important near term objectives are (1) determine which analytical services will be retained in the MSC; (2) assess the operational costs for the various analytical services; and (3) develop a fee schedule for these services; and (4) have it approved by the UI Service Center Committee. As part of this transition we will also work to inform users and potential users of the newly developed and inclusive fee-for-service model that will insure sustainability and continued operation of the MSC in the years ahead.

The capabilities of the MSC are not widely known by UI investigators, and this is particularly true among biological scientists who might wish to expand there research past genomics to include proteomics or metabolomics. We have not yet developed a specific plan for how we might best 'draw in' these investigators, but surely a more prominent presence on the web by inclusion of the MSC on the IBEST core facilities web-site will be a part of this effort, as will 'infomercials' to various groups in various venues. As with the other IBEST cores, the core director will be expected to contact prospective users and engage them in discussions of how the analytical capabilities of the MSC might be exploited by their research programs in the future.

As with the OIC we will promote two different fee-for-services models. The first will be a "Self-Service Model" in which the principal investigator or a member of their research group acquires their own data. In this case only usage of instruments will be billed to the investigator. The MSC Director will provide training on instrument use to all investigators, and the time required for this instruction will be billed to the investigator. The second is referred to as the "Full-Service Model" in which the MSC Director consults with investigators from experimental design through to publication of the study findings. Under this model, the MSC Director will be personally responsible for sample processing, as well as data acquisition and analysis. His time for consulting, sample preparation, and usage of instruments will be billed to the investigator. In essence an investigator can pay for the MSC director's time and the costs of sample analysis, and by doing so they can easily acquire the technical know-how needed to add new facets to their research programs.

Strategic Analysis

An abbreviated analysis of MSC strengths, weaknesses, opportunities and threats is presented below.

Strengths

- The MSC has sophisticated instruments with a wide range of capabilities
- Strong financial underpinning from university support
- Exceptionally qualified and dedicated core director
- The MSC is well equipped with other resources (glassware, chemicals, and small equipment) for sample preparation and other related tasks

Weaknesses

- The acting core director does not have the training and experience needed to fully exploit the capabilities of the instruments
- Service calls for repairs not covered by service contracts are more expensive because of the UI's remote location
- There is a single staff person to do all of the tasks necessary (instrument operation, maintenance, method development, etc.) and this fragments his time and effort

Opportunities

- LC-MS is especially suited to biological samples and the resources of the MSC for these sorts of analyses is largely untapped
- Analyses performed by the MSC require minimal sample preparation but yield considerable information relative to the effort involved
- UI investigators will have the opportunity to easily expand the kinds of analytical methods that can be incorporated into their research projects

Threats

- Problems growing the user base
  - UI researchers are unaware of the MSC
  - Projects are typically small and this this tends to inflate the total costs for sample analysis because the relative personnel costs increase as the number of samples analyzed decreases.
  - Development of new applications can be time consuming and may be reluctant to pay for custom method development
- LC-MS and GC-MS instrumentation is becoming more advanced and affordable
  - This could lead 'heavy users' to acquire their own instruments, which would erode revenues to the MSC
  - Customers may seek out analyses that require capabilities found only on newer instruments not available in the MSC.

Appendix I

IBEST SEMINAR SERIES 2012

Institute for Bioinformatics and Evolutionary Studies

ibest

Seminars Spring 2012

January 19, Thursday

Elhanan Borenstein
University of Washington

Computational research in evolutionary systems biology

January 26, Thursday

Dee Denver
Oregon State University

How forces of evolution shape patterns of variation & divergence in genomes

March 29, Thursday

Tomi Pastinen
McGill University Health, Montreal Canada

Understanding which common variation of genes lead to different human diseases

April 5, Thursday

Cedric Feschotte
University of Texas-Arlington

Mobile DNA - a diverse array of genetic elements able to integrate within the genome

May 3, Thursday

Steve Horvath
University of California Los Angeles

Weighted gene co-expression network analysis using microarray data

Institute for Bioinformatics & Evolutionary Studies

www.ibest.uidaho.edu

Thursdays at 12:30 p.m.
Engineering Physics Building
Room 214

University of Idaho

This seminar series was made possible by NIH Grant P20 RR016448 from the COBRE Program of the National Center for Research Resources.

National Center for Research Resources

IBEST

The IBEST Fall Seminar Series

Fall 2012

8.30 Rustom Antia, EMory University
"Developing quantitative undersatnding of the dynamics of pathogens and immune responses."

9.13 Cedric Feschotte, University of Utah
"Genomes without borders: horizontal transposon transfer and the misfit origins of genetic novelty."

10.4 Jose Clemente, University of Colorado Boulder
"The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites."

10.18 Michael Turelli, University of California Davis
"Theoretical population and quantitative genetics, speciation, and population biology of Drosophila."

11.2 Andrew Clark, Cornell University
"Population genetics of insect immunity and sperm displacement, and the evolution of the Y chromosome in drosophila."

11.8 Chris Oehmen, Pacific Northwest National Laboratory
"Biological research approached by using high-performance computing."

12.6 James Cai, Texas A&M
"Elucidation of genotype-phenotype relationships using computational genomics approaches."

All seminars are Thursdays at 12:30 in McClure 209
Friday, November 2nd location to be announced.

The Institute for Bioinformatics and Evolutionary Studies
www.ibest.uidaho.edu

ibest

Appendix 2

IBEST Publications 2012

Amish, S. J., Hohenlohe, P. A., Painter, S., Leary, R. F., Muhlfeld, C., Allendorf, F. W., & Luikart, G. (2012). RAD sequencing yields a high success rate for westslope cutthroat and rainbow trout species-diagnostic SNP assays. *Molecular ecology resources*, 12(4), 653–660. doi:10.1111/j.1755-0998.2012.03157.x

Anderson, J. L., Rodríguez Marí, A., Braasch, I., Amores, A., Hohenlohe, P., Batzel, P., & Postlethwait, J. H. (2012). Multiple sex-associated regions and a putative sex chromosome in zebrafish revealed by RAD mapping and population genomics. *PloS one*, 7(7), e40701. doi:10.1371/journal.pone.0040701

Blanquart, F., Gandon, S., & Nuismer, S. L. (2012). The effects of migration and drift on local adaptation to a heterogeneous environment. *Journal of evolutionary biology*, 25(7), 1351–1363. doi:10.1111/j.1420-9101.2012.02524.x

Brotman, R. M., Bradford, L. L., Conrad, M., Gajer, P., Ault, K., Peralta, L., Forney, L. J., et al. (2012). Association Between Trichomonas vaginalis and Vaginal Bacterial Community Composition Among Reproductive-Age Women. *Sexually transmitted diseases*, 39(10), 807–812. doi:10.1097/OLQ.0b013e3182631c79

Bunge, J., Woodard, L., Böhning, D., Foster, J. A., Connolly, S., & Allen, H. K. (2012). Estimating population diversity with CatchAll. *Bioinformatics* (Oxford, England), 28(7), 1045–1047. doi:10.1093/bioinformatics/bts075

Clay, D., SJ Novak, MD Serpe, DC Tank, and JF Smith. (2012). Homoploid hybrid speciation in a rare endemic Castilleja from Idaho (Castilleja christii, Orobanchaceae). *American Journal of Botany*. In Press.

Copeland, W. K., Krishnan, V., Beck, D., Settles, M., Foster, J. A., Cho, K.-C., Day, M., et al. (2012). mcaGUI: microbial community analysis R-Graphical User Interface (GUI). *Bioinformatics* (Oxford, England), 28(16), 2198–2199. doi:10.1093/bioinformatics/bts338

Daughdrill, G. W., Kashtanov, S., Stancik, A., Hill, S. E., Helms, G., Muschol, M., Receveur-Bréchot, V., et al. (2012). Understanding the structural ensembles of a highly extended disordered protein. *Molecular bioSystems*, 8(1), 308–319. doi:10.1039/c1mb05243h

Drew, R. E., Settles, M. L., Churchill, E. J., Williams, S. M., Balli, S., & Robison, B. D. (2012). Brain transcriptome variation among behaviorally distinct strains of zebrafish (Danio rerio). *BMC genomics*, 13, 323. doi:10.1186/1471-2164-13-323

Dziedzic, S. A., & Caplan, A. B. (2012). Autophagy proteins play cytoprotective and cytocidal roles in leucine starvation-induced cell death in Saccharomyces cerevisiae. *Autophagy*, 8(5), 731–738. doi:10.4161/auto.19314

Egger, J. M., JA Ruygt, and DC Tank. (2012). Castilleja ambigua var. meadii (Orobanchaceae): A new variety from Napa County, California. *Phytoneuron*, 68, 1–12.

Eikmeyer, F., Hadiati, A., Szczepanowski, R., Wibberg, D., Schneiker-Bekel, S., Rogers, L. M., Brown, C. J., et al. (2012). The complete genome sequences of four new IncN plasmids from wastewater treatment plant effluent provide new insights into IncN plasmid diversity and evolution. *Plasmid*, 68(1), 13–24. doi:10.1016/j.plasmid.2012.01.011

Evans, J., & Sullivan, J. (2012). Generalized mixture models for molecular phylogenetic estimation. *Systematic biology*, 61(1), 12–21. doi:10.1093/sysbio/syr093

Foster, J. A., Bunge, J., Gilbert, J. A., & Moore, J. H. (2012). Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. *Briefings in bioinformatics*, 13(4), 420–429. doi:10.1093/bib/bbr080

Foster, J. A., Moore, J. H., Gilbert, J. A., & Bunge, J. (2012). Microbiome studies: analytical tools and techniques. Pacific Symposium on Biocomputing. *Pacific Symposium on Biocomputing*, 200–202.

Funk, W. C., McKay, J. K., Hohenlohe, P. A., & Allendorf, F. W. (2012). Harnessing genomics for delineating conservation units. *Trends in ecology & evolution*, 27(9), 489–496. doi:10.1016/j.tree.2012.05.012

Gajer, P., Brotman, R. M., Bai, G., Sakamoto, J., Schütte, U. M. E., Zhong, X., Koenig, S. S. K., et al. (2012). Temporal dynamics of the human vaginal microbiota. *Science translational medicine*, 4(132), 132ra52. doi:10.1126/scitranslmed.3003605

Garrison, E., Treeck. M., Ehret, E., Butz, H., Garbuz, T., Oswald, BP, Settles, M., Boothroyd, J. and Arrizabalaga, G. (2012). A forward genetic screen reveals calcium-dependent protein kinase 3 regulates egress in Toxoplasma. *PLoS Pathogens*. In Press.

Gilman, R. T., Nuismer, S. L., & Jhwueng, D.-C. (2012). Coevolution in multidimensional trait space favours escape from parasites and pathogens. *Nature*, 483(7389), 328–330. doi:10.1038/nature10853

Godsoe, W., & Harmon, L. J. (2012). How do species interactions affect species distribution models? Ecography. Goldberg, C. S., TANK, D. C., & Uribe-Convers, S. (2012). Species designation of the Bruneau Dune tiger beetle (Cicindela waynei) is supported by phylogenetic analysis of mitochondrial DNA sequence data. *Conserv Genet*. 13:373-380. doi:10.1007/s10592-011-0295-9

Guerrero-Bosagna, C., Covert, T. R., Haque, M. M., Settles, M., Nilsson, E. E., Anway, M. D., & Skinner, M. K. (2012). Epigenetic Transgenerational Inheritance of Vinclozolin Induced Mouse Adult Onset Disease and Associated Sperm Epigenome Biomarkers. *Reproductive toxicology* (Elmsford, N.Y.). doi:10.1016/j.reprotox.2012.09.005

Harmon, L. J. (2012). An inordinate fondness for eukaryotic diversity. *PLoS biology*, 10(8), e1001382. doi:10.1371/journal.pbio.1001382

Hayles, A., K Boland, H Sheng, CJ Hovde, and K Lahmers. (2012). Bovine cellular immune response to Escherichia coli O157:H7 proteins. *Clin.Vaccine Immunol*, 13(12): 1322-1327. doi:10.1128/CVI.00205-06.

Heuer, H., Binh, C. T. T., Jechalke, S., Kopmann, C., Zimmerling, U., Krögerrecklenfort, E., Ledger, T., et al. (2012). IncP-1ε Plasmids are Important Vectors of Antibiotic Resistance Genes in Agricultural Systems: Diversification Driven by Class 1 Integron Gene Cassettes. *Frontiers in microbiology*, 3, 2. doi:10.3389/fmicb.2012.00002

Hohenlohe, P. A., Bassham, S., Currey, M., & Cresko, W. A. (2012). Extensive linkage disequilibrium and parallel adaptive divergence across threespine stickleback genomes. Philosophical transactions of the Royal Society of London. *Series B, Biological sciences*, 367(1587), 395–408. doi:10.1098/rstb.2011.0245

Hohenlohe, P. A., Catchen, J., & Cresko, W. A. (2012). Population genomic analysis of model and nonmodel organisms using sequenced RAD tags. *Methods in molecular biology* (Clifton, N.J.), 888, 235–260. doi:10.1007/978-1-61779-870-2_14

Hoisington-Lopez, J. L., Waits, L. P., & Sullivan, J. (2012). Species limits and integrated taxonomy of the Idaho ground squirrel (Urocitellus brunneus): genetic and ecological differentiation. *Journal of Mammalogy*, 93(2), 589–604. doi:10.1644/11-MAMM-A-021.1

Hughes, J. M., Lohman, B. K., Deckert, G. E., Nichols, E. P., Settles, M., Abdo, Z., & Top, E. M. (2012). The role of clonal interference in the evolutionary dynamics of plasmid-host adaptation. *mBio*, 3(4), e00077–12. doi:10.1128/mBio.00077-12

Hunt, K. M., Williams, J. E., Shafii, B., Hunt, M. K., Behre, R., Ting, R., McGuire, M. K., et al. (2012). Mastitis Is Associated with Increased Free Fatty Acids, Somatic Cell Count, and Interleukin-8 Concentrations in Human Milk. *Breastfeeding medicine : the official journal of the Academy of Breastfeeding Medicine*. doi:10.1089/bfm.2011.0141

Hunt, K. M., Preuss, J., Nissan, C., Davlin, C. A., Williams, J. E., Shafii, B., Richardson, A. D., et al. (2012). Human milk oligosaccharides promote the growth of staphylococci. *Applied and environmental microbiology*, 78(14), 4763–4770. doi:10.1128/AEM.00477-12

Ingram, T., Harmon, L. J., & Shurin, J. B. (2012). When should we expect early bursts of trait evolution in comparative data? Predictions from an evolutionary food web model. *Journal of evolutionary biology*, 25(9), 1902–1910. doi:10.1111/j.1420-9101.2012.02566.x

Jones, A. G., Bürger, R., Arnold, S. J., Hohenlohe, P. A., & Uyeda, J. C. (2012). The effects of stochastic and episodic movement of the optimum on the evolution of the G-matrix and the response of the trait mean to selection. *Journal of evolutionary biology*. doi:10.1111/j.1420-9101.2012.02598.x

Joyce, P., Genz, A., & Buzbas, E. O. (2012). Efficient simulation and likelihood methods for non-neutral multi-allele models. *Journal of computational biology : a journal of computational molecular cell biology*, 19(6), 650–661. doi:10.1089/cmb.2012.0033

Kashtanov, S., Borcherds, W., Wu, H., Daughdrill, G. W., & Ytreberg, F. M. (2012). Intrinsically Disordered Proteins: Volume I. *Experimental Techniques*. New York: Humana Press Inc.

Kimmel, C. B., Hohenlohe, P. A., Ullmann, B., Currey, M., & Cresko, W. A. (2012). Developmental dissociation in morphological evolution of the stickleback opercle. *Evolution & development*, 14(4), 326–337. doi:10.1111/j.1525-142X.2012.00551.x

Klionsky, D. J., Abdalla, F. C., Abeliovich, H., Abraham, R. T., Acevedo-Arozena, A., Adeli, K., Agholme, L., et al. (2012). Guidelines for the use and interpretation of assays for monitoring autophagy. *Autophagy*, 8(4), 445–544.

Kolodziejek, A. M., Hovde, C. J., & Minnich, S. A. (2012). Yersinia pestis Ail: multiple roles of a single protein. Frontiers in cellular and infection microbiology, 2, 103. doi:10.3389/fcimb.2012.00103

Król, J. E., Penrod, J. T., McCaslin, H., Rogers, L. M., Yano, H., Stancik, A. D., Dejonghe, W., et al. (2012). Role of IncP-1β plasmids pWDL7::rfp and pNB8c in chloroaniline catabolism as determined by genomic and functional analyses. *Applied and environmental microbiology*, 78(3), 828–838. doi:10.1128/AEM.07480-11

Kudva, I. T., Davis, M. A., Griffin, R. W., Garren, J., Murray, M., John, M., Hovde, C. J., et al. (2012). Polymorphic Amplified Typing Sequences and Pulsed-Field Gel Electrophoresis Yield Comparable Results in the Strain Typing of a Diverse Set of Bovine Escherichia coli O157:H7 Isolates. *International journal of microbiology*, 2012, 140105. doi:10.1155/2012/140105

Lee, K. H., & Ytreberg, F. M. (2012). Effect of Gold Nanoparticle Conjugation on Peptide Dynamics and Structure. *Entropy*, 14(4), 630-641. doi:10.3390/e14040630

Lu, T., Park, J. Y., Parnell, K., Fox, L. K., & McGuire, M. A. (2012). Characterization of fatty acid modifying enzyme activity in staphylococcal mastitis isolates and other bacteria. *BMC research notes*, 5, 323. doi:10.1186/1756-0500-5-323

Madan, J. C., Salari, R. C., Saxena, D., Davidson, L., O'Toole, G. A., Moore, J. H., Sogin, M. L., et al. (2012). Gut microbial colonisation in premature neonates predicts neonatal sepsis. *Archives of disease in childhood. Fetal and neonatal edition*. doi:10.1136/fetalneonatal-2011-301373

Madan, J. C., Koestler, D. C., Stanton, B. A., Davidson, L., Moulton, L. A., Housman, M. L., Moore, J. H., et al. (2012). Serial Analysis of the Gut and Respiratory Microbiome in Cystic Fibrosis in Infancy: Interaction between Intestinal and Respiratory Tracts and Impact of Nutritional Exposures. *mBio*, 3(4). doi:10.1128/mBio.00251-12

Minozzi, G., Williams, J. L., Stella, A., Strozzi, F., Luini, M., Settles, M. L., Taylor, J. F., et al. (2012). Meta-analysis of two genome-wide association studies of bovine paratuberculosis. *PloS one*, 7(3), e32578. doi:10.1371/journal.pone.0032578

Nagel, A. C., Joyce, P., Wichman, H. A., & Miller, C. R. (2012). Stickbreaking: a novel fitness landscape model that harbors epistasis and is consistent with commonly observed patterns of adaptive evolution. *Genetics*, 190(2), 655–667. doi:10.1534/genetics.111.132134

Nuismer, S. L., Jordano, P., & Bascompte, J. (2012). Coevolution and the architecture of mutualistic networks. *Evolution*. DOI: 10.1111/j.1558-5646.2012.01801.x

Ouyang, B., Fei, Z., Joung, J.-G., Kolenovsky, A., Koh, C., Nowak, J., Caplan, A., et al. (2012). Transcriptome profiling and methyl homeostasis of an Arabidopsis mutant deficient in S-adenosylhomocysteine hydrolase1 (SAHH1). *Plant molecular biology*, 79(4-5), 315–331. doi:10.1007/s11103-012-9914-1

Pearson, V. M., Miller, C. R., & Rokyta, D. R. (2012). The Consistency of Beneficial Fitness Effects of Mutations across Diverse Genetic Backgrounds. *PloS one*, 7(8), e43864. doi:10.1371/journal.pone.0043864

Peever, T. L., Chen, W., Abdo, Z., & Kaiser, W. J. (2012). Genetics of virulence in Ascochyta rabiei. *Plant Pathology*, 61(4), 754–760. doi:10.1111/j.1365-3059.2011.02566.x

Pennell, M. W., Sarver, B. A. J., & Harmon, L. J. (2012). Trees of unusual size: biased inference of early bursts from large molecular phylogenies. *PloS one*, 7(9), e43348. doi:10.1371/journal.pone.0043348

Pennell, M. W., Stansbury, C. R., & Waits, L. P. (2012). Capwire: a R package for estimating population census size from non-invasive genetic sampling. *Molecular Ecology*. DOI: 10.1111/1755-0998.12019

Peterson, S. E., Rezamand, P., Williams, J. E., Price, W., Chahine, M., & McGuire, M. A. (2012). Effects of dietary betaine on milk yield and milk composition of mid-lactation Holstein dairy cows. *Journal of dairy science*. doi:10.3168/jds.2011-4808

Pham, M., Raymond, J., Hester, J., & Kyzar, E. (2012). Assessing social behavior phenotypes in adult zebrafish: shoaling, social preference and mirror biting tests. *Zebrafish protocols for neurobehavioral research*. 66(2) 231-246, DOI: 10.1007/978-1-61779-597-8_17

Pina, J. E., Lee, K. H., & Ytreberg, F. M. (2012). Effects of the binding of calcium ions on the structure and dynamics of the ΦX174 virus investigated using molecular dynamics. *Journal of Biological Physics*, 38(3), 397–404. doi:10.1007/s10867-011-9260-6

Rastogi, S. K., Gibson, C. M., Branen, J. R., Aston, D. E., Branen, A. L., & Hrdlicka, P. J. (2012). DNA detection on lateral flow test strips: enhanced signal sensitivity using LNA-conjugated gold nanoparticles. *Chemical communications* (Cambridge, England), 48(62), 7714–7716. doi:10.1039/c2cc33430e

Reid, N., Demboski, J. R., & Sullivan, J. (2012). Phylogeny estimation of the radiation of western North American chipmunks (Tamias) in the face of introgression using reproductive protein genes. *Systematic biology*, 61(1), 44–62. doi:10.1093/sysbio/syr094

Ritzenthaler, K. L., Shahin, A. M., Shultz, T. D., Dasgupta, N., McGuire, M. A., & McGuire, M. K. (2012). Dietary Intake of c9, t11-Conjugated Linoleic Acid Correlates with Its Concentration in Plasma Lipid Fractions of Men but Not Women. *The Journal of Nutrition*, 142(9), 1645-1651. doi: 10.3945/ jn.111.156794

Robison, B. D., & Thorgaard, G. H. (2012). Prospects and Pitfalls of Clonal Fishes in the Postgenomic Era. *Aquaculture Biotechnology*, 55-67. ISBN 0813810280

Rosenblum, E. B., Poorten, T. J., Settles, M., & Murdoch, G. K. (2012). Only skin deep: shared genetic response to the deadly chytrid fungus in susceptible frog species. *Molecular ecology*, 21(13), 3110–3120. doi:10.1111/j.1365-294X.2012.05481.x

Rosenblum, E. B., Sarver, B. A. J., Brown, J. W., Roches, Des, S., Hardwick, K. M., Hether, T. D., Eastman, J. M., et al. (2012). Goldilocks Meets Santa Rosalia: An Ephemeral Speciation Model Explains Patterns of Diversification Across Time Scales. *Evolutionary biology*, 39(2), 255–261. doi:10.1007/s11692-012-9171-x

Rosindell, J., Hubbell, S. P., He, F., Harmon, L. J., & Etienne, R. S. (2012). The case for ecological neutral theory. *Trends in ecology & evolution*, 27(4), 203–208. doi:10.1016/j.tree.2012.01.004

Krone, S. M. (2004). Spatial models: stochastic and deterministic. *Mathematical and computer modelling*, 40(3-4), 393–409. doi:10.1016/j.mcm.2003.09.037

Sanapareddy, N., Legge, R. M., Jovov, B., McCoy, A., Burcal, L., Araujo-Perez, F., Randall, T. A., et al. (2012). Increased rectal microbial richness is associated with the presence of colorectal adenomas in humans. *The ISME journal*, 6(10), 1858–1868. doi:10.1038/ismej.2012.43

Sau, S. P., & Hrdlicka, P. J. (2012). C2′-Pyrene-Functionalized Triazole-Linked DNA: Universal DNA/RNA Hybridization Probes. *The Journal of organic chemistry*, 77(1), 5–16. doi:10.1021/jo201845z

Sau, S. P., Kumar, P., Sharma, P. K., & Hrdlicka, P. J. (2012). Fluorescent intercalator displacement replacement (FIDR) assay: determination of relative thermodynamic and kinetic parameters in triplex formation--a case study using triplex-forming LNAs. *Nucleic acids research*. doi:10.1093/nar/gks729

Sen, D., Brown, C. J., Top, E. M., & Sullivan, J. (2012). Inferring the Evolutionary History of IncP-1 Plasmids Despite Incongruence among Backbone Gene Trees. *Molecular biology and evolution*. doi:10.1093/molbev/mss210

Seo, K. S., Kim, J. W., Park, J. Y., Viall, A. K., Minnich, S. S., Rohde, H. N., Schnider, D. R., et al. (2012). Role of a New Intimin/Invasin-Like Protein in Yersinia pestis Virulence. *Infect. Immun*. 80(10) 3559-3569. doi: 10.1128/ IAI.00294-12

Settles, M. L., Coram, T., Soule, T., & Robison, B. D. (2012). An improved algorithm for the detection of genomic variation using short oligonucleotide expression microarrays. *Molecular ecology resources*, 12(6), 1079–1089. doi:10.1111/1755-0998.12006

Shringi, S., García, A., Lahmers, K. K., Potter, K. A., Muthupalani, S., Swennes, A. G., Hovde, C. J., et al. (2012). Differential Virulence of Clinical and Bovine-Biased Enterohemorrhagic Escherichia coli O157:H7 Genotypes in Piglet and Dutch Belted Rabbit Models. *Infect. Immun*. 80(1) 369-380. doi: 10.1128/ IAI.05470-11

Silva, S., & Foster, J. A. (2012). Guest editorial: special issue on selected papers from the European conference on genetic programming. *Genetic Programming and Evolvable Machines*, 1-3.

Slater, G. J., Harmon, L. J., & Alfaro, M. E. (2012). Integrating fossils with molecular phylogenies improves inference of trait evolution. *Evolution*. DOI: 10.1111/j.1558-5646.2012.01723.x

Slater, G. J., Harmon, L. J., Wegmann, D., Joyce, P., Revell, L. J., & Alfaro, M. E. (2012). Fitting models of continuous trait evolution to incompletely sampled comparative data using approximate Bayesian computation. *Evolution*. DOI: 10.1111/j.1558-5646.2011.01474.x

Solomon, M., Soule, T., & Heckendorn, R. B. (2012). Proceedings of the fourteenth international conference on Genetic and evolutionary computation conference - GECCO '12 (pp. 153–160). Presented at the the fourteenth international conference, New York, New York, *USA: ACM Press*. doi:10.1145/2330163.2330185

Speybroeck, N., Williams, C. J., Lafia, K. B., Devleesschauwer, B., & Berkvens, D. (2012). Estimating the prevalence of infections in vector populations using pools of samples. *Medical and veterinary entomology*. doi:10.1111/j.1365-2915.2012.01015.x

Stewart, J. E., Abdo, Z., Dumroese, R. K., Klopfenstein, N. B., & Kim, M. S. (2011). Virulence of Fusarium oxysporum and F. commune to Douglas-fir (Pseudotsuga menziesii) seedlings. *Forest Pathology*, 42(3), 220–228. doi:10.1111/j.1439-0329.2011.00746.x

Stolze, Y., Eikmeyer, F., Wibberg, D., Brandis, G., Karsten, C., Krahn, I., … others. (2012). IncP-1\beta plasmids of Comamonas sp. and Delftia sp. strains isolated from a wastewater treatment plant mediate resistance to and decolorization of the triphenylmethane dye crystal violet. *Microbiology*, 158(Pt 8), 2060-2072. PMID: 22653947

Van Meervenne, E., Van Coillie, E., Kerckhof, F.-M., Devlieghere, F., Herman, L., De Gelder, L. S. P., Top, E. M., et al. (2012). Strain-specific transfer of antibiotic resistance from an environmental plasmid to foodborne pathogens. *Journal of biomedicine & biotechnology*, 2012, 834598. doi:10.1155/2012/834598

Wagner, C. E., Harmon, L. J., & Seehausen, O. (2012). Ecological opportunity and sexual selection together predict adaptive radiation. *Nature*, 487(7407), 366–369. doi:10.1038/nature11144

Wang, G., Papasani, M. R., Cheguru, P., Hrdlicka, P. J., & Hill, R. A. (2012). Gold-peptide nanoconjugate cellular uptake is modulated by serum proteins. *Nanomedicine: Nanotechnology, Biology and Medicine*, 8(6), 822–832. doi:10.1016/j.nano.2011.10.007

Wojtowicz, A. J., Miller, C. R., & Joyce, P. (2012). Estimating the number of one-step beneficial mutations. *Statistical applications in genetics and molecular biology*, 11(4). doi:10.1515/1544-6115.1788

Zhong, X., Droesch, J., Fox, R., Top, E. M., & Krone, S. M. (2012). On the meaning and estimation of plasmid transfer rates for surface-associated and well-mixed bacterial populations. *Journal of Theoretical Biology*, 294, 144–152. doi:10.1016/j.jtbi.2011.10.034

Yano, H., Deckert, G. E., Rogers, L. M., & Top, E. M. (2012). Roles of long and short replication initiation proteins in the fate of IncP-1 plasmids. *Journal of bacteriology*, 194(6), 1533–1543. doi:10.1128/JB.06395-11

Yano, H., Genka, H., Ohtsubo, Y., Nagata, Y., Top, E. M., & Tsuda, M. (2012). Cointegrate-resolution of toluene-catabolic transposon Tn4651: Determination of crossover site and the segment required for full resolution activity. *Plasmid*. doi:10.1016/j.plasmid.2012.07.004

Yuan, S., Cohen, D. B., Ravel, J., Abdo, Z., & Forney, L. J. (2012). Evaluation of methods for the extraction and purification of DNA from the human microbiome. *PloS one*, 7(3), e33865. doi:10.1371/journal.pone.0033865

Zhao, L., Stancik, A. D., & Brown, C. J. (2012). Differential Transcription of Bacteriophage\varphiX174 Genes at 37° C and 42° C. *PloS one*, 7(4), e35909. doi: 10.1371/journal.pone.0035909