

INSTITUTE FOR BIOINFORMATICS AND EVOLUTIONARY
STUDIES

2015 ANNUAL REPORT

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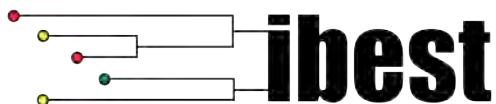
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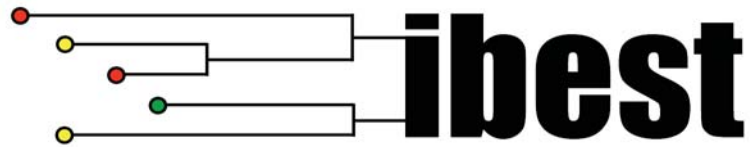
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PREFACE: TRANSITIONS

2015 has been a year of transition with respect to leadership and IBEST personnel. The founding director, Dr. Larry Forney, stepped down and Dr. Jack Sullivan, an original IBESTian, has assumed the Director position via a two-year appointment. Dr. Forney's leadership during his tenure as IBEST Director has been exceptional, and IBEST ascended to its current position of strength and vibrancy under his vision and guidance; we owe him a great deal of gratitude. He will remain as PI of the COBRE.

In response to the change in leadership, the Research Oversight Team (Drs. Holly Wichman, James Foster and Barrie Robison, the Associate Director) has been renamed to the Strategic Planning Committee and have assumed a broader role.

Furthermore, we have a new Business Manager, John Grimes; a new Communications Coordinator/Administrative Assistant, Amberly Beckman; and we are conducting a search for a new Director of the Genomics Resources Core (as a Clinical Assistant Professor).

Nevertheless, IBEST retains its major strengths going forward: our dynamic interdisciplinary environment; the vibrant, interactive, and exceptionally productive faculty; and strong support (financial and otherwise) from the Office of Research and Economic Development. These will allow us to weather the current transitions, maintain our momentum and broaden our impact across campus.



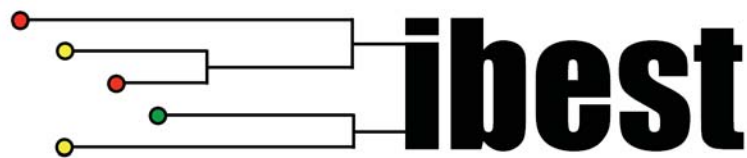


OVERVIEW

Here we report the accomplishments of the Institute for Bioinformatics and Evolutionary Studies (IBEST) for fiscal year 2014-15 for financial information, and for the calendar year 2015 for programmatic activities. The report is organized according to the four elements of IBEST's mission, namely:

- Facilitate interdisciplinary research on evolutionary processes at different levels of 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.

University of Idaho



FACILITATE INTERDISCIPLINARY RESEARCH

STRATEGIC REINVESTMENTS

During FY2015, \$392,951 was reinvested into IBEST-related research. This included (a) investment into recruitment of faculty, (b) investment directly into research through pilot (and bridge) grants, technology access grants (TAGs), and travel/collaboration grants, and (c) professional development workshops and seminars.

Intramural Revenue Sources

IBEST receives revenue from three main sources: 50% of the F&A on grants submitted through IBEST (listed in Appendix X), direct support from the Office of Research and Economic Development (ORED), and payment for services provided by our three core facilities. Revenues generated by the core facilities are funneled back into the budgets of the individual cores with the goal of improving financial sustainability. Revenues provided by ORED are used primarily to subsidize salaries of IBEST administrative and core facility staff, as well as to support the Bioinformatics and Computational Biology (BCB) graduate program. The F&A generated by IBEST grants is used to reinvest in personnel and activities that promote research in real-time evolution.

The majority of F&A received by IBEST is earned from the Phase III COBRE grant that will end in a little over two years; this revenue will need to be replaced and we're implementing a transition strategy. First, we will continue to pursue large program-scale grants. In addition, we will increase the number of investigator-initiated grants (e.g., standard NSF and NIH grants) from across campus. In order to encourage submission of these grants through IBEST, we have erected a new policy for distribution of the 50% of F&A that IBEST receives. This policy is detailed below and will also be followed by the newly established UofI Center for Modeling Complex Processes (CMCI), a new strategic partner.

Expenditure of Intramural Revenues

In FY2014-2015, IBEST largely continued investing revenues in personnel and programs. Hires conducted in previous years had IBEST funds committed to start-up packages (see Appendix 1) to recruit and foster new faculty. In addition,

small distributions of F&A were returned to IBEST investigators. Future investments will follow a more standardized approach. This policy has been implemented to increase transparency to other units on campus (i.e., colleges that house IBEST participants), with the goal of increasing the impact of IBEST across campus. Furthermore, this policy will facilitate strategic planning by academic units by making the IBEST reinvestment more predictable.

IBEST F&A distribution policy (Figures are % of total F&A from each grant).

Investigator-initiated grants & projects within a program-project grant	
Institute	30%
Colleges/Departments	15%
PD/PI	5%
Total	50%

Program-project and similar grants			
<i>Portions designated for administration</i>		<i>Portions designated for cores</i>	
Institute	40%	Institute/Center	40%
College	0%	College	0%
PI	10%	PI	5%
		Core Director	5%
Total	50%	Total	50%

Targeted and Cluster Hires

Efforts by the College of Science to build strength in Systems Biology have continued from prior years. In addition to last year's targeted hire of Dr. Chris Marx in the Department of Biological Sciences and the cluster hires of Drs. Andreas Vasdekis (Physics), Chris Remien (Mathematics), and Audrey Fu (Statistics), the department of Biological Sciences has hired Dr. Paul Rowley, a biochemist from UT-Austin. The collaborative environment that IBEST cultivates has been a tremendous advantage in recruiting these young scientists.

EXTRAMURAL FUNDING

Extramural Research and Administrative Funding

Research grant proposals that are related to the theme "real time evolution" may be submitted through IBEST by UofI faculty from any unit. In these instances the IBEST Business Manager assists principal investigators to prepare and submit their grant applications to the UI Office of Sponsored Programs (OSP) who in turn review and submit the application to the granting agency. The level of support provided investigators varies depending on their level of experience and the agency requirements. At a minimum, the Business Manager works with the PI to prepare the budget and budget justification in accordance with UI policies and those of the granting agency. Once a grant is awarded the IBEST administrative staff help the PI

recruit personnel, handle all purchasing and travel expenditures, and help the PI manage their budget.

In FY2015, grant applications requesting \$9.1 million were submitted and a total of \$2.8 million in new funds were awarded. The COBRE received another year of funding. In addition, since the beginning of FY2016, \$500,422 in new funds have been awarded on BEACON grants. Both the BEACON and COBRE grants also provide administrative funding.



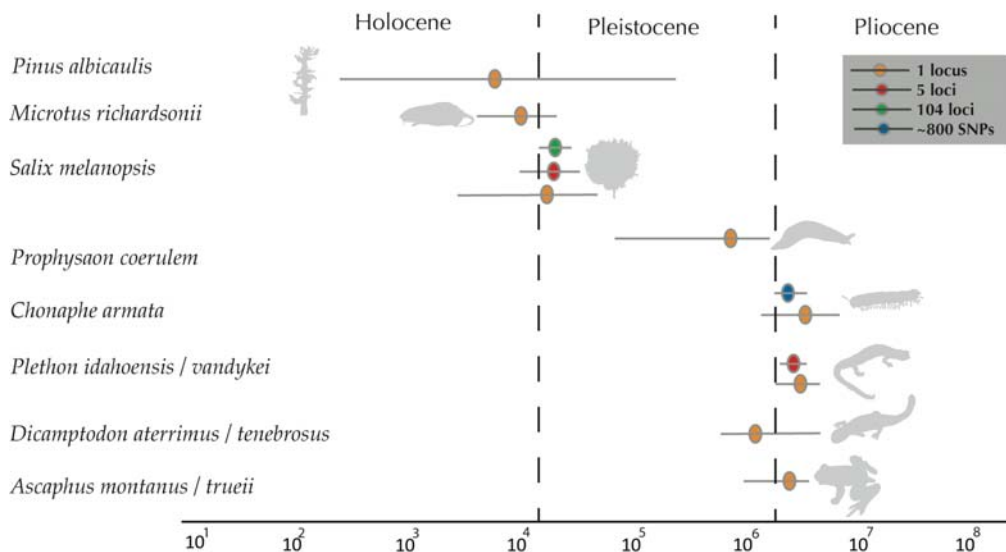
COLLABORATIVE RESEARCH: A COMPARATIVE PHYLOGEOGRAPHIC APPROACH TO PREDICTING CRYPTIC DIVERSITY - THE INLAND TEMPERATE RAINFOREST AS A MODEL SYSTEM

Drs. Jack Sullivan, David Tank and Anahí Espíndola (NSF Grant Submitted through IBEST)

Given the myriad threats to the earth’s biodiversity it is clear that biodiversity discovery can no longer proceed on a species-by-species basis. Rather, rapid discovery and characterization of biodiversity is needed. The proposed work will develop a **predictive framework for the discovery of cryptic biodiversity** that can be applied to entire ecosystems. The proposed research will develop a predictive framework for the discovery of cryptic biodiversity that can be applied to entire ecosystems. In this two-phase framework we will (i) gather environmental, taxonomic, functional, and genetic data from a *reference set of taxa* endemic to our model ecosystem and identify which of these harbor cryptic diversity, (ii) conduct a discriminant function analysis (DFA) to identify characteristics of the data shared by *reference taxa* that harbor cryptic diversity, (iii) apply the DFA to an *experimental set of taxa* to make predictions about which of these species contain cryptic diversity, and (iv) validate these predictions via phylogeographic analyses of *experimental taxa*.

The temperate rainforests of the Pacific Northwest of North America will serve as the model system for this comparative phylogeographic work. This ecosystem is rich in endemics and harbors the potential for substantial cryptic diversity. The disjunction of conspecific populations or putative sister- species pairs between Pacific coastal and interior Rocky Mountain habitats presents clear hypotheses regarding this potential: either pre-Pleistocene vicariance, which predicts high cryptic diversity, or post- Pleistocene dispersal where we predict a lack of cryptic diversity. Our predictive framework will move the field from descriptive, pattern-matching comparative analyses towards a rigorous evaluation of ecosystem-level patterns. Second, this framework will improve the efficiency with which cryptic diversity is discovered by allowing researchers to target taxa that are predicted to harbor cryptic diversity.

This work has been funded by the Biodiversity Discovery and Analysis program of The National Science Foundation for three years (2015 – 2018) and will use the IBEST GRC and CRC; we will collaborate with Dr. Bryan Carstens at the Ohio State University.



IBEST GRANTS

COBRE-funded Pilot Grants

The objective of the IBEST Research Pilot Project Program is to (a) increase the number and success rate of grant applications submitted to NIH and other federal and private funding agencies by faculty at the University of Idaho for biomedically relevant research in the fields of computational and evolutionary biology by enabling faculty to generate preliminary data that will make them more competitive for external funding, and (b) increase the usage of the core facilities as investigators conduct research that relies on the resources available in these cores.

All tenure track and non-tenure track faculty of any rank at the University of Idaho are eligible to apply for the IBEST Pilot Project Research Grant. The proposal may be collaborative with individuals at UI or at other institutions; non-UI collaborators can generally not receive COBRE funds, but funds can be used for collaborator travel. The research proposed must be consistent with the scientific theme of the NIH COBRE and have clear relevance to human health. (For proposal criteria see Appendix 4)

2015 Pilot Grant Award

The call for IBEST Research Pilot Project proposals was advertised campus wide, and four proposals were received. Four external peer reviewers who had no conflict of interest with the applicants were selected. Three reviewers were selected for each proposal; one of the three was an expert in the subject of the proposal. The review criteria were identical to those used by NIH, with the additions of incorporating the relevance of the proposed work to the 'evolution theme' of our COBRE grant and assessment of whether the investigator would use IBEST core facilities. Members of the IBEST Research Oversight Team read the reviews and met to discuss the scores. The proposal with the lowest (best) score was "A novel system for the genetics of inflammation and cancer" that was submitted by Dr. Paul Hohenlohe from the Department of Biological Sciences (see description on following page).

Dr. Hohenlohe's proposal was then distributed to the IBEST External Advisory Committee (EAC) who endorsed the recommendation before it was forwarded to NIH for final approval. In August 2015 Dr. Hohenlohe was awarded the IBEST Pilot Research Grant for year one, which can be renewed for a second year if progress is satisfactory.

In addition, the Research Oversight Team decided to award Dr. Deb Stenkamp a portion of her request for the project "Evolutionary mechanisms underlying regulation of tandemly replicated opsin genes." Dr. Stenkamp's proposal scored nearly as well as well as did Hohenlohe's; furthermore, this award was viewed by the ROT as an excellent opportunity to bridge Dr. Stenkamp to competitive renewal of her NIH R01 grant.

A NOVEL SYSTEM FOR THE GENETICS OF INFLAMMATION AND CANCER

Dr. Paul Hohenlohe and Sarah Hendricks (2015 IBEST Pilot Grant)

The relationship between inflammation and tumorigenesis remains a complex and multifaceted challenge in oncology. While a wide range of genetic and environmental factors may lead to tumorigenesis, chronic inflammation plays a critical role in tumor initiation, promotion, and progression. Host defense due to infection, or tissue repair due to massive cell death as a result of infectious or non-infectious tissue injury, illicit inflammatory responses. The resulting inflammation, when prolonged, can lead to genomic lesions and tumor initiation. This response to chronic inflammation is partially attributed to lifestyle-related factors in humans; yet, wildlife populations also experience inflammation-induced cancers. Understanding genetic variation that links inflammation and cancer in a novel system could provide new insight into this complex interaction.

We propose to identify genomic regions and differential gene expression patterns associated with tumorigenesis resulting from inflammation. We will test the hypothesis that genetic variation in immune response is responsible for variation in carcinoma prevalence. We will test this hypothesis in the California channel island fox (*Urocyon littoralis*), for which more than half of adult foxes on one island (Santa Catalina) suffer from ceremonious gland carcinoma induced by inflammation due to mite infection. Foxes on two other islands suffer high rates of infection with the same mites, and although this causes inflammation, cancer does not result. This observed variation in carcinoma status in hosts and their response across islands allows for the unique opportunity to investigate the role of inflammation and cancer in a controlled, comprehensive analysis of natural populations. We propose to use RAD sequencing, RNA sequencing, and sequence capture to develop a novel system for understanding variation in the immune response to infection, inflammation, and tumor development.

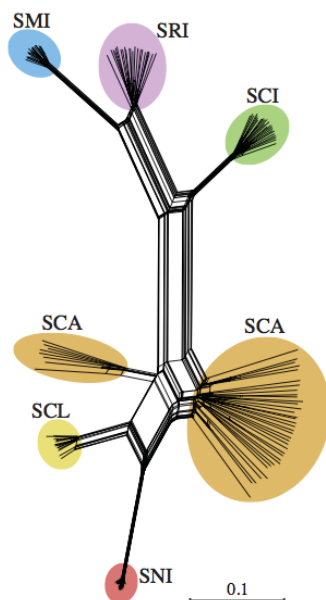


Figure 1. Genetic clustering of individual foxes from the six Channel Islands, based on over 5,000 SNPs identified and genotyped with RAD sequencing (Funk, Hohenlohe et al. unpublished). Northern Islands: San Miguel Island (SMI); Santa Rosa Island (SRI); Santa Cruz Island (SCI). Southern Islands: Santa Catalina Island (SCA); San Clemente Island (SCL); San Nicolas Island (SNI). Despite strong differentiation among islands, SCA retains significant within-population genetic variation.

IBEST Technology Access Grants (TAGS)

As in years past, IBEST has partnered with the Idaho-INBRE to administer and fund the Technology Access Grant (TAG) Program. This is essentially a small 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.

Proposals related to the IBEST theme of 'real time' evolution or the INBRE theme of 'cell-cell signaling' are accepted at anytime during the year and the review process is simplified and expedited; requiring only the review by members of the IBEST Steering Committee and the INBRE leadership. 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. 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.

So far in 2015 three Technology Access Grants totaling \$32,794 have been awarded.

1. "Pathophysiology of diabetic nerve cell injury (neuropathy) in the gut." Onesmo Balemba, Department of Biological Sciences.
2. "Host/pathogen interactions of human cytomegalovirus." Lee Fortunato, Department of Biological Sciences
3. "An integrated approach to understand eco-evolutionary invasion dynamics in an alpine system." Dave Tank, Department of Biological Sciences

The progress reports for these TAGs can be found in Appendix 5.

IBEST Travel and Collaborative Grants

The Travel and Collaborations Grant Program allows investigators to explore new collaborative research opportunities, spur the productivity of an existing collaboration, or facilitate the preparation of research grant proposals. These awards can also be used by IBEST faculty to attend scientific conferences that focus on topics outside of their area of research; this will add breadth to their expertise. 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. These small grants will typically not exceed \$2,000.

We received and awarded a single grant application in 2015. Dr. Celeste Brown traveled to Indianapolis to re-establish a collaboration with Dr. Keith Dunker at the Indiana University Center for Computational Biology and Bioinformatics. This research involves the evolution of disordered proteins and her travel should assist her efforts to write NIH and NSF proposals on these molecules.

EVOLUTIONARY MECHANISMS UNDERLYING REGULATION OF OPSIN GENES

Dr. Deborah L. Stenkamp (IBEST Bridge Funding)

The tandem replication of genes to generate arrays of paralogs is an established evolutionary process underlying functional diversification in vertebrate sensory systems. The tandem array on the human X chromosome harbors genes encoding a long wavelength-sensitive (LWS; red) opsin and 1-9 genes encoding medium wavelength-sensitive (MWS; green) opsins, and is an excellent example of a recent outcome of such a process. Heritable defects in the *LWS/MWS* array result in various forms of color blindness, and in X-linked retinal degenerations. The current model for human *LWS* vs. *MWS* opsin regulation states that a stochastic event favors an association of an upstream regulatory region with the *LWS* or most proximal *MWS* opsin promoter or exon. However, spatiotemporal patterns of human *LWS* vs. *MWS* opsin expression suggest that a nonrandom, *trans* regulatory mechanism may be involved. In this IBEST-supported project we focus upon ***evolutionary mechanisms underlying regulation of tandemly replicated opsin genes***. Our studies include two Specific Aims: **1)** Test the hypothesis that endogenous RA signaling regulates differential expression of zebrafish *LWS1* vs. *LWS2*; **2)** Test the hypothesis that RA signaling is a co-opted mechanism for patterning of tandemly replicated opsins in vertebrates.

Benefit of IBEST Funds for This Project: IBEST funding has allowed us to retain a Research Specialist in the laboratory who has and will continue to contribute significantly to this project. This support was necessary for the completion of several experiments related to Aim 1 of the project, which were incorporated into a re-submission of a manuscript to *PLOS Genetics* (Mitchell et al., 2015). This paper provides the first report of a developmental cell signaling system regulating differential expression of tandemly-replicated opsin genes, and provides support for the hypothesis that endogenous RA signaling regulates these genes.

The IBEST funding now supports two avenues of further study on this project. The first is the pursuit of Aim 2, in which we evaluate the distribution of RA signaling components, and expression of additional tandemly replicated opsin arrays in zebrafish, other fishes, and in primates. We have determined that RA signaling is a likely regulator of expression from the tandemly *quadruplicated* array of *RH2* (green-sensitive) cone opsins in zebrafish. We have also obtained stickleback tissues from a collaborator to determine the distribution of RA signaling components, and the tandemly duplicated *RH2* cone opsins in this teleost. We will obtain cichlid, medaka, and human tissues from other collaborators and central repositories to continue our progress on Aim 2. Over the summer, an NSF-REU-supported undergraduate performed pilot studies that suggest endogenous *thyroid hormone* signaling constitutes a secondary, co-opted mechanism for patterning of tandemly replicated opsins in vertebrates. We will next gather and generating genetic tools to explicitly test this hypothesis. Our studies have high potential to dramatically shift the existing paradigm for the regulation of tandemly replicated opsin genes to an alternative model involving *trans* regulatory mechanisms that suggest opportunities for therapeutic manipulation of cone phenotype, and for revealing evolutionary processes that underlie differential expression. Our experiments will generate preliminary data for proposals to the NIH (National Eye Institute) and the NSF (Division of Integrative Organismal Systems).

DISSEMINATION OF INFORMATION

IBEST/BCB Seminar Series

The IBEST Seminar Series continues to attract excellent scientists from across the nation and world to the campus of the University of Idaho. 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 research done at the University of Idaho and the collegial and collaborative atmosphere within IBEST. This has bolstered our reputation in the scientific community and helped us recruit students. See Appendix 6 for a listing of seminar speakers and topics in 2014.

These seminars (about four per semester) 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. The graduate students of the Bioinformatics and Computational Biology program choose and invite speakers for the seminar series and organize their itinerary.

IBEST Lunch Series

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) Thunder Thursdays, where three IBEST investigators present an informal “lightening talk” of 8 minutes on their work, followed by 8-10 minutes of group discussion; (b) invited speakers present formal seminars (described above); (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.

Inland Northwest Genomics Research Symposium

The third annual Inland Northwest Genomics Research Symposium (INWGRS) was held in May 2015. The symposium was a one-day event used a lecture format and included presentations by IBEST core facility directors, vendors, regional and national researchers. The symposium keynote address was given by Dr. Jim Seeb of the University of Washington. Dr. Seeb's research focuses upon identifying gene markers that distinguish populations, demes, or individual Pacific salmon. He currently has projects or is collaborating on projects to use these markers to study migration of adults in the Bering Sea or migration of juveniles in complex lake systems.

The objectives of the Symposium were to provide the University of Idaho research community an opportunity to learn more about IBEST GRC and CRC core facilities, potential uses of newly introduced technologies and approaches to data analysis, increase awareness of leading edge research projects at both the local and national level, and to

provide insights into emerging technologies. It provided opportunities for local researchers to interact with invited nationally renowned scholars and interact with technology representatives. The Symposium provided benefit to IBEST cores by increasing awareness of their capabilities and highlighting local research programs that utilize core services.

The symposium had 145 attendees. Of those 68 were from the University of Idaho, 31 were from Washington State University, with the remainder coming from further away (Appendix 8 for more details).



INNOVATION

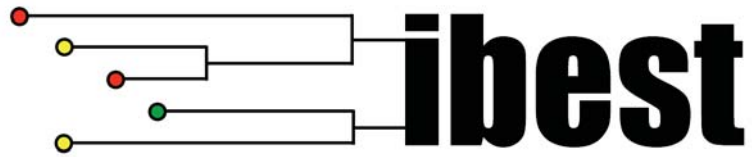
Business for Scientists

In 2015, we offered the “Leading and Sustaining Your Research program” workshop for the second time. This workshop has been designed in partnership with the University of Idaho College of Business and Economics and teaches skills that are not part of traditional graduate and postdoctoral programs. These include project management, budget development, human resources administration, strategic planning, risk assessment, team building, communication with stakeholders and especially lay people. The course was advertised across the Moscow campus, and this year we extended eligibility to postdoctoral fellows; thus, IEST faculty can include this course to enhance Postdoctoral Mentoring Plans in successful NSF and NIH proposals (one such NSF proposal was funded in 2015). Importantly, there is no cost for attendance.

“This workshop provided me with a new perspective of how to present my research, plan my research strategy, and areas I should seek for career development and/or collaboration.” Katie Brown

This year, we had a full roster of 22 attendees from 16 departments (Appendix 9) and representing four colleges (College of Sciences, College of Agricultural and Life Sciences, College of Natural Resources, and College of Engineering). As was the case last year, the workshop was delivered in 5 morning sessions over the course of a week (June 1st -5th; see schedule in Appendix 8). Our assessment from this year indicated that the workshop was very well received again. Attendees rated the overall effectiveness of the workshop 4.2 (out of five), and provided suggestions that will allow us to improve the 2016 edition of the workshop.





STRATEGIC COLLABORATIONS & PARTNERSHIPS



BEACON

The BEACON Center for the Study of Evolution in Action is an NSF Science and Technology Center (SCT) founded in 2010 with the mission of illuminating and harnessing the power of evolution in action to advance science and technology and benefit society. NSF STCs are multi-institutional consortia funded for up to 10 years at up to \$5M per year. BEACON is a consortium of universities led by Michigan State University, and including IBEST at the University of Idaho along with the University of Texas at Austin, the University of Washington, and North Carolina A&T State University. 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.

BEACON promotes research on “Evolution in Action” that crosses academic areas (biological, artificial, engineering) and thematic boundaries (networks, communities, and behavior) by providing competitive research grants to participating institutions. Ideally the projects funded transcend geographic boundaries and engage investigators from multiple participating institutions.

The BEACON STC was renewed this year, for five more years and \$22.5 million in additional funding. IBEST has received over \$3 million in competitive funding from BEACON, to date. These funds have supported 38 projects, 17 faculty members from across campus, over two dozen graduate students and postdocs, and many undergraduate students. We have research capacity by funding new labs such as the fly-virus co-evolution facility, and individual lab enhancements. These projects are interdisciplinary, and many are cross

institutional. In the last year alone, IBEST faculty and postdocs had 11 new projects funded, at over \$500,000 (listed in Appendix 9).

The competitive renewal of the BEACON STC this year was a major accomplishment. IBEST personnel participated in NSF site visits, and helped prepare and submit the proposal itself. IBEST was originally asked to help form BEACON in 2010 because of our established excellence in evolutionary engineering and experimental evolution in biology. IBEST's continued active involvement in BEACON remains a testament to the high regard in which our real-time evolution activities are held by top universities nation wide, and by NSF.

A complete listing of the projects funded to date can be found in Appendix 11.



CENTER FOR MODELING COMPLEX INTERACTIONS (CMCI)

The Center for Modeling Complex Interactions (CMCI) is an NIGMS-funded Center of Biomedical Research Excellence (COBRE). CMCI was awarded a \$10.6 million 5-year grant in March 2015, with Dr. Holly Wichman as PI on the grant and the Director of the Center. CMCI funds projects led by three early-career faculty working in the area of viral co-infection. It also funds a Collaboratorium for modeling that houses four postdocs. These postdocs and participating faculty work with the three project directors on modeling for their projects and also do modeling for other biomedically-related research. One long-term goal is to extend this modeling paradigm beyond biomedical projects to other areas of research in at the university.

CMCI is an independent program, but it is complementary to and synergistic with IBEST. For example, the two programs have complementary pilot grant programs and access grants, have agreed to use the same formula for resource distribution to PIs and colleges, and have put protocols in place so that PIs can submit grants with shared credit between CMCI and IBEST when appropriate. CMCI has funding to add additional bioinformatics expertise in the IBEST Genomic Core and the IBEST Computational Core houses and maintains CMCI's high-end graphical processing node for molecular dynamic modeling. Furthermore, IBEST committed some funds to assist construction of CMCI's Collaboratorium.



CORE FACILITIES

COBRE PHASE III

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. Using COBRE funds, we have established and expanded the Computational Resources and Genomics Resources Core facilities at the University (the CRC and GRC, respectively). 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. We are completing year 3 of this five year third phase of COBRE funding that began in February 2013 and brings an additional \$5,096,846 in funding to the university. This final phase of COBRE funding, along with institutional investments in IBEST as a strategic institute, will help the core facilities become self-sustaining and maintain the momentum of the highly competitive research programs built during the first ten years of COBRE funding.

IBEST GENOMICS RESOURCES CORE

Mission and Vision

The *mission* of the IBEST Genomics Resources Core (GRC) is to provide researchers at the University of Idaho access to cutting edge genomics technology and the bioinformatics tools needed to acquire, analyze, and visualize data. The *vision* of the GRC is to stay current in genomics technology and bioinformatics, remaining agile with respect to new techniques and approaches, and to build partnerships with research groups and other regional core facilities.

Summary of Accomplishments

- Tailoring molecular techniques to accommodate the unique needs of each researcher.
- Custom two-step PCR process for generating amplicons and sequencing up to 2,976

amplicons per MiSeq run or HiSeq lane resulting in drastically reduced cost and increased coverage.

- To allow clients to assemble genomes without a reference the GRC is testing Illumina's new method for making and sequencing 10kb reads. Success would allow the GRC to produce PacBio-competitive data without a significant capital investment.
- The GRC's unique practices and capabilities have resulted in a very large number of first-time clients from word-of-mouth advertising.
- Bioinformatics workshops as part of outreach programs - Held in February of 2015 for internal users of the GRC.

Infrastructure and Personnel

The IBEST GRC is the only comprehensive facility on the University of Idaho campus that houses all the equipment and personnel necessary to aid researchers in every aspect of high-throughput genomics research. It provides the molecular expertise and equipment needed for most high-throughput sequencing studies, and develops partnerships with other service facilities when additional capacity or other specialized equipment are warranted. The real benefit of the IBEST Genomics Resources Core facility, however, has been the integration of bioinformatics data analysis with data generation. The GRC offers consultation on experimental design, appropriate and best use of technologies, and bioinformatics support to perform analysis, quality assurance, interpretation, and visualization. Through a unique strategy known as "*the triangle of collaboration*," an investigator, molecular scientist, and bioinformatician meet regularly as a team to discuss the goals and objectives for a project. This strategy helps improve the success rate of GRC projects, and reduces costs by generating informative data on the first attempt for a given experiment.

The GRC also maintains equipment that is accessible to faculty, staff and students of University of Idaho. This equipment, collectively called the "GRC User Core", is primarily designated for high throughput sample preparation and quality assurance. Users are trained by GRC laboratory staff before scheduling time to use the equipment, and are responsible for any reagents needed to run their samples. When needed, GRC staff are available to help troubleshoot.

Existing Infrastructure

The Genomics Resources Core Facility has the equipment necessary for applications of DNA sequencing technology, high throughput sample preparation and quality assurance, and bioinformatics analysis. The Core facility occupies approximately 1530 square feet of laboratory space in Gibb Hall 242, 775 sq. feet of laboratory space in the GRC User Core, Gibb Hall 116, and approximately 300 sq. feet of office space in Life Sciences South at the University of Idaho main campus in Moscow, Idaho. The Core facility infrastructure is described in more detail below.

GRC DNA Sequencing Laboratory:

DNA sequencing has become an indispensable tool for basic biological research,

biomedical research, diagnostics, and molecular systematics. Current applications using DNA sequencing include whole genome shotgun sequencing and synthetic long reads, including *de novo* sequencing of previously unknown genomes; transcriptome sequencing; targeted re-sequencing; transposable element enrichment; single nucleotide polymorphism (SNP) discovery; metagenomics and amplicon sequencing for studies on microbial community composition; and many other applications. The Core facility also has equipment and robotics for high throughput sample preparation associated with activities upstream of DNA sequencing, such as library preparation. This approach reduces the need to hire additional staff, thereby reducing the costs of operating the core. Presently, the core has the following equipment in its DNA Sequencing Laboratory:

- DNA Sequencing

ILLUMINA MiSeq Sequencing Platform: Paired-end sequencing of up to 600bp per library-fragment and 15Gb of DNA sequence per run.

ILLUMINA HiSeq Sequencing Service: Paired-end sequencing for projects requiring higher-than-MiSeq read-density; outsourced to collaborating facilities.

- Library Qualification and Quantification

LIFE Technologies StepOnePlus: Quantification of sequenceable libraries via qPCR.

ADVANCED ANALYTICAL TECHNOLOGIES FRAGMENT ANALYZER: Capillary array based high-throughput quality assessment of all DNA and RNA samples.

AGILENT 2100 BIOANALYZER: Sizing, quantification, and quality control of DNA, RNA, proteins and cells in low-throughput fashion.

- Library Preparation and Size-Selection

FLUIDIGM ACCESS ARRAY: Creates 2304 amplicon libraries per 48 sample chip for targeted-resequencing.

WAFERGEN APOLLO 324: Automates next generation sequence library preparation workflows for Illumina, Ion Torrent, and 454.

SAGE BIOSCIENCES BLUEPIPPIN: Automated and customizable PFGE-based size-selection of DNA fragments between 90bp and 50kb with no cross-contamination.

COVARIS M220: Highly reproducible DNA-shearing between 150bp and 5kb.

INVITROGEN E-GEL SYSTEM: Size-selection and visualization of library and DNA respectively.

- Sample Quantification

MOLECULAR DEVICES PLATE-READER AND INVITROGEN QUBIT 2.0: Fluorometric quantification of DNA and RNA (hundreds of samples or single samples depending on device) yielding more accurate and reliable concentrations than NanoDrop.

GRC User Core: High Throughput Sample Preparation and Quality Assurance

By acquiring new instruments in the GRC User Core for high-throughput sample preparation and quality assurance, the GRC provides researchers with the ability to

increase sample quality while simultaneously reducing sample-to-sample variability and the time required for procedures. Equipment in the GRC User Core used for high sample throughput and quality assurance include:

- DNA, RNA, and Library Qualification

Qiagen QIAxcel: Providing “digital gels” for all DNA and RNA less than 3000 bp in high throughput fashion.

Molecular Devices SpectraMax Paradigm: Multimode modular microplate reader currently capable of high-throughput quantification of DNA & RNA.

- Sample -prep DNA & RNA purification

Thermo Scientific KingFisher Flex: Automated high speed purification of nucleic acids, proteins, and cells in a 96well format using agnostic reagents and kits.

Qiagen QIAgility: Highly customizable liquid handler for qPCR assay setup and other tasks benefitting from accurate and reproducible pipetting.

Boreal Genomics Aurora: Gel based isolation, purification, and concentration of DNA from highly contaminated sources using Boreal’s proprietary SCODA electrophoresis.

Diagenode Bioruptor Plus (UCD-300): High-volume sonication/shearing of DNA, chromatin, cells, and tissue.

BioRad T100: Basic touch-screen thermal-cycler for labs lacking this capability.

GRC staff continuously monitor current technological methods and trends for potential new equipment that will contribute to the mission of the GRC, both in the DNA sequencing laboratory and the GRC User Core. Each piece of equipment is evaluated for its ability to increase potential service offerings, improve the quality of existing services, increase automation and throughput, and/or augment the existing equipment in the GRC User Core. These features are considered from the perspective of the stated mission – to facilitate cutting edge research in “real time evolution.”

Planned Infrastructure Investments

The GRC is currently evaluating the purchase of the following equipment for addition to the GRC Sequencing Laboratory:

BioRad C1000 Touch: 384 well thermal cycler required for Illumina’s synthetic long read workflow.

Personnel

The IBEST Genomics Resources Core facility operates as a “turnkey” facility in which project design, sample preparation, data generation, and data analysis are integrated within a single facility. Therefore, the GRC has two main components: the “wet” lab and the “dry” lab, with the GRC Director overseeing both laboratories. The “wet” laboratory is staffed by professionals with molecular biology expertise and is where data are generated from samples provided by investigators. The “dry” laboratory is staffed by bioinformatics data scientists and is where data generated in the “wet” lab are analyzed, summarized and interpreted. A significant amount of communication and coordination occurs between the

“wet” and “dry” laboratories.

The GRC stays nimble by continuing to develop new partnerships with other service facilities and by purchasing equipment to automate molecular methods, allowing a small staff to perform the same quantity and quality of work as a core facility with a larger staff that lacks as many automated workflows.

Genomics Resources Core Director

The former GRC Core Director, Dr. Matthew Settles, left the UI this summer to take a position as the Director of Bioinformatics at UC Davis. The GRC has restructured the position of Director, and is now conducting a national search for a new Director at the rank of Clinical Assistant Professor.

Bioinformatics Data Scientist

This position is responsible for bioinformatics and analysis of genomics data, and was filled in the summer of 2015 by Dr. Alida Gerritsen. Dr. Gerritsen earned a Ph.D. in Biology from the University of Oregon after earning a B.S. degree in Biology from St. Lawrence University. Dr. Gerritsen originally joined the GRC in the summer of 2014 as a Genomics Laboratory Scientist and worked in a hybrid role in both the “wet” and “dry” labs. Her current duties involve sequence analysis and bioinformatics support for a variety of projects.

Genomics Laboratory Manager

Mr. Daniel New is responsible for the day-to-day operation of the GRC “wet” laboratories which includes the DNA Sequencing Laboratory and USER CORE. Dan earned B.S. degrees in Microbiology and Molecular-Biology/Biochemistry from the University of Idaho in 2005 while concurrently working as an undergraduate research to learn basic molecular techniques from 2003-2005. Prior to joining the Core in 2010, Mr. New was a Research Associate at Washington State University in the College of Veterinary Medicine where he gained experience in RNA extraction, relative-qPCR, mammalian cell-culture and transfection, microarray printing/processing, Sanger sequencing/instrumentation, PFGE, MLVA, and Kirby-Bauer assays.

Genomics Laboratory Scientist

This position is currently vacant, and we will conduct a search after the new GRC director has been hired.

Bioinformatics Research Assistant

David Streett is a graduate student in Bioinformatics and Computational Biology. He has a half time appointment in the GRC, where he is responsible for the development of bioinformatics software and analysis pipelines. He received his B.S. in Biochemistry in May of 2015.

Bioinformatics Analysis Resources

The GRC does not maintain any specialized equipment for data management or

bioinformatics analysis; instead, it maintains a strong partnership with the University of Idaho IBEST Computational Resources Core facility. This tight integration between the GRC and CRC has numerous advantages. First, the CRC provides the storage and computational power necessary for the analysis of the large-scale genomic data sets that are produced by the GRC. Second, the collaboration between the cores provides a great deal of agility with regard to the development of new bioinformatics techniques and analyses. This fosters innovation and creative activity that are the hallmark of IBEST, and differentiates the GRC from other more “traditional” genomics core facilities around the US and the world.

Services and Innovation

The Genomics Resources Core offers “*genomics project management*” to customers by integrating services in all three phases of genomics research: project planning and consultation, genomic data generation, and bioinformatics data analysis. In contrast, most core facilities around the country focus mainly on data generation, leaving investigators to struggle with immense data sets with little help. Our integrated approach is very unusual, and a key component to our continued success. This has led to a large amount of off-campus clients (both U.S. and International) through “word-of-mouth advertising” which is balanced with our on-campus workload (see Figure 1). To track and manage the growing GRC user base, the Core implemented iLab project management and billing system in late FY2014. Over the past year, the Core has been able to use iLab to accurately track usage data from internal and external users and effectively bill for bioinformatics time.

Top 10 Institutions (by total cost)

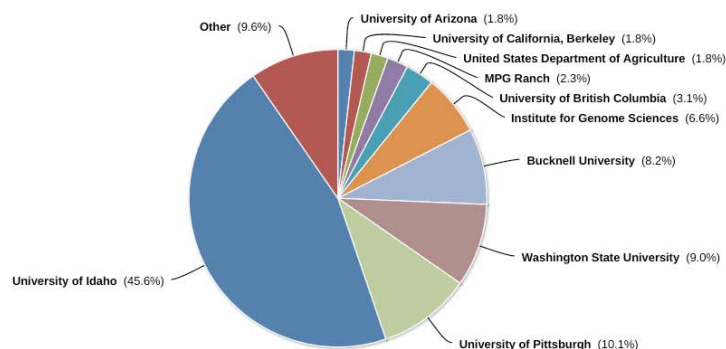


Figure 1. The top 10 institutions (by total expenditures) commissioning work from the GRC in 2015.

Project Consultation

Core facility staff consult with investigators to discuss project aims and expectations, experimental design, appropriate and best use of technology, sample quantity and quality issues, and data analysis needs. During consultation, a project timeline is formed and expected costs are discussed. Having these discussions early in a project provides an

opportunity for Core personnel to offer their expertise, advice, and assistance to enhance the proposed project and sidestep potential problems. Initial consultation is a service that the GRC currently provides free of charge, even to researchers in the grant proposal process. Providing this service free of charge ensures that researchers come to the GRC to develop a detailed plan at an early stage of their project and can develop a cost structure for proposed experiments, including bioinformatics. This approach helps keep overall costs low, expectations realistic, and potentially costly problems minimal in the latter stages of a project.

Genomics Data Generation

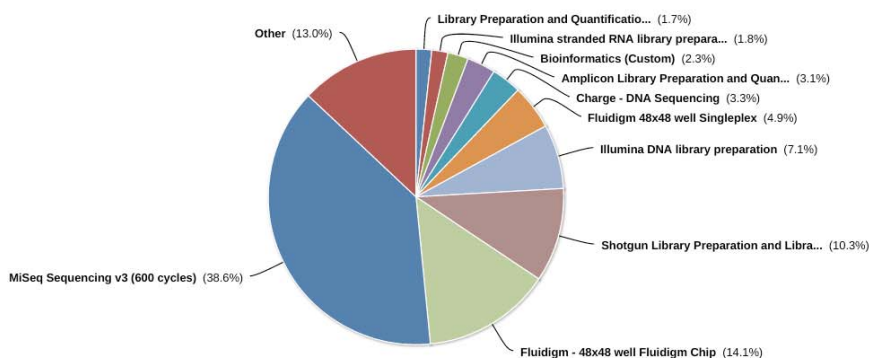
The Genomics Resource Core facility operates and maintains equipment (described above) that allows high throughput sample preparation and quality assurance, and generates high throughput DNA/RNA sequence data. While the Genomics Resources Core operates much of the equipment necessary to perform the work proposed by its clients, there are instances when projects require technologies that are not present in the facility. In these cases, the GRC facilitates access to the technology through cooperation and collaboration with other regional core facilities. For example, when investigators require the additional capacity provided by the Illumina HiSeq platform, the GRC staff prepares Illumina libraries that are sent to other institutions for sequencing (such as University of California - Berkeley or the University of Oregon), and the data are then sent back to the GRC for processing and analysis. The fact that the sequencing was done “off-site” is seamless and causes no additional work for the investigator. This expands the range of services the GRC can offer without incurring additional capital expense. A time series of expenditures by type is shown in Figure 2.

Top 10 Services by month (by total cost)



Figure 2. Time series of expenditures (by type of service) in the GRC in 2015.

Top 10 Services (by total cost)



Highcharts.com

Figure 3. Summary of types of services.

Bioinformatics and Data Analysis

The GRC continues to increase its user base for genomic data generation and as a result has increased charges associated with bioinformatics analysis. Bioinformatics data analysis is often the most challenging aspect of any experiment, and until very recently was often overlooked. The current system accurately tracks personnel hours on independent projects and reflects the effort that is expended for analysis.

The GRC offers bioinformatics services through staff bioinformaticians and can perform a full range of analysis tasks to address questions in areas such as population genetics, genomics, microbial community dynamics, functional genomics and systems biology. GRC bioinformaticians begin with raw output from genomics equipment and proceed through quality assurance, data processing and analysis, data interpretation and visualization. Analyses are conducted using pipelines in the public domain or those developed by Core staff members. Core personnel have developed analytical techniques and pipelines for microbial community analysis, genome assembly, transcriptome assembly, population variant analysis, SNP/INDEL detection, and RNAseq analysis. These pipelines transform and manipulate raw data into a form and format that can be mined by investigators.

Data processing occurs through a feedback loop with investigators. The GRC bioinformaticians seek feedback from investigators after preliminary data analysis, so that adjustments in output content, form, and format can be made. Data are then re-analyzed or additional analyses are performed until the project's goals are met, figures are generated, and summary tables are provided to the investigators in a form that is useful to them. The Core staff provides investigators with detailed knowledge of the laboratory protocols and bioinformatics methods used so they can be included in reports and publications as needed. As a result, core staff members are often included as co-authors on publications because of their significant intellectual contributions to research projects.

Innovative New Methods

GRC staff has participated in the design and development of new methods and techniques for genomics research. Example projects are briefly described below.

Assembly by Reduced Complexity (ARC)

As a part of his PhD dissertation, previous Data Scientist Dr. Samuel Hunter developed Assembly by Reduced Complexity (ARC), a software package for targeted assembly of homologous sequences. The algorithm works by comparing reads to a set of reference targets similar and bins them based on the results of these comparisons. Assemblies are then performed on sequences from each bin. ARC works effectively with divergent references, functions well with short low quality sequence reads, and compares favorably to *de novo* assembly in terms of CPU and memory requirements.

A Modular, Highly Multiplexed Design for Illumina Amplicon Sequencing

Dr. Matthew Settles, in collaboration with Mr. New and Dr. Gerritsen, developed a laboratory protocol and data analysis platform for performing highly multiplexed Illumina amplicon sequencing. PCR amplicon sequencing is an important tool used to query genetic variation and structure in individual samples and ecological communities. Applications range from determining the composition and structure of bacterial and fungal communities to determining allele frequencies in a set of genes across many individuals. This methodology provides a way to simultaneously sequence and analyze hundreds of samples across one or many targeted regions in the same sequencing reaction while significantly reducing experimental costs.

The analysis platform is a comprehensive application that starts with raw sequence reads and ends with abundance tables of taxonomically assigned sequences for community analysis. Additionally, the application is able to prepare reads for input into phylogenetic tree building software. The software project is ongoing, relying on user comments and feedback to continue improving the functionality and efficiency of the program.

Long-Read Sequencing Technology

Mr. New invested a significant amount of time learning Illumina's new "TruSeq Synthetic Long-Read DNA Library Prep" method. This method produces 10kb pseudo-reads, which allow rapid *de novo* genome assembly of plants and animals as well as phased genome sequencing (allows allelic discrimination). The GRC chose to utilize long-read technology for many local researchers who use non-model organisms and therefore lack reference genomes. At best, these researchers must use the genome of a "nearest-neighbor" when designing an experiment or NGS project. The GRC's ability to produce 10kb reads on the Illumina platform should eliminate the need for use of the costly PacBio platform, except when detection of methylation is required.

The GRC currently uses the long-read technology for *de novo* genome assembly of Wireworm (an emerging crop pest) and Galapagos endemic land snails.

Transposable Element Enrichment

The GRC identified a lack in existing library preparation methods for enriching Transposable Elements (TEs) which occur only once per genome. Clients typically use commercially available and home-brew TEs as simple but useful tools in order to study evolution in action. The problem comes when trying to sequence a TE which inserts itself only once per genome. Even when the host genome has only 4Mb, this makes sequencing the insertion site at reasonable coverage cost-prohibitive for the client.

The GRC provides order-of-magnitude TE insertion site enrichment services for clients with a minimal increase in cost-of-library over standard Illumina shotgun libraries. This allows clients to complete projects at a fraction of the sequencing cost, or where project completion was not possible otherwise.

Experimental High-Throughput Sequencing processing (expHTS)

expHTS is a multi-functional sequence analysis pipeline designed to quickly handle the large amount of data generated from Illumina sequencing, and is the current workhorse for many of the experiments coming through the GRC. The software pipeline can process reads from a variety of experiments including transcriptomic, RNAseq, amplicon, and genomic studies. The pipeline removes PCR duplicates from the data, trims off low-quality ends, removes contaminant sequences, removes poly-A tails from RNA reads, and joins overlapping ends of reads all in one process. *expHTS* runs in a fraction of the time it would take to execute these functions individually. *expHTS* also reduces memory demands by eliminating intermediate files in these processes. As sequencing technology improves and datasets become larger, the time and memory required to process the data become an important consideration for researchers with limited amounts of both.

Sustainability

Service center fees are established based on the estimated costs of consumables, instrument maintenance agreements and personnel time associated with each service and updated on a semi-annual basis. Clients who request custom bioinformatic analyses or new method development are provided a cost estimate based on the amount of time expected to complete the proposed work.

During FY 2013-2014 there was a significant shift in the types of services the GRC offered. Specifically, the GRC phased out equipment for DNA microarrays (purchased 2011), DNA genotyping (purchased 2011), and Roche 454 Pyrosequencing (purchased 2009). Each of these technologies was displaced by new, less expensive technology (such as the Illumina MiSeq). These upgrades produced a 'more data for lower cost' effect, which resulted in a decrease in GRC annual revenue from \$369,314 in FY2013 to \$204,022 FY2014. Even so the number of users and projects in the GRC increased by ~20%.

Plans

The GRC is currently conducting a national search for a Director, with the rank of Clinical Assistant Professor. The new director will face the challenge of beginning to transition the Core to a new business model more focused on sustainability. New protocols, decreasing reagent costs, and time efficiency will all factor into the implementation of a sustainable business plan; additionally, increasing the user base both on and off campus will become an important consideration.

Because of its small staff size relative to other research institutions, the GRC is constantly investigating ways to introduce its users to their data. One of these ways is through analysis workshops that lead researchers through the process of data generation to a final interpretable product. Previous workshops have been very successful, as detailed below, and the GRC plans on expanding the workshop options to cover a wide range of experiments and to include off-campus users.

Outreach

The Genomics Resources Core engages in a number of outreach activities across the University of Idaho campus, the state of Idaho, and across the nation. Examples of outreach activities include:

Educational Workshops: In February 2015 a workshop was held to lead users through a GRC-developed analysis pipeline to determine community structure. Workshop participation was at maximum capacity (24) and participants represented six departments across the UI and WSU campuses.

Genomics technology partnerships and close consultation with the University of Oregon, University of California-Berkeley, University of California-Irvine, University of Montana, and Washington State University.

Travel to technological and administrative conferences aimed at similar cores, including the Association of Biomolecular Resource Facilities and the Western Association of Core Directors. Novel approaches to analysis, budgeting, customer service, and technological innovations are all topics that are encountered at these conferences.

Assisting with organizing and participating in the annual Genomics Research Symposium held at the University of Idaho in Spring of 2015. Speakers and attendees were from a wide range of research backgrounds, and the GRC was able to provide Illumina sequencing kits as poster prizes.

The previous Core Director served in the program organizing committee for the Western Association of Core Directors (WACD) in 2013, 2014, and 2015, and gave a talk at the 2014 annual WACD meeting in Davis, CA on the GRC's innovative and unique structure.

Opportunities

The Genomics Resources Core continues to look for opportunities for new customers and collaborations. Of particular interest are the potential synergies with center-type research programs. For example:

- The Idaho INBRE is developing bioinformatics projects for undergraduate researchers. The GRC has been collaborating with the INBRE Bioinformatics Core to develop these projects at institutions across the state.
- The new NIH Center of Biomedical Research Excellence (COBRE), called the CMCI, includes projects that will require genomics technologies and a systems biology modeling collaboratorium that will engage both the GRC's "wet" and "dry" labs.

The GRC is also exploring collaborations and partnerships with regional entities to provide genomics support in the form of data generation and bioinformatics expertise. These include:

- St. Luke's Mountain States Tumor Institute in Boise, ID
- Idaho Wheat and Grain Commissions
- Kootenai Medical Center in Coeur d'Alene, ID
- Pathology Associates Medical Laboratories (PAML) in Spokane, Washington

Future Objectives

Challenges

Maintaining a balance between accessibility and financial sustainability continues to be the biggest challenge for the GRC. The GRC operates under a unique structure that integrates all three phases of genomics project management - combining data generation and bioinformatics like few other facilities in the United States. This is both its greatest strength and its greatest ongoing challenge. Because the GRC is so unique, there are few (if any) other facilities that can serve as a model for growth and sustainability. In addition, the scope of research facilitated by the GRC is complex and highly varied, working with a wide variety of data types, non-model organisms, and a range of experimental protocols. This challenges staff to develop expertise pertinent to a wide range of technologies and methodologies, and can limit the ability to develop high volume standardized workflows. Despite these challenges, the integrated approach remains the GRC's signature characteristic and is a key component to continued success.

Another challenge for the GRC that is related to financial sustainability is the lack of recognition the GRC receives for molecular and bioinformatics work. Many PI's assume that because GRC services are paid, the GRC staff is not part of the publication process. However, the investment of time through multiple consultations with researchers the GRC staff has a significant intellectual impact on many of the projects submitted to the core, and these impacts should be attributed. This recognition will help favorably increase the core's reputation amongst the scientific community, and will also justify the continuing University investment into this shared resource.

Perhaps the most significant threat to the Genomics Resources Core continues to be its ability to hire new staff and retain them. Existing classification and pay scales at the UI significantly hinder efforts to hire well-qualified people with experience because it cannot offer competitive salaries. This is of immediate concern because in the fall of 2015 the GRC lost its Director to the Genomics Core at University of California - Davis, and a suitable replacement still needs to be recruited.

Future Directions

The IBEST Genomics Resources Core will continue to offer state-of-art services in genomics and bioinformatics that will enable University of Idaho investigators to overcome the "barriers to entry" posed by their own lack of expertise in these fields. Collaborating with the GRC will allow them to pursue new avenues of research that leverage the resources available within IBEST. The goal is to continue to provide integrated services to IBEST researchers - facilitating cutting edge research in real time evolution.

The GRC constantly evaluates the portfolio of offered services, a critical activity because the field of genomics changes remarkably fast. New technologies emerge every year, and the capacity for data generation is now outpacing the capacity to store, analyze, and interpret these data. Because the GRC's most important offering is intellectual capital and expertise, it may be necessary to shift efforts away from "data generation" and into consultation and analysis - areas that have fewer capital costs and more personnel costs.

The University of Idaho has begun construction of the new Integrated Research and Innovation Center (IRIC) on the Moscow campus. The Genomics Resources Core has worked with the architects and designers of NBBJ Architects of Seattle to design space in

the new building that the GRC will occupy once the construction of IRIC is completed in mid-2016. This new building presents numerous exciting opportunities for the GRC to reach more customers and facilitate the research of investigators within and beyond IBEST.

IBEST COMPUTATIONAL RESOURCES CORE

Vision

The *mission* of the CRC is to provide state of the art computing and data management services to our customers. Our *vision* is to remain technologically current in hardware, software and services while partnering with customers to help them perform and disseminate their research, in a fiscally sustainable way. Our guiding principles are to maximize the reliability, availability, and effectiveness of our services while minimizing administrative costs.

Infrastructure

The CRC contains an advanced mix of high performance computing clusters, powerful servers and reliable data storage components and is staffed by personnel with the knowledge and technical skills required to compress years of analysis into days. Our 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 our core. This room has a dedicated Uninterruptable Power Supply (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. The features of our primary systems are described below.

High Performance Computing

CRC has one main compute cluster for research and genomic data analyses. The main cluster provides 616 processor cores and over 2 terabytes of system memory. Cluster nodes are connected with 40Gb/s QDR Infiniband connections, providing fast, low latency data transmission for increased performance of HPC bioinformatics applications. The CRC also maintains nine servers (344 total cores and 2.5 terabytes total system memory) for applications that require large amounts of memory on a single system but do not take advantage of the parallel cluster resources. Two of our most powerful servers in this group contain 256 times the system memory of a standard desktop (1TB or 1024GB) and are used primarily for sequence assembly of next-generation sequencing data.

Data Storage

The CRC maintains two tiers of primary storage. The first tier is comprised of fast but more expensive disk arrays totaling 52TB and 40Gb/s networking. The second tier, uses slower disks and totals 214TB. Additionally, we have approximately 300TB disk available for data archiving and backup storage. In addition the core provides in-house developed solutions to maintain data integrity and restoration.

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 Enterprise Computing services. Our support infrastructure includes 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.

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. 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.

New Infrastructure

To increase the data throughput within the CRC to our users, we have:

- Doubled our data storage capacity by installing new data storage and networking hardware, and upgraded the storage backbone networking to Infiniband for the main cluster and standalone servers.
- Added five computational nodes - 136 processor cores and 19,968 GPU cores, to our main cluster.
- Added a new standalone server with 3TB PCIe based high-speed storage.
- Improved our internal and external documentation systems by developing a streamlined web-based system.
- Streamlined billing system
- Improved data integrity by moving our primary and backup storage systems to ZFS based file systems.
- Continued to upgrade the network connections between CRC servers and the campus network by upgrading switches and installing fiber optic cables. These new resources connect the CRC servers directly to the 10G campus backbone at 10G speeds instead of the final link being 1G.

Planned Infrastructure

- We intend to start replacing our aging cluster nodes (purchased in 2008) with modern, more efficient compute nodes.
- Add new standalone servers with additional co-processors for increased computational efficiency.

Under Consideration

We are considering various other changes to our infrastructure, including the following:

- Moving from existing computing technology to more “green” alternatives that

- use power more efficiently and require less cooling.
- We are also considering new systems with powerful Graphic Processing Units (GPU) that allow specific analyses to be done at greater speed than those using only the Central Processing Unit (CPU). This modification would support applications such as BEAST or rendering software that could expand our customer base.

Innovation

Continuing Innovation in Technology and Services

The primary function of the CRC is to facilitate the innovation of our customers. We have deployed existing technology in innovative ways, offer services that are not available from most other computational core facilities, and developed unique in-house solutions to address user needs.

Examples of our innovative use of existing technology include:

- We use configuration management systems (the modules environment) to provide customized software services, including versioning. Most cores provide only one version of software, which makes it difficult to replicate prior work or to test new user-developed software. This mechanism is uniform across 78 systems, so the learning curve for users is very shallow. This mechanism also makes it possible for us to install and test new software without disrupting system availability.
- Some of our hardware, such as the very large memory servers, are not commonly available. These enable users to pursue specialized applications such as alignments of very large genomic datasets, intense agent-based simulations, and visualization rendering.
- Our existing data backup system was developed in house.
- Internal Software development – We employ several technologies and write a significant amount of code (Figure 4) to maintain our complex infrastructure with a small staff.

Examples of our innovative services include:

- The tight integration of the CRC and GRC in terms of personnel, hardware, software, and administration is highly innovative relative to most other computational core facilities.
- We provide a high level of support for customized software installation, configuration, script development, and *ad hoc* user services.
- We offer a local, secure file-sharing system as an alternative to DropBox and similar cloud storage services.
- We offer our own web-based account management, poster printing, and online documentation systems. These systems were developed in-house, and offer streamlined interfaces to our services and documentation and are easier for CRC staff to maintain. Thorough documentation of our services allows novice users a consistent reference, and reduces CRC staff user support load. Last year we

added almost 34,000 lines of documentation to our user website (Figure 4).

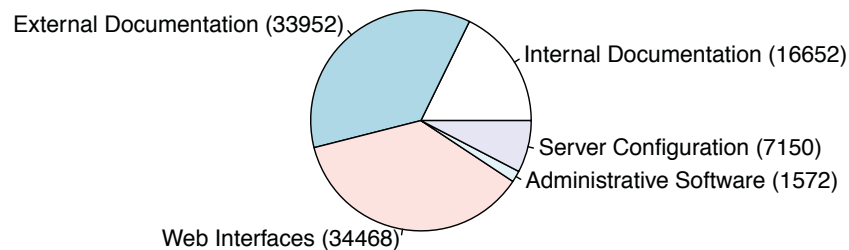


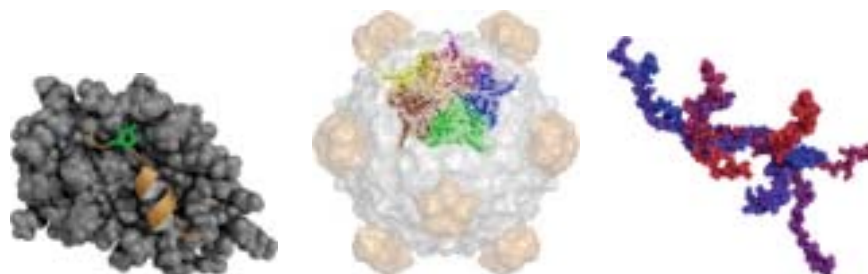
Figure 4 – Number of lines of code and documentation added for various CRC projects in 2015.

Impact on Research

The CRC seeks to facilitate innovative research across a wide array of research disciplines. As examples of research that is facilitated by the CRC, we offer summaries from Dr. Marty Ytreberg and Tyler Hether.

MARTY YTREBERG – PHYSICS DEPARTMENT

The 2014 Ebola virus outbreak in West Africa was the largest in recorded history and resulted in over 11,000 deaths. It is important to develop strategies for treatment and containment to avoid future epidemics of this magnitude. One strategy is to anticipate how the evolution of the virus might compromise treatment efforts. We have used the IBEST CRC to perform molecular modeling simulations of the Ebola virus glycoprotein. The simulations were used to estimate how the folding and binding stabilities of the glycoprotein are modified due to amino acid mutation. As a result of this study we have initiated a watch list of mutations that could potentially reduce the effectiveness of vaccines and therapies. The list was generated by considering every possible mutation of the glycoprotein and including those that disrupt binding to protective antibodies but do not disrupt the protein function.



TYLER HETHER – BCB GRADUATE PROGRAM

Details of the processes that generate biological diversity have long been of interest to evolutionary biologists. A common theme in nature is diversification via divergent selection with gene flow. Empirical studies find variable genetic differentiation throughout the genome, that genetic differentiation is non-randomly distributed, and that loci of adaptive significance are often found within “genomic islands of divergence” (GIs). A model has emerged to explain these empirical patterns in which these islands are expected to form when a balance exists between divergent selection, gene flow, and recombination. Though the GI model fits the data, we still lack any expectations of the dynamics of GIs.

At the same time, functional data from model systems are shedding light on the ubiquity of genetic interactions. However, we still know relatively little how such epistasis affects rates of adaptation. While the current working GI model considers *physical* genetic interactions it does not give predictions on how *epistatic* interactions influence the size, width, and dispersion of GIs across the genome. Our research not only provides a crucial test of the current GI model, but it also promises to generalize it by discerning how *both* physical and epistatic interactions shape the “genomic island architecture” -- the number, extent, formation of GIs.

Our work attempts to address how adaptation is influenced by physical and epistatic interactions using two general methods. **First**, we model genetic regulatory networks and investigate how these networks produce genetic correlations that structure multivariate phenotypes in populations under selection. Thus far our findings have characterized how network architecture shapes mutational (co)variance and constrains local adaptation.

The **second** – experimental – approach provides a crucial test of the GI model by experimentally evaluating the conditions of island formation and maintenance in the face of migration. We examine island dynamics when adaptation is from standing genetic variation, a phenomenon commonly found in nature yet to be incorporated in theoretical models. In addition, the experimental design provides a unique opportunity to expand the GI model further by relating island formation with yeast epistasis networks, thereby bridging population genomics and quantitative genetics. This work is timely because there is need to transform the field of population genomics into a more predictive science.



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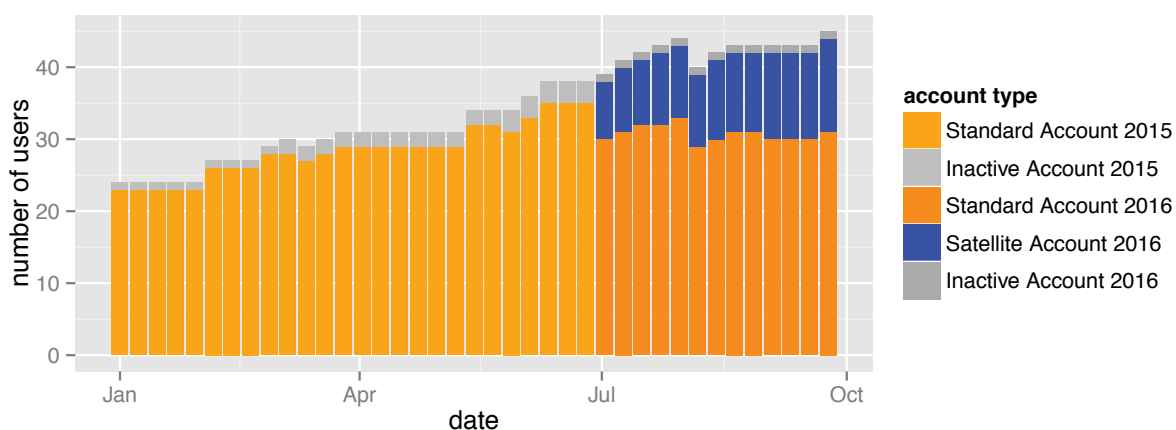
Sustainability

To sustain the level of service required by investigators we must continually update hardware and software to remain an attractive option for researchers. There are two dimensions to sustainability in the CRC: maintaining our current services and updating services to remain on the cutting edge.

Maintaining Current Status

In June 2014, we implemented a fee for service model with a single user fee for access to all systems, and hourly charges for custom services. A single standard user subscription currently costs \$2000 per year, and can be acquired on a quarterly basis. We have increased from 23 paid users last year, to 42 this year, and introduced a new account option – the Satellite Account – intended as a lower cost (\$300 annually) account that will be more feasible for larger labs, see Figure 5.

Figure 5 – The number of users with active accounts for each week in 2015.



Pursuant to federal guidelines, user fees fund personnel costs associated with administering the CRC, not hardware. The breakdown of financial support to the CRC is summarized in Table 1. The CRC is currently heavily subsidized by the COBRE and ORED.

Table 1. FY 2014 Financial support to the CRC.

CRC FY2014 Financial Support from Budgets								
Budget	Salary	Fringe	Travel	Expense	Capital	Tuition	Total	Revenue
Core	\$0	\$0	\$0	\$0	\$48,055		\$48,055	\$29,422
COBRE	\$71,019	\$27,467	\$7,947	\$10,865	\$106,124		\$223,422	
ORED	\$42,150	\$16,360					\$58,510	
State - Direct	\$40,150	\$13,847					\$54,374	
Total Revenue								\$29,422
Total Expense	\$153,696	\$57,674	\$7,947	\$10,865	\$154,179	\$0	\$384,361	

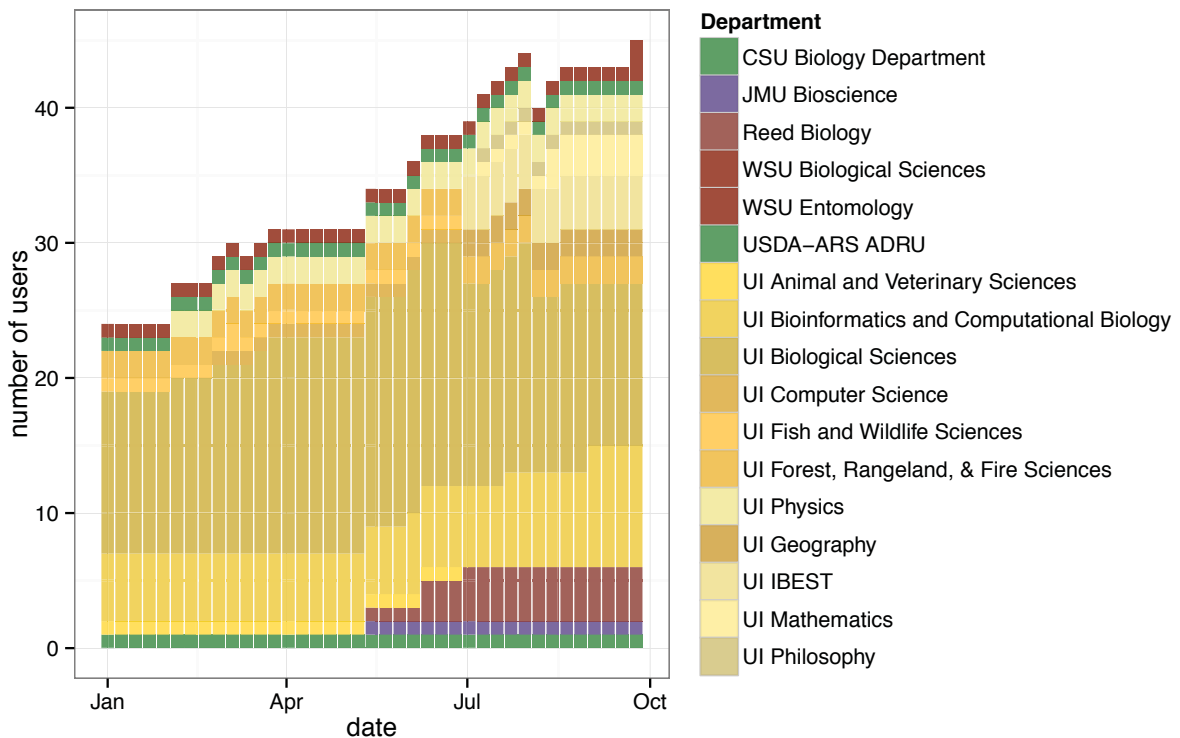
In order to increase our campus wide impact and overall number of paid accounts, we have started to support additional departments with the UI College of Science. Besides making use of our existing computational resources, some of these researchers have

existing hardware that we will assimilate into our infrastructure over time. Additionally, we have gained external users from Reed College, and James Madison University (Figure 6). The CRC is a particularly attractive option for institutions such as Reed College that do not have their own computational infrastructure.

We at Reed College chose to use IBEST for our computational needs because they provide the optimal environment for performing bioinformatics analyses. They offer the necessary data storage, memory, and power for performing computationally intensive tasks, such as genome assemblies, and at a reasonable price. They provide amazing administrative support, with quick response to questions. Not to be taken lightly, they also pre-install and regularly update many of the most common bioinformatics programs, saving valuable time for the user. As an undergraduate university, IBEST also offers Reed a financially reasonable option for undergraduates to have the computational resources to perform their own bioinformatics projects.

We will continue to court external users, while keeping our core user-base on the University of Idaho campus.

Figure 6 – The number of users with active accounts for each week in 2015, colored by institution and department.



Usage pattern trends and prospectus

In the fast-paced and intensely competitive research environment now common to higher education, our users tend to pick the shortest path to quick results rather than spend the time required to learn complex application programming interfaces. Thus, being able to simply log onto a powerful server and immediately run several threads of a

bioinformatics application has proven more attractive for our users than taking extra time to write additional scripts to make use of our primary HPC cluster. Additionally, the nodes that compose our HPC cluster have an order of magnitude less system memory than our standalone servers. Unfortunately, in a multi-user environment, it is depressingly easy for users to overload a simple standalone server if they do not monitor the current system usage before starting their own jobs. This necessitates extra vigilance on the part of CRC systems administrators to detect when systems are overloaded and manually stop user jobs that threaten system stability and negatively impact other users. This common conflict between finite system resources and seemingly infinite user demands is not unique to our core, and the generally available solution is job-scheduling software, which we use to manage user jobs on our main HPC cluster. Thus, as we add more users, we will likely need to move several of the standalone servers into a cluster framework to avoid overloading individual servers and to ensure equal access to compute resources. To help CRC users overcome the intimidating knowledge barrier presented by job-scheduling software, we plan to offer regular workshops where researchers can get one-on-one help converting

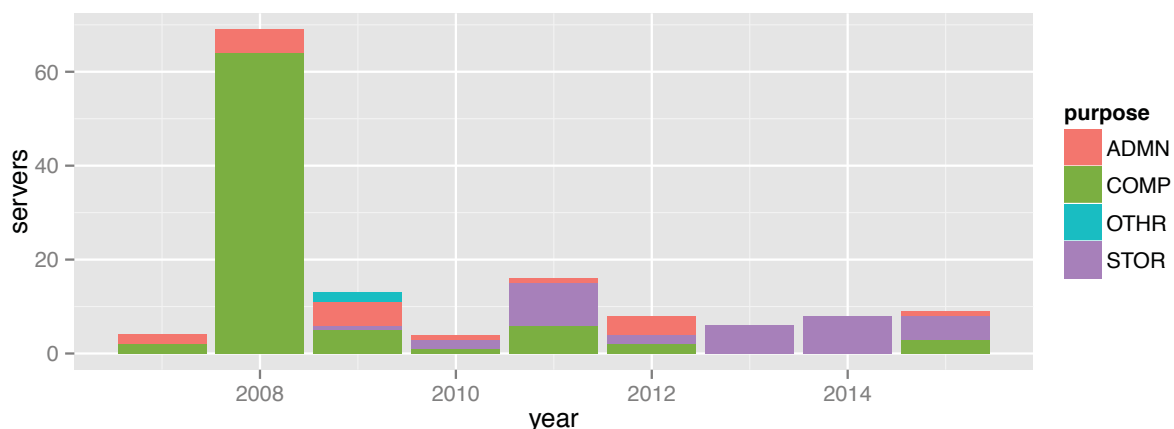


their scripts and application calls to cluster enabled scripts.

Keeping Current

Maintaining current hardware is a continuous challenge. Academic and corporate data centers assume a half-life of about two years for high-end equipment like ours. Thus, after approximately four years, the equipment is fully depreciated. HPC equipment depreciates much faster than laptops, for example, because it often runs at high load in unusually hot environments 24/7. So, even though an individual user may find a four year old or older laptop adequate for basic computational needs, the equipment in the CRC is effectively at or near end of life after four years. Our two most powerful systems were purchased 2 years ago (Nov 2012) and our primary cluster nodes are now 7 years old. (purchased Nov 2008). As the data storage needs of our users have grown faster than their computational needs, we have focused our new equipment purchases on ever-larger data storage capacity (Figure 8). Some of the storage expansion was funded by INBRE as part of our collaboration with them. However, as we add additional users, we will now need to update our computational infrastructure as well.

Figure 8 – The number of servers purchased each year, colored by their primary purpose.



In 2012, we upgraded the main cluster nodes, and future upgrades to these systems are not possible. It will thus be necessary to replace these cluster nodes to realize increased performance. Helpfully, though data storage technology has failed to keep up with data storage needs, processor technology has made significant gains and replacing the computational infrastructure will be comparatively less costly.

Because our primary user data storage is a distributed file system composed of several individual servers that each store a part of the overall file system, a high-speed network is necessary to ensure adequate performance. As the amount of data stored and accessed by our users has increased, the standard networking technologies employed have struggled to deliver consistent performance. We therefore purchased higher speed network interfaces (Infiniband) to decrease latency and increase throughput by 4000% and are in the process of installing that equipment.

Additionally, working with UI technology services, we are in the process of upgrading

our external facing switches from 1G to 10G so that our servers will be able to connect to the campus 10G network at full speed instead of the final link being only 1G. This project is funded by NSF.

Plans

The sustainability of the CRC over the long term will require that we increase self-generated revenue and retain institutional financial support. User fees alone cannot maintain centers such as the CRC given their high capitalization and maintenance costs. Therefore, institutional support will always be part of the core's revenue. Our goal is to support 50% of personnel expenses with self-generated revenue. With our current cost structure this will require approximately 25 Standard user accounts, and 20 Satellite user accounts. We currently have 30 and 12 accounts respectively.

To bridge the gap between our current number of accounts and our goal, we plan to actively advertise our services and to identify new customers, especially on the UI campus. We will seek customers who are not necessarily evolutionary biologists, though we will need to balance new user research area support with the IBEST mission that focuses on "real time evolution". See "Opportunities" below for some specific examples.

We will also continue to seek ways to minimize expenditures. In particular, we will use the finer granularity of usage data that is now available to target our efforts to high-volume activities and users.

Outreach

The CRC is less active with outreach than the other cores within IBEST. This is in part due to the departure of the CRC Director in June 2014. The outreach activities described by the GRC are often facilitated by the tight integration between the CRC and GRC.

Opportunities

There are many on campus resources, both current and potential, that could increase the CRC user base or simplify CRC operations.

- Potential synergies with program projects or infrastructure efforts, which are part of the University's strategic plan. For example:
 - The new COBRE Center for Modeling Complex Interactions includes a modeling collaboratorium and several potentially computationally intensive projects which has led to five user accounts, and computational nodes for the HPC cluster.
 - We have begun to support other research units within the College of Science, including Geographical Sciences, and Geology Researchers.
- Reduce duplication with existing campus units.
 - Strategic integration with ITS. For example, using the university authentication services would benefit users (who could log into CRC resources with their university accounts) and remove the need for administering authentication services and some systems security responsibilities.
 - UI Media services may be able to help with teleconferencing (such as the BEACON conference room) and the IBEST classroom.

We are also considering other opportunities to take advantage of existing on-campus resources. For example:

- We have resumed the practice of hiring undergraduate assistants for tasks such as inventory, classroom and communications support, hardware installation, and systems monitoring. In the past, this has been a reliable pipeline for developing and training future CRC staff.
- Work with the College of Business and Economics to help develop and implement a marketing strategy and a formal business plan for the CRC.
- Tap existing users to recruit new customers, for example at IBEST lunches or new faculty orientation.
- Include a university-funded CRC “gift certificate” as part of the startup package for new faculty.

We could also consider expanding our mission to support educational activities such as undergraduate research, courses, and workshops, or to support research from non-evolutionary scientists such as physicists and computer scientists.

Challenges

User Accounts

The CRC strives to provide quality, cutting edge research computing to researchers within the UI and beyond. However, sustaining this effort is a constant challenge. We are now in our second year charging for services using a user account model, but these fees cannot currently be used to charge for hardware usage and depreciation. In our first year, we had a single user account type, which was prohibitively expensive for less demanding users and larger research groups. Therefore, we added a second user account level with access to fewer resources and data storage, at 15% of the cost of a standard account. These ‘satellite accounts’ have proven quite popular – and have increased our overall number of users. Adding additional user accounts is not a catchall solution, as additional users will eventually require additional staff. Nevertheless, we are striving to minimize and recover costs when possible. Our goal is to reach 50 user accounts, a number that can be sustained at our current staffing level. This should recover ~50% of the personnel costs of the CRC.

Data Storage

As the cost of DNA sequencing has fallen, the amount of data available to researchers from both on campus resources such as the GRC, and from public databases such as NCBI has increased dramatically. This readily available sequence data has found its way to our servers *en masse*, enabling CRC users to study previously intractable evolutionary processes. We now have the data storage capacity to accommodate current users. However, as our primary data capacity increases, backups of that data have become increasingly difficult to manage using open source backup solutions. We are currently employing large hard disk arrays with advanced file systems that allow for file compression, and reducing the number of backup copies currently being maintained.

Providing energy demands of the CRC systems is a challenging task. Energy needs to be clean and uninterrupted for proper operation of the systems and supporting infrastructure. This challenge is met by our 3-phase 80KV power supply battery backup system. But this system was purchased in 2012 and the batteries will be reaching end of life in 2016.

IBEST OPTICAL IMAGING CORE

The IBEST Optical Imaging Core (OIC) provides instrumentation and expertise in optical imaging and flow cytometry. Our complete services begin with experimental design and choice of instrumentation that best fits the needs of the science, yet, is not more complex or expensive than necessary. This is critical to providing quality results in an efficient manner and at a reasonable cost. Investigators may then choose to be trained on the instrumentation independently or use the full services of the director of the Optical Imaging Core, Ann Norton, for acquisition, analysis and publication preparation. The breadth of applications available can be increased as a result of sharing expenses across the campus and throughout the region.

Existing Infrastructure

The microscopes, flow cytometer and analysis computers are all located in Life Science South 450. This space also provides basic laboratory prep needs, including a fume hood and biosafety cabinet. The OIC offers a breadth of fluorescent imaging options to stay abreast of the rapid development of fluorescent labels and to match the speed and resolution needs of the scientific inquiries.

- Currently there are two confocal microscopes: a laser scanning system that is best suited for high resolution imaging of static samples and a spinning disk confocal that is best suited for live imaging.
- A fluorescent stereoscope provides an efficient option for imaging of larger samples and larger fields of view. It has also become useful for images of a full slide to choose useful areas prior to high-resolution imaging.
- Analysis computers contain sophisticated image and flow cytometry software that would be cost-prohibitive for an individual laboratory. Having these stations in a shared resource facility also provides available expertise and sharing of ideas among active users.
- A flow cytometer that can be used to analyze and characterize dissociated cells as well as to sort-selected cells into a variety of vessels provides the only flow cytometry option on campus.

Potential Infrastructure

Though the breadth of applications available in the OIC are adequate, the older instruments do not provide the most efficient detection systems nor a full breadth of laser options for some experiments. In the case of the flow cytometer, there are new options that are much simpler for independent users to master.

- The OIC director has initiated discussions with flow cytometry users to consider replacement options for the aging and complex cell sorter. It may be more efficient and versatile to purchase a simpler analysis table top system for independent users and a more robust cell sorter with multiple lasers. Outside maintenance service that is less expensive is also driving this consideration.
- The laser-scanning microscope is also aging and inefficient. New solid state lasers, improved detectors, smaller footprints and the need for longer wavelength lasers for developmental biology inquiries are driving the need to replace that system.
- Whenever a microscope system is fully replaced with a new system, the basic

microscope from the older system is an excellent option for use in an individual laboratory. This option has allowed new investigators to save their start-up funds for other uses.

Innovation

Instrumentation alone does not provide innovation; people provide innovation. Experienced users of a shared facility can provide new application ideas for other investigators and new avenues for the director to serve. New instruments, such as the spinning disk confocal microscope, provide novel approaches for inquiry.

Grand Scale

- The characterization of cells and tissues is a critical component of understanding what is happening in a biological system. Scientists make comparisons. They examine change over time, change under different conditions, change following specific treatments. Imaging and flow cytometry are powerful tools for capturing and quantifying those changes.
- The University of Idaho faculty are very generous in their willingness to provide research opportunities for undergraduates. Many of those undergraduates use the facilities of the OIC. This is a wonderful opportunity for them to get advanced technical skills, to work through problems with experts on an intimate scale and to present their work at a professional meeting. These experiences make them better prepared for the work environment or graduate school.
- In the fall of the year, new investigators that have arrived on campus are searching for what shared resources may be available to them. They are often surprised, and certainly relieved, to see that there are quality instruments and personal assistance available to help them get their research programs initiated.
- Many inquiries in science require multidisciplinary approaches and the use of multiple resource facilities. Exploration of how the Optical Imaging Core can provide services that feed projects into the other shared facilities, and vice versa, will allow for efficient approaches to more complex scientific inquiries.

Person Scale

The main role of the OIC director is to facilitate research on our campus. That includes taking good care of the instruments so they are ready for use, understanding the scientific goals of the investigators, providing appropriate training for all users and being available to assist when problems arise. At times, the most needed assistance is simply to provide a full service for an investigator when they need a professional job done in a timely fashion or they are short on staff.

- As the expert on the instrumentation, it is also very useful to stay abreast of new applications and to present those options to the researchers. The director does presentations at the IBEST lunches at least annually, workshops on microscopy and flow cytometry each semester and to other groups on campus when requested. Webinars, scientific journals and an annual scientific meeting provide new ideas and inspiration.
- The director is also active in the Western Association of Core Directors (WACD), a

chapter of the Association of Biomolecular Resource Facilities (ABRF). In addition to learning new discoveries in science, the organization actively assists core directors in the business side of running a core, including opportunities for funding new acquisitions and dealing with the high costs of maintaining these complicated tools.

- A unique offering at the IBEST Optical Imaging Core is the 'Outside Service'. This service is provided by the director and may include advice on purchasing decisions in microscopy, training staff and graduate students on instrumentation in their own laboratory or cleaning and maintaining microscopes outside of the OIC. The complexity of newer microscopes and associated software can be overwhelming so providing assistance and advice from an expert creates a better understanding of the potential and limitations of their new instruments.
- The OIC requires that each individual user be trained directly by the director. This allows for training that is more tailored to the experience and interest level of the new user. It also allows the director to have a sense of which users may require a longer period to master the use of the systems.

Sustainability

When investigators are short on funds, research does not move forward and service centers suffer financially. As the characterization of cells and tissue is a critical component to fully understanding biological systems, institutional investment is not just for the immediate users but provides opportunities to future students and researchers, as well. It is much more expensive and inefficient to try to repair damaged or poorly maintained instruments, start up a new imaging facility or to have investigators supply their own, compromised instrumentation.

Current Status

- Funding for individual investigators that have been heavy users of the OIC was down significantly. IBEST Technology Access Grants provided some temporary assistance to keep their research programs going.
- The new spinning-disk confocal microscope was used by many investigators, yet, in the grant proposals that funded the system, we had committed to not charging for that system for the first year of use. This also ate into potential income and provided a free alternative for users that might have used a fee-based instrument.
- Service centers on campus are annually reviewed to determine that rates are appropriate and federal guidelines are followed. After many years of attempting to offer a 'flat rate' charge, the newly appointed service center committee approved such an approach. Since July 1 2015, the OIC now offers 3-month passes for particular applications at a fixed rate, in lieu of charging hourly. This allows users to work more carefully at getting good results without feeling rushed because 'every minute counts'. This also allows principal investigators to better predict their expenses, brings some money into the OIC during these financial lulls and keeps projects moving forward.
- The graph below shows the actual income from hourly charges in FY2014 and FY2015, broken down into 1st quarter income + income from the 2nd, 3rd and 4th

quarters compiled. These incomes are compared to the hourly charges + the pass charges that were purchased during the 1st quarter of FY2016. If the pass option continues to be attractive, we should improve our total income as compared to last year and also achieve higher quality results as the user is not on the clock.

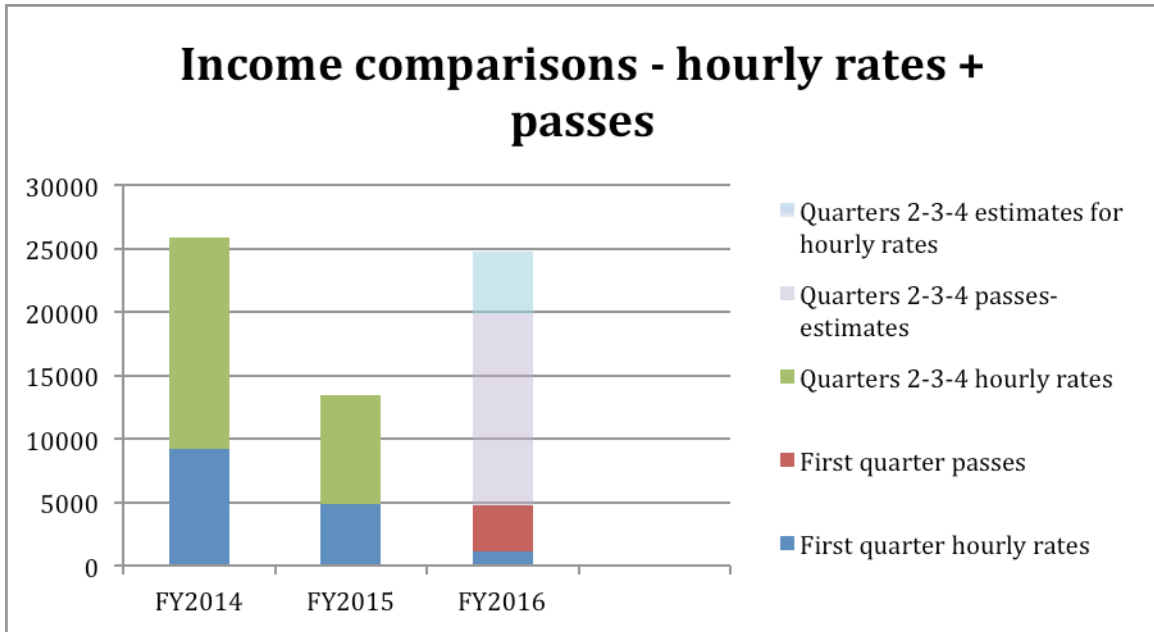


Figure 9 – OIC income for 2014-15 and projected for 2016.

As the instrument costs don't greatly change based on hours of use and the instruments in the OIC are underutilized, the pass option should work. The table below shows a comparison of hours of use for the first quarter of FY2014, FY2015 and FY2016. Interestingly, the PIs were certain that they would use the instruments many more hours given this opportunity and so far that has not proven to be true.

Comparison of hours of instrument use for the first quarter			
	2014	2015	2016
Hours of Use	338	243	350

Plans

- Service Centers can be reviewed, by request, in less than a year. The new pass options will be reviewed mid-year for possible increases.
- Instrument maintenance costs are fairly fixed and very expensive. In flow cytometry, there are options for providing service from an outside group. During the discussions on options for updating the flow cytometry configuration and services, this lower priced option will be considered.
- In November 2015, there will be a new service contract initiated on the new Spinning Disk Confocal microscope. In February 2016, the FACS Aria maintenance contract will not be renewed. This will reduce KNOWN operating expenses by

\$10,000, though, there are likely to be out of pocket expenses for the flow cytometer. The age of the instrument and the high demand for the simpler method of analysis only suggests that the OIC would satisfy the majority of users with a simpler, less expensive analysis instrument. More discussions on this issue will be had during a user meeting in the near future.

- New investigators are expecting to start using the Optical Imaging Core this year. Specifically, investigators from the newly formed Department of Bioengineering as well as others from Chemistry and Forestry.

Below are two graphs comparing the known income from fees for FY2014 and FY2015 and estimates of income for FY2016. This past year we had a greatly reduced income from fees. This change is likely due to a few things:

- Generally, major users did not have strong funding last year
- Flow Cytometry – WSU purchased 2 new systems so less need to come here for flow cytometry
- Confocal Microscopy – A major user from previous years was low on funds and temporarily used their own, less robust, system in their lab
- Confocal Microscopy – as was mentioned earlier, the OIC was not charging for the use of the new confocal microscope, the spinning disk.

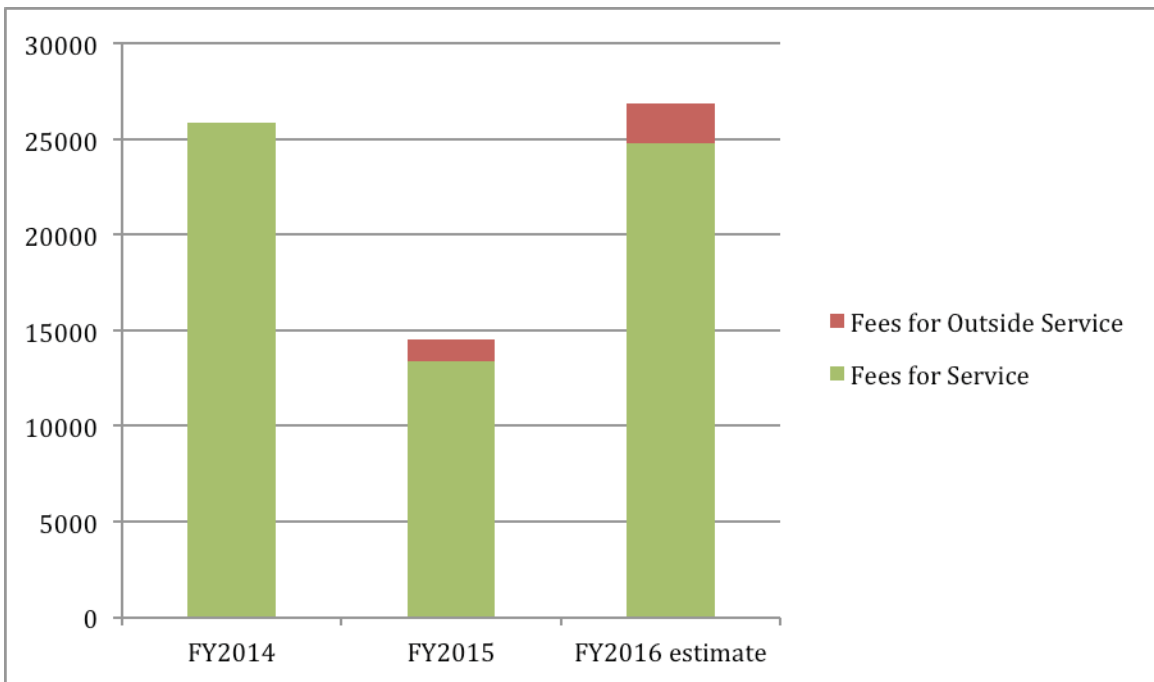


Figure 10. – Fee usage for internal and external OIC users.

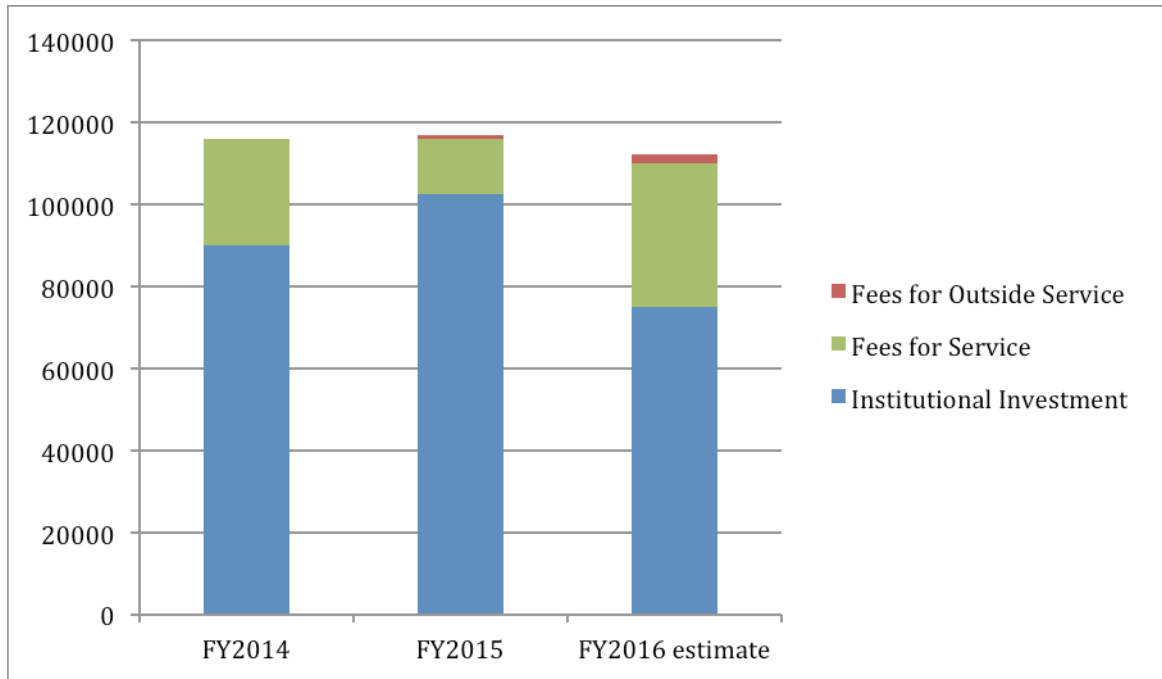


Figure 11. Total OIC operating revenue.

Outreach

Despite efforts to reach investigators by workshops, e-mailings, guest lectures and posters, the most effective approach to creating professional relationships that have led to facilitating investigators in their research has been by personal contact. Making suggestions to a PI that they might try something novel in their research program can be a delicate subject to broach, yet, the offer of only a 3-month commitment to exploring something new at a fixed price should make the effort more fiscally attractive.

- As an active member of the Western Association of Core Directors, the OIC director has created professional associations and increased awareness of the service options and high quality results offered at the University of Idaho's core facilities. In the case of the Optical Imaging Core facility, this is not likely to create specific increases in usage, yet, it does make potential faculty, graduate students and collaborators aware of what we have to offer. In addition, as the Program Chair of the recent regional meeting, the OIC director organized a program of speakers that emphasized collaborative projects between institutions and with industry partners.
- Idaho is an INBRE state and has a very active program of opportunities for undergraduate students in research. The OIC Director has had a significant presence within the summer INBRE Fellows program for many years. This year, there were also undergraduates working in the OIC on projects funded by the National Science Foundation's Research for Undergraduates Program (REU). Again, these are short term projects and funding, yet, the students come from other undergraduate institutions and their positive experiences while visiting here, may bring them back for graduate studies and create a broader awareness of the quality

and personal opportunities available in research at the University of Idaho.

- On campus, there will continue to be workshops in flow cytometry and microscopy offered each semester, yet, the formats for the workshops will vary. More hands-on options will be made available to compliment the background lecture. Additional advertising by posting flyers directly in other buildings will be added this year and e-mail advertising will be extended to all faculty at the four major colleges, College of Science, College of Agricultural and Life Sciences, College of Engineering and College of Natural Resources, as well as the graduate school.
- A group of investigators from the College of Engineering, College of Natural Resources and the College of Science plan to actively pursue a new imaging device, an x-ray computed tomography system (micro CT). The OIC director has been consulted on this project as a result of the recent success in obtaining funds for a shared instrument (the spinning disk confocal microscope). Reaching out to these investigators to be a part of the discussion of this acquisition helps them become aware of potential crossover imaging projects as well as the expertise that the OIC has to offer in the long term vision for this new instrument.
- An unexpected surprise is how the offer of 'Outside Services' has also made the OIC more visible on campus. The quality and attention that is given to this service is intended to reflect the quality and attention that one would receive both personally and professionally at the OIC.

Opportunities

The existing systems in the Optical Imaging Core offer a breadth of platforms for imaging and characterizing activities in cells and model organisms. The new spinning disk system offers choices in dynamic imaging of cells in action. Investigators receive personal attention, flexible scheduling and payment options, as well as the choice of working independently or having a professional do the work. The environment at the OIC also creates camaraderie between scientists of all ages and experiences and opportunities for advanced learning of technical skills to young scientists.

New instrumentation on campus that may cross over into other imaging platforms may create increased collaboration on projects and possibly the sharing of skills and experiences across disciplines. Perhaps analysis tools and staff can be shared and reduce the overall cost and space issues for all users.

Future Objectives

Challenges

- The existing configuration of the OIC provides a breadth of applications, yet, instrumentation must be replaced to keep those options available. Tough choices must be made on whether to continue to offer all these platforms, as the maintenance expense is quite high and the volume of researchers will always be too low to cover those costs with reasonable fees.
- If service contracts are terminated, more time will be spent by the OIC director to repair instruments rather than assist users or move forward seeking new instruments and applications offerings. Directors wear many hats, yet, being a trained engineer is stretching their skills.

Vision

Telling the story of a biological system will always be aided by imaging and cytometry. Teaching young investigators the tools of today and the future adds to their overall educational experience. Creative scientists will continue to design experiments that explore novel aspects of disease, evolution or development. Having the talent, tools and funding to keep trying to answer the tough questions is the ultimate goal of the OIC.

IBEST ADMINISTRATIVE CORE

Institute Leadership

Dr. Larry Forney served as IBEST Director for virtually all of this reporting period; he stepped down in mid-June, when Dr. Jack Sullivan took the reins. Sullivan now 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. Dr. Sullivan devotes an average 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.

Since the transition of leadership occurred, the Research Oversight Team (ROT) has been renamed to the Strategic Planning Committee (SPC) to recognize the increased breadth of topics on which they advise the director (i.e., to include efforts to broaden our impact, integrate with the BCB graduate program, and interface with strategic partners such as BEACON, CMCI, the Idaho Wheat Commission, etc.). Drs. Wichman and Foster are currently members of the Strategic Planning Committee, and a third member (to replace Sullivan) is being sought. As in the past, these individuals meet with the Director and Associate Director on a weekly basis and devote 5% of their effort to service on SPC.

Associate Director

Dr. Barrie Robison continues to serve as Associate Director of IBEST. He is charged with assisting the Director in developing and implementing plans to achieve sustainability of the core facilities, ensure the continued growth and high quality of IBEST research programs and reach out to companies, government agencies, and foundations to identify interesting opportunities for research and funding that are viable alternatives to federal agencies. Dr. Robison has demonstrated exceptional leadership skills, and has a broad understanding of the research done by IBEST investigators and the services provided by the IBEST core facilities. Dr. Robison will continue to contribute 25% of his annual effort to this position.

Key Administrative Staff

We have experienced turnover in two of our three administrative staff positions. Business Manager Rose Poulin has retired and been replaced by John Grimes, who started in June. Communications Coordinator Whitney Schroeder left for a job in the Alumni office and has been replaced by Amberly Beckman, whose employment begins 28 September. We are very fortunate to retain Lisha Abendroth, the IBEST program coordinator.

External Advisory Committee

For more than a decade we have relied on our External Advisory Committee to help shape our vision for IBEST, provide advice on administrative challenges, and to develop strategies to capitalize on new opportunities in our research. 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 following individuals are the current members of the EAC:

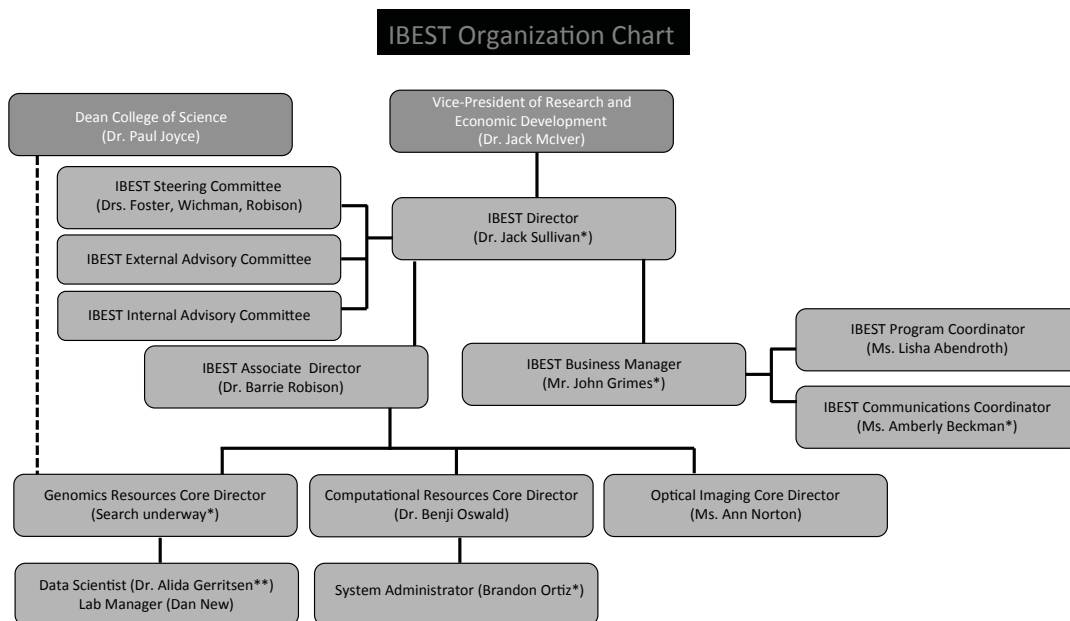
Dr. Bruce Levin
 Samuel C. Dobbs Professor of Biology
 Emory University
 Member of the National Academy of Science.

Dr. Maggie Washburn-Werner
 Professor
 University of New Mexico

Dr. John Roth, Chair
 Distinguished Professor
 University of California-Davis
 Member of the National Academy of Science.

Dr. Owen White
 Professor & Director of Bioinformatics
 University of Maryland School of
 Medicine

Dr. Michael Turelli, Vice-Chair
 Distinguished Professor
 University of California-Davis.



*New appointments

**Dr. Gerritsen moved into the Data Scientist position from a lower classification via a normal search.

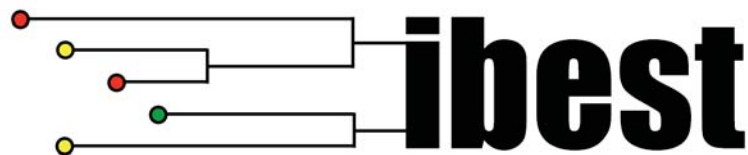
Internal Advisory Committee

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 following individuals are the current members of the IAC:

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



The Idaho state amphibian, the Idaho giant salamander (*Dicamptodon aterrimus*), first sequenced in 2005 by IBESTians.



GRADUATE AND UNDERGRADUATE EDUCATION

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY GRADUATE PROGRAM

The BCB program plays a unique role within the university and worldwide because it prepares graduates who are at the forefront of a booming field, that of bioinformatics and computational biology. The major challenge today for mathematicians, statisticians, computer scientists and biologists is to develop ingenious ways to analyze and interpret the daunting big data sets in ways that will not just incrementally increase our understanding, but allow big leaps forward.

To address this challenge investigators will need to be fluent in more than one disciplinary 'language' so they can communicate about research goals, discuss experimental design, data analysis options and technical limitations, and interpret the final result of a large data analysis exercise with all caveats in mind. Our unique contribution to this exciting area of science is to provide BCB students with a strong shared educational foundation and a required rotation in a research group outside their area of expertise. In combination with in-depth training in one specific area (Biological Sciences or Computer Sciences/Mathematical Sciences) and conducting cutting edge research, this formula makes the students fluent enough to successfully interact with collaborators in the other disciplines and thus perform true interdisciplinary research.

In the fall of 2013, the BCB Program was reviewed by a panel of three experts. The panelists were extremely impressed with the program and wrote the following in the report:

"The BCB program is a stellar program at the University of Idaho and one that is distinctive nationally. While there are many excellent programs in evolutionary biology throughout the country as well as exceptional informatics programs, the BCB program is unique in combining expertise and opportunities in bioinformatics, mathematics, statistics and evolutionary biology."

Currently there are 24 students in the BCB program (21 PhD, 3 MS). Four students graduated in academic year 14-15 (Table 1) and we admitted nine new students for the academic year 15-16 (Table 2), clearly showing a growing trend in the student pool. Data from last academic year also show that our BCB students scored well above the average of the University of Idaho students based on GRE scores. In fact, most of their percentile scores look quite impressive (Table 3).

Table 1: BCB students who graduated during academic year 14-15

Graduate	Degree	Major Professor and their department
Ailene MacPherson	MS	Dr. Scott Nuismer (Biol. Sci.)
Roxana Hickey	PhD	Dr. Larry Forney (Biol. Sci.)
Matthew Pennell	PhD	Dr. Luke Harmon (Biol. Sci.)
Ilya Zhbannikov	PhD	Dr. James Foster (Biol. Sci.)

As there are only five BCB student fellowships per year; most students are funded by extramural grants and other sources. IBEST provided \$105,000 toward these five fellowships (covering about 3.5 fellowships, including in-state tuitions/fees and health insurance) and the University provided \$34,000 and waives out-of-state tuition like it does for all research assistantships. Thus most institutional support for BCB students is provided by IBEST. We think this is a valuable investment because the vast majority of BCB students work in the laboratories of IBEST faculty. Therefore, this investment is consistent with the institute’s charter because it directly supports interdisciplinary research on evolutionary processes at different levels of biological complexity. The investment is important in at least two other ways. First, the availability of these fellowships allows faculty to recruit outstanding students even if they do not have funded positions on extramural grants. Since fellowship support is limited to four semesters, the faculty must find alternative means to support their students, which releases the funding for future recruitment. Secondly, students supported by BCB fellowships can work on ‘not yet funded’ research and collect preliminary data to support future grant applications. Thus student support ‘primes the pump’ for extramural grant funding. Since IBEST faculty derive large benefits from the BCB program – mostly through the recruitment and training of truly exceptional students –we will continue to pursue ways to grow and sustain the program. One such effort was made in the summer of 2014 through the NSF Research Traineeship (NRT) program but was unfortunately not funded. We will try to pursue an NIH training grant.

Table 2: New students, fall 2015

Student	BCB Degree	Previous Institution	Current Major Professor and their Department
Sarah Brooker	PhD	Whitman College	Dr. M. McGuire (Animal and Veterinary Science)
Joseph DeAgüero	PhD	University of New Mexico	Drs. Bert Baumgartner (Philosophy) and Stephen Krone (Mathematics)
Brenda Hanley	PhD	Central Washington University/LCSC	Dr. Brian Dennis (Statistics)
Bethel Kohler	MS	University of Idaho	Dr. Eva Top (Biol. Sci.)
Jacek Maselko	PhD	University of Alaska Fairbanks	Dr. Michelle Wiest (Statistics)
Megan Ruffley	PhD	Miami University	Drs. Dave Tank and Jack Sullivan (Biol. Sci.)
Amanda Stahlke	PhD	Colorado Mesa University	Dr. Paul Hohenlohe (Biol. Sci.)
David Streett	MS	University of Idaho	Dr. Barrie Robison (Biol. Sci.)
Robert Week	PhD	University of Idaho	Dr. Scott Nuismer (Biol. Sci.)

Table 3: GRE scores (in percentiles) for '14-'15: BCB students compared to all graduate students at the University of Idaho (UI).

Average GRE Percentile	BCB Graduate Students	All UI Graduate Students
GRE Analytical %	57%	49%
GRE Quantitative %	87%	59%
GRE Verbal %	81%	62%

BCB Certificate Program

At the suggestion of the external review committee, the leadership of the BCB graduate program developed plans for a BCB certificate program. It will provide students

who are getting their graduate degrees in other areas with recognition for taking core course of the BCB curriculum. Graduates with this certificate will 1) have improved their understanding in bioinformatics, mathematical and computational sciences, and 2) will be able to participate in interdisciplinary research and in academia, industry, or government agencies thanks to the common 'language' they will learn. They will be able to explain BCB concepts to people with widely varying backgrounds, from professionals in other fields to lay people. The Idaho State Board of Education approved the proposal in the spring of 2015.

NSF INTERDISCIPLINARY TRAINING FOR UNDERGRADUATES IN BIOLOGICAL AND MATHEMATICAL SCIENCES

The University of Idaho (UI) and Washington State University (WSU) have established a collaborative program offering interdisciplinary training opportunities for undergraduates in mathematics and biology. The program capitalizes on extensive collaborations between mathematics and biology faculty at both institutions, providing undergraduates an educational experience well beyond what would be possible at either institution alone. IBEST has been central to developing many of the collaborations between math and biology faculty that are foundational to the success of the UBM program.

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 with modern research tools and methods. Projects are therefore designed to be genuine research experiences rather than rehearsals of research methods. Projects also involve students from both 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.

The UBM program has completed its fifth year. To date, UBM has funded 26 students (18 women and eight men), and many of these students were enrolled in the program for two full years. This long-term research experience is designed to facilitate the realization of research objectives, and emphasis is placed on the publication and presentation of results at scientific meetings. Students have presented their work at institutional (UI and WSU), regional (Pacific Northwest), and national scientific meetings, and in some cases published a peer reviewed journal article. Other article submissions are currently in preparation.

Several students who have completed the program have enrolled in graduate programs in mathematical biology. Recruitment of students has been broad, particularly from the

biological sciences. The program now includes mentors and students from five colleges at the UI (Agriculture, Science, Letters Arts and Social Sciences, Natural Resources, and Engineering).

We have also begun institutionalizing the curricular aspects of the UBM program at the UI. A new degree track in Mathematical Biology has been approved in the Mathematics department. The creation of this option in Mathematical Biology is consistent with the University of Idaho's strategic plan. In addition, the UBM program has proven to be a useful track of preparation for our graduate program in Bioinformatics and Computational Biology. We have recruited one of the UBM graduates (Ailene MacPherson) into the BCB program, while many other graduates have enrolled in graduate programs around the US.

APPENDIX 1 – HISTORY OF IBEST

The institute was founded in 2011 following a competitive internal selection process. But IBEST, which was formerly known as the Initiative for Bioinformatics and Evolutionary Studies, has a much longer history that extends back more than 20 years to when it was a grassroots effort of faculty from different disciplines that had common research interests and a desire to collaborate across disciplines. The growth of IBEST over the past decade has been spurred by funding from Center of Biomedical Research Excellence (COBRE) awards from the NIH-IDEA Program that have enabled us to fund research, recruit new faculty (see below), build impressive core facilities, and support students in our Bioinformatics and Computational Biology Graduate program. Participants in IBEST are now nested within a vibrant community of scientists in which intellectual interactions and collaborations are many and varied.

IBEST itself has evolved, most notably in terms of the increasing breadth and scope of research being done by IBEST investigators. While research on the molecular processes of evolutionary change and experimental evolution remain strong, there are increasing numbers of projects that focus on community and landscape-level evolutionary processes. We will continue to foster and encourage these because evolutionary processes play out at various levels of temporal and spatial complexity that range from speciation and adaptive evolution within populations at different spatial scales, interactions between populations that range from co-evolutionary processes to community-level ecological interactions, to broader scales within and between landscapes. The broader scope of IBEST research will bridge research between disciplines and lead to integration of concepts and principles from an even wider spectrum of disciplines.

IBEST	STRETEGIC REINVESTMENTS IN DIRECT SUPPORT FOR NEW FACULTY			2012 - 2015
PAST INVESTMENTS				
	INVESTMENT	FACULTY RECIPIENT	AMOUNT	SOURCE OF FUNDING
FY 2012	BIO/STATS START UP	PAUL HOHENLOHE	\$100,000	COBRE
	BIO/STATS START UP SUMMER SAL	PAUL HOHENLOHE	\$12,885	COBRE
	BIOLOGY LABORATORY SET UP	PAUL HOHENLOHE	\$15,000	IBEST OVERHEAD
	NEW FACULTY MOVING EXPENSE	PAUL HOHENLOHE	\$5,738	IBEST OVERHEAD
	STATISTICS START UP	ERKAN BUZBAS	\$35,000	IBEST OVERHEAD
	BIOLOGY START UP REPAYMENT	CRAIG MCGOWAN	\$10,000	IBEST OVERHEAD
	2012 TOTAL		\$178,623	
FY 2013	BIOLOGY START UP	PAUL HOHENLOHE	\$200,000	COBRE
	BIO/STATS START UP SUMMER SAL	PAUL HOHENLOHE	\$7,075	COBRE
	BIOLOGY START UP	PAUL HOHENLOHE	\$50,000	IBEST OVERHEAD
	BIOLOGY START UP REPAYMENT	CRAIG MCGOWAN	\$10,000	IBEST OVERHEAD
	2013 TOTAL		\$267,075	
FY 2014	BIOLOGY START UP	PAUL HOHENLOHE	\$82,866	COBRE PILOT
	EVOL BIOLOGIST START UP	CHRISTINE PARENT	\$65,000	IBEST OVERHEAD
	BIOLOGY FACULTY	DAVE TANK	\$41,000	IBEST OVERHEAD
	STATISTICS HIRE START UP	TBD (FU)	\$50,000	IBEST OVERHEAD
	2014 TOTAL		\$238,866	
2015	EVOL BIOLOGIST START UP	CHRISTINE PARENT	\$50,000	IBEST OVERHEAD
TOTAL IBEST INVESTMENT IN UNIVERSITY FACULTY:			\$734,564	
FUTURE COMMITMENTS				
2016	EVOL BIOLOGIST START UP	CHRISTINE PARENT	\$50,000	TBD
INCLUDING FUTURE PARENT STARTUP			INVESTMENT TOTAL	\$784,564

APPENDIX 2 – RESEARCH PUBLICATIONS

2015 Publications

Amador JM, & Soule T. Girls build excitement for math from scratch. *Mathematics Teaching in the Middle School*. 2015; 20:408-415.

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APPENDIX 3 – AWARDS RECEIVED IN 2015

IBEST AWARDS RECEIVED IN 2015			
Sponsor	PI	Award Title	Award Amount
Embassy of France	Tank	Chateaubriand fellowship	\$14,865
FioTec -Foundation for Scientific & Tech Development in Health	Forney	Influence of the vaginal microbiome	\$49,192
Michigan State University	Foster	BEACON Administration Yr 2	\$57,883
Michigan State University	Fuerst	BEACON Yr2 Fuerst	\$31,878
Michigan State University	Hagey	BEACON Yr 2 Hagey	\$52,690
Michigan State University	Heckendorn	BEACON Yr2 Heckendorn	\$363
Michigan State University	Marx	BEACON Yr2 Marx	\$31,240
Michigan State University	McGowan	BEACON Yr2 McGowan	\$19,624
Michigan State University	Nuismer	BEACON Yr2 Nuismer	\$6,974
Michigan State University	Soule	BEACON Yr2 Soule	\$21,959
Michigan State University	Wichman	BEACON Yr2 Wichman	\$62,432
National Institutes of Health	Forney	COBRE III Administration Yr 3	\$494,345
National Institutes of Health	Forney	COBRE III Computational Res. Core Yr 3	\$232,115
National Institutes of Health	Forney	COBRE III Genomics Res. Core Yr 3	\$229,100
National Institutes of Health	Forney	COBRE III Tech Access Yr 3	\$43,590
National Institutes of Health	Johnson	COBRE III Pilot Project	\$8,718
National Science Foundation	Harmon	Workflows for the Tree of Life	\$542,969
National Science Foundation	Nuismer	Strength of Coevolution	\$86,557
National Science Foundation	Settles	Fungal Pathogen Vertebrate Host	\$30,000
National Science Foundation	Sullivan	Predicting Cryptic Diversity	\$222,337
National Science Foundation	Tank	Contributors to Plant Species	\$18,738
National Science Foundation	Tank	Graduate Research Fellowship - H. Mar	\$6,000
National Science Foundation	Tank	Hybrid Swarm Hypothesis Testing	\$18,743
University of Florida	Forney	Vaginal Microbial Communities	\$30,270
University of Maryland	Forney	Ecopathogenomics of Infections	\$28,245
USDA Forest Service	Settles	USFS Soil Metagenomic Study	\$2,000
Washington State University	Foster	Inspire Milk Project	\$111,350
Washington State University	Hohenlohe	Tasmanian Facial Tumor	\$177,973
# of Awards Received: 28		Total Amount of Awards Received:	\$2,632,150

APPENDIX 4 – IBEST Pilot Project Grant Program

The IBEST Pilot Grant Program fosters research at the University of Idaho in all aspects of evolutionary and computational biology that are pertinent to human health. The objective of the Pilot Project Grants Program is to provide faculty with personnel, financial resources and time to collect preliminary data needed for a competitive external proposal.

Proposals will be accepted until February 1, 2015 with an expected award of funding by April 1, 2015.

ELIGIBILITY CRITERIA

All tenure track and non-tenure track faculty of any rank at the University of Idaho are eligible to apply for the IBEST Pilot Project Grant. The proposal may be collaborative with individuals at UI or at other institutions but non-UI collaborators can generally not receive COBRE funds. Funds can be used for collaborator travel.

Individuals are not eligible to submit a pilot grant proposal if they are current recipients of a pilot grant or if that have received a pilot grant in the past three years. The research proposed must be consistent with the scientific theme of the COBRE – processes of evolution – and have clear relevance to human health. Proposals outside this field will be deemed unacceptable and will be returned to the applicant without being sent out for review. To better determine if your project might be NIH-fundable and to place it in the context of other funded NIH grants, search the NIH RePORT site of grant abstracts at: <http://projectreporter.nih.gov/reporter.cfm>.

The maximum allowable request is \$75,000 (direct costs) per year for up to two years. Allowable costs are detailed below in (4).

The second year of funding is contingent on satisfactory progress and submission of a progress report as detailed in the letter of award. Other conditions apply as described below.

INSTRUCTIONS

1. All applications should be accompanied by a cover letter that contains:
 - A brief statement of how their research is relevant to the thematic focus of the COBRE
 - A description of the projected use of COBRE subsidized Core Facilities
 - A statement of the plan for developing and submitting a proposal for external funding
 - A statement that explains compliance with the necessary university and NIH regulations concerning research on Human Subjects, Animal Care and Use, Biohazard and Select Agents, if these are relevant. For details on how to comply at the University of Idaho, see the Office of Research Assurances website. Investigators must comply with all assurances and certifications listed in the PHS Supplemental Grant Application Instructions to be found online at: <http://grants.nih.gov/grants/forms.htm>.

2. The letter should be not more than 1.5 pages in length and will be included with the proposal for external review.

3. Grant proposals submitted to the IBEST Pilot Grant Program must be prepared using the following forms from PHS 398 (Revised 8/2012). Forms and instructions for completing these forms are available online at:

<http://grants.nih.gov/grants/funding/phs398/phs398.html>.

4. Page limits for the project description are indicated below in (3).

- Form Page 1: Face Page
- Form Page 2: Summary, Relevance, Project/Performance Sites, Senior/Key Personnel, Other Significant Contributors
- Form Page 3: Research Grant Table of Contents
- Form Page 4: Detailed Budget for Initial Budget Period
- Form Page 5: Budget for Entire Proposed Project Period (and budget justification)
- Biographical Sketch Format Page
- Resources Format Page
- Continuation Format Page (for Specific Aims and Research Strategy)

5. The project description should include the following elements within the indicate page limits:

- Specific Aims (1 page; see section 5.5.2 in PHS 398)
- Research Strategy (3 pages; see section 5.5.3 in PHS 398)
 - Significance
 - Innovation
 - Approach

6. Budgets should be prepared and justified following PHS 398 guidelines. Allowable costs include personnel (PI, postdoctoral fellow, technician or graduate student); supplies; core facility costs; small equipment; publication costs; and research-related travel (e.g., field work, collaborative travel, but not conferences).

Special guidelines for the project budget:

The person(s) who will do the research must be UI employee(s) by the time funds are awarded. If necessary the start date will be delayed until hiring is complete. In accordance with university guidelines, PIs are required to budget for and cover at least 2% of their academic year salary for the period of the grant.

7. Proposals should be submitted via email as a single PDF file that includes the cover letter and all forms in the appropriate order. They should be submitted to IBEST via email ibest@uidaho.edu before February 1, 2015. The subject line should be 'IBEST Pilot Grant Proposal.'

8. A non-competitive renewal application for year 2 funding should be submitted 60 days prior to the end of year 1 using forms and instructions from PHS 2590 (Revised 8/2012) available at: <http://grants.nih.gov/grants/funding/2590/2590.htm>.

9. Pilot grant recipients are obligated to acknowledge this support in presentations and publications that emanate from this funding. They must agree to provide IBEST with information about their publications, presentations, and grant submissions during and after the funding period. Recipients are also expected to attend IBEST sponsored seminars and will be asked to present their research findings and their plans for submission of a grant proposal in an oral presentation to the IBEST group around 9 months into the first funding year.

10. A final report that describes their research findings (2 pages) and a list of publications and manuscripts submitted, presentations, proposals submitted and grants funded is due within one month after funding concludes.

EVALUATION PROCEDURE

The Research Oversight Team will identify potential reviewers for the applications based on the subject matter of the proposals. Two referees from outside the University of Idaho will review each application and each reviewer will be asked to evaluate multiple proposals. The reviewers will be asked to prepare an anonymous written review that will subsequently be provided to the applicant. The proposals will be scored based on NIH guidelines (see section 6 in PHS 398):

Overall impact based on:

- Significance
- Investigator(s)
- Innovation
- Approach
- Environment

Reviews will also be asked to comment on:

- Consistency with the scientific theme of the COBRE – processes of evolution – and clear relevance to human health.
- Appropriateness of the budget
- Plans to comply with policies for research on Human Subjects, Animal Care and Use, Biohazard and Select Agent policies and procedures, if applicable
- Potential to lead to extramural funding from NIH or other agencies or foundations
- Use of the COBRE Core Facilities

After receipt of the written reviews, the Research Oversight Team will discuss the reviews and choose the most meritorious proposal.

APPENDIX 5 – TECHNOLOGY ACCESS GRANT PROGRESS REPORTS

Onesmo Balemba - Pathophysiology of Diabetic Nerve Cell Injury (Neuropathy) in the Gut

IBEST TAG Grant supports a research project whose goal is to elucidate the pathophysiology of diabetic nerve cell injury (neuropathy) in the gut. Funds cover the costs of using the IBEST Optical imaging core, Genomics Resources Core and Computational Resources Core to collect and analyze data.

Type two diabetes (T2D) is a chronic, debilitating illness affecting approximately 29 million Americans, and over 85 million prediabetic Americans are at risk of developing T2D. Roughly, 60-75 % T2D patients have disease complications arising from neuropathy; as such it is thought to be the major factor leading to debilitation. According to new research, neuropathy occurs during prediabetes stages. In the gut, injuries to the enteric nervous system (ENS) underlie symptoms of diabetic gut dysfunction, including gastroparesis (nausea, vomiting, bloating, delayed gastric emptying, weight loss, erratic blood glucose levels, spasms of stomach wall and gastroesophageal reflux disease), diarrhea, constipation, and pain. These symptoms are commonly manifested by a proportion of pre-diabetic patients and over 75% of T2D patients. Unfortunately, the pathogenesis and the exact nature of cellular changes leading to diabetic ENS neuropathy and subsequent alterations in neurotransmission are not fully understood. Importantly, the role of diet-gut microbiota-host interactions is not known fully; and at present, there no effective medications to mitigate diabetic ENS nerve cell damage. Therefore, TAG grant supports my lab to study gut nerve injuries in C57BL/6 mice with high fat diet-induced induced T2D. Our objectives are to: 1) identify whether the antimotility ileocecal supernatants of T2D mice inflict injury to inhibitory motor neurons, and how the effects correlate with the abundance of specific members of the microbiota; (2) identify changes in synaptic transmission in the myenteric plexus of diabetic mice and the underlying cellular mechanisms; and (3) determine the efficacy of oligofructose, mannoflavanone, GB-2 and alpha lipoic acid combination therapy to counteract the production of antimotility molecules, and mitigate HFD-induced diabetic ENS neuropathy.

IBEST TAG Grants have enabled us to obtain new findings showing that ileocecal supernatants of T2D mice inhibit gut motility. This suggests that the ileocecal content of T2D mice contain molecules that could damage ENS neurons. Likely, the damaging molecules are produced by high fat diet-microbiota-host interactions and could be the etiology agents and biomarkers of host ENS neuropathy. Pilot results suggest that the combination therapy mitigates ENS nerve cell damage in T2D mice. Preliminary data were used in a pending grant application to NIH (R03).

APPENDIX 5 (CONT.)

Lee Fortunato - Host/Pathogen Interactions of Human Cytomegalovirus

Human Cytomegalovirus (HCMV) can induce two site-specific breaks in the host cell's chromosomes at positions 1q23 and 1q42. We observe the breaks at a frequency of roughly 30% of the cells as early as 15 minutes post infection. As time proceeds, many of these breaks appear to be "repaired." However, since HCMV can interact with the DNA damage machinery of the host cell, it is not clear whether or not the DNA is repaired properly. In addition, the methodology we utilized to see breaks, fluorescence in situ hybridization, is a rather "blunt force" method and there may be smaller breaks/damage that we do not see with these types of assays.

With our TAG grant, we were able to use dual barcoded primers to amplify our break site region on 1q42 to generate amplicons for Illumina MiSeq deep sequencing. Amplification of both mock infected and virus infected samples at various time points between 24 and 120 h post infection were performed for comparison. Variation in sequence between mock and virus samples is being assessed. Variations are being assessed both for their frequency and for the actual sequence variations that occur. This analysis should reveal if small breaks (undetectable by FISH analysis) occur at the majority of the break sites in more cells that we can currently see. We would expect that a disproportionate number of improperly repaired breaks might be present in the virus-infected cells. The stability of the genome should suggest whether the cellular DNA is repeatedly breaking and rejoining at the break sites.

There may be only changes of a few base pairs from the mock infected sequences or there may be reasonably sized insertions/deletions. We want to assess the percentage of cells with aberrations and whether this increases or decreases over the course of infection. We also want to know if certain sequences come up more frequently, which would be indicative of the use of a particular type of repair.

Dr. Alida Gerritsen of the IBEST Genomic Resources Core is currently assisting us with analysis of the data from the latest time point post-infection, as this would potentially be the time point that shows the most differential between mock and viral samples. The data gathered here will serve to support my renewal application for my NIH R01 grant.

APPENDIX 5 (CONT.)

Dave Tank - An Integrated Approach to Understand Eco-Evolutionary Invasion Dynamics in an Alpine System

Modern species introductions are becoming somewhat of a ‘model system’ to understand diversity dynamics such as community assembly in natural systems. Studies over the past decades have used a variety of different measures to describe this diversity (i.e., species richness, functional traits, phylogenetic diversity) and attempt to explain evolutionary and ecological processes that drive the patterns of community assembly and species coexistence we observe. Still, they assume only a few functional traits and a phylogeny to be a proxy for all underlying ecological diversity in the community, and have yet to elucidate generalizable rules to explain—or even compare—the assembly processes that drive diversity dynamics of species across continents.

Transcriptomes describe the total diversity of expressed genes in an ecosystem, and in microbial communities transcribed gene products have been used as ‘functional traits’ to characterize the community by clustering orthologous transcripts into protein functional categories. These functional genes describe all products of the organism in their environment, and therefore, may provide insights into the relevant phenotypes that are important for the ecological function of a species—such as its invasibility—within a community more accurately than a few measurable functional traits. While gaining importance within microbial ecosystems, complete transcriptomes have not been used to understand diversity dynamics in macro-systems.

Advances in next-generation sequencing techniques make it possible to sequence transcriptomes for whole communities and explore the underlying genetic diversity, however despite its acceptance in microbial systems, RNAseq is still rarely used in macro-systems, especially at the level of a community. In collaboration with a research group in Grenoble, France, plants were surveyed from two adjacent streamside plots at the Lautaret Alpine Research Station in Grenoble, France—one from a community that has been recently invaded from the alpine botanic garden above that contains collections from across the globe, and one that remains a pristine alpine streambed. RNA was extracted from leaf tissue, and quality assessment was conducted at the IBEST Genomic Resources Core Facility. We are currently preparing Illumina-quantified libraries for 40 diverse plant species, and Illumina sequencing will be conducted through the GRC by the end of the year.

Transcriptome cleaning, assembly, and annotation will be done with the assistance of the IBEST Computational Resources Core Facility. With this data, we will 1) compare the total transcribed diversity between the invaded and native plots, and 2) compare the diversity of native-invasive congeneric species pairs within and between plots. We aim to extend community genomics into macro-ecosystems, and use the underlying transcribed diversity of co-existing alpine plants to describe functional differences between invaded and pristine plots at the genetic level. Ultimately, we will compare these patterns of diversity to those that are routinely used—phylogenetic diversity and “ecologically relevant” phenotypic trait diversity—and gain insight into mechanisms that allow species to become invasive within a community, and some communities to be more susceptible to invasions than others.

APPENDIX 6 – IBEST/BCB SEMINAR SERIES

Spring 2015



The poster features a dark, textured background with the word "IBEST" in large, bold, white letters at the top. Below it, the text "THE IBEST SEMINAR SERIES" and "SPRING 2015" is displayed in a smaller, white, serif font. A central white box contains a list of five seminars, each with a date, speaker name, affiliation, and topic. At the bottom of the poster, there is a white box with the text "THE INSTITUTE FOR BIOINFORMATICS AND EVOLUTIONARY STUDIES" and "WWW.IBEST.UIDAHO.EDU". In the bottom right corner, there is a logo for "ibest" with a stylized circuit diagram.

IBEST

THE IBEST SEMINAR SERIES
SPRING 2015

01.22 DR. FOLKER MEYER, ARGONNE LABORATORY - U.S. DEPARTMENT OF ENERGY
"ANALYZING SHOTGUN METAGENOMIC DATA."

02.12 DR. DOUGLAS EMLEN, UNIVERSITY OF MONTANA
"INSIGHTS INTO THE DEVELOPMENT AND EVOLUTION OF ANIMAL WEAPONS."

02.26 DR. SALLY OTTO, UNIVERSITY OF BRITISH COLUMBIA
"IDENTIFYING WHEN AND WHETHER PARTICULAR EVOLUTIONARY TRANSITIONS ARE POSSIBLE."
THIS SEMINAR IS CO-SPONSORED BY THE RANDALL WOMEN IN SCIENCE SEMINAR SERIES.

03.26 DR. NOAH ROSENBERG, STANFORD UNIVERSITY
"STUDYING PROBLEMS IN EVOLUTIONARY BIOLOGY AND GENETICS THROUGH MATHEMATICAL MODELING AND COMPUTER SIMULATION."

04.30 DR. JOSHUA PLOTKIN, UNIVERSITY OF PENNSYLVANIA
"MATHEMATICS AND COMPUTATION TO STUDY ADAPTATION IN POPULATIONS."

ALL SEMINARS ARE THURSDAYS AT 12:30PM IN MCCLURE 209

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APPENDIX 6 (CONT.)

Fall 2015



The poster features a dark, textured background with the word "IBEST" in large, bold, white letters at the top. Below it, the text "THE IBEST SEMINAR SERIES" and "FALL 2015" is displayed in a smaller, white, serif font. A central white box contains the seminar details, and a dark grey box at the bottom contains the institute's name, website, and logo.

IBEST

THE IBEST SEMINAR SERIES
FALL 2015

9.3 DR. ERIN LANDGUTH –
UNIVERSITY OF MONTANA
“An eco-evolutionary metapopulation simulation model for population viability analysis in riverscape genetics: Case examples in the Sullivan watershed, Washington, USA”

11.5 DR. LOREN RIESEBERG –
UNIVERSITY OF BRITISH COLUMBIA
“Sexual Selection and Plant Speciation”

11.12 DR. JEFF LEEK –
JOHNS HOPKINS UNIVERSITY
“How to go from raw data from next generation sequencing machines to results, turning public genomic data into clinically useful tools, and understanding how people use data analysis in real life”

11.19 DR. JESSE SHAPIRO –
UNIVERSITY OF MONTREAL
“The evolution of acute cholera infections on “human” time scales”

ALL SEMINARS ARE THURSDAYS AT 12:30PM IN ENGINEERING-PHYSICS 122

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APPENDIX 7 – 2015 IBEST NEWSLETTER





Did you know.....

The Bioinformatics and Computational Biology (BCB) program at the University of Idaho provides interdisciplinary training required to tackle the most cutting edge problems in genetics, genomics, population biology, mathematical modeling, statistics and computer science.

This highly flexible, research-intensive program provides a common language and understanding critical to interdisciplinary research. It prepares students to conduct and oversee research in academics, health sciences, agriculture and other industries. It integrates research and coursework in Computer Science, Biological Sciences, and Mathematical and Statistical Sciences. Students benefit from having faculty advisors that work across disciplines.

Instead of training students to be skilled in one specific area, the BCB program equips students with a set of quantitative tools and conceptual skills that prepare them to integrate theoretical and empirical research projects. It focuses on critical thinking and problem solving that can be applied across the spectrum of challenges in biological research.

There are 38 faculty members affiliated with the program (most of which are also affiliated with IBEST), from 13 departments and 6 colleges.

208-885-6010
bcb@uidaho.edu
www.uidaho.edu/cogs/bcb

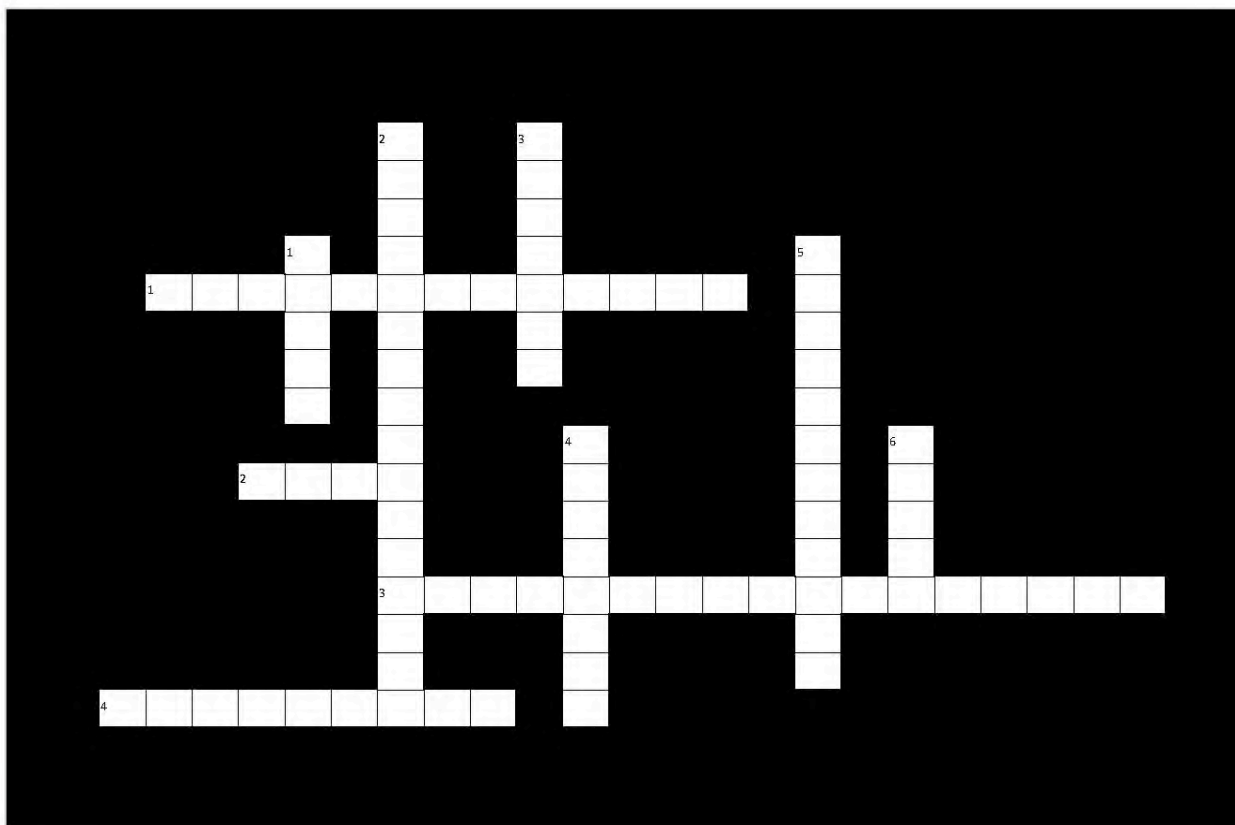
"The dilemma is this. In the modern world knowledge has been growing so fast and so enormously, in almost every field, that the probabilities are immensely against anybody, no matter how innately clever, being able to make a contribution in any one field unless he devotes all his time to it for years. If he tries to be the Rounded Universal Man, like Leonardo da Vinci, or to take all knowledge for his province, like Francis Bacon, he is most likely to become a mere dilettante and dabbler. But if he becomes too specialized, he is apt to become narrow and lopsided, ignorant on every subject but his own, and perhaps dull and sterile even on that because he lacks perspective and vision and has missed the cross-fertilization of ideas that can come from knowing something of other subjects."

- Henry Hazlitt

University of Idaho
College of Graduate Studies

© Dreamstime

Now You Know!



Across

1. Necrotizing _____ is when the lining of the intestinal wall dies, sometimes causing holes in the intestinal wall.
2. Robert _____ was a German physician in the late 1800s famous for identifying specific causative agents of tuberculosis, cholera, and anthrax.
3. Bioinformatics is highly _____.
4. Bacterial _____ is the most common vaginal infection in women.

Down

1. Tiny, malleable hair-like structures called _____ cover the toes of geckos.
2. Human milk _____ are a diverse group of sugars that make up a lot of breast milk solids components.
3. There are 38 _____ members affiliated with the BCB program.
4. White Sands National Monument is in the _____ basin.
5. _____ boosts an ecosystems productivity with each species playing an important role.
6. A volume pixel is called a _____.

What is annoying about the Geico gecko. (According to a scientist.)

Besides the fact that he interrupts your TV shows of course!

For one thing, it blinks in the commercials currently ran. "Which is just flat out wrong," says Dr. Travis Hagey (see article on page 3). Geckos don't have eyelids, they must lick their eyes to clear them of any debris or disturbance.

The Geico gecko first aired in 1999 as a result of the Screen Actors Guild Strike that prevented the use of live actors. In his debut, he was less anthropomorphic, crawling on all fours and indeed, licking his eye. His ability to talk has existed from the beginning, his famous plea to "stop calling him" cementing his position as a Geico mainstay.

Dr. Hagey says the Geico gecko looks most similar to the Day Gecko, which is appropriate, since it is primarily active in the day rather than at night like many geckos. The Geico gecko has been given more human characteristics over the years, such as the ability to walk on his hind legs and an other human mannerisms. Instead of a Malagasy or French accent that reflects the Day gecko's natural habitat (Mauritius or Madagascar), the Geico gecko speaks with a British Cockney accent.

Despite appearances by the Geico caveman and Maxwell the Pig, the Geico gecko remains the leading and longest running mascot, likely sticking around in anthropomorphic glory for years to come.



Where can Bioinformatics and Computational Biology take you?

Jason Evans ('09)
Computer Software Engineer
Facebook
Menlo Park, CA

Sam Hunter ('14)
Computational Biologist
Dana Farber Cancer Research Institute
Boston, MA

Craig Beisel ('07)
Senior Modeler
AIG - Global Casualty
New York, NY

Armand Bankhead ('06)
Bioinformatics Scientist
Compendia Bioscience
Ann Arbor, MI

Yongtao Guan ('06)
Assistant Professor
Baylor College of Medicine
Houston, TX

Andrzej Wojtowicz ('12)
Postdoctoral Fellow
Washington State University
Pullman, WA

Matt Settles ('11)
Director, IBEST Genomics
Resources Core
University of Idaho
Moscow, ID

Stephen Bent ('08)
Assistant Professor
University of Adelaide
Adelaide, AUS

Zaid Abdo ('05)
Statistician
USDA Research Service
Athens, GA

STICKY Fingers

By Whitney Schroeder

In one way or another we have all been exposed to the web-slinging, wall climbing, upside down kissing hero that has a history of swinging through the pages of comic books. It is probably a safe assumption that many, if not all of us have thought, “wouldn’t it be cool to be able to...” in regards to Spiderman’s skill set. Unfortunately, unless genetics enter the realm of fantasy, you won’t see anyone scurrying up walls anytime soon. However, the mechanism supposedly allowing this superhero to cling to a variety of surfaces – tiny hairs sprouting from his fingertips – lends him more credibility than those fantasies utilizing suction cups or plungers.

At the end of a spider’s legs are thousands of tiny, malleable hairs. It is these hairs that allow them to access nearly any surface at any angle. Geckos share this characteristic, although we are yet to see a superhero in their honor. Each gecko toe is covered in microscopic hair-like structures. It is large groups of these hair-like structures that give gecko feet their layered appearance. These tiny hairs are called “setae.” Each setae have thousands of even tinier flat tip structures called “spatulae” (pronounced like spatula). Small enough to interact with van der Waals forces, these hairs are the key to a gecko’s super-hero like abilities. van der Waals are the attractive and repulsive forces between molecules. Geckos literally walk at a molecular level.

“It is kind of a novel evolutionary characteristic,” says Dr. Travis Hagey, a postdoctoral researcher at the University of Idaho, “Gecko’s adhesive capabilities influence how they walk, how they use their environment, how they catch food, how they get away from predators.

It really lets them move through their environment in a way few other animals can.”

Hagey is currently funded by a grant from the BEACON Center for Evolution in Action to study the optimization of the gecko adhesive system. His first goal

Did you know geckos, like most things, cannot stick to Teflon?

is to develop 3D reconstructions of the setae.

“Previous research has really only considered simplified hair-like structures, modeled as cantilever beams, to understand how they work,” says Hagey.

While these simplifications are fairly accurate in theory, they can easily be violated by the variable realities surrounding an actual gecko’s setae – the fact that they are not perfectly straight, they are not made from the same material all the way through and they can vary greatly from gecko to gecko. This means that the current approach for mathematical modeling leaves out a lot of information and does not exactly mirror real life mechanics. By making 3D reconstructions, Hagey will be able to make fewer simplifications. If there are differences in the hair length or how they are shaped, those can be incorporated into the 3D model. Using engineering software Hagey can also incorporate more things like material make-up and stiffness, allowing him to simulate how the hair will bend and deform when outside forces are applied to it. By reconstructing these hairs, Hagey can explore the different variables that play a role in the



TRAVIS HAGEY

Dr. Hagey’s research investigates why animals are shaped the way they are shaped, integrating biomechanics, evolution and ecology, using comparative methods and engineering simulations along side field observations and lab-based experiments.

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Department of Biological Sciences
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Roches.

Genetically speaking, these three lizard species are indistinguishable from their dark soil counterparts. But phenotypically and behaviorally Des Roches has started to notice some differences. These differences are unique between each species of lizards, despite all of them living in the same location and being distantly related to one another. For example, in comparison to their dark soil counterparts, two of the White Sands species morphs exhibit larger body size and longer limbs. The White Sands morphs also have different escape responses. In all three species, the dark morphs are less likely to immediately sprint from a predator when on the White Sands ecotone and all sprinted faster on the stable terrain of the dark soils as compared to the unstable White Sands substrate. Des Roches findings suggest that these differences in escape responses and sprint performance in the two different habitats may signify that behavioral differences play an important role in speciation in new environments.

The mark-recapture project also allowed Des Roches to study prey availability and diet along with the performance and morphology of the three lizard species. With the differences in the prey available on the White Sands, the species of lizards living there exhibited different

diets from their dark soil counterparts. Corresponding with these differences in diet were phenotypic traits, such as stronger bite force and larger head size, reflecting the need to accommodate the harder bodied prey more prevalent in the White Sands environment.

The why in all of this resides in the importance of biodiversity, or the variety of life on earth. Biodiversity boosts an ecosystems productivity with each species playing an important role. For example, healthy diverse ecosystems can withstand and recover better from a variety of disasters. Diversity also ensures sustainability of all life forms, as species depend on each other through the variety of services each species provides. Understanding this diversity – especially in the age of advanced agricultural, industrial and rural development – and how it develops in the face of environmental change is essential in effective management of biological diversity that will ensure a sustained, balanced world in the future.

“I am interested in knowing more about what is around us, the natural systems around us and I believe that gives us an appreciation for nature,” says Des Roches, “I think there is a lot we can learn from it in terms of how we treat the environment and to me that is as noble a cause as anything else.”



evolutionary change is a bit unprecedented.

Three species of lizards have colonized the White Sands. The Lesser Earless Lizard (*Holbrookia maculata*), the Eastern Fence Lizard (*Sceloporus undulatus*), and the Little Striped Whiptail Lizard (*Aspidoscecis inornata*). All three species have developed white coloration as compared to their darker neighbors found in the regular, dark soils desert that surrounds White Sands. Des Roches PhD advisors, Dr. Brie Rosenblum and Dr. Luke



Drawing by Simone Des Roches

Harmon, have studied the genetic mechanism behind the color change – called a morph – in the populations of these lizards that live within White Sands. Des Roches research focus has not been limited to just the color, but on whether or not survivorship is associated with some sort of phenotypic trait in the lizards, such as limb length. For example, if lizards that have longer legs are recaptured more over time than their shorter legged counterparts, this data might signify a short-term directional selection

towards longer legs in the species.

“I’m interested in the evolutionary ecology, so stuff like how they run, what they eat and those sorts of things,” says Des Roches, “I am interested in traits that have an ecological implication or function.” By exploring what traits enable organisms to colonize a new environment, Des Roches hope to better understand adaptation and the process of speciation.

Along with the obvious changes to their coloration, changes have been documented in their body shape, limb length, what they eat, where they hang out during the day, and population size and make-up. Des Roches has spent the last three years, and the focus of her dissertation on this data, conducting a marker-capture experiment every summer. With a team of undergraduate researchers, Des Roches traps lizards on White Sands, marking them with a fluorescent identification marker, documenting a wide array of characteristics and releasing them in hopes of capturing them again the following year.

Des Roches marker-capture project has focused on a region called the ecotone, the transitional area between two different ecosystems. White Sands is unique in that it is constantly moving, slowly migrating in a southeasterly direction. On the windward side the ecotone is gradual, but on the leeward side it is an abrupt line, meaning you could literally stand with one foot in White Sands and one foot in the dark soil habitat. Des Roches has focused her marker-capture to this abrupt ecotone on the leeward side, because the interface between the two habitats is probably the most reflective of how things were when White Sands first formed, with higher predation and competition pressures. At this abrupt line, more species abound that might come on to the edge of the dunes, but not make it into or spend much time in White Sands proper. It is the perfect environment to study the White Sands selective environment and the evolutionary changes this causes in the lizards.

“Why that is interesting is because on the ecotone these lizards are a mix of colors, like a range, so you can get really dark ones or really light ones,” says Des



SIMONE DES ROCHES

Dr. Des Roches graduated from the University of Idaho with a Ph.D. in Biology, she is currently a postdoctoral fellow at the University of California, Berkeley. Along with a love for evolutionary ecology and lizards of the White Sands, Dr. Des Roches also has a talent and passion for drawing.

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© Travis Hagey

many diverse gecko species (over 1500 different species to be exact) ability to stick to walls and other habitats. Likewise, it will allow him to build reconstructions that don't exist in real life and to ask questions, such as "why isn't a gecko shaped like this or that."

He will also be able to build synthetic structures. Meaning if an engineer came to Hagey wanting to build a gecko-like adhesive out of a particular material with a specific diameter, density and length, Hagey could



build a similar digital model, run a simulation and tell the engineer how the synthetic adhesive would work before it is ever built, as well as suggest improvements.

But how does one go about getting a 3D image of something so tiny? The incredibly small tip structures of the spatulae are only 200 nanometers wide. For reference, the human eye is only able to see wavelengths of light between 400 and 700 nanometers, meaning anything smaller will not reflect light and not be visible to the naked eye. (Red blood cells are roughly 10 thousand nanometers in diameter. Consequently the width of a spatulae is 50 times smaller than the width of a red blood cell.) They are so small that even high-powered light microscopes struggle to capture their detail.

Hagey first utilized the Confocal Microscope in the IBEST Optical Imaging Core. He was able to get images of the hairs showing how they are shaped relative to each other, but their density blocked the imaging of some details. This led Hagey to the University of California – San Francisco dentistry department. They had an X-ray micro CT scanner capable of passing through and imaging densely packed setae. The micro CT scanner (envison a desktop cat scan machine appropriate for small samples) takes hundreds of imaged slices of the structure, producing a stack of digital cross sections. Once they are all "glued" back together, you have a 3D image. While this approach had rather high resolution, it did not meet the desired quality Hagey envisioned for imaging the tiny tip structures necessary for truly accurate 3D modeling.

Hagey's current focus has been in Chicago,

specifically at the Argonne National Laboratory, a Department of Energy research site run in conjunction with the University of Chicago. Argonne houses a particle accelerator as part of the Advanced Photon Source facility. This particle accelerator supports 34 different sectors that investigate things from Microscopy, physics and engineering, magnetism, biological structure, and nanoscale materials just to name a few. Each sector utilizes a beamline of the accelerator.

During Hagey's first visit to the lab Hagey was able to utilize beamline 21, allowing him to do elemental analysis. This allowed him to see what elements the hairs are made of and where the elements are in each hair. His interest is focused on sulfur and phosphorus. These elements are important because they relate to the stiffness of proteins, and since the hairs on gecko toes are made up of proteins, the elemental content can provide insight into the behavior of the hairs.

Hagey's second visit utilized beamline 32. This beamline specialized in nano x-ray tomography, or nano-CT.

The nano-CT functions like a traditional CT scanner used in hospitals, only the voxel size (3-D pixel) is in the nanometer range as opposed to the millimeter range. (There are 1,000,000 nanometers in one millimeter.) Hagey is currently working with the beamline 32 staff in order to refine the imaging process and recreate a virtual model detailed enough to run accurate simulations.

So why all this interest in gecko feet? Is science fueled by the imaginings of comic books and sci fi movies? Maybe a little, but Hagey feels there is a lot of interest from the human point of view outside of biomimicry (such as scaling buildings). There are potential industrial applications, such as trying to replace

In digital imaging, a pixel is a physical point in the image. Pixels are the smallest unit of information that makes up a picture. In 3D imaging, one works in Voxels or a volume pixel (think of 1 cubic inch versus 1 square inch). One might compare voxels to bricks, which are stacked and used to build bigger structures. The smaller the bricks you use, the more detail the bigger structure can have (Lego vs Duplo blocks).

Velcro on the space station or creating a strong, easily removable, and non-damaging adhesive. Already researchers are implementing gecko-like adhesives in a product called GeckSkin™, developed at the University of Massachusetts-Amherst. Unlike adhesives developed so far, GeckSkin™ leaves no sticky residue and is easy to release. According to their website, an index-card

IMPORTANCE of Biodiversity

By Whitney Schroeder



Imagine if we woke tomorrow to a brand new island in the Pacific, not far off the coast of California. It has unique vegetation and resources, unlike anything we have seen on our planet. Over time, small groups of people start to inhabit the island. Because of the uniqueness of this island, many of the traditional living techniques we are accustomed to cannot be utilized. The habits of the people on the island change from those of the mainland and only a few groups of people care to stay there permanently. Fast-forward a few thousand years and changes begin to be noticed in the posterity of the populations who settled there. Perhaps their eyes are consistently lighter and their skin consistently darker; or small structural changes to their feet, hands and mandibles. They are still homo sapiens like those on the mainland, but they are also different.

While an island complete with established flora and fauna suddenly appearing over night is something of fantasy, new habitats on this planet do appear, becoming – over millions of years – what we see today. The life that slowly develops with these habitats is studied in a broad biological model called evolution. In a single human lifetime, these changes can be challenging to explore, as roughly 80 years is but a minuscule blip on the timeline of millions. But what about changes that are relatively recent, say

“I am interested in knowing more about what is around us...I believe that gives us an appreciation for nature.”

in the thousands of years or even on the scale of a few generations of a species? This is evolution in action, and this is why Simone Des Roches, a recent PhD graduate from the University of Idaho, has been visiting the White Sands National Monument for the last three summers.

White Sands exists in the south central region of New Mexico. Bright white, glistening gypsum dunes rise and fall over 275 square miles of the Chihuahuan desert in the Tularosa Basin. Part White Sands National Monument, part White Sands Missile Range, the white sands make up the world's largest gypsum dunefield. The second largest – Cuatro Ciénegas in central Mexico – covers only eight square miles. Evolutionarily speaking,

it is also young.

The Tularosa Basin used to be a large inland sea, fed by the runoff from the Sacramento and San Andres Mountains. After the last glaciation event, the lake slowly evaporated, leaving gypsum deposits behind. Weather and winds reduced these deposits

to fine, sand-like grains and concentrated them into the dunes we observe today.

“We know that everything that happened must have happened within the last 7,000 years,” says Des Roches, “and that’s even more recent than what we consider recent in terms of a lot of people who study evolution.” For vertebrates, such a short timespan of

"The ultimate goal is to clarify what *Gardnerella vaginalis* looks like in healthy individuals so that we can make better sense of its possible role in BV," says Hickey, "if it turns out specific strains are more highly associated with BV then we could develop therapies that specifically target those bacteria without wiping out the whole microbiota because we know the vaginal

microbiota is necessary for health."

Sources:

<http://www.funtrivia.com/en/subtopics/Gardnerella-is-Not-the-Farmers-Daughter-297668.html>

http://www.cdc.gov/std/bv/stdfact_bacterial_vaginosis.htm

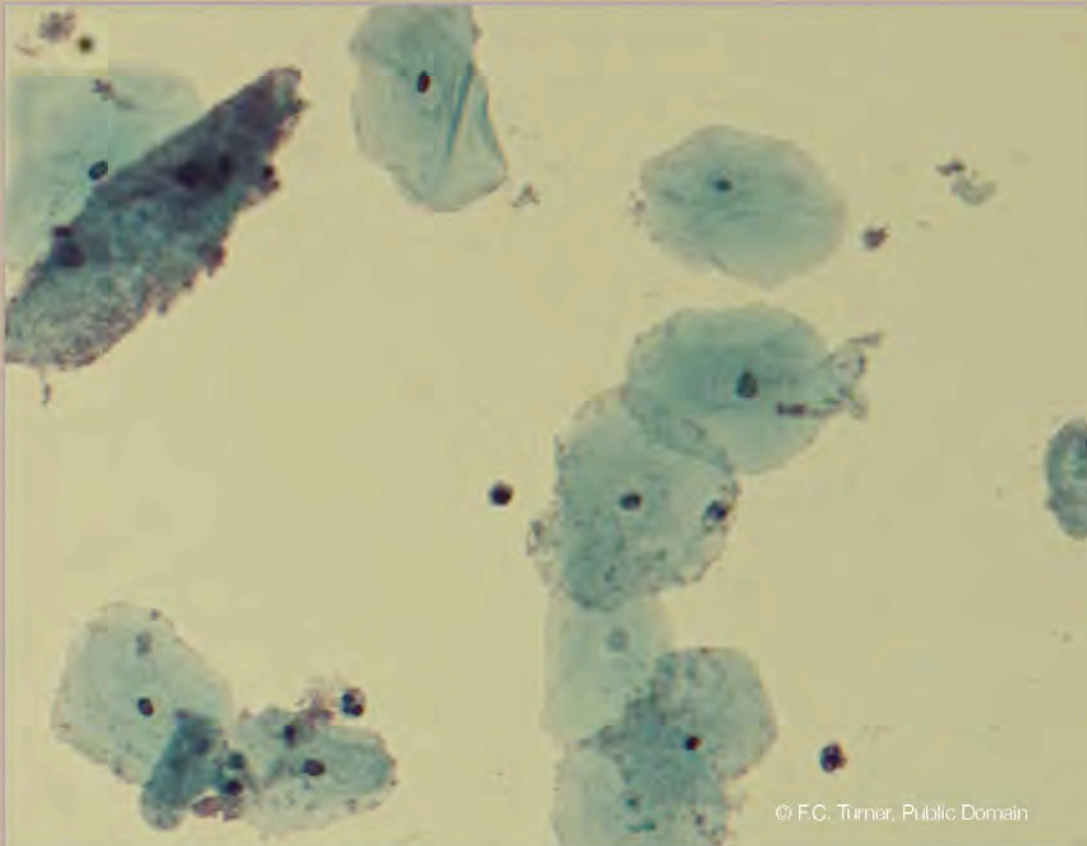
http://www.genomenewsnetwork.org/resources/whats_a_genome/Chp2_2.shtml

Metagenomic what?

Shotgun Metagenomic sequencing is a technique that is performed on environmental samples (including human). Metagenomic means "more than one genome." Shotgun sequencing is the process of taking all DNA in a sample and chopping it up into small pieces 200-800 base pairs (A, C, G, T) long. Metagenomic shotgun sequencing determines the DNA sequence from the many genomes by first chopping them into many smaller pieces and then piecing them back together.

Still confused? Imagine a sequencing machine is a wood chipper (see page 10). Now imagine each genome is a book of yellow page directories, one from New York, another from L.A., another from Seattle, etc., etc. All these books are in a sealed box (a sample) and in order to open the box you have to throw it in the wood chipper. When the box is thrown in, everything comes out the other end of the wood chipper in millions of tiny pieces. The goal is to then piece each directory back together. It becomes complicated when you have the same item - say an ACME Cleaning Service - that shows up in multiple yellow page directories.

By sequencing the samples, Hickey can see what genomes are in the environment and what it might be doing (what genes are there).



© F.C. Turner, Public Domain

sized piece of GeckSkin™ can hold 700 pounds on a smooth surface. The researchers took more of a mathematical modeling approach to engineering their product, involving a fair amount of trial and error to reach a finished product. Hagey hopes his technique of 3D modeling and simulation will make the development of new adhesives easier in the future, as the “trial and error” part will be done digitally.

But most interesting to Hagey is finding out how geckos work within their unique evolutionary ecological system. They are a group that is 200 million years old, extremely diverse, and spanning multiple continents. They are nocturnal and diurnal; some have eyes 350 times more sensitive than ours; they range in size from

2 centimeters to the length of a human forearm; they lack eyelids; many can lose their tail, some manually, and it keeps wiggling after doing so; some species are parthenogenic, meaning a female can reproduce without mating; like many reptiles, they shed their skin; some geckos can glide (similar to a flying squirrel) over 195 feet; many geckos live well over ten years; and of course, they have unique and highly specialized toe pads allowing them to traverse walls and ceilings.

“They have unique morphology which can allow for unique performance and unique habitat use,” says Hagey, “I think they are special in every kind of way, in every dimension.”

Move Like Spiderman - not yet.

Geckos can support their own body weight in inverted and vertical situations. Human bodies weren't designed to do that, and even the strongest among us could not suction cup up a wall very far without additional support. (Sorry all of you Mission Impossible fans.)

This has not stopped researchers at Stanford from trying though. In a study published in the Journal of the Royal Society Interface this past November, researchers at Stanford University reported on a dry adhesive system they created modeled after the gecko. Using this system – made of silicones, plastics, carbon nanotubes and other materials – a 154-pound man was able to crawl vertically up a glass wall nearly 12 feet. Their system resembles a VersaClimber you would find at the gym, better accommodated to the human build.

Read more about Stanford here: <http://rsif.royalsocietypublishing.org/content/12/102/20140675>



Three frames from a video (electronic supplementary material, move S1) showing a 154 lb climber ascending a 12 ft vertical glass surface using a synthetic adhesion system with degressive load-sharing and gecko-inspired adhesives. The time between (a) and (c) is about 90 seconds and includes six steps.

WHAT IS BIOINFORMATICS?



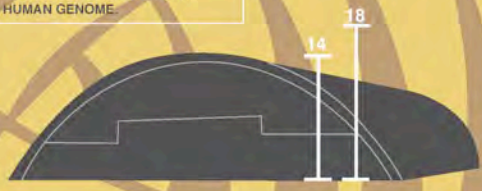
4 PRIMARY FIELDS WORKING TOGETHER TO DEVELOP TOOLS FOR UNDERSTANDING BIOLOGICAL DATA (DNA)

4 LETTERS REPRESENT DNA
A, T, G, C

3 BILLION OF THESE LETTERS MAKE UP THE HUMAN GENOME

1,000
COPIES OF TOLSTOY'S WAR AND PEACE HAVE ROUGHLY THE SAME AMOUNT OF LETTERS AS THE HUMAN GENOME.

18 STORIES HIGH, IF EACH BOOKED WAS STACKED ON THE OTHER
(HIGHER THAN THE UK KIBBIE CONE)



TO SEQUENCE THE HUMAN GENOME...

IMAGINE...

1,000

COPIES OF WAR AND PEACE THROWN INTO A WOODCHIPPER (SEQUENCER)

WHY THE WOODCHIPPER?
CURRENT TECHNOLOGY IS NOT CAPABLE OF SEQUENCING THE ENTIRE LENGTH OF THE HUMAN GENOME. PIECES MUST BE USED TO PUT IT ALL TOGETHER. THE MORE TIMES IT IS RESEQUENCED OR CHIPPED, THE HIGHER THE ACCURACY.

MILLIONS

OF PIECES WITH HUNDREDS OF LETTERS ARE PRODUCED



IN BIOINFORMATICS THESE PIECES ARE CALLED "READS"



+190

SOFTWARE PROGRAMS USED TO HELP PROCESS THE INFORMATION (READS)

CHALLENGES

- DISTINGUISHING BETWEEN INDIVIDUAL DIFFERENCES & THOSE THAT CAUSE DISEASE
- INTERPRETING WHAT THE DATA TELLS US ABOUT BIOLOGY
- NAVIGATING THE SHEER VOLUME OF DATA
- ASSEMBLING LARGE GENOMES INTO CHROMOSOMES



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APPENDIX 8 – 2015 INLAND NORTHWEST GENOMICS RESEARCH SYMPOSIUM

Inland Northwest Genomics Research Symposium, MAY 21, 2015

Speakers topics and institutions

Oral presentations	Total	Topics				Keynote	
		Genomics	Computation	Vendors			
Number presentations	9	4	2	2	1		
Speaker Institution	U Idaho	Washington State U	University of California - Davis	University of Oregon	Reed College	Univeristy of Washington	Industry
Number speakers	2	1	1	1	1	1	2
Posters	39						

Institutions/Vendors Represented

Eastern Washington University	3	Thermo Fisher	2
Montana State University	2	Hamilton Robotics	1
University of California Davis	1	Florigenex	1
USDA	6	Fluidigm	1
University of Oregon	4	Advanced Analytical Technologies	1
PNNL	1	Illumina	3
Reed College	16		
Washington State University	31	Subtotal	9
Northwest Nazarene University	1		
University of Idaho	68		
University of Montana	1		
University of Washington	1		
University of Quebec	1		
Subtotal	136	TOTAL ATTENDEES	145

Funding

Source of funds	COBRE I	BEST F&A	Vendors	Total cost
	\$6,300	\$8,200	\$1,500	\$16,000

Vendors: ThermoFisher, Hamilton Robotics, Illumina, Advanced Analytical Technologies

APPENDIX 8. THE INLAND NORTHWEST GENOMICS RESEARCH SYMPOSIUM (CONT.)

Schedule

INWGRS Agenda 2015	
Thursday, May 21	
International Ballroom, Bruce M. Pitman Center University of Idaho	
8:00 – 8:50	Continental Breakfast Registration
8:50 – 9:00	Welcome Remarks – Dr. Barrie Robison, University of Idaho
9:00 – 10:15	Session One - Moderator: Dr. Barrie Robison
9:00 – 9:25	Dr. Stacy Musone – Illumina, Inc. <i>Illumina's Sequencing Portfolio</i>
9:25 – 10:15	Dr. Thomas Desvignes – University of Oregon <i>Studying microRNA-Seq data using Prosti!: applied example to stickleback and other fish</i>
10:15 – 12:00	Poster Session and Lunch
11:15	Lunch served
12:00 – 1:00	Keynote Address - Introduction by Dr. Paul Hohenlohe Dr. Jim Seeb – University of Washington <i>Why has genome science had such a profound effect on the conservation of Pacific salmonids?</i>
1:15 – 2:30	Session Two - Moderator: Dr. Benji Oswald
1:15 – 1:40	Dr. Jason Boone – Floragenex, Inc. <i>300 Strong: Leveraging Ion AmpliSeq™ and Ion Torrent™ sequencing for targeted genotyping studies</i>
1:40 – 2:30	Dr. Joanna Kelley – Washington State University <i>Opportunities and Challenges in Ecological Genomics</i>
2:30 – 2:45	Break
2:45 – 4:00	Session Three – Moderator Dr. Alida Gerritsen
2:45 – 3:10	Bridget McLaughlin, M.S. – University of California, Davis <i>Linking Flow Cytometry with Single Cell Genomics: A Case Study at UC Davis</i>
3:10 – 4:00	Dr. Christopher Marx – University of Idaho <i>Evolution with an engineered metabolism: mutations, gene expression, and models pushing towards prediction adaptation</i>
4:00 – 4:15	Break
4:15 – 5:30	Session Four - Moderator: Dr. Matthew Settles
4:15 – 4:40	Dr. Matthew Settles – University of Idaho <i>The Data Science in Bioinformatics</i>
4:40– 5:30	Dr. Sarah Schaack – Reed College <i>Paleovirology in rattlesnakes: Scouring the genomic fossil bed for endogenous viruses</i>
5:30 – 5:45	Closing Remarks - Dr. Larry Forney, University of Idaho
5:45 – 6:30	Reception

APPENDIX 9 – BUSINESS FOR SCIENTISTS

ATTENDEES

2015 Business for Scientists	
Name	Department
Barrie Robison	Biological Sciences
Bert Baumgaertner	Philosophy
Andreas Vasdekis	Physics
Tara Hudiburg	Forest, Rangeland, and Fire Sciences
Krishnan Raja	Chemical & Materials Engineering
Sarah Koerber	ORED
Ekaterina Vorotnikova	Agriculture
Joel Perry	Mechanical Engineering
Benji Oswald	IBEST
Katie Brown	Family and Consumer Sciences
Dojin Ryu	Food Science
Alida Gerritson	IBEST
James Moberly	Chemical & Materials Engineering
Robert Heckendorn	Computer Science
James Stoutenborough	EPSCoR (Postdoc)
Jackie Maximillian	Environmental Science (Postdoc)
Karol Gliniewicz	Biological Sciences (Postdoc)
Sudheesh Ponnerassery	Fish and Wildlife (Postdoc)
Anahí Espíndola	Biological Sciences (Postdoc)
Carrie Roever	Forest, Rangeland and Fire Sciences (Postdoc)
Dorah Mtui	College of Natural Resources (Staff)
Inna Popova	Plant, Soil and Entomological Sciences (Staff)

APPENDIX 9 – BUSINESS FOR SCIENTISTS (CONT.)

SCHEDULE

2015 Leading and Sustaining Your Research Program

Commons Clearwater Room

	Mon. June 1	Tues. June 2	Weds. June 3	Thurs. June 4	Fri. June 5
8:00 AM	Introduction	Business Model Discussion (Day 1 Follow-Up) <i>George Tanner</i>	Communications Discussion (Day 2 Follow-Up) <i>George Tanner</i>	Research Lab Management: Behavioral Aspects of Decision Making <i>Ray Dacey</i>	From Research to Industry: Market Feasibility <i>Steve Peterson</i>
9:00 AM	Business Model <i>George Tanner</i>	Communicating Your Research: The Elevator Pitch <i>George Tanner</i>	Research Lab Management: Managing the Team <i>Dan Eveleth</i>		
10:00 AM					Business Model Exercise
11:00 AM					
12:00 PM					

Required Reading	
May 2015 Issue of Harvard Business Review, pages 52 through 85	http://db.lib.uidaho.edu/ereserve/show_course.php?pointer=4450

** Please note, if you are off campus you must use the UI VPN client: <https://www.uidaho.edu/its/Self-Help/Security-and-AntiVirus> **

APPENDIX 10 – BEACON AWARDS

UI PI	PROJECT TITLE
Foster	Idaho Administrative Budget
Foster	Idaho Administrative Budget
Heckendorn	Sabbatical Support
Soule 1	Evolutionary Games K - 6
Harmon 1	Mystery of Mysteries
Sullivan	An integrated approach to testing divergence with gene flow model of speciation
Wichman 1	Evolution of synthetic genomes
Harmon	The Genetic Architecture of Multidimensional Adaptation and Speciation
McGowan	Why hop? Morphology, mechanics, and natural selection in bipedal hopping
Hohenlohe	An experimental evolution model for genomic islands of speciation
Top	Slow and steady wins the race? Adaptation in structured worlds
Tank	The genetic basis of weediness: rapid evolution of flowering time in wild radish,
Heckendorn	Cross-fertilization of techniques: epistasis from evolutionary computation and biology
Foster	Teaching evolution through action: the Avida challenge
Heckendorn	BEACON Summit to Catalyze Diversity
Foster	The role of symbiotic bacteria in a predator-prey coevolutionary arms race
Hagey	Optimization of the Gecko Adhesive System
Marx	
Fuerst	
Baumgaertner	Simulating signals and security
Top	Use it and lose it: Alternating selection promotes horizontal gene transfer
Heckendorn	Landmark Guidance: An integrated study in bees, Avida, and physical robots
Top	Source-sink population dynamics facilitate plasmid host range evolution
McGowan 2	The Price of Performance: The Evolution of Efficient Locomotion in Quadrupeds
Tank 2	Evolutionary and ecological consequences of polyploidy
Nuismer	Predicting the evolution of synthetic genomes: transmissible viral defense (phase 2)
Murdoch	Has evolution of human milk sugars responded to selection
Foster	Administration
Fuerst	
O'Rourke	Developing a virtue-based approach to RCR training
Soule 2	Evolution curriculum for elementary classrooms: LadyBug and supporting activities
Soule 3	Distributed, Onboard Evolution in a Robotic Cloud
Harmon 2	Evolution of mechanisms enabling the use of a neurotoxin as a pheromone
Harmon3	Long-term consequences of evolution in action examined over a phylogeny
Wichman 2	A tractable animal model for experimental viral evolution
Foster	Avida-ED Infrastructure Maintenance and Development
Foster	Avida-ED Curriculum Development and Assessment Pilot Study
Hagey 2	Optimization of the Gecko Adhesive System