IBEST

ANNUAL REVIEW 2016

The Institute for Bioinformatics and Evolutionary Studies

Supported by the National Institutes of Health under Award Number P30 GM103324

University of Idaho

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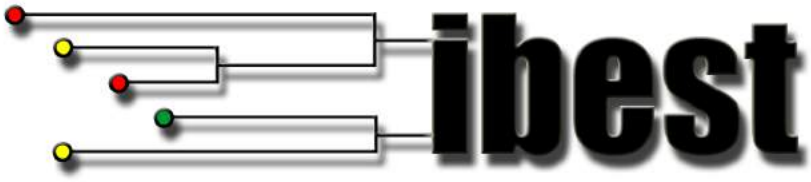
Appendices

I. IN MEMORIAM

In FY 2016, we experienced a terrible loss; as is well known, College of Science Dean Paul Joyce, our dear friend and cherished collaborator, passed away tragically while driving back to his hotel from an IBEST retreat event at the High Country Inn. Paul was one of the original IBEST faculty and one of his great delights was sharing his mathematical brilliance to elevate his colleagues' research programs. We can take solace from acknowledging that his last evening was spent with IBESTians discussing science, politics, and his family and celebrating our history of shared success. We will miss Paul in so many ways, but one of the most meaningful ways to honor and cherish Paul's legacy of intellectual generosity is to continue to have fun doing great science together.

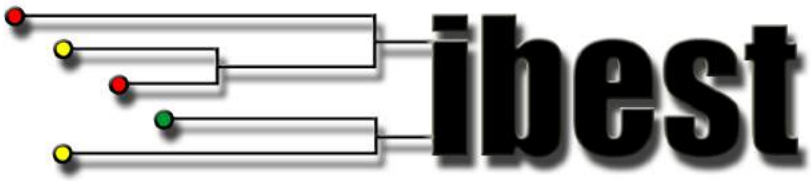


II. EXECUTIVE SUMMARY

The Institute for Bioinformatics and Evolutionary Studies (IBEST) was established as a Level III Research Institute at the University of Idaho in August of 2011, for a period of 5 years. The mission of IBEST is to facilitate and accelerate interdisciplinary research in evolutionary science, inclusive of all scholarly disciplines and across administrative units. IBEST faculty, staff, and students conduct *basic research* in evolution, as well as evolutionary modeling and *applied* evolutionary research in *biomedical*, *agricultural*, *computational* and *conservation* sciences. IBEST provides a collegial and inclusive environment defined by a shared commitment to understanding evolution.

There have been four original goals of IBEST: 1) enhance interdisciplinary research in evolutionary processes, 2) establish and nurture strategic collaborations and partnerships, 3) maintain and enhance IBEST's core facilities in Genomics and Computational Resources, and 4) promote interdisciplinary training in evolutionary science to undergraduates, graduate students and postdoctoral fellows. Detailed reports for the last fiscal year on the assessment metrics linked to each of these goals form the basis of this report and are summarized here.

1) IBEST reinvested $381,876 in programs to accelerate research in evolutionary science in FY 2016. This has occurred via contribution to faculty start-up, funding Pilot and Technology Access Grants, and hosting workshops and symposia.
   IBEST faculty have reported 62 publications supported by IBEST to date in 2016.
   IBEST has generated $3.2M in research expenditures in FY2016
   IBEST faculty have secured over $3.4M in external funding (including BEACON) in FY2016.
2) We have continued our participation in BEACON, an NSF Science and Technology Center that focuses on "Evolution in Action." In addition, we have strengthened our partnership with the Center for Modeling Complex Interactions (CMCI) by co-funding a paid bioinformatics intern and merging seminars. Further, we have established a new partnership with the Idaho Wheat Commission through genomic studies of pesticide resistance in crop pests.
3) We have expanded usage of the Genomics Resources and Computational Resources Core facilities, and hired a new GRC director as a Clinical Assistant Professor.
4) We have continued to support BCB fellowships, funded BCB seminars, and supported workshops for graduate students and postdoctoral fellows.



III. IBEST MISSION AND GOALS

A. MISSION

The Institute for Bioinformatics and Evolutionary Studies (IBEST), a Level III Institute at the University of Idaho, facilitates research in evolutionary science, inclusive of all scholarly disciplines. IBEST faculty, staff, and students conduct basic research in evolution, as well as evolutionary modeling and applied evolutionary research in biomedical, agricultural, computational and conservation sciences. IBEST provides an interdisciplinary, collegial and inclusive environment defined by a shared commitment to understanding evolution.

The process of evolution, descent with modification leading to diversification, is the unifying principle of life sciences - but it is also much more. Understanding evolution is essential to improving human well-being because evolutionary processes drive critical health challenges such as emerging infectious diseases, antimicrobial resistance, and even the origin and treatment of diseases such as cancer, mental illness, and obesity. Evolution also underlies agricultural challenges such as the emergence of pesticide resistance, the effects of invasive species, and improving the effectiveness of domestication. Furthermore, understanding evolution helps protect our natural heritage by informing conservation policy, and providing insight into adaptation to climate change and how and why organisms respond to changing environments. Less obviously, computers can use evolution to solve complicated problems and to design both software and hardware and evolution has even proven important to understanding the diversity of languages and cultures.

B. GOALS

IBEST activities are focused around our major goals:

1. Broaden and accelerate interdisciplinary research in evolutionary science.
2. Establish strategic partnerships with research groups across the state, nation and world.
3. Maintain and enhance research infrastructure.
4. Promote education and research training at all career stages.

C. CHARTER & FIVE-YEAR REVIEW

IBEST was established as an official Institute in August of 2011, with a 5-year charter. We have recently submitted a 5-year review, accompanied by an application for renewal of our

charter for an additional 5 years. The review document is available from the IBEST website: http://www.ibest.uidaho.edu/media/42262/IBEST-Five-Year-Reviewcompressed.pdf; it details our success over the initial charter tenure.

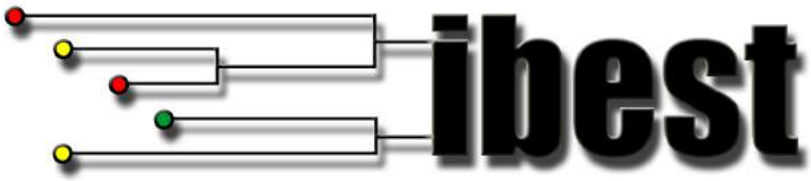
Some salient points from that document are as follows:

- Since 2011, IBEST has invested nearly $785,000 in recruitment and start-up (and, in one case, retention) for seven UI faculty.
- IBEST has invested $4,481,614 in faculty development grants through BEACON, Pilot Grants and Technology Access Grants.
- IBEST faculty have published 283 peer-reviewed papers (2012-2015).
- IBEST faculty (14) have requested $49,122,424 in external grant funding through the Institute and have been awarded $11,899,610 in external funds. This is an astonishing ratio of awarded to requested funding (nearly one out of four).

In addition, we have created and maintained core facilities that specialize in high-performance computing and genome research and by supporting a vibrant interdisciplinary graduate program in Bioinformatics and Computational Biology.

Our efforts to accelerate the productivity and impact of interdisciplinary research in evolutionary science align precisely with the UI Strategic Plan, and our goal of expanding the quantity and impact of research conducted at UI to that characteristic of of Carnegie Highest Research Activity (R1) institutions.

University of Idaho
A LEGACY OF LEADING



IV. FINANCIAL OVERVIEW

A. REVENUE SOURCES

IBEST receives operating revenue from four main sources. First, two programmatic grants support IBEST administrative activities as direct-cost: Phase III of the NIH COBRE (Forney, PI); and the NSF BEACON Science and Technology Center grant to Michigan State University (Foster is the UI lead). Second, many salary lines receive support from the Office of Research and Economic Development ($234,090; ORED). Third, 50% of the F&A on grants submitted through IBEST ($340,460) is returned to IBEST to accelerate research in evolutionary science. Fourth, revenue is generated by services provided by our three core facilities; these are funneled back into the budgets of the individual cores with the goal of improving financial sustainability.

B. SALARY EXPENDITURE OF ORED INVESTMENT AND COBRE DIRECT COST

Revenues provided by ORED are used primarily to pay large portions of the salaries of IBEST administrative and core facility staff, as well as to support the Bioinformatics and Computational Biology (BCB) graduate program. In addition, several administrative and scientific staff positions receive salary support from direct costs in the COBRE. The positions these support and the portions of each salary derived from these sources are listed in Table 1.

C. EXPENDITURE OF F&A REVENUES

The majority of F&A received by IBEST is earned from the Phase III COBRE grant that will end in a little over a year; this revenue will need to be replaced and we are 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 was detailed in our application for renewal and will also be followed by the UofI Center for Modeling Complex Processes (CMCI), a new strategic partner

The F&A generated by IBEST grants is used to reinvest in personnel and activities that promote research in evolutionary science (detailed below). In FY2016, IBEST largely continued investing returned F&A into personnel and programs. Hires conducted in previous years had FY2016 IBEST funds committed to start-up packages ($50,000 to Christine Parent) to recruit and foster new faculty and foster their success. In addition, F&A distributions totaling $39,112 were returned to IBEST investigators and $20,000 was returned to the Department of Biological Sciences. Other expenditures of F&A included a BCB fellowship ($26,272), IBEST operating expenses ($50,314), the annual EAC meeting ($9718), and a one-time contribution to the INBRE Conference ($11,158). Thus, a total of $220,925 in F&A was expended, leaving $119,535 to be

carried forward. These carry-forward funds are critical to our transition to the post-COBRE funding environment.

Table 1. IBEST Staff FY16 Labor Distribution*

Staff		Funding source	%
Sullivan	ABX003	Biological Sciences	80.3%
	KGK080	NSF Predicting Cryptic Diversity	2.3%
	KGX001	IBEST Support "Student Tuition and Fees"	17.4%
Foster	ABK918	BEACON Admin	9.0%
	ABX003	Biological Sciences	62.6%
	IAK301	NIH INBRE 3 Yr 2 Prog Foster	20.5%
	KGK599	WSU NSF Inspire Milk Project	2.7%
	KGK930	NIH COBRE III Admin Yr 4	5.2%
Robison	ABK824	NSF UBM UI--WSU Math Bio	13.1%
	ABX003	Biological Sciences	58.4%
	ABX515	BioSci Robison Salary Release	5.1%
	KBU012	Research Compliance	3.1%
	KGK931	NIH COBRE III CRC Yr 4	20.3%
Grimes	KGK930	NIH COBRE III Admin Yr 4	25.0%
	KBU302	ORED Research Support	14.4%
	KGX001	IBEST Support "Student Tuition and Fees"	60.6%
Abendroth	KAX003	BCB	29.8%
	KBU302	ORED Research Support	5.0%
	KGK930	NIH COBRE III Admin Yr 4	24.8%
	KGX001	IBEST Support "Student Tuition and Fees"	40.4%
Beckman	KGK930	NIH COBRE III Admin Yr 4	50.0%
	KGX001	IBEST Support "Student Tuition and Fees"	50.0%
Oswald	ABX003	Biological Sciences	62.4%
	KGK931	NIH COBRE III CRC Yr 4	10.0%
	KGX001	IBEST Support "Student Tuition and Fees"	27.6%
Hunter	KGX001	IBEST Support "Finance & Admin revenues"	72.7%
	ABK824	UBM course development	9.6%
	ABY095	IBEST GRC Off Campus	9.6%
	KGK932	NIH COBRE III GRC Yr 4	8.1%
Gerritsen	KGK932	NIH COBRE III GRC Yr 4	35.0%
	ABY091	IBEST Sequencing Center	65.0%
New	ABY091	IBEST Sequencing Center	25.0%
	KGK932	NIH COBRE III GRC Yr 4	35.0%
	KGX001	IBEST Support "Student Tuition and Fees"	40.0%
Norton	KBX022	ORED Research Support	20.0%
	KBY100	Optical Imaging Center	14.8%
	KGX001	IBEST Support "Student Tuition and Fees"	65.2%

* Gray shading alternates between staff members and is intended to group all sources of each staff member's salary.

V. FACILITATE RESEARCH IN EVOLUTION

A. STRATEGIC REINVESTMENTS

During FY2016, $381,876 was reinvested into IBEST-related research. This included (a) investment into faculty start-up, (b) investment directly into research through pilot grants and technology access grants (TAGs), and (c) student support, workshops and seminars (see Appendix 1 for details). This continued our history of reinvestment into evolutionary science (shown in Figure 1).

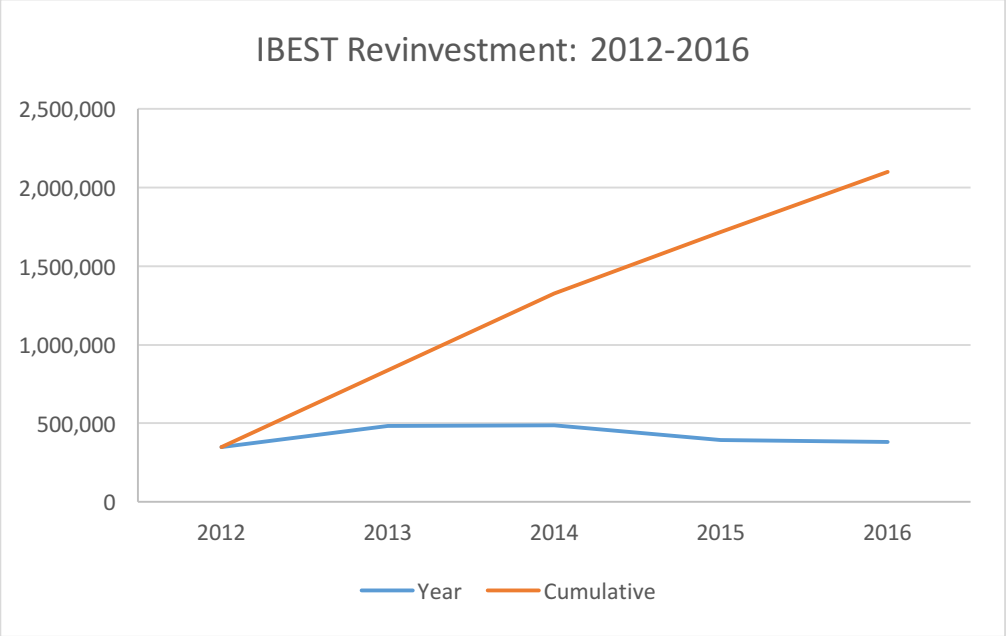


Figure 1. Reinvestment of IBEST resources into accelerating evolutionary science.

1. Faculty Start Up

In FY 2016, IBEST completed our contribution to the start-up package of Dr. Christine Parent, an Assistant Professor in the Department of Biological Sciences. This concludes our commitment of contributing $165,000 to Dr. Parent's start up package over three years. Among Dr. Parent's research interests is the study of speciation on island systems, including Galapagos snails, and our contributions have been provided entirely out of returned overhead. This constitutes a major investment in evolutionary science at UofI, and in fact, over the past 5 years, IBEST has contributed $784,564 to start-up (and in one case, retention) packages for 6 new faculty in three departments (see Appendix 2).

Figure 2. A major focus of Dr. Christine Parent's research is diversity and speciation in Galapagos snails, including *Naesiotus darwini* from Santiago Island.

2. IBEST Grants

In addition to providing the stimulating intellectual environment, IBEST has provided a large number of direct grants to faculty to serve as seed grants. Funds for these have come from two sources; the Technology Access and Pilot Grants are funded by the COBRE grant and the BEACON STC (see below) provides another source of seed grant funding.

a. Pilot Grants – The objective of the IBEST Research Pilot Project Program is to increase the number and success rate of grant applications submitted to NIH and other federal and private funding agencies. Our scientific focus for pilot grants is on biomedically relevant research in the fields of computational and evolutionary biology. Pilot grants enable UI faculty to generate preliminary data that will make them more competitive for external funding. 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.

In FY 2016, we provided $143,089 in direct costs to two Pilot Grants. Dr. Jill Johnson received $75,000 in direct costs for the second year of her project *"Directed Evolution of the Molecular HSP90 and Its Clients."* In addition, Dr. Paul Hohenlohe and his co-PI Sara Hendricks (a BCB student) received $68,819 in direct costs for the first year of his project *"A Novel System for the Genetics of Inflammation and Cancer."* Progress reports on one of these projects are included below.

Pilot Grant - A Novel System for the Genetics of Inflammation and Cancer

Dr. Paul Hohenlohe and BCB Student Sarah Hendricks - 2015-2016 Pilot Grant

While a wide range of genetic and environmental factors may lead to cancer, chronic inflammation plays a critical role in tumor initiation, promotion, and progression. Understanding genetic variation that links inflammation and cancer could provide new insight into this complex interaction. In this study, we are making use of a remarkable natural system for addressing this issue. Channel Island foxes (*Urocyon littoralis*) live in several isolated populations off the coast of California. Most populations are affected by ear mites, and in several populations these parasites cause chronic inflammation of the ear canal. In just one population (Santa Catalina Island; SCA), however, this chronic inflammation is associated with a high incidence of carcinoma or adenoma of the ceruminous gland. With over 50% of untreated adults affected, this is one of the highest incidences of cancer known in any species. We are testing the hypothesis that this high incidence of cancer in SCA foxes is the result of genetic differences among populations caused by recent population bottlenecks, and that identifying the genetic basis of this difference in SCA foxes will provide novel insights into the inflammation-cancer link.

To date we have begun testing for genomic associations with cancer using existing RADseq data previously generated in the Hohenlohe lab (Funk et al. 2016), focusing on 14 case and control individuals. Pairwise F_{ST} values comparing 14 case and control individuals suggest that there are several highly differentiated SNPs, which may be linked to causal polymorphisms. The most differentiated SNP is located within the intronic region of C10orf90, a fragile-site associated tumor suppressor homolog. We have designed primers and are conducting targeted sequencing of this region in a much larger sample of individuals. Second, we have generated whole-genome sequence data for 28 case and 10 control individuals, taking a two-tiered approach to get high sequencing coverage (10-15x) for a set of case and control individuals, and lower coverage (2-6x) for additional case individuals. We are currently analyzing these data to identify genetic polymorphisms (single-nucleotide as well as insertion/deletion and copy number variants) associated with cancer. We will use the dog reference genome, which was successfully used in alignment of the RADseq data above, to identify annotated candidate genes linked to cancer susceptibility.

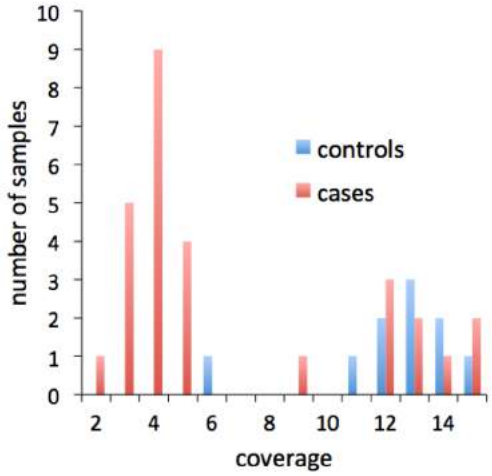


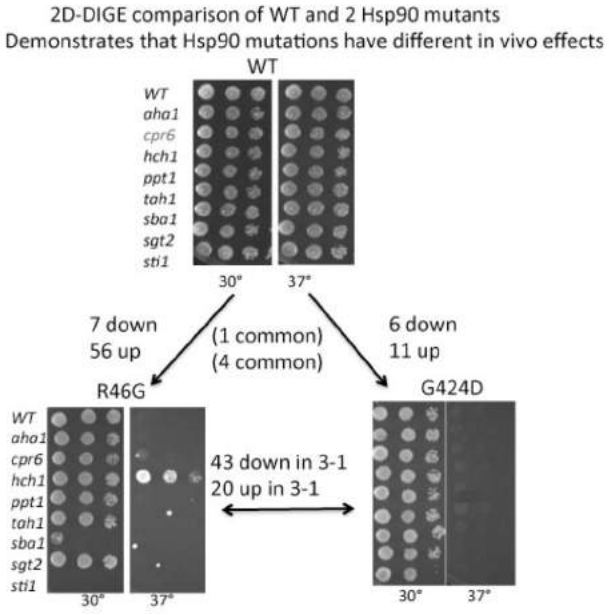
Figure: Sequencing coverage for 38 samples subject to whole-genome shotgun sequencing.

Directed Evolution of the Hsp90 Molecular Chaperone

Dr. Jill L. Johnson - 2014-2015 IBEST Pilot Grant.

The essential Hsp90 molecular chaperone is a global cellular regulator of protein folding, transport and assembly of multiprotein complexes. Hsp90 inhibitors that target the ATP-binding pocket affect hundreds of proteins and broad inhibition of Hsp90 is toxic to healthy cells. Genome wide studies in yeast and human cells treated with Hsp90 inhibitors identified changes in mRNA and/or protein levels. Clients become unstable and are targeted for degradation. Moreover, disruption of Hsp90 interaction with transcription factors and MAP kinases affects mRNA levels of downstream targets.

Our goal was to identify Hsp90 mutations that affect different functions of Hsp90. We identified a novel set of Hsp90 mutations that cause similar growth defects when expressed in cells lacking wild-type Hsp90. The mutations are located throughout all three domains of Hsp90, and affect surface exposed residues, suggesting they alter interaction with nucleotide, clients and/or cochaperones. We then used 2D-DIGE to identify proteomic differences between yeast strains. We identified about 25 specific proteins that exhibited altered accumulation in cells expressing different Hsp90 mutations. This includes stress-responsive genes, ribosomal proteins, metabolic enzymes and likely clients. These studies provide preliminary results for an R21 proposal to design new reagents and assays that will allow us to rapidly assess the effect of these and additional Hsp90 mutations and/or small molecules on target proteins. We will also pursue mechanistic studies to determine the basis for selective effects. For example, the R46G mutation induces a strong stress response, while other mutations do not, and the G424D mutation affects primarily ribosomal functions. Together these studies will help identify Hsp90 functions that promote client selection, providing a clearer understanding of how Hsp90 regulates diverse cellular functions.



The call for proposals for the 2016 IBEST Research Pilot Project was advertised campus wide (Appendix 4), and four proposals were received. Two reviewers were selected for each proposal, one of whom 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 Steering Committee read the reviews and met to discuss the scores. The proposal with the lowest (best) score was "*Determining the natural reservoirs of antibiotic resistance genes.*" From Dr. Eva Top in the Department of Biological Sciences (see description on following page). Dr. Top'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 September 2016 Dr. Top was awarded the IBEST Pilot Research Grant for year one, which can be renewed for a second year if progress is satisfactory. The summary from that proposal is highlighted on the next page.

A yellow-pine chipmunk (*Tamias amoenus canicaudus*) that carries heterospecific mtDNA that has introgressed from red-tailed chipmunks *(T. ruficaudus*). IBESTians are studying divergence-with-gene-flow in this group.

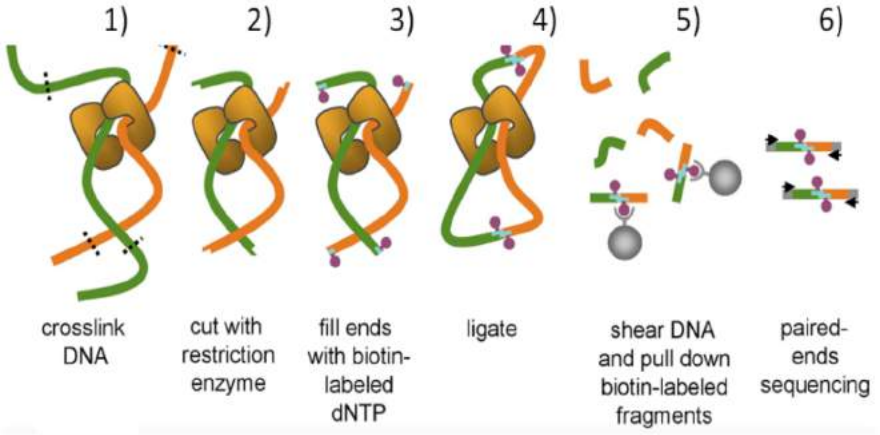
Determining the Natural Reservoirs of Antibiotic Resistance Genes

Dr. Eva Top – Summary of IBEST Pilot Grant Awarded in 2016

The evolution of multidrug resistant bacteria has become a serious global human health threat that requires immediate action. The alarming rate at which bacteria adapt to antimicrobial compounds is partly due to their ability to acquire antibiotic resistance genes (ARG) through horizontal transfer of mobile genetic elements (MGE) such as plasmids. A great example is the recent, unsettling news of plasmid-encoded colistin resistance genes found in pathogenic *E. coli*. Equally disturbing is that one plasmid can often serve as a vector for multiple ARG, allowing bacteria to acquire multidrug resistance through a single genetic transfer event. In spite of this major health care crisis, we still do not really understand the origins of these ARG in today's deadly pathogens and their trajectories from environment to clinic. To design efficient strategies that can contain ARG dissemination we need to understand the reservoirs of ARG and the pathways through which they spread from the environment to human pathogens.

It has become clear that the environment is an abundant source of ARG that are potentially transferable to pathogens, and that anthropogenic activities likely foster this reservoir. This has resulted in a spike of recent research aimed at detecting ARG and their MGE beyond clinical settings. Metagenomic studies have identified and characterized ARG in a diverse range of habitats such as soil, rivers, human/animal guts, etc. Similarly, numerous antibiotic resistance plasmids have been detected and isolated from such. However, there is typically limited information linking the ARG and their plasmids to the bacterial hosts in a cultivation-independent manner.

To fill this knowledge gap, we propose to adopt an innovative approach using chromosomal conformation capture, or Hi-C. By analyzing nucleotide sequences that are in close physical proximity within a cell and therefore likely to cross-link before cell lysis, Hi-C has been recently shown capable of reconstructing species' genomes from rather simple mixed bacterial cultures, and correctly linking plasmids to their bacterial host. By applying this Hi-C method to environmental samples like manure, activated sludge, and soil our long-term goal is to determine the reservoirs of ARG of greatest concern and their likelihood of spreading by MGE. To achieve this, we first need to determine the potential and limits of the method when applied to real ecosystems. Therefore, the central hypothesis of this pilot project is that the Hi-C method will allow the identification of hosts and plasmids that carry ARG in natural bacterial communities.



Hi-C protocol: (1) Crosslink DNA with formaldehyde; (2) lyse cells and cut DNA with restriction enzyme; (3) fill and label ends; (4) ligate blunt ends; (5) purify, shear DNA and isolate biotin labeled fragments; (6) sequence. (From Le *et al.* 2013. Science 342, 731–734).

b. Technology Access Grants - As in years past, IBEST administers and funds 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 evolution are accepted at any time 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. Thus far in 2016 a single Technology Access Grant totaling $1,675 has been awarded to Nathan Schiele (Department of Biological Engineering) and Craig McGowan (Department of Biological Sciences); see Appendix 3 for a progress report.

3. External Grants

Research grant proposals that address evolutionary science may be submitted through IBEST by UofI faculty from any unit. In such cases, 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 to 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 FY2016, 17 grant applications requesting $7.2 million in extramural funds were submitted (Appendix 5) and a total of $2.5 million were awarded (Appendix 6). In addition, in FY2016 $500,422 in new funds (direct cost) were awarded from BEACON grants. The most recent round of BEACON applications (FY 2017) resulted in $348,297 in new awards.

Elucidating Causes of Vaginal Symptoms Using a Multi-omics Approach
Dr. Larry Forney - an NIH Grant submitted through IBEST

Vaginal discharge, discomfort, and malodor are pervasive symptoms among reproductive-age women that negatively impact their self-esteem and quality of life, cause extreme anxiety, and disrupt social and sexual functioning. Despite the severity of the problem, many women do not seek medical attention because of the costs of taking time off from work or concerns that they will be judged as being sexually promiscuous. This leads them to resort to self-help strategies such as douches, medicated wipes, anti-itch creams, powders and manual vaginal washes that can exacerbate the underlying problem by altering the vaginal microbiota. That is a significant health risk because it predisposes the women to developing bacterial vaginosis and is also associated with other serious gynecologic outcomes, including increased risk of cervical cancer, pelvic inflammatory disease, endometritis, as well as increased risk for sexually transmitted infections, including HIV. There is a clear need to better predict and understand the underlying causes of vaginal symptoms so that targeted and effective strategies can be developed to prevent or treat vaginal discharge, discomfort, and malodor.

Dr. Larry Forney and colleagues were recently awarded an NIH grant to define changes in the composition, structure and function of vaginal bacterial communities and host responses that elicit symptoms. This will increase our knowledge of factors that contribute to healthy vaginal microbiomes. The team will leverage a unique set of samples and metadata that were prospectively collected daily by 135 women for 10 weeks as part of the Human Microbiome Project (HMP) between 2009-2010. From this repository, it will be possible to discern three categories of women: 1) those with clear episodes of vaginal symptoms, 2) those with chronic and persistent symptoms and 3) those who are asymptomatic. The study design affords a unique opportunity to use 'omics technologies to understand features of the vaginal microbiome and host gene expression that occur before, during and after episodes of vaginal symptoms and compare these to women with chronic symptoms and to those who were asymptomatic.

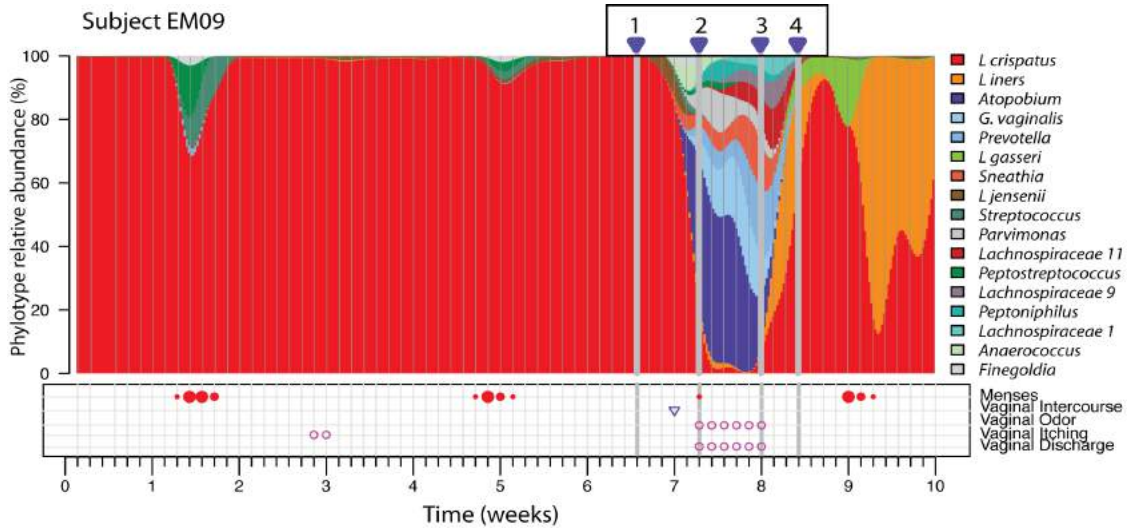


Figure. Interpolated bar plot of phylotype relative abundances observed daily over 10 weeks in subject EM09. Color key for each phylotype represented is shown on the right. Selected metadata are shown below the graph. The metagenomes and metatranscripomes of samples labeled 1, 2, 3, and 4 have been sequenced.

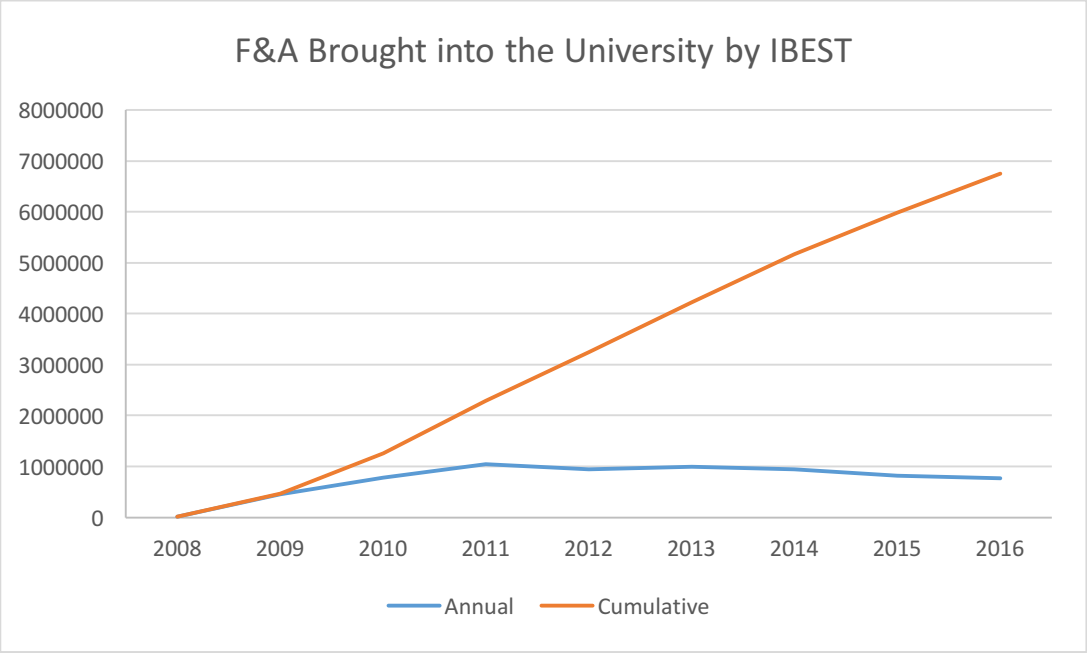


Figure 3. IBEST grants have generated substantial F&A revenue to UofI over the last several years.

B. DISSEMINATION OF INFORMATION

1. IBEST/BCB Seminar Series

The IBEST/BCB Seminar Series once again attracted 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, helped us recruit students, and attracted new customers to our core facilities. See Appendix 7 for a listing of seminar speakers and topics in 2016.

These seminars (about four per semester) have been 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 scientist invited typically spends 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 (BCB) program choose and invite speakers for the seminar series and organize their itinerary. Beginning in FY 2017, we are merging our seminar series with that of CMCI as part of efforts to ensure that IBEST and CMCI are synergistic rather than competitive.

Figure 4. Dr. Tracy Heath (Iowa State University) presenting a BCB seminar. During her visit, Dr. Heath also taught a workshop to BCB students on use of her software RevBAYES for integrating fossil and genomic data in evolutionary analyses.

2. IBEST Lunch

The IBEST Lunch Series is the hidden key to our success. Each week at the same time and same place IBESTians – which include all individuals affiliated with IBEST including faculty, students, postdoctoral fellows and technicians – meet one hour for lunch. This occurs every week, all year long. These lunch meetings come in four basic flavors: (a) Thunder Thursdays, where three IBEST investigators present an informal "lightning 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.

3. Inland Northwest Genomics Research Symposium

The fourth annual Inland Northwest Genomics Research Symposium (INWGRS) was held in May 2016. As in the past, the symposium was a one-day event, used a lecture format and included presentations by IBEST core facility directors, vendors, regional and national researchers. Broadly, the Symposium provides the University of Idaho research community an opportunity to learn more about IBEST's GRC, CRC, and OIC 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 keynote speaker this year was Dr. Megan Dennis, of UC-Davis. Her research focuses on identifying genomic regions associated with complex phenotypes, especially disease phenotypes. we focused on agricultural application of genomics. Other speakers were invited to focus attention on agricultural genomics, and we specifically coalesced a wireworm genomics working group using the Symposium as a gathering point. This has led to grant funding from the Idaho Wheat Commission to assess geographic variation in genomic regions associated with pesticide resistance (Dr. Alida Gerritsen will give an oral presentation on this project this during the EAC meeting). The symposium had 143 attendees. Of those 76 were from the University of Idaho, 46 from Washington State University, with the remainder coming from further away (See Appendix 8 for details on the INWGRS).

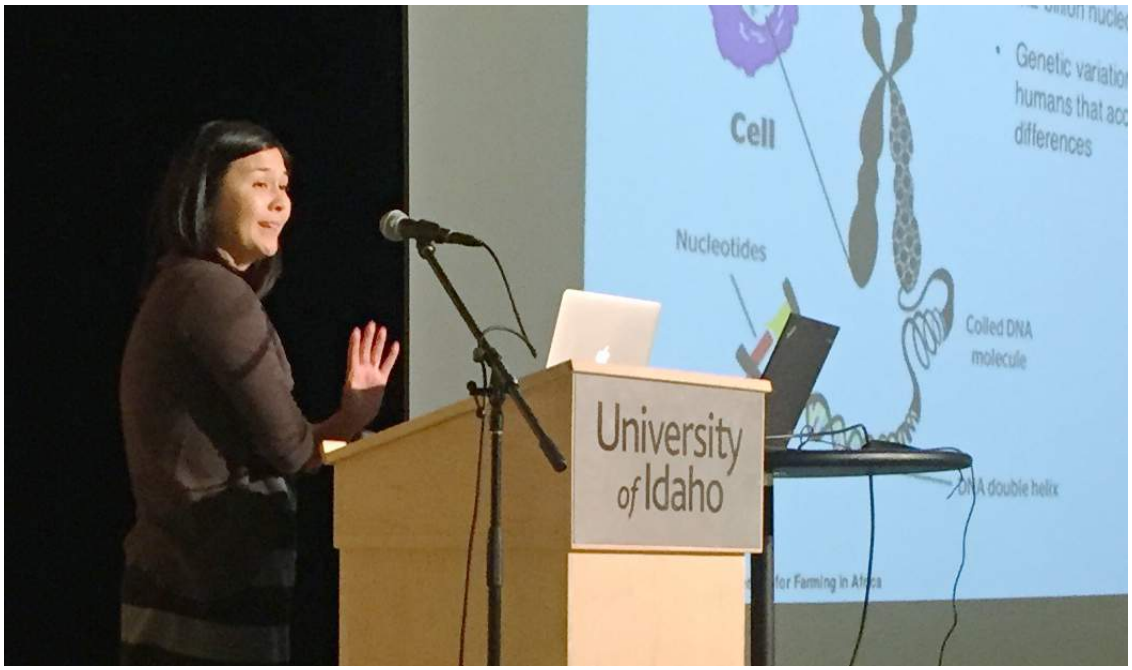


Figure 5. Dr. Megan Dennis (UC-Davis) giving her keynote address at the 2016 Inland Northwest Genomic Research Symposium.

4. Publications

Publications are the primary means of dissemination of science and are therefore the currency for judging research output. IBEST faculty have been enormously productive in this key metric. The list of IBEST publications from 2015 (60 publications) and 2016 (70 publications to date, including 4 book chapters) are presented in Appendix 9. Indeed, over the past five years (2012-2015), IBEST faculty have published 283 peer-reviewed journal articles and these have appeared in a large diversity of high-impact journals. Indeed, the area of "Ecology, Evolution, Behavior and Systematics" has been uniquely identified as nationally prominent in a study of UofI research competencies from Elsevier commissioned as part of the Strategic Plan. Furthermore, Elsevier recognized the central role that IBEST has played in accelerating this impressive publication record. This recognition by an independent third party reiterates past evaluations from our External Advisory Committee (EAC) that have emphasized our national prominence in these areas.

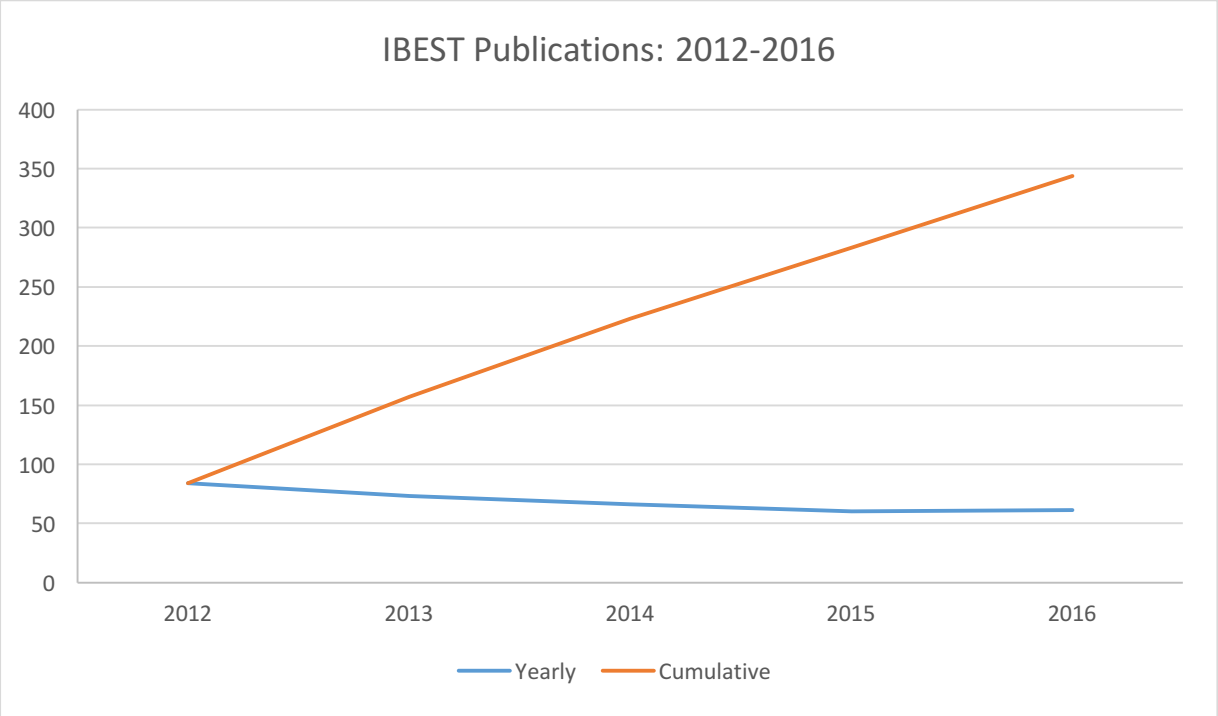


Figure 6. Publications by IBEST faulty that cite IBEST support. The 2016 figure (62 publications) only includes those published or in press as of 09/18/16.

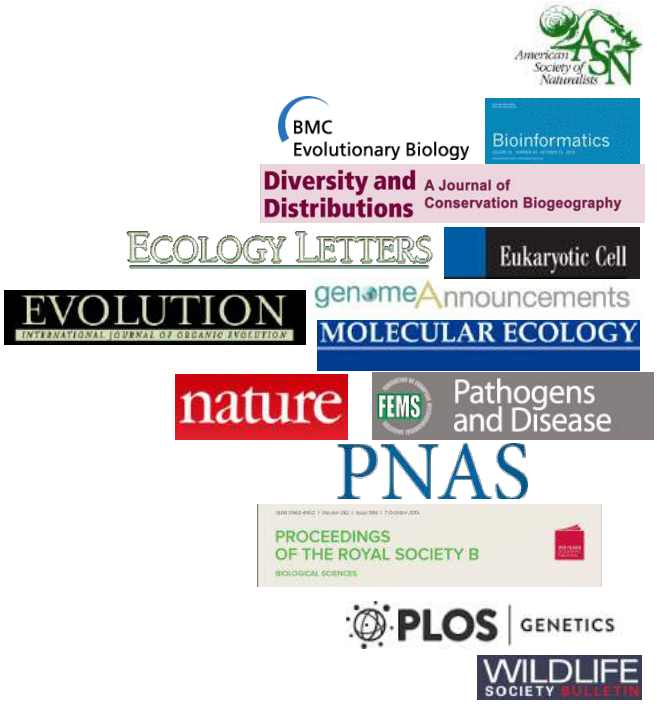


Figure 7. A sample of the journals in which IBEST faculty have published.

C. INNOVATION - Polymorphic Games – An extension of the IBEST interdisciplinary culture.

In 2016, Professors Terry Soule (Computer Science) and Barrie Robison (Biology) were awarded two grants to establish Polymorphic Games – a video game design studio for University of Idaho undergraduate and graduate students. Video game design is an inherently interdisciplinary activity, requiring close collaboration between programmers, designers, artists, musicians, and entrepreneurs. Polymorphic Games adds a unique component to this collaboration by incorporating the principles of evolutionary biology into video games. To create an innovative video game based on evolutionary biology requires the addition of collaborators in the biological and mathematical sciences, and educators to help develop learning based achievements appropriate to developmental levels of students. This unique combination of students and faculty working across disciplines to advance the ways we facilitate learning does not exist in any game studio or academic unit of which we are aware. Fortunately, fostering this culture of interdisciplinarity is one of the core values of IBEST.

Polymorphic Games embraces the inherent interdisciplinarity of video game design. Creating an evolutionary game requires more than just students familiar with programming. It requires students from across the sciences and humanities to write the story elements, design the look of the game, score and play the soundtrack, ascertain the knowledge level appropriate for specific games, and create a marketing plan for the distribution of the game. In this process, students learn how to collaborate across disciplines contributing their particular expertise to the project. They discover that other disciplines often speak a different "language," and that these kinds of collaborations take time and perseverance to cultivate. They also discover that interdisciplinary collaborations produce unique ***emergent properties*** that could not be achieved with a less diverse team. In the two years we have been developing this idea, we have witnessed: ***Undergraduates from music and biology discuss whether music can evolve; entrepreneurs and artists grappling with the complexities of marketing art; and programmers struggling to describe their algorithms to writers and educators.*** These experiences are invaluable for undergraduates and graduate students seeking jobs in a world where knowledge of how to navigate interdisciplinary interactions is assumed.

Evolutionary Video Games

Polymorphic Games uses the principles of biological evolution to develop better video games. Traditional video games are usually scripted, featuring "*waves*" of enemies that have defined and predictable characteristics. A player's success in such games is based on learning the predictable, rote script necessary to advance to subsequent levels. By integrating principles of evolutionary biology, video games can be made more compelling. For example, our games feature *generations* of enemies that undergo adaptation through natural selection. The enemies with the traits that best counter the player's strategies survive to reproduce, and their offspring feature prominently in the next generation (analogous to a game level or wave). We essentially *create an evolutionary arms race* between the player and the enemy population. The success of the player is based on her comprehension and application of principles of evolutionary biology. The parallels to real world examples are numerous, and include the rapid evolution of antibiotic resistance in microbial pathogens, adaptation of crop pests to chemical and biological control

measures, and behavioral adaptation to captivity in domesticated animals. Adding biological evolution to video games makes the games better for the game player and facilitates player comprehension of complex concepts that are hard to teach.

In its inaugural summer (May to August 2016), Polymorphic Games hired 12 students from across campus to develop an evolutionary space shooter. "Darwin's Demons" is now in the advanced beta testing stage. It has been approved ("Greenlit") to be sold on STEAM, an online gaming platform with hundreds of millions of users across the globe. The full soundtrack for Darwin's Demons is now available on iTunes and Spotify. We have presented the science underlying the game at international conferences, and have been invited to Steam Developer Days in October of this year.

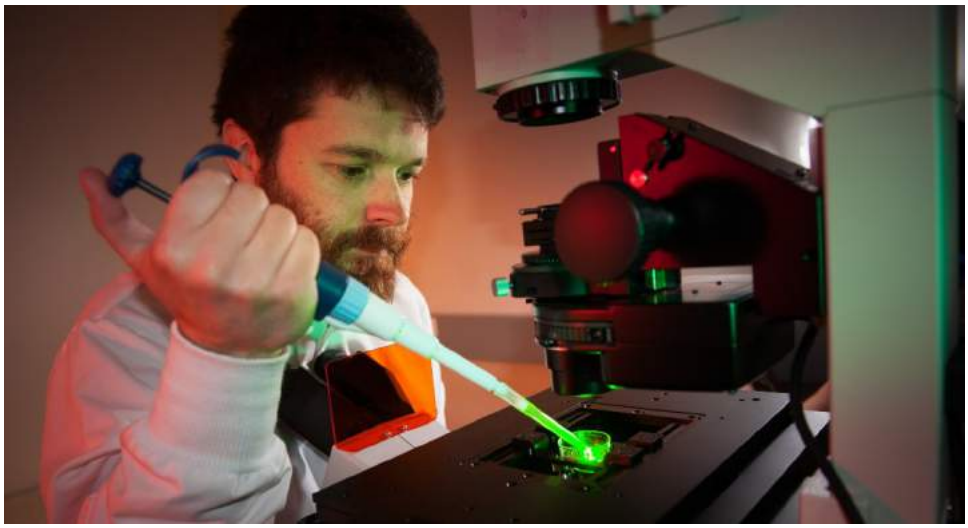
The Polymorphic Games development team now includes 26 undergraduates from Biology (3), Computer Science (4), Virtual Technology and Design (4), Business and Economics (4), Theater and Performing Arts (7), English (1), Journalism and Mass Media (1), and Music (2). We are also actively recruiting students from Education, Foreign Language, and Law. To learn more about Polymorphic Games, you can visit our website at www.polymorphicgames.com.


POLYMORPHIC
GAMES
DARWINS DEMONS
Download the Demo!
www.polymorphicgames.com
In this arcade style space shooter, defend against an encroaching horde of evolving enemies. At the end of each wave, only the fittest enemies reproduce to create the next generation, causing the population to adapt to your play style.
How long will you survive against the evolving swarm?
Polymorphic Games is a University of Idaho Game Design Studio
Vote for us on Steam Greenlight!
http://www.polymorphicgames.com/greenlight.html

Report on Results from IBEST Bridge Funding for Stenkamp Research Program.

The Stenkamp research program is focused upon the development, regeneration, and evolution of the vertebrate visual system, using zebrafish and stickleback as model organisms. In 2014, IBEST provided our research program with bridging funds, as our longstanding (14 years) NIH R01 award, "Patterning Genes in Retinal Development," was nearing the end of a no-cost extension. At the time, we also awaited the outcomes of several pending proposals and generated several additional grant applications. This bridging support was essential for maintaining key personnel and continuity of the research program, for paying publication costs associated with new papers from the lab, and for generating preliminary data for more proposals.

The IBEST investment was essential to the successful outcomes of these proposal efforts. We have since been awarded the following external grants. 1) In fall 2015, the National Eye Institute (NEI) awarded our research program with $250,000 (direct) in bridging funds for "Patterning Genes in Retinal Development," in recognition of its centrality to the recently-announced Audacious Goals Initiative: "to regenerate retinal neurons and their connections in the visual system." 2) In spring 2016, we were awarded a new R21 ($275,000 direct, two years), "Synapses in Regenerated Retina," again directly supporting the Audacious Goals Initiative. 3) In fall 2016, we were awarded another new R21, "Ocular Vasculature and Retinal Neurogenesis." 4) Also in fall 2016, we were successful in obtaining an NSF Dimensions of Biodiversity award, collaboratively with investigators who are involved in the BEACON consortium. This NSF award provides approximately $2,000,000 to the multi-institution team and $400,000 to the Stenkamp research program. This new project pursues the evolutionary correlates of the colonization of visually challenging environments, tested in populations of threespine sticklebacks collected from glacially-fed and highly turbid lakes, vs. spring-fed and clear lakes of Iceland.



VI. STRATEGIC PARTNERSHIPS AND COLLABORATIONS

A. BEACON, AN NSF SCIENCE AND TECHNOLOGY CENTER

The BEACON Center for the Study of Evolution in Action is an NSF Science and Technology Center founded in 2010 with the mission of illuminating and harnessing the power of evolution in action to advance science and technology and benefit society. 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 includes 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. To date, IBEST has received over $3.3 million in competitive funding from BEACON. These funds have supported 48 projects, 18 faculty members from across campus, over two dozen graduate students and postdocs, and may undergraduate students. These projects are interdisciplinary, and many are cross-institutional. In the last year alone, IBEST faculty and postdocs had 10 new projects funded, at over $500,000 (listed in Appendix 8). In addition, we received an NSF supplement to fund this year's IBEST Business for Scientists course.

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. Several IBEST faculty contributed large portions of text for the original BEACON STC proposal and for the recent application for renewal.

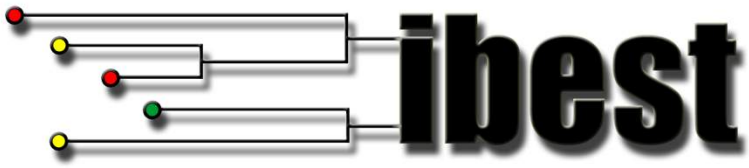
B. CENTER FOR MODELING COMPLEX INTERACTIONS

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. Furthermore, we have put protocols in place so that PIs can submit grants with shared credit (and F&A) between CMCI and IBEST when appropriate. CMCI and IBEST have partnered to jointly fund additional bioinformatics expertise in the form of IBEST GRC intern. This person was selected from among several BCB students who applied. In response to feedback from faculty, students and postdocs, CMCI and IBEST have merged our seminars. This will provide greater opportunity for cross fertilization. Finally, the IBEST Computational Core houses and maintains CMCI's high-end graphical processing node for molecular dynamic modeling.

C. IDAHO WHEAT COMMISSION

The Idaho Wheat Commission (IWC) was established in 1959 by the Idaho Grain Growers Association to help maximize profitability for Idaho wheat producers by investing funds in market development, research, and information and education. The Commission recognizes that investing in new approaches to problem solving and into innovative ideas will help Idaho wheat growers adjust to changing situations. In recognition of this, IBEST, in collaboration with Dr. Arash Rashed (University of Idaho Aberdeen extension researcher) has been awarded a grant from the IWC. This will enable the IBEST GRC to take the lead in studying the genomics of an emerging agricultural pest. Collaborations developed during this project are expected to lead to multiple new clients, opportunities for collaborative grant submission, and continued collaboration with the Idaho Wheat Commission. This collaboration grew out an IBEST TAG that funded sequencing the wireworm genome to provide the genomic resources that will enable this research.



VII. CORE FACILITIES

A. COBRE PHASE III

The Center of Biomedical Research Excellence (COBRE) for Research on Processes in Evolution at the University of Idaho has received over $22M in funding over 12 years from the NIH IDeA program. This funding has been critical to the growth and success of IBEST and we have used COBRE funds to establish and expand 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 4 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.

B. IBEST GENOMICS RESOURCES CORE (GRC)

1. 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.

2. Summary of Accomplishments

- Provided custom molecular and bioinformatic techniques to accommodate the unique needs of each researcher.
- Created a unique, 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.
- Tested new long-read technology including developing skills for generating and analyzing both Oxford Nanopore and PacBio long reads.
- Leveraged the GRC's unique practices and capabilities, resulting in a very large number of

first-time clients from word-of-mouth advertising, and an increasing number of repeat clients.

- Filled two empty positions, returning the GRC to a fully staffed status.
- Established a successful collaboration with the Idaho Wheat Commission resulting in a grant to carry out research on wireworm phylogeography and genomics.

3. Infrastructure

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.

a. 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.

i. 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:

- DNA Sequencing

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

Illumina MiSeq Flow Cell

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

  PacBio Sequencing Service: Third generation sequencing for *de novo* assembly and other experiments requiring long read sequencing are outsourced to collaborating facilities, however PacBio library preparation can be done in the GRC.

  Oxford Nanopore Sequencing Platform: Due to the experimental nature of the Oxford Nanopore platform, the GRC does not offer this type of sequencing for a fee. However, the GRC has developed the expertise to be able to assist clients interested in this technology by preparing libraries, running the sequencer, and providing basic bioinformatics.

- 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 Juno : Creates sequencing libraries of up to 2400 amplicons per 192 sample chip for targeted-resequencing. Highly automated for minimal hands-on time and high throughput.

  Fluidigm Access Array**:** Creates sequencing libraries of up to 480 amplicons 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 3.0: Fluorometric quantification of DNA and RNA (hundreds of samples or single samples depending on device) yielding more accurate and reliable concentrations than NanoDrop.

ii. 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 benefiting 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.

  Qubit 2.0 Fluorometer: Fluorometric quantification of DNA and RNA (hundreds of samples or single samples depending on device) yielding more accurate and reliable concentrations than NanoDrop.

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."

b. Recent Infrastructure Investments.

Fluidigm Juno

The GRC recently acquired the Fluidigm Juno targeted NGS library preparation device. This device will enable the GRC to significantly reduce the cost and hands-on time associated with creating targeted amplicon libraries. At the same time, it will greatly improve throughput, making it possible for the GRC to keep up with customer demand and accept very large scale projects.

c. Planned Infrastructure Investments.

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

Fluidigm Biomark HD: Complimenting the recently acquired Fluidigm Juno, the Biomark would allow the GRC to offer expanded services including gene expression, genotyping and digital PCR.

Oxford Nanopore PromethION or PacBio Sequel: Long read sequencing technologies are poised to significantly change the world of high throughput sequencing. The GRC continues to evaluate these emerging technologies and assess their utility to GRC customers.

Illumina MiSeq Sequencer: Currently the GRC relies on a single MiSeq sequencer to serve most sequencing needs of clients both on and off campus. The MiSeq is a sensitive machine prone to occasional failure. Although the GRC maintains a service contract, repairs and issue resolution can occasionally require weeks to complete. These delays can lead to large queues and slow turnaround times. A second MiSeq would remove this single point of failure and allow the GRC to deliver high quality, reliable service even in the case of sequencer failure.

4. 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 (and in other facilities) 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. This allows a small staff to perform the same quantity and quality of work as core facilities with larger staffs.

a. Genomics Resources Core Director

The current GRC Core Director, Dr. Samuel Hunter, joined the core in January 2016. Dr. Hunter earned a Ph.D. in Bioinformatics and MS in Statistics from the University of Idaho after earning a B.S. degree with a double major in Biology and Computer Science from the College of Idaho. Dr. Hunter worked for the GRC as a Bioinformatics Data Scientist from 2011 to 2014 focusing on Microarray data analysis and high throughput sequencing analysis, especially genome assembly, variant calling, and methods development. In 2014 Dr. Hunter left the GRC to work as a Computational Biologist at Dana-Farber Cancer Institute in Boston, Massachusetts. While there he focused on methods development for clinical cancer sequencing, creating a software tool for CNV detection which was integrated into the Dana-Farber/Brigham and Women's Hospital personalized cancer sequencing pipeline to aid in clinical diagnosis. His current duties with the GRC include management of day to day operations, existing projects and client relations, outreach, identification of new opportunities, technologies, and clients, retaining and recruiting staff, data analysis, and advising students.

b. 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 consulting with clients, R&D (both wet and dry lab), sequence analysis and bioinformatics support for a variety of projects, billing and some administrative duties. Dr. Gerritsen's continued development of bioinformatics skills, wet lab R&D experience, administrative skills, and role as co-PI on a recently funded grant from the Idaho Wheat Commission are consistent with a GRC objective to improve staff retention, redundancy and stability.

c. 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 GRC User Core. Dan earned a 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. Starting in early 2016, Mr. New has worked closely with Dr. Gerritsen to learn basic bioinformatics skills necessary for preliminary analysis and data delivery, Mr. New has also enrolled in an R-programming course with the UofI Statistics Department, consistent with a GRC objective to improve staff retention, redundancy and stability.

d. Genomics Laboratory Scientist

In May 2016 the GRC hired Matthew Fagnan as a temporary employee. Mr. Fagnan completed a B.S. in Bioengineering at WSU in May 2016 and spent the summer working closely with Mr. New and Dr. Gerritsen to gain the necessary skills for working in a high-throughput sequencing laboratory. These skills include training and familiarity with Qubit, TBS-380, Fluidigm 48.48 Access Array, Fluidigm Juno, Fragment Analyzer, aPCR, Wafergen Apollo, Ampur Bead cleaning, Linux, as well as experience with customer service and research and development. Following this successful evaluation/training period, the GRC is now in the final stages of hiring Mr. Fagnan as a permanent employee to fill the Genomics Laboratory Scientist position. As part of an ongoing GRC objective to address recruitment and retention difficulties, as well as to improve redundancy and stability, Mr. Fagnan will continue to work with Mr. New, Dr. Hunter and Dr. Gerritsen to develop more advanced wet lab and bioinformatics skills.

e. 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.

f. Bioinformatics Intern

Christopher Mirabzadeh is a graduate student in Physics who joined the GRC in the Spring of 2016 in order to learn about high throughput sequence analysis and bioinformatics. He has worked on bioinformatics software development and testing during his time with the GRC.

5. 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.

6. 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 8). To track and manage the growing GRC user base, the Core implemented iLab project management and billing system in late FY2014. Over the past two years, the Core has been able to use iLab to accurately track usage data from internal and external users and effectively bill for bioinformatics time.

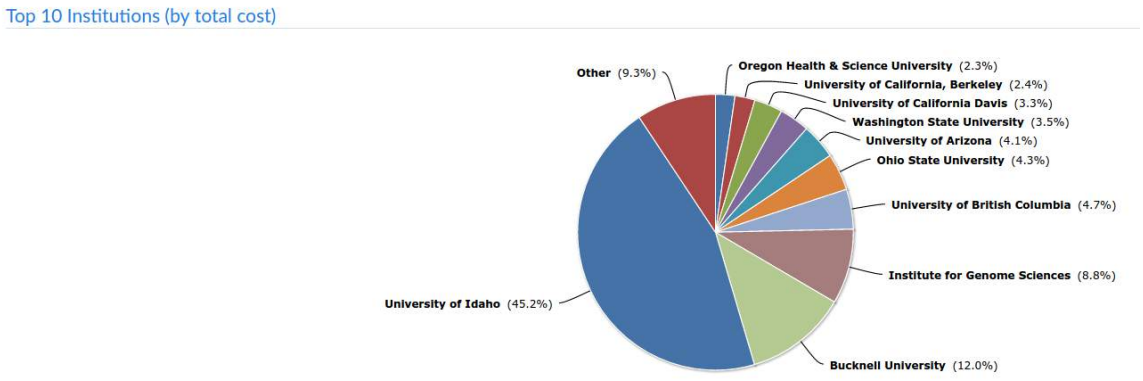


Figure 8. The top 10 institutions (by total expenditures) in billed work from the GRC during FY2015.

7. Project Consultation

Core facility staff consult with investigators to discuss project aims, expectations, experimental design, appropriate and best use of technology, sample quantity and quality issues, and data analysis needs. During consultation, a project time line is formed, expected costs are discussed, deliverables are identified, and a user agreement is reviewed. 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. This service is especially important to researchers developing grant proposals, where a detailed quote and sophisticated understanding of the protocols and analysis are likely to increase chances for funding and ensure accurate budgeting. In 2016, the GRC has provided letters of support and/or consultation for Dr. Eigenbrode (UofI), Dr. Fortunato (UofI), Dr. Rowley (UofI), Dr. Top (UofI) Dr. Raboy (USDA), and Dr. Soltis (UF) among others. 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 sequencing and bioinformatics. This approach helps keep overall costs low, expectations realistic, and potentially costly problems minimal in the latter stages of a project.

8. Genomics Data Generation

The Genomics Resource Core facility operates and maintains equipment (described above) that allows high throughput sample preparation, quality assurance, and generation of 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 GRC has also developed a relationship with the University of Washington PacBio sequencing core in expectation of the need for long-read sequencing in the future. 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 9 and and top ten services by total cost in Figure 10.

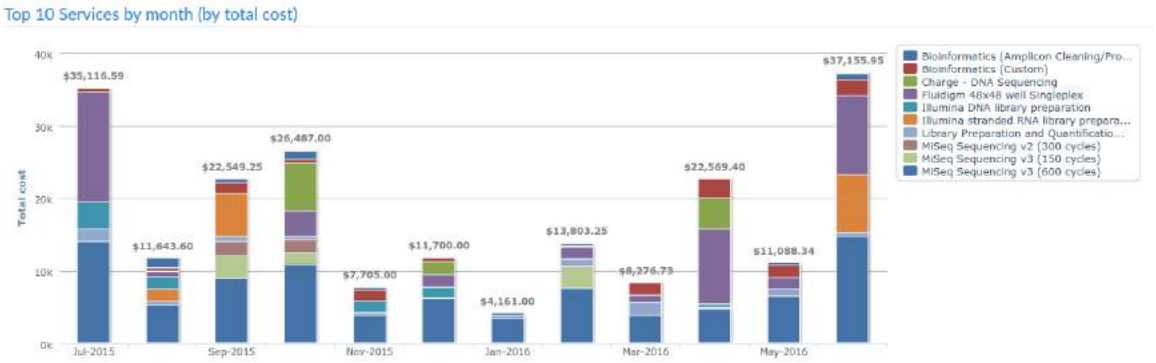


Figure 9. Time series of expenditures by type of service, FY2015.

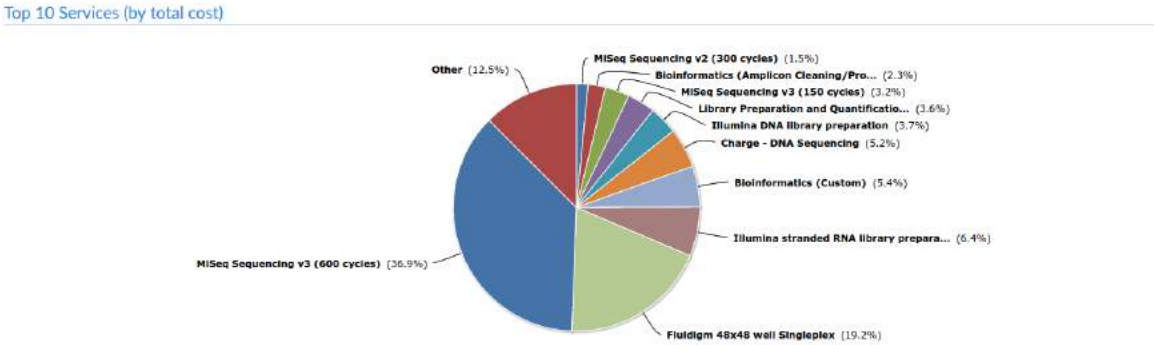


Figure 10. Summary of top ten types of service by cost, FY2015.

9. 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 in budgeting for experiments. 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.

10. 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.

a. Assembly by Reduced Complexity (ARC)

As a part of his PhD dissertation, 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 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 sequence reads, and compares favorably to *de novo* assembly in terms of CPU and memory requirements.

b. 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.

c. 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.

11. 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 $203,198 in FY2014. A slight increase in demand for services was reflected by a total revenue of $219,688 in FY2015, however the GRC was severely understaffed during much of this fiscal year, limiting the amount of time that could be spent on outreach developing new opportunities. Ongoing R&D efforts and new acquisitions continue to be targeted at decreasing reagent costs and improving efficiency in order to offer updated services while maintaining competitive pricing for existing and new clients. Outreach efforts and a renewed focus on identifying new opportunities for collaboration (made possible by achieving a full level of staffing within the GRC) are expected to result in further improvements towards sustainability.

12. Plans

IBEST successfully completed a search for a new GRC Director in late 2015. The new director has continued to transition the Core towards a business model focused on long term sustainability. Included in this transition is continued investment in key strengths such as multi-locus targeted amplicon sequencing. Based on extensive research online, discussions with Fluidigm, clients, and other core directors, this service is offered for non-model organisms by only one other sequencing center in the country. Limited availability, in combination with presentations at conferences and publications by early adopters has led to increased demand for this service. This increased demand will be met by the acquisition of the Fluidigm Juno platform which will significantly reduce reagent cost per sample and hands-on time by quadrupling throughput as compared to our existing Access Array system (a close collaboration with Fluidigm research scientists has enabled us to maintain backwards compatibility with assays run on the Access Array improving redundancy of key service).

Another key strength of the GRC, metagenomic community analysis using 16s and other targets, has also been an area of continued focus. As well as continuing to invest heavily in training clients to prepare libraries using our custom set of dual barcode indexes, we have launched an initiative to improve reproducibility and consistency across runs by developing a set of positive controls consisting of an internal (standardized library) and external (mock community) control which will be sequenced at low depth on each amplicon run. These controls will allow us to monitor for run-to-run variations within the GRC, as well as simplify trouble shooting library prep for new clients as well as variation between library preps for existing clients.

The GRC has continued to look for new ways to expand the applications of this targeted amplicon strategy by identifying researchers at WSU and the UofI who can employ this strategy

to characterize mutations generated by the exciting new CRISPR/Cas9 gene editing technology. Additional research and development objectives aimed at increased sustainability include adopting new protocols for decreasing costs and increasing efficiency of shotgun and RNAseq library preparation, both of which are currently in progress. Finally, increasing the user base continues to be a major objective. Efforts on campus have included consulting, sequencing, analysis and grant writing support for members of the College of Agriculture and Life Sciences as well as members of the College of Natural Resources. Fostering collaborations with off campus researchers has included collaborations with faculty at UofI extension offices and USDA facilities in Idaho, as well as with researchers in neighboring states. As well as “word of mouth” advertising, our collaboration with the Idaho Wheat Commission has facilitated these efforts, opening up many opportunities to work with a variety of agricultural researchers across the Northwest.

A second component of sustainability is recruitment, retention, and minimizing the damage caused by losing a staff member. The increasing popularity of next generation sequencing methods has led to high demand for experienced staff. This represents a serious concern for the GRC which has a small staff and has traditionally had little redundancy in skills and significant risk associated with losing a staff member. A major objective of the new Director has been to address these problems through a combination of strategies.

The GRC currently (and historically) has been staffed entirely by members who gained a large portion of their training in High Throughput Sequencing techniques within the GRC. Although recruiting highly skilled staff members is always a possibility, the rapid growth and popularity of High Throughput Sequencing has created consistent demand for experts in this area. Rather than relying on recruitment of such skilled staff, the GRC will continue the strategy of developing capacity by hiring entry level positions, investing in professional development and training, and promoting when appropriate. As mentioned earlier, this model was used for the current Director, Bioinformatics Scientist, and Genomics Laboratory Manager as well as the new Genomics Laboratory Scientist (who was hired as a summer intern with no previous HTS or genomics experience).

To reduce the threat posed by loss of a staff member, redundancy in job roles has been improved by training wet-lab staff in basic bioinformatic and data delivery procedures, ensuring that a subset of services would continue to be available even in the absence of bioinformatic staff. Redundancy in wet-lab procedures has been improved by hiring a Genomics Laboratory Scientist who has been trained in nearly all critical wet-lab procedures, and by continued involvement in laboratory procedures and research and development by the Bioinformatics Scientist Dr. Gerritsen. Redundancy in administrative tasks is ensured by continued involvement of Dr. Gerritsen and Mr. New in developing new business, billing, and other administrative decisions where appropriate. Concerns about retention have been partially addressed by somewhat reducing workload and stress through hiring additional core staff and by working with IBEST and University administration to provide above baseline salary increases for existing staff members. Although these measures in no way solve this concern they represent a small step in the right direction.

13. Outreach

The Genomics Resources Core engages in a number of outreach activities across the

University of Idaho campus, the state of Idaho, across the nation. Examples of outreach activities include:

Collaboration with the Idaho State University Molecular Research Core Facility. The GRC was able to step in and successfully complete a number of delayed projects following the departure of the bioinformatics scientist from the ISU MRCF. Successful resolution of these projects has led to continued collaboration on new projects with the GRC contributing to new project design and analysis, and generally serving as bioinformatics support for the ISU core.

Educational Workshops: Following the departure of the previous Director, the GRC was understaffed and suspended educational workshops in order to focus on core operations. Previous workshops have been attended at maximum capacity however, and every indication suggests that demand remains high. Plans are in progress to begin offering workshops again in the future. In the interim, the GRC remains dedicated to educational activities by acting as a resource for wet lab and bioinformatics support, especially for BCB graduate students learning to prepare samples and analyze HTS data.

Professional associations: Genomics technology partnerships and consultation with service centers and researchers at the University of Oregon, University of California-Berkeley, University of California-Irvine, University of Montana, Washington State University, and the University of Washington.

Conferences: Travel to technological and administrative conferences developed for service centers and core facilities, including the Association of Biomolecular Resource Facilities and the Western Association of Core Directors. Novel approaches to analysis, budgeting, customer service, sustainability, and technological innovations are all topics that are encountered at these conferences.

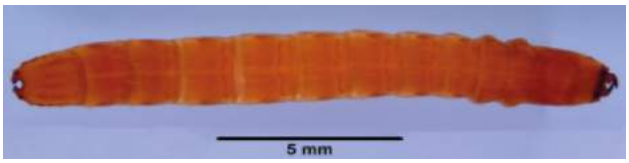
Symposium: Assisting with organizing and participating in the annual Genomics Research Symposium held at the University of Idaho in Spring of 2016. Many Speakers and attendees were GRC customers from a wide range of research backgrounds and institutions. The GRC was able to partner with vendors who supported the event, paying for food and providing gift cards as poster prizes.

14. 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 WSU Functional Genomics Initiative, a recently funded ($10m) five year initiative to develop service centers providing CRISPR gene editing technology and infrastructure with a focus on improving food resources. Preliminary discussions with the PI for this initiative have indicated a good opportunity to partner with the planned service centers in order to provide characterization of CRISPR mutation sites, RNAseq, and followup bioinformatics support.

- *A recently funded grant from the Idaho Wheat Commission will fund the GRC to carry out original research on the phylogeography and population genomics of the Sugarbeet wireworm, Limonius californicus.* In collaboration with the Idaho Wheat Commission and Dr. Arash Rashed (University of Idaho Aberdeen extension researcher) the GRC has taken a leadership role in studying the emerging wireworm agricultural pest, first by organizing a wireworm workshop in Spring 2016 which was attended by ~28 researchers from Washington, Idaho, Montana and Canada, and second by continuing to work with researchers to gather a representative sampling of *Limonius californicus* and other species of wireworm from across the Northwest. Collaborations developed during this project are expected to lead to multiple new clients, opportunities for collaborative grant submission, and continued collaboration with the Idaho Wheat Commission, and possibly similar groups representing wheat and other crops in this and neighboring states.



Sugar beet wireworm (*Limonius californicus*)

- 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 will occupy space in the same building as CMCI following a planned move to the new IRIC building in January 2017.

15. Future Objectives

a. 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 work flows. 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 clients assume that because GRC services are paid, the GRC staff should not receive recognition as part of the publication process. However, because of the investment of time through multiple, (typically free) consultations with researchers, the GRC staff has a significant intellectual impact on many of the projects submitted to the core. These intellectual contributions often result in completely

redesigned projects which take better advantage of modern technologies and more effectively address the research question. These impacts should be attributed and will help favorably increase the core's reputation amongst the scientific community, and will also justify the continuing University investment into this shared resource. The GRC has taken steps towards addressing this problem by requesting that new and existing clients review and sign a document acknowledging these contributions, and also reminding clients of the necessity of citing the COBRE grant which has supported development of the core facility.

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. Upcoming changes to UofI hiring policies may help to alleviate this problem somewhat, however recruitment is likely to continue to be a problem due to high demand in the field and the location of the University of Idaho.

b. 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 genomics and 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 outpacing the capacity to store, analyze, and interpret these data. Staying on top of emerging technologies and trends enables the GRC to continually identify novel business and collaborative opportunities while focusing on key existing services ensures financial stability, at least in the short term. Balancing these two competing interests will ensure that the GRC is sustainable, and adaptable as old technologies are replaced by new ones. The GRC's most important offering is in identifying and developing solutions to facilitate scientific discovery, particularly in areas where less integrated or more entrenched cores may be unwilling to innovate. To this end, the intellectual capital, expertise, and adaptability represented in the GRC are its biggest asset. So, while purchasing new equipment may be necessary to stay current or increase capacity, continued investment in personnel is the best way to ensure long-term viability of the core.

The University of Idaho has nearly finished 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 this building to design space that the GRC will occupy. A move in date of early January 2017 is currently planned. Because it is centrally located between the College of Science, College of Natural Resources, and College of Agriculture and Life Sciences, this new building presents numerous exciting opportunities for the GRC to reach more customers and facilitate the research of investigators within and beyond IBEST.

C. IBEST COMPUTATIONAL RESOURCES CORE (CRC)

1. 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.

2. 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.

a. High Performance Computing

CRC has one main compute cluster for research and genomic data analyses. After adding 32 new nodes at the end of 2015, the main cluster now provides 1160 processor cores and over 6 terabytes of system memory. Along with the new nodes, we have deployed new cluster scheduling software that is better able to allocate jobs to our now more heterogeneous cluster. 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 (416 total cores and over 3 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.

b. 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 2016, we added a robust offsite backup system by working with UI ITS to co-locate two IBEST data servers with 360TB combined capacity in the UI Library datacenter. In addition, the core provides in-house developed solutions to maintain data integrity and restoration.

c. 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.

d. Education and Training

To support educational programs and inter-institutional collaborations we maintain three 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

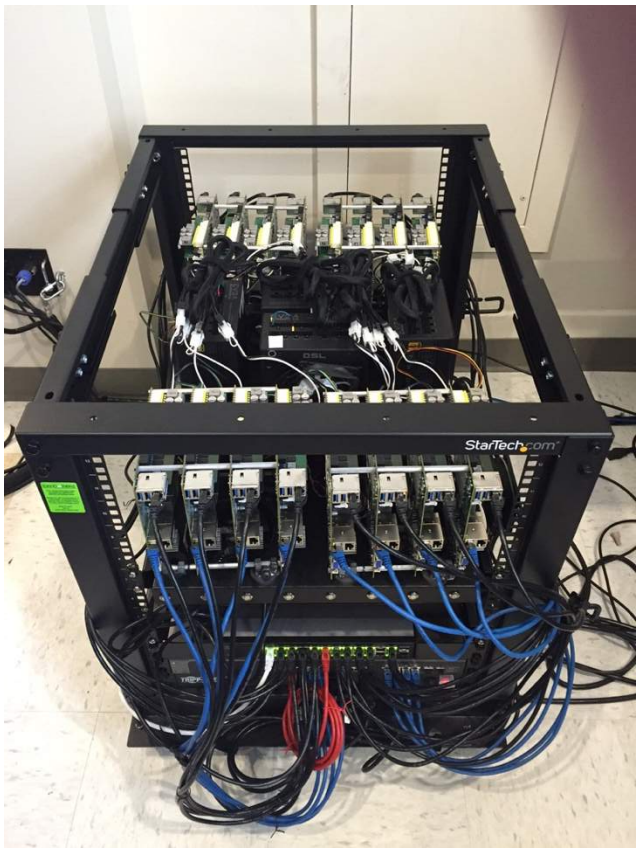


Figure 11. The classroom cluster.

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 in 2016 is our classroom cluster – an 8 node (64 core) unit with 10G networking, specifically designed to fit in a half-size rack and operate quiet enough for classroom use (Figure 11).

e. Power

Providing the energy demands of the CRC systems is a challenging task. The 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. This system was purchased in 2012 and we replaced the batteries in the fourth quarter of 2015.

f. New Infrastructure

To increase the capacity, throughput, and reliability within the CRC for our users, we have over the past year:

- Added 32 computational nodes - 512 processor cores and 4TB system RAM to our main cluster, along with new scheduling software.
- Added two new standalone servers, each with four Intel Phi coprocessor cards.
- Continued to improve our in-house developed billing system.
- Improved data integrity by implementing an offsite backup system.
- Upgraded the CRC network, adding a second 10G switch and higher speed switch interconnects. Also, added redundancy to the CRC network infrastructure to reduce the danger of outages cause by network equipment failures.
- Replaced our aging database server with a more fault-tolerant master-slave database server pair.
- Added an increased capacity Owncloud (file-sharing) server.
- Designed and built a 'classroom-cluster' to train UI students in HPC management and administration, with the support of INBRE and the Computer Science Department.
- Configured and deployed new cluster scheduling software
- With the support of INBRE, replaced 14 iMac's in the IBEST technology classroom.
- Installed a digital billboard in the IBEST common area to display CRC server usage, highlight IBEST research, and advertise seminars.
- Replaced the batteries in our main UPS.

g. Planned infrastructure

- We intend to continue adding additional data storage capacity to accommodate increasing numbers of users and their increasing data requirements.
- Add new standalone servers with additional co-processors and/or GPUs for increased computational efficiency.

h. Under Consideration

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

- New support for users of the Optical Imaging Core. These users generate exceptionally large datasets and need a reliable and cost-effective means of long-term storage.
- 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.

3. Innovation

a. 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 over 100 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 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.

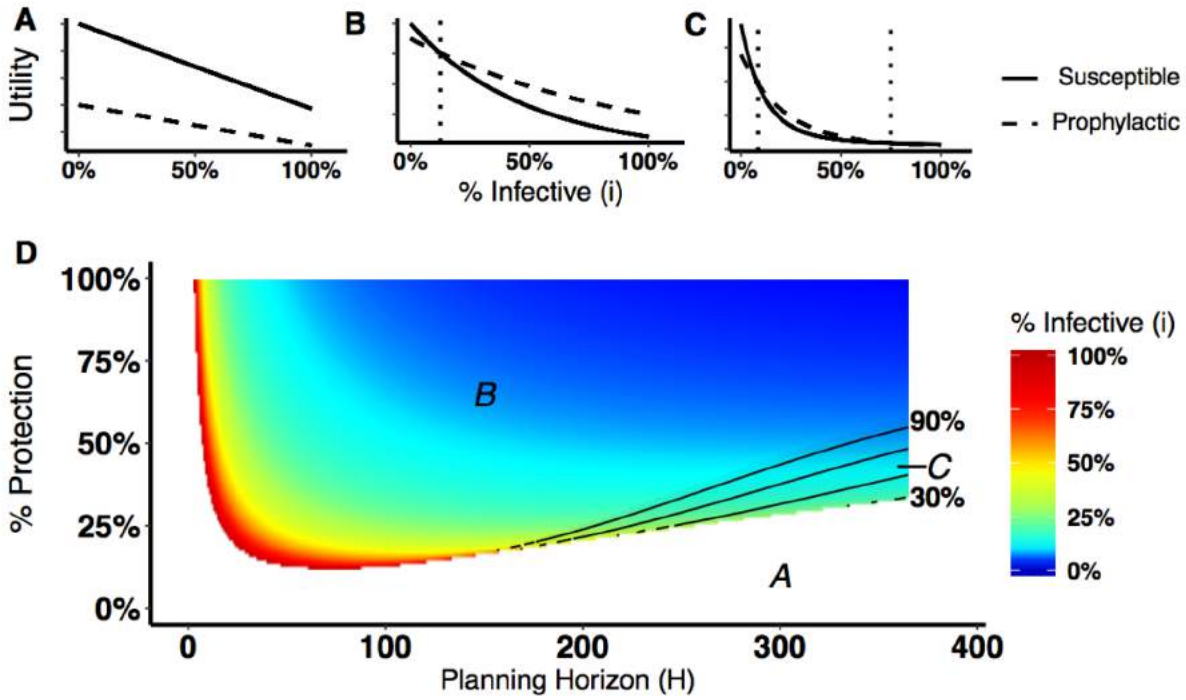
b. Impact on Research

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 a summary from Luis Gustavo Nardin:

Modeling Behavioral Responses to Disease

Luis Gustavo Nardin, Postdoctoral Fellow, Center for Modeling Complex Interactions

Human behavioral response to disease spreading has been recognized to have great influence on epidemic dynamics. It is important to understand how human behaviors and social factors influence the spreading of infectious disease in a population in order to identify how we can intervene to reduce the negative impact of outbreaks. We use several mathematical and computational modeling and simulation approaches to study the dynamics of this coupled behavior-disease model, such as ordinary differential equations and agent-based modeling. We have used the IBEST CRC to perform calculations to identify and understand how the planning horizon and fear influences the decision to adopt prophylactic measures. We additionally used the IBEST CRC to perform simulations to understand how different planning horizons and fear values influence the spread of the infectious disease in a population.



4. 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. First, we must maintain our current services and, second, we must update services to remain on the cutting edge.

a. Maintaining Current Status

In June 2014, we implemented a fee for service model with a single user fee for access to all systems. A single standard user subscription currently costs $2000 per year, as it did in 2014. We have been able to control costs through the extensive use of automation, commodity hardware, and a growing user base. We currently have 65 paid users (39 standard accounts, and 26 satellite accounts). Last fiscal year, we introduced a new account option – the Satellite Account – intended as a lower cost (now $320 annually) account that has proven popular for larger labs, see Figure 12.

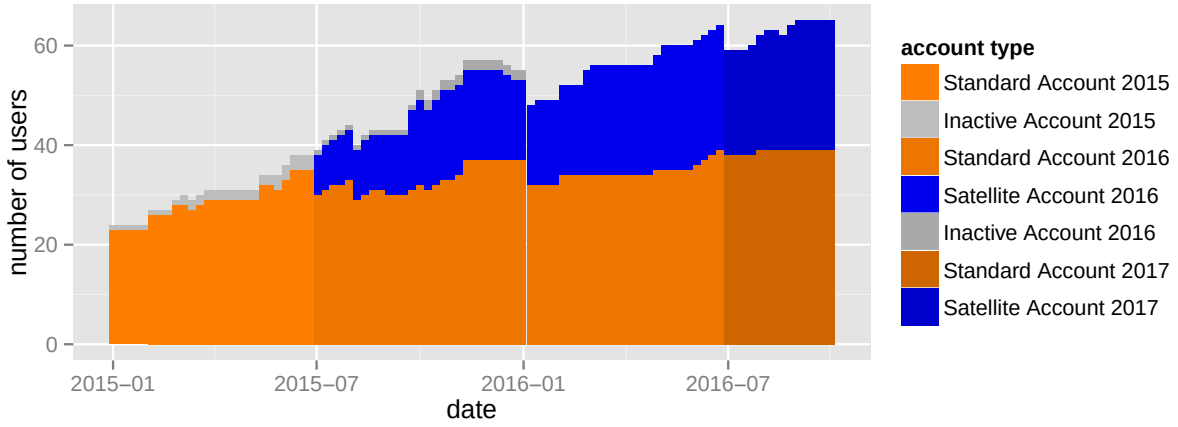


Figure 12. The number of users with active accounts for each week in 2015-present.

The bulk of the CRC equipment was purchased using COBRE funds, and so pursuant to federal guidelines, user fees fund personnel costs associated with administering the CRC, not hardware. In 2011 however, the CRC used University funds to lease several servers with the intent of billing users for the computational time used. This year we made the final payment to the University for this leased equipment, and have incorporated the leased servers into various CRC systems. We are now in a position to support our staff on user fees (40 standard accounts, and 30 satellite accounts) provided that: 1) the significant salary support from the Dept. of Biological Sciences for the CRC Director position continues, and 2) we continue to use undergraduate students to fill the role of systems administrators.

We have continued to increase our campus wide impact and overall number of paid accounts and now have users in 12 different UI Academic Departments. We continue to support external users from Reed College, and Colorado State University, and have added a private company out of Wisconsin (Figure 13). We intend to continue to court external users, while keeping our core user-base on the University of Idaho campus.

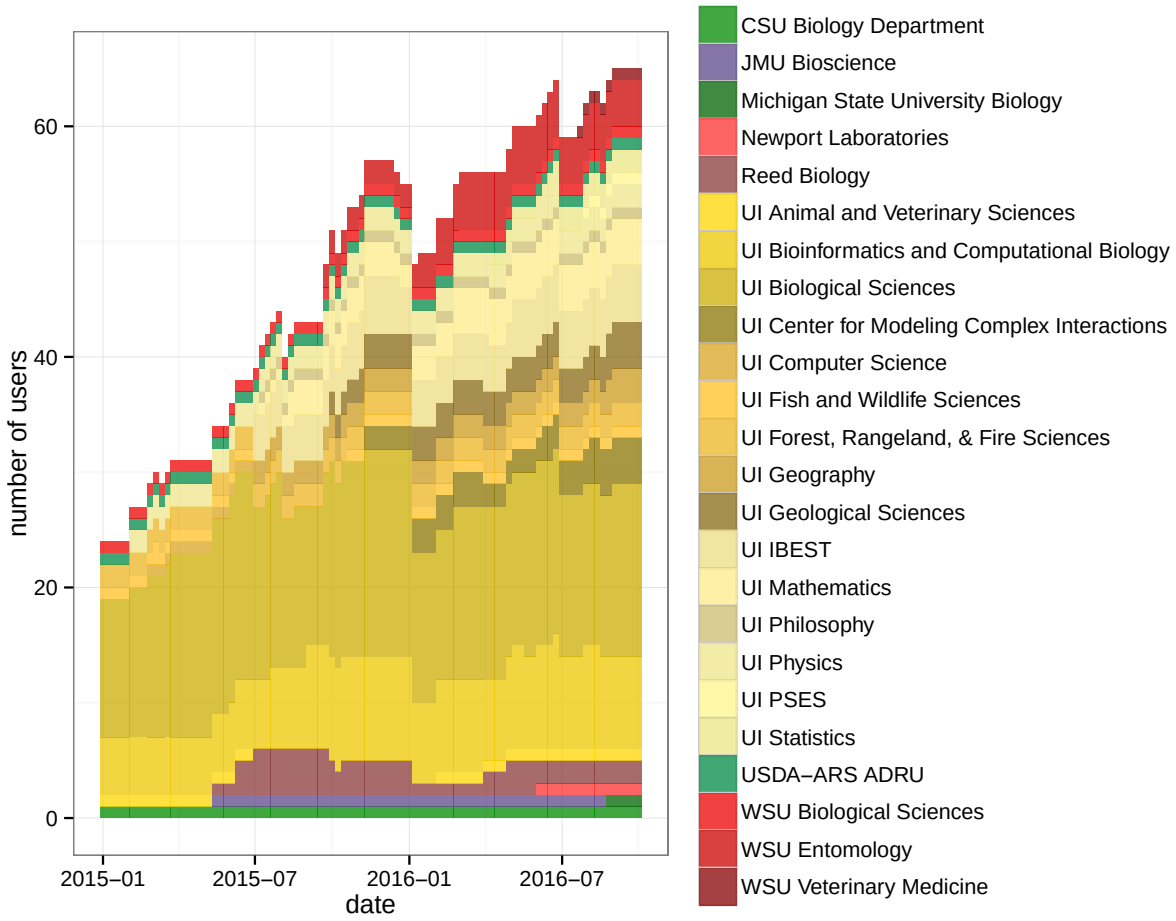


Figure 13. The number of users with active accounts for each week in 2015 and 2016, colored by institution and department.

b. 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 offer regular workshops where researchers can get one-on-one help converting their scripts and application calls to cluster enabled scripts.

c. 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. Our two most powerful systems were purchased nearly 4 years ago (Nov 2012) and the bulk of our cluster nodes are now 8 years old (purchased Nov 2008). With the purchase of 32 new cluster nodes this year, we have the computational resources to keep our current user base satisfied for the near future. As the older cluster nodes fail however, it has not been cost-effective to repair them. At this time, about 10% (6/64) of the original cluster nodes have failed without being replaced. 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 14). However, as we add additional users, we will now need to continue to update our computational infrastructure as well.

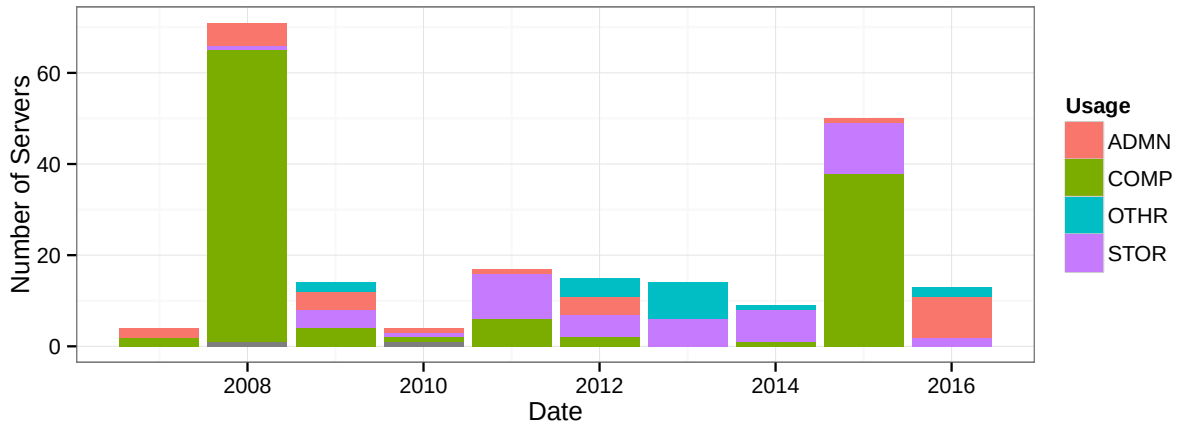


Figure 14. The number of servers purchased each year, colored by their primary purpose.

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 installed that equipment in late 2015. Additionally, working with UI technology services, we updated 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 increased bandwidth makes an offsite daily backup feasible, and we implemented such as system in 2016.

d. 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 the bulk of salary expenses with self-generated revenue, and rely on future grant funding to continue to replace aging hardware. In order to avoid costly maintenance contracts with hardware vendors, we rely heavily on commodity hardware with warranties included at the time of purchase. However, we keep hardware in service well beyond typical warranty periods (3-5 years), and so ongoing maintenance costs will likely increase (Figure 15).

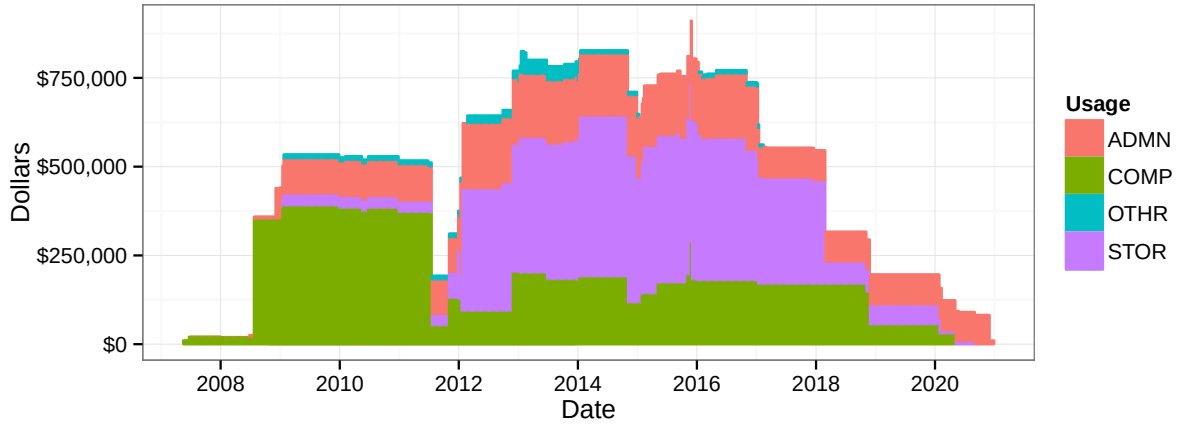


Figure 15. Dollar value (adjusted for inflation) of hardware currently in service and under warranty.

Besides relying on commodity hardware, we also rely on open-source software almost exclusively. While this reduces overall operating costs, it places a greater burden on our staff in both time and education. With the current compensation levels at the UI, we have found it impossible to attract systems administrators with previous experience in HPC and configuration management tools. Thus, we have historically settled for systems administrators with little experience - but high aptitude - and trained them up over the period of a couple years. However, these now experienced systems administrators have then promptly moved on to private industry or higher education institutions that can compensate them at market rates. We have therefore decided to instead focus on our undergraduate staff. The amount of training necessary to get a talented undergraduate to the level of competency required for systems administration in our environment is comparable to the amount required for an individual with a bachelor's degree. The undergraduate students get the benefit of hands-on systems administration experience, and the CRC benefits from a simplified hiring process and reduced salary expenditures. This type of training requires a hardware environment tolerant of system administrator errors – which our production environment is not. We therefore built a unique 'classroom cluster' which has nearly all the complexities of our production cluster – but fits nicely in the IBEST classroom. This classroom cluster uses modern hardware similar to that used in our production environment, and provides an ideal environment for testing new technologies and software. Solutions developed for the classroom cluster can be translated directly to our production environment. We intend to offer undergraduate classes for credit on HPC administration using the classroom cluster. These classes will serve as a talent pool for future CRC staff.

5. Outreach

Do to staffing constraints, the CRC is less active with outreach than the other cores within IBEST. We provide workshops every Fall semester for CRC users and non-users. We hope to expand our educational reach with the undergraduate HPC administration class. The outreach activities described by the GRC are often facilitated by the tight integration between the Computation and Genomics Resources Cores.

6. Opportunities

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

- The new COBRE Center for Modeling Complex Interactions includes a modeling collaboratorium and several potentially computationally intensive projects which has led to fourteen user accounts, and computational nodes for the HPC cluster.
- We are now supporting other research units within the College of Science, including Geographical Sciences, and Geology Researchers. With the required software for these users now installed, we are in a better position to offer services to other faculty members.
- A 'bring your own node' program could be a viable option for replacing computational equipment in the future. In this model, researchers would include computational hardware in grant applications, which would become part of the CRC managed infrastructure with the understanding that the researcher would have first priority using that equipment. In this way, the researcher avoids the complexities of managing their own hardware and software, and idle cycles on the server would be available to all CRC users. The researcher would be granted a low- or no-cost account with the CRC so they would also have access to computational resources beyond their own hardware. The CRC would benefit from a broader pool of grant applications, and potential expanded user base.
- Federal grants increasingly require data management plans to be submitted with any large grant. The CRC has the expertise to offer data management services for researchers, but would need to invest in additional hardware and formalize a service center category to offer this service.

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

- We have expanded the use of 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.

6. Challenges

a. 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 third 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 hardware. Nevertheless, we are striving to minimize and recover costs when possible. Our goal is to reach 70 user accounts, a number that can be sustained at our current staffing level. This should recover the bulk of the staffing costs of the CRC.

b. 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.

A 5 million year old leaf from the Clarkia Flora.

D. IBEST OPTICAL IMAGING CORE

The IBEST Optical Imaging Core (OIC) provides expertise, training and instrumentation for characterizing tissue, cells and particles via optical microscopy and flow cytometry. By training faculty, staff, graduate students and undergraduate students to become independent users of these complex instruments, they are allowed personal flexibility and optimum timing for best results. For the students, this experience also provides a learning opportunity beyond simply preparing the samples. They play an active role in the acquisition of the imaging and flow cytometry data, the analysis of that data and final preparation for publications and presentations. They learn what is happening inside the machine, how to modify their preparation and acquisition techniques to get accurate, quality results and the experience of being a part of the project, from experimental design to interpretation and publication. Ann Norton, director of the Optical Imaging Core, is also available to provide full service when faculty require professional results quickly or do not have staff or students available.

1. Existing Infrastructure

To provide a breadth of optical imaging and flow cytometry services to all university researchers, the OIC instruments are more complex and versatile than is typically available in an individual laboratory. The instruments are all located in Life Science South 450 and include both acquisition and analysis services with an emphasis on characterization of samples using fluorescent biomarkers.

- **Confocal Laser Scanning Microscope** – this system provides the best option at the OIC for high resolution imaging of multiple fluorescent labels using visible wavelength lasers. A multiphoton laser on this system provides the only option for deep tissue and second harmonic imaging.
- **Spinning Disk Confocal Microscope** – this recently purchased system provides similar visible wavelength lasers for imaging multiple fluorescent labels, yet, is much faster than the Laser Scanning system. The addition of an on-stage environmental chamber allows cells and embryos to be kept alive during long imaging sessions. A third camera provides improved wide-field imaging and allowed us to sunset an older, less efficient fluorescent microscope.
- **Fluorescence Activated Cell Sorter** (FACS) – dissociated cells can be characterized and sorted for downstream processing, based on both fluorescent and non-fluorescent parameters, using this system. This system is limited by few lasers, older detectors, a software program that is not very robust and it is expensive to run. It is mainly used only for counting and characterizing cells, not sorting.
- **Histological and Stereo Microscopes** – most individual laboratories that may use a stereomicroscope for preparation of samples do not have the added feature of fluorescence excitation or image capture. The color camera can be easily transferred to an adjacent transmitted light microscope for imaging of histological samples. Though not extremely sophisticated systems, they are the only option for those

investigators that need this documentation and cannot justify an investment in a full imaging system.

- **Analysis Computers and Advanced Software** – the imaging and cytometry systems in the OIC create complex data sets that require advanced software for analysis and publication preparation. These software programs are expensive and require robust computers to work effectively, therefore, sharing of these programs is an efficient approach for multiple investigators.

2. Potential Infrastructure

At the Optical Imaging Core, we strive to stay abreast of new technologies and improvements that may be available for improved imaging, analysis and flow cytometry. As the instrumentation is expensive to acquire and maintain, it is critical to carefully review the needs of investigators at the University and match those needs with the appropriate tools and configurations. We cannot provide all of the newest opportunities and expect to find enough users to secure the funds to purchase and maintain them. Most modern imaging and flow cytometry are done on live or recently fixed samples and the fluorescent biomarkers are light, time and temperature sensitive, so we cannot expect to find users from off-campus to offset our costs. That said, to satisfy the needs of current investigators at the University, we plan to pursue some modern instrumentation.

- **Flow Cytometer** – investigators in the NIH funded Center for Modeling of Complex Interactions (CMCI) on our campus would be better served with a flow cytometer that has more lasers and is simpler to use than our existing Fluorescent Activated Cell Sorter. Many potential users brought samples to an on-campus demonstration of a flow cytometer of interest and had successful results. Funding from CMCI has been approved and a Request for Proposals has been sent out to vendors. The CMCI has chosen to house this new flow cytometer in the OIC, as the expertise and potential additional customer base are already in place.
- **Upgrade/Replacement of Confocal Laser Scanning Microscope** – recently hired, as well as experienced faculty, are in need of a modern multiphoton imaging system for deep, live imaging and second harmonic imaging. Our existing multiphoton laser is aged, inefficient and unsupported at this time. New projects are proposed that require this imaging, so new infrastructure must also be proposed to improve the chances of funding these projects. The Director is actively working with researchers, including an experienced investigator as the administrative PI, to seek instrumentation funding to replace our aging system.
- **Improved Data Transfer** – in an effort to keep data off of the acquisition stations, yet, available to investigators, the director is creating an internal network to transfer data from each acquisition to one computer within the OIC. From this station, investigators will be able to transfer their data off of the OIC computers to other storage locations. One storage option being considered is to purchase dedicated support for a data

appliance from the IBEST Computational Resources Core and share the cost among major users of the OIC.

3. Innovation

Researchers often contact the OIC with new ideas that they are not certain can be done on our campus. We take the approach that if it may be even remotely possible on our instruments, 'let's try it'. New and experienced faculty members came to the OIC this year with new, innovative imaging ideas. In each case, it took a couple of attempts to determine the best instrument and configuration. The newer faculty members are writing grant proposals using this preliminary data. One project received an IBEST/INBRE Technology Access Grant to develop that idea further. Innovative projects may reinforce the need to update an existing instrument, yet, now that need will be more clearly defined and make a stronger instrumentation proposal.

a. Grand Scale

- Biological processes can be characterized, imaged, and quantified using fluorescent biomarkers. Careful experimental design, matching of the research goals to the best instrument and training of users to know what quality results should look like are key to getting dependable, publishable data.
- Most of the work done in the Optical Imaging Core is performed by students, both graduate (33% of the independent users) and undergraduate (37% of the independent users). The summer is very active with undergraduate students that are part of the INBRE Fellows or NSF Research Experience for Undergraduate (REU) programs. This facility provides an amazing opportunity for young scientists to learn advanced skills and to gain confidence by working independently.
- Innovative investigations often involve multidisciplinary approaches. Researchers goals may include further exploration downstream of what is done in the Optical Imaging Core. This involves some new skills and, in some cases, new instrumentation. We are working with investigators to perform more demanding and sensitive experimentation on our instruments and, if necessary, collaborating with colleagues at Washington State University to determine if instruments on their campus may be the most appropriate or, perhaps, only option.

b. Person Scale

- The director of the Optical Imaging Core is the direct contact for users and potential users of the facility. The director works with new and experienced faculty, staff, graduate and undergraduate students who come to the OIC with vast differences in training and theoretical understanding of the available systems. The director must be able to make them feel both comfortable and confident about what the OIC can offer them. It is also critical not to make promises that are unrealistic or untenable.
- As most of the work done at the OIC is done by independent users, training sessions must be tailored to the experience level of the user and the expectations of the principal investigator. This may require multiple sessions or simply being readily

available during early sessions for inexperienced users. Occasionally the director will encourage the Principal Investigator to 'drop in' on an inexperienced user to make sure the user is following guidelines and protocols that are specific to their research goals.

- Some instruments in the OIC are old, inefficient and not what a young investigator would consider user-friendly. As funds for maintenance support are inadequate, the director must be able to run standardized testing and make adjustments, if possible, more frequently than would be likely on a newer system. Despite these disruptions and challenges, the OIC director must maintain a professional and confident atmosphere for the users. Instrument breakdowns are likely to become more frequent and demand some tough decisions on what services will need to be terminated.
- The IBEST Optical Imaging Core will not be able to offer a full breadth of the latest instrumentation in optical imaging or flow cytometry, yet, the director does strive to be aware of new technologies and management approaches. The director is the current president of the Western Association of Core Directors (WACD), a chapter of the Association of Biomolecular Resource Facilities (ABRF). In this capacity, the director organizes an annual meeting that offers sessions on topics, such as, challenges of sustainability, new technologies, writing of instrumentation grant proposals and reports and vendor updates. These meetings also create professional networking opportunities. The director also learns of new instrumentation by attending corporate-sponsored visits to demo sites and arranges for on-campus demonstrations.

4. Sustainability

Over the last few years, the Director of the Optical Imaging Core has tried a variety of fee structures to provide opportunities for as many investigators as possible, yet, balance the offerings with equitable service charges. It is clear that there is a breakpoint, whereby the cost is too much for investigators. For an investigator that requires careful imaging and analysis and strives to train developing scientists in proper technique, high hourly rates can force those investigators to have to do the work themselves. It costs too much to get quality results from inexperienced student users and the students miss out on a wonderful training opportunity.

The Service Center Committee of the University of Idaho and the OIC Director have worked to develop multiple fee structures that are available to everyone. Last year we introduced a 'pass' structure allowing for users to purchase the right to a service for a fixed period of time (3 months), yet, not be charged hourly. This has allowed more use of the facility, more research moving forward and more young scientists being trained. It created increased predictability in budgeting for investigators and research fund providers. Though the number of unique users did not increase over the last year, the income did increase significantly. Despite these positive changes, the income does not come anywhere near paying for salary, required maintenance or updates and replacements at the Optical Imaging Core.

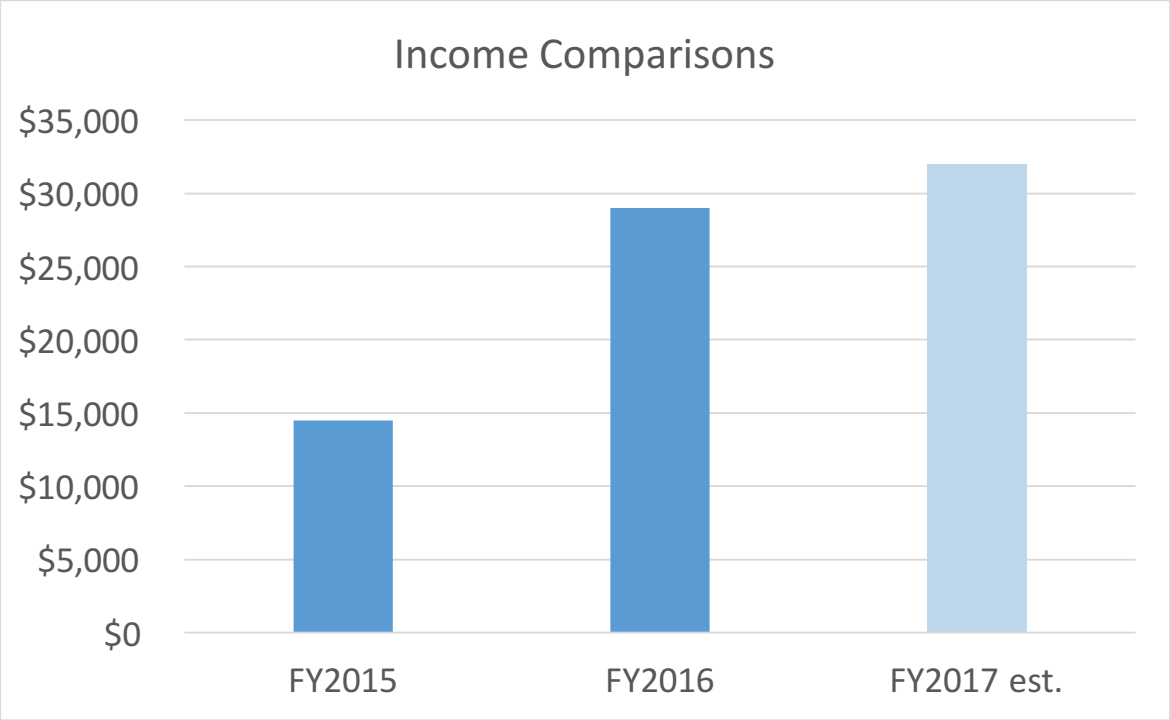


Figure 16. OIC income for FY2015 and FY2016. Anticipated income for FY2017.

a. Current status

- We anticipate some increase in income due to more users and more hours of use of the new flow cytometer and the spinning disk microscope, yet, as the Confocal Laser Scanning Microscope is likely to become inoperable and too expensive to repair, there will be reduced usage of that critical service. See Figure 1.
- The Spinning Disk microscope is seeing a huge increase in usage since the beginning of FY2016. Usage rose by 400% (30 hours to 150 hours) between the first quarter to the third quarter. The current quarter appears to be staying at a high usage rate of approximately 150 hours/quarter.
- As seen in Figure 2, the option to choose to pay for usage at a flat rate for 3 months allowed individual laboratories to afford to use the facility for more hours of work. This option also allowed Principal Investigators to send students to do the work, as there was less expense involved for them to become experienced enough to produce quality results. It is much more financially prudent for the principal investigator to use the students in this fashion and provides the students with added skills.

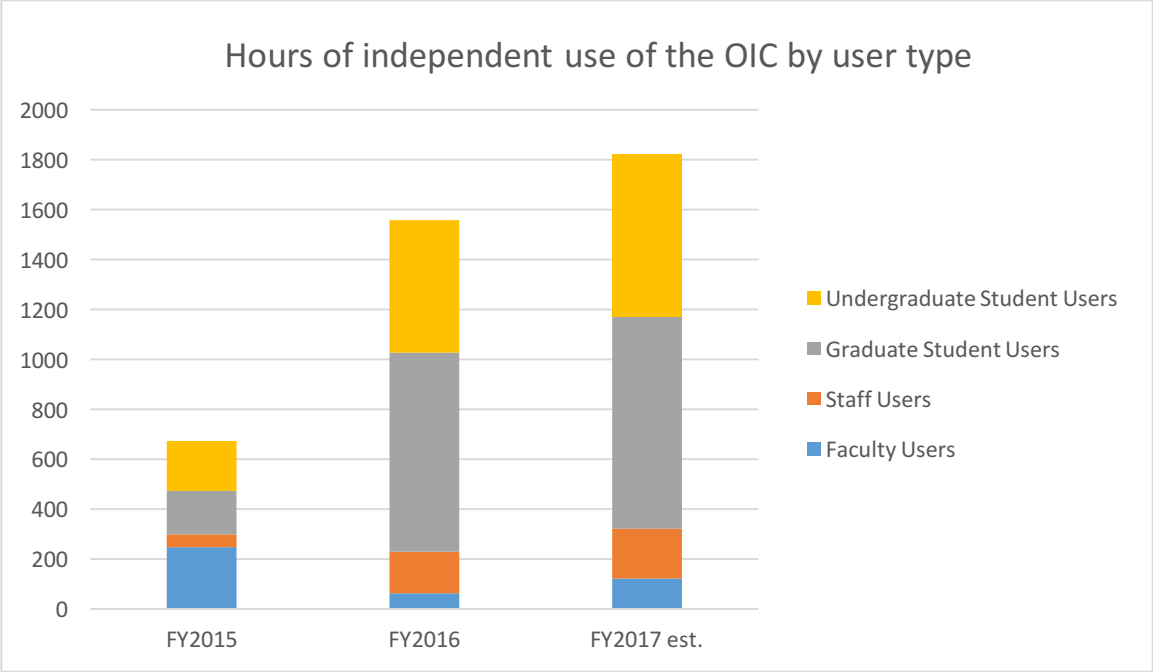


Figure 17. Hours of independent use of the OIC by user type during FY2015 and FY2016. Estimated usage for FY2017.

b. Plans

- The Service Center fee structure will be reviewed early in 2017. The results of this review will likely find the pass fees to be raised. Yet, if they are raised too much, principal investigators will have to consider slowing down the pace of their research, purchasing their own imaging and flow cytometry systems, requesting collaborators on other campuses do this work or doing more of the work in the OIC themselves.
- The older systems, the Olympus Laser Scanning Microscope with associated multiphoton laser and the BD FACSAria Cell Sorter, will likely not get repaired and the small maintenance budget will need to be applied to the Spinning Disk system and new analysis computers. Having no laser scanning system or multiphoton laser will completely stop research programs for those investigators that require high resolution and second harmonic imaging. The loss of the cell sorter will greatly inconvenience a few users that will have to go to WSU to get that work done.
- Increase usage will likely come from newer faculty members as they get funds to perform additional work and take on students to do the work. There is the risk that the instruments they plan to use will no longer be functioning and not yet replaced.
- New instrumentation, specifically a multiphoton imaging system, will be pursued by writing an NIH S10 instrumentation grant proposal and perhaps one to MJ Murdock Charitable Trust. The Murdock option does require a much higher match from the institution than previously, so this will not be the first option to pursue.

- We will continue to provide friendly and professional service to as many UI investigators as we can serve with existing infrastructure. We will provide a smoother approach to storing data and new options in flow cytometry while seeking new collaborations with Washington State University service centers for services that can no longer be offered.

The operating expenses of the OIC were reduced this past year, as there were no expenditures toward service contracts and anticipated computer expenses were facilitated by a new analysis-only computer that arrived with the Spinning Disk Confocal microscope package. Image and flow cytometry analysis needs are likely to grow with the increase in use of the spinning disk and new flow cytometer. At least one new analysis computer, as well as, upgrades and support costs for existing software packages is anticipated this year. Though we will not likely repair the oldest instruments this year, maintenance costs for newer instruments and others that were ignored last year to keep costs down, will likely come about this year and are estimated in the FY2017 budget in Figure 18 below. Training costs for an extensive course from the chosen cytometer vendor are also highly desirable.

What is missing from Figure 18 is the contribution made by faculty to acquire funding for new instrumentation. The faculty write instrumentation grant proposals, attend on-campus instrumentation demos and presentations to better understand the options and participate in the final purchasing decisions. Those purchasing decisions are very critical to the success of the OIC, as there are no dollars available to make additions or changes once the grant has closed. The Optical Imaging Core could not offer imaging and flow cytometry services to university researchers without this major contribution from some very dedicated faculty.
This is still an extremely lean budget and does not plan well for any increase or upgrade in services or professional training. There are new technologies in imaging and flow cytometry that would be welcome by our researchers that we are not pursuing due to their expense to maintain with a low volume of users.

5. Outreach

Creating a responsive and professional atmosphere and responding quickly to the needs of the OIC users provides an efficient pipeline for scientific inquiry. Additionally, the OIC director reaches out to the research community by providing workshops on imaging and flow cytometry, presenting new tools and techniques at IBEST lunches and working closely with the NIH-Idaho INBRE Fellows Program. Investigators also use the professional services of the OIC director in their own laboratories, at a fee, for consultation on purchases, repair of instruments and installation of new technologies.

6. Opportunities

In recent years, faculty candidates and new faculty have come to the IBEST Optical Imaging Core early in their exploration of opportunities available at the university. This provides a direct savings to the faculty, as they are less likely to spend their initial dollars on instruments and expertise that are already in place on campus. These new and innovative investigators provide collaboration opportunities to existing faculty that are already using the OIC and may not

have met each other in their home colleges or departments. These collaborations also increase the likelihood of funding success.

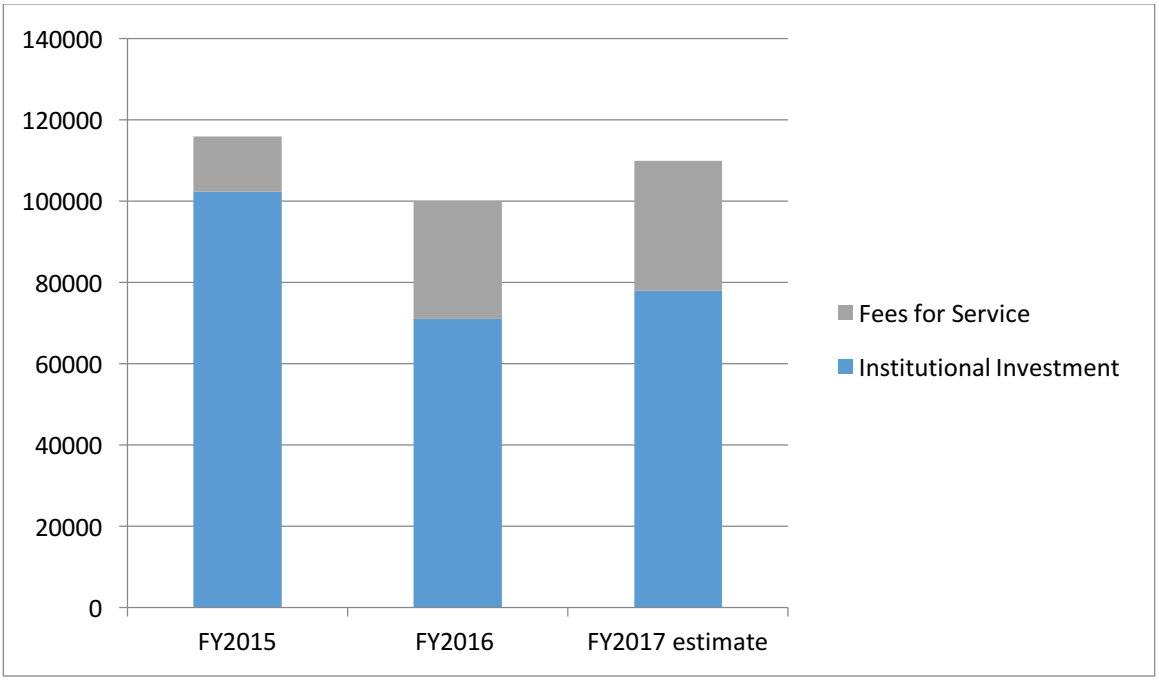


Figure 18. Total OIC operating revenue.

The OIC is available 24 hours a day, 7 days a week to independent users. This provides incredible flexibility and the ability for researchers to work when they (or their research subjects) can anticipate the best results for the experimental design and is critical for the new service of live imaging available on the Spinning Disk microscope. The extensive development of engineered fluorescent proteins has created numerous bright and stable biomarkers for longer experiments and a larger breadth of colors. We are 'machine ready' for these new tools with our recent and upcoming instrument purchases. The power of a flow cytometer is how much data can be obtained very quickly. With the addition of an efficient new instrument and extended breadth of biomarker labels that can be excited by the new configuration, those experiments can also be more complex and answer more questions in each run.

7. Future Objectives

a. Challenges

- Providing a breadth of quality services at reasonable costs to all researchers at the University of Idaho is an important mission that will help increase research funding and innovation, yet, providing these services during lean times is especially challenging.
- New instruments are designed to be more integrated, safer and generally more user friendly. This provides more efficiency for the investigator, as long as all is going well. The integration and safety aspects of newer instruments make them less accessible

for repair and configuration modifications. That makes them less flexible when trying to satisfy different experimental designs with one instrument and harder to repair for those that do not have access to proprietary diagnostic tools. This forces most owners of complex systems, such as confocal microscopes and flow cytometers, to purchase a service contract or pay the vendor service technician to do repairs at an unpredictable expense.

- Staff at an imaging or flow cytometry shared resource facility need to be skilled in science, teaching, outreach, administration and regular maintenance of instruments. Finding staff to do all of these things well and also be prepared to diagnose instrument breakdowns and possibly perform sophisticated repairs will be a significant challenge.

b. Vision

Visualizing living cells at full resolution in real time tells a cinematic story. Seeing is believing and having the tools to tell that story, training people on how to use those tools well and how to design their experiments to make the most of those tools will always help tell that story better. Publishing our scientific stories requires multiple ways of characterizing, counting and comparing our biological and material objects. Providing the tools and expertise to study disease, development and evolution and to offer opportunities for young scientists to train is an important mission of a research university.

In collaboration with Dr. Deb Stenkamp, Dr. Mitchell is probing the roles of microglia during regeneration of retinal neurons after damage, which occurs in zebrafish, though not in mammals. These findings may contribute to therapeutic therapeutic and restorative strategies that could result in functional retinal regeneration in humans.

The Mitchell and Stenkamp labs use the Nikon/Andor Spinning Disk microscope in the IBEST Optical Imaging Core extensively to observe the microglia and associated synaptic components. In Figure a, the cell nuclei are labeled in blue and the microglia in red. This shows a microglia engulfing SV-2+ presynaptic vesicles (in green) at the edge of the inner plexiform layer of a normal zebrafish retina. (20X magnification).

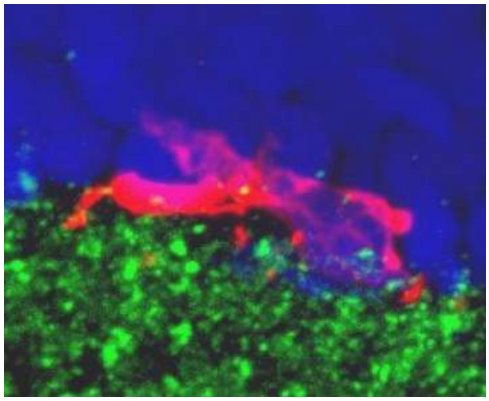


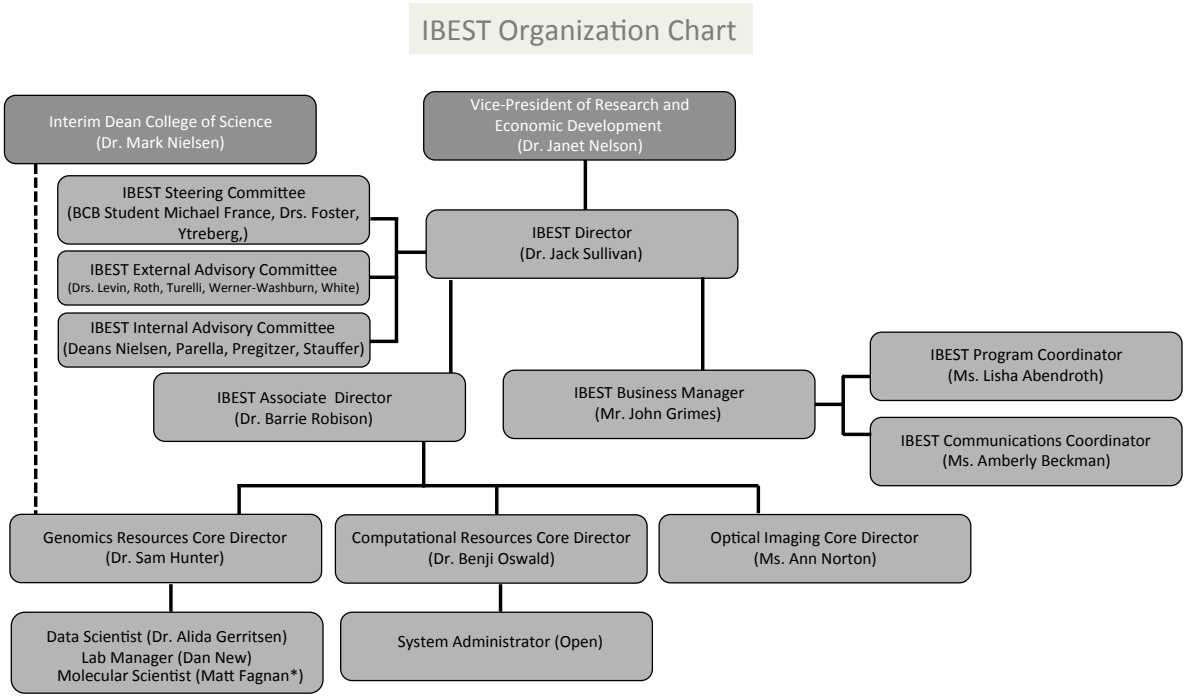
Figure a. Cell nuclei (blue) and microglia (red).

E. IBEST ADMINISTRATIVE CORE

1. Institute Leadership

Dr. Jack Sullivan is in his second year as IBEST Director. He has 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 and 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.

The Strategic Planning Committee has been reorganized to replace Drs. Soule and Top, who are on sabbatical leave. Dr. Marty Ytreberg will serve in the Fall 2016, and BCB Michael France has been elected as the graduate student representative.



*New appointment

2. 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.

3. Key Administrative Staff

John Grimes continues as Program Manager. Amberly Beckman has recently finished her first year serving as Communications Coordinator. We are very fortunate to retain Lisha Abendroth, the IBEST Program Coordinator.

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

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

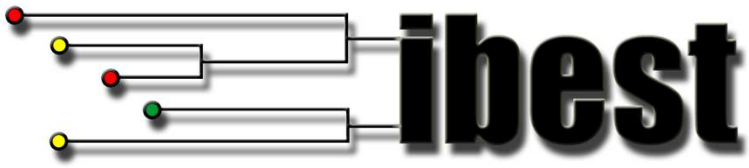
Dr. Maggie Washburn-Werner
Professor
University of New Mexico

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

5. 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:

Interim Dean Mark Nielsen, College of Science,
Dean Michael Parella, College of Agriculture and Life Sciences
Dean Kurt Pregitzer, College of Natural Resources
Dean Larry Stauffer, College of Engineering



VIII. GRADUATE AND UNDERGRADUATE EDUCATION

A. BIOINFORMATICS AND COMPUTATIONAL BIOLOGY PROGRAM

The Bioinformatics and Computational Biology (BCB) graduate program plays a unique role within the university and worldwide, preparing graduates who are at the forefront of the booming field 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 for 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 lab rotation in a research group outside their area of expertise or industry internship for those looking to gain experience outside of academia. 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 22 students in the BCB program (17 PhD, 5 MS). Five students graduated in academic year 15-16 (Table 2) and we admitted four new students for the academic year 16-17 (Table 3). 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 4).

Table 2: Graduated Students academic year 15-16

Graduate	Degree	Major Professor and their department
Yingqian Zhan	MS	Dr. Marty Ytreberg (Physics)
Hua Feng	PhD	Dr. Celeste Brown (Biol. Sci.)
Tyler Hether	PhD	Dr. Paul Hohenlohe (Biol. Sci.)
Hannah Marx	PhD	Dr. David Tank (Biol. Sci.)
Janet Williams	PhD	Dr. Mark McGuire (Animal Vet Sci.)

Because there are only five BCB student fellowships awarded per year, most students are funded by extramural grants, teaching assistantships, or other external sources. IBEST provided $105,000 toward these five fellowships (covering about 3.5 fellowships, including in-state tuition/fees and health insurance) and the University provided $34,000 and waived 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. Second, students supported by BCB fellowships can work on 'not yet funded' research projects and collect preliminary data to support future grant applications. Thus student support 'primes the pump' for extramural grant funding. Because 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 are currently discussing future training grant submissions (e.g., NIH).

Table 3: New Students Fall 2016

Student	BCB Degree	Previous Institution	Current Major Professor and their Department
Heather Clendenin	MS	Bowling Green State University	Dr. Lisette Waits (Fish & Wildlife)
Mariah Eckwright	MS	University of Idaho	Dr. Christopher Remien (Mathematics)
Evan Martin	PhD	University of Idaho	Dr. Audrey Fu (Mathematics)
Andrew Rankin	PhD	Northern Michigan University	Dr. Jack Sullivan (Biol. Sci.)

Table 4: GRE scores (in percentiles) for '15-'16: 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 %	58%	47%
GRE Quantitative %	82%	58%
GRE Verbal %	81%	64%

1. BCB Certificate Program

At the suggestion of the external review committee, the leadership of the BCB graduate program developed a BCB certificate program. This certificate provides students who are getting their graduate degrees in other areas with recognition for completing the core courses of the BCB curriculum. Graduates with this certificate will 1) have improved their understanding in bioinformatics, mathematical and computational sciences, and 2) be able to participate in interdisciplinary research in academia, industry, or government agencies thanks to the common 'language' they will learn. They will be able to explain the core BCB concepts to people with widely varying backgrounds, including professionals in other fields to lay people. The Idaho State Board of Education approved the proposal in the spring of 2015.

2. Increasing exposure to non-academic professionals

Increasingly, the BCB students have indicated that they would like more explicit exposure to and/or training for futures outside of academia. In January 2015 industry speaker Dr. Folker Meyer, a computational biologist at Argonne National Laboratory, visited IBEST and BCB to present a seminar and special question and answer session for BCB students. In 2016, two additional "industry speakers" visited IBEST and BCB, Dr. Jason Evans (Facebook) and Dr. Nigel Delaney (Pacific Biosciences), and we continue to receive feedback from the BCB students that these sessions are very informational regarding careers alternative to academia. Because these visits include dedicated question and answer forums with the BCB students, there have been some unforeseen outcomes that demonstrate the success of these interactions. For example, following the student-speaker forum with Dr. Nigel Delaney, one of our graduating PhD students was recruited to interview for a position with Pacific Biosciences. Following these successes, IBEST and BCB will continue to bring at least one non-academic professional to campus each year, and we currently have another scheduled for December 2016.

B. NSF INTERDISCIPLINARY TRAINING FOR UNDERGRADUATES IN BIOLOGICAL AND MATHEMATECAL SCIENCES

We have recently completed our 6-year Undergraduate Program in Biology and Mathematics, supported by the National Science foundation. This grant supported research activites of more than 30 undergraduates across four colleges at the UI. It created lasting impacts on the UI, including a new biological mathematics track in the Math curriculum, sparked numerous new collaborations, and provided transformational experiences to talented undergraduates.

For example, for the last two years, UBM has supported the research of Dr. Ryan Long

(Department of Fish and Wildlife Sciences, College of Natural Resources) by funding two students in the CNR. In the summer of 2016, Elyce Gosselin (a Goldwater scholarship awardee) conducted field research in Gorongosa National Park, Mozambique. She studied African elephants with Ryan's Master's student Paola Branco. Paola's work focused on human-elephant conflict, specifically the conflict created by crop-raiding elephants. Many elephants (mostly males) cross the river (the barrier between the national park and the local communities) at night and raid crops, and they can destroy massive proportions of a family's subsistence crops by eating or trampling them. Paola was working to get a monitoring program set up to collect data about crop-raiding this year before implementation of mitigation strategies next summer. Paola and Elyce trained local community members to monitor the crop damage, and also trained a Mozambican intern in computer use and data entry software. Elyce also participated in other studies, helping capture and collar elephants, cape buffalo, waterbuck, and bushbuck.

Now back from Africa, Elyce is continuing her work on the elephant project. National Geographic placed "crittercams" on 6 of the elephants that the team collared and the team will soon receive two weeks of footage from National Geographic. Elyce will be processing the footage and using the data to study crop raiding behavior and micro climate usage.

Elyce's work builds on that of another UBM student, math major Savannah Kollasch. Savannah and Elyce worked together on the modeling and data analysis for a thermal biology project focused on African antelope. Savannah, Elyce, and Dr. Long are preparing a manuscript for submission to Nature Climate Change, and Elyce is presenting a poster at the national Wildlife Society Meeting in Raleigh in October.

A robust lancetooth (*Haplotrema vacouverense*) being sequenced by IBESTians.

Appendix 1. Strategic Reinvestment of IBEST Resources, FY 2016.

DATE	DESCRIPTION	College/Department	Amount
2016	2015 F&A RETURN TO PIs	Various	39,112
	2015 F&A RETURN TO DEPTS	Biol. Sci.	20,000
	TOTAL F&A RETURNED		**59,112**
2016	**FACULTY SUPPORT**		
	JOHNSON PILOT Yr 2	COS/Biol. Sci.	75,000
	HOHENLOHE PILOT YR 1	COS/Biol. Sci.	75,000
	C PARENT START UP	COS/Biol. Sci.	50,000
	FACULTY PUB CHARGES	COS	2,000
	TOTAL FACULTY SUPPORT		**202,000**
2016	**RESEARCH SUPPORT**		
	TECH ACCESS GRANTS	COE & COS	1,675
	IBEST FACULTY RESEARCH	University/COS	3,554
	iLab SOLUTIONS	University	7,514
	GOTOMEETING SUBSCRIPTION	University/COS	525
	INWGR SYMPOSIUM	University/NW US	13,177
	TOTAL RESEARCH SUPPORT		**26,445**
2016	**STUDENT SUPPORT**		
	BCB FELLOWSHIPS	COS/Biol. Sci.	78,430
	BCB STUDENT TRAVEL GRANTS	COS/Mathematics	1,717
	BCB STUDENT GROUP	COS/Biol. Sci.	310
	UBM SUMMER STUDENTS	COS/Mathematics	122
	BEACON 101 STUDENTS	COS/Biol. Sci.	198
	IBEST SEMINAR SERIES SUPPORT	University	13,542
	TOTAL STUDENT SUPPORT		**94,319**
2016	**TOTAL**		**381,876**

Appendix 2. IBEST Investment in Faculty Recruitment and Retention.

IBEST Strategic Reinvestments in Faculty Recreuitmet/Retention				2011-2016
Investment		Faculty	Amount	Source
FY 2012	Biol/Stats Start Up	Hohenlohe	$100,000	COBRE Direct
	Biol/Stats Summer Sal.	Hohenlohe	$12,885	COBRE Direct
	Biol. Lab Set UP	Hohenlohe	$15,000	IBEST F&A
	Moving Expense	Hohenlohe	$5,738	IBEST F&A
	Stats Start Up	Buzbas	$35,000	IBEST F&A
	Biol. Start Up	McGowan	$10,000	IBEST F&A
		2012 Total	**$178,623**	
FY 2013	Biol. Start Up	Hohenlohe	$200,000	COBRE Direct
	Biol/Stats Summer Sal.	Hohenlohe	$7,075	COBRE Direct
	Biol. Start Up	Hohenlohe	$50,000	IBEST F&A
	Biol. Start Up	McGowan	$10,000	IBEST F&A
		2013 Total	**$267,075**	
FY 2014	Biol. Start Up	Hohenlohe	$82,866	COBRE Pilot
	Biol. Start Up	Parent	$65,000	IBEST F&A
	Biology Retention	Tank	$41,000	IBEST F&A
	Stats Start Up	Fu	$50,000	IBEST F&A
		2014 Total	**$238,886**	
FY 2015	Biol. Start Up	Parent	$50,000	IBEST F&A
		2015 Total	**$50,000**	
FY 2016	Biol. Start Up	Parent	$50,000	IBEST F&A
		2015 Total	**$50,000**	
Total Reinvestment into IBEST Faculty			**$784,584**	

Appendix 3. Technology Access Grant (TAG) Progress Report

Identifying Links Between Tendon Structure and Function
Drs. Nathan Schiele and Craig McGowan

The high incidence of tendon injury and tendon's poor healing capacity significantly impair human motion. Limited treatment options drive the need for novel regenerative therapies, biomechanical models, and tendon tissue engineering approaches. However, a major challenge for developing these strategies is an incomplete understanding of the normal tendon structure and mechanical function. The general assumption is that all tendons are the same at the material and structural levels. Specifically, it is unknown if the material and structural properties of tendons scale with applied load (e.g., body mass) or specific task (e.g., flexor vs. extensor tendons). The goal of this project is to identify how the collagen structure of tendons may have adapted to accommodate different functional demands. This project has two aims: 1) identify how body mass scaling influences the collagen structure of tendon and 2) identify how functional task associated with locomotion influences the collagen structure of tendon. This will provide a foundation for understanding how tendons have evolved to meet different functional demands, provide insight into the evolution of tendon structure, and advance understanding structure-function relationships.

This Technology Access Grant supports this collaborative project between biological engineering and biological science by providing access to the IBEST Optical Imaging Core. In the Optical Imaging Core, we are using the unique capability of the Olympus Fluoview 1000 confocal/multiphoton microscope to take second harmonic generation (SHG) images of the tendon tissues. SHG is an imaging modality to visualize and identify collagen fibers. This TAG has provided initial microscope training, and two 3-month confocal microscope passes. To date, we have developed a SHG imaging protocol, verified the efficacy of using SHG to visualize collagen fibers in tendon, and established an image analysis protocol. Imaging and analysis of the collagen structure of tendon as a function of body mass and functional task is in progress.

The data generated as a result of this Technology Access Grant will provide the preliminary data needed to submit a competitive R01 proposal to the NIH to investigate structure-function relationships in tendon as a function of task. Additional proposals focused on the design and modeling of tendon structure and function for applications ranging from movement biomechanics to prosthetics and robotics will be submitted to the NSF.

Appendix 4. IBEST Pilot Project Grant Program RFP

The IBEST Pilot Project Grant Program, which is funded by the Center of Biomedical Research Excellence (COBRE), fosters research at the University of Idaho by funding 1-2 grants to support pilot research on aspects of evolutionary and computational biology that are pertinent to human health. All tenure track and non-tenure track faculty of any rank at the University of Idaho are eligible to apply for the Pilot Project Grant. The maximum amounts of each award will $75,000 (direct costs) per year for up to two years. This funding will be restricted to new initiatives and used to collect preliminary data needed to support a competitive extramural proposal.

Proposals will be accepted until February 1, 2016 with an expected award of funding by mid-April 2016.

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; and
- 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.

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

2. 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. 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)

3. 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

4. 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 employees by the time funds are awarded; this should be addressed in the budget justification. 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.

5. Proposals should be submitted via email as a single PDF file that includes the cover letter and all forms in the appropriate order. Send to IBEST via email ibest@uidaho.edu before February 1, 2016. The subject line should be 'IBEST Pilot Research Proposal.'

6. 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. Details will be provided in the award letter.

7. 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.

8. A final report that describes their research findings (2 pgs) 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 Strategic Planning Committee 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

- Reviewers 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 IBEST Strategic Planning Committee and Dr. Forney (COBRE PI) will discuss the reviews and choose the most meritorious proposal.

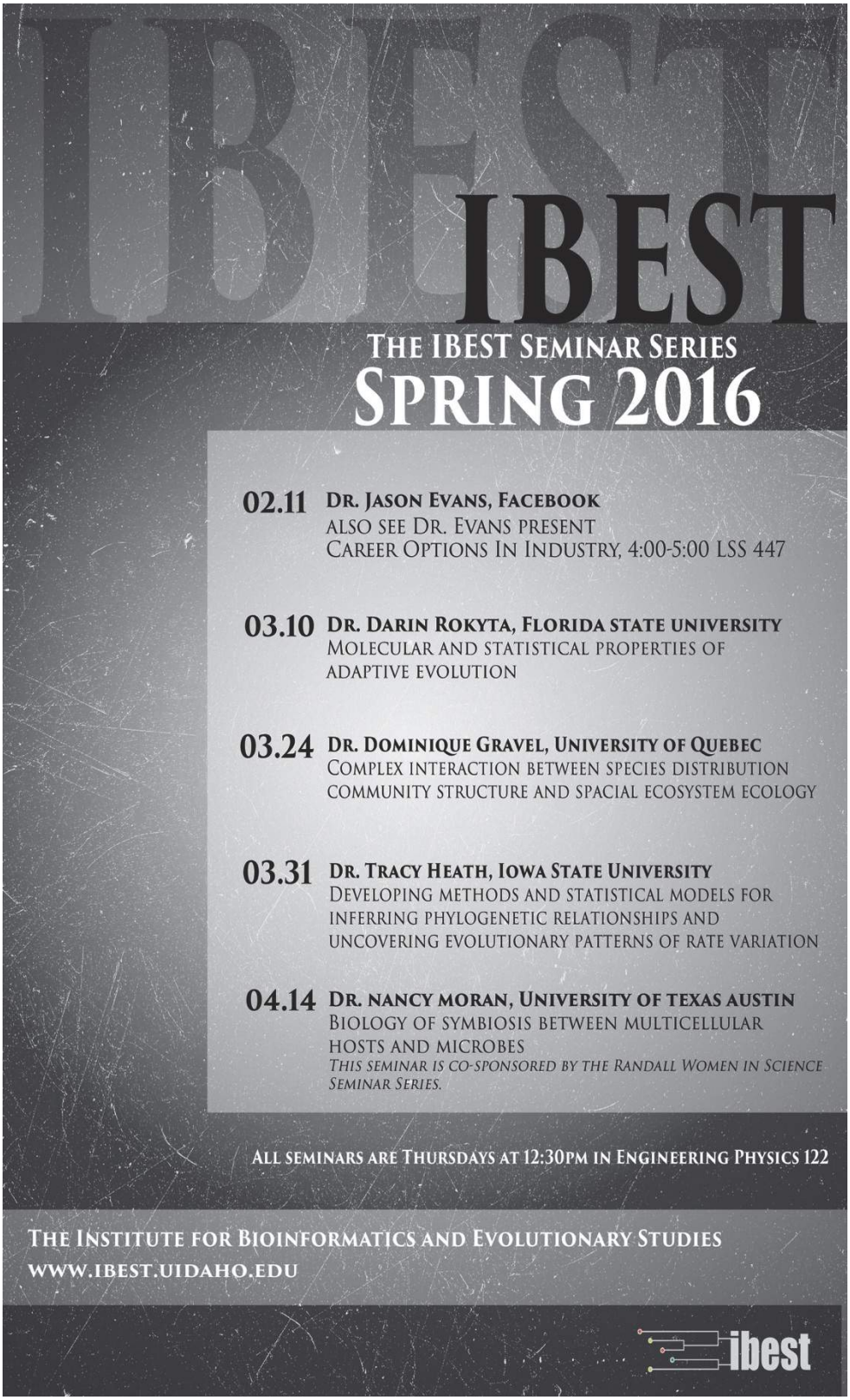
Appendix 5 - 2016 Proposals for External Funding Submitted through IBEST

PI	SPONSOR	Total
Brown, Celeste J.	Dept. Health and Human Services	1,862,138
Forney, Larry J.	The Procter & Gamble Fund	222,846
Forney, Larry J.	The Procter & Gamble Fund	49,120
Forney, Larry J.	Dept. Health and Human Services	350,600
Forney, Larry J.	The University of Michigan	119,161
Forney, Larry J.	Dept. Health and Human Services	316,011
Forney, Larry J.	Keck Foundation	1,200,000
Harmon, Luke J.	National Science Foundation	116,297
Harmon, Luke J.	National Science Foundation	93,678
Harmon, Luke J.	National Science Foundation	411,281
Harmon, Luke J.	National Science Foundation	18,446
Hohenlohe, Paul	USDA	297,852
Hohenlohe, Paul	National Science Foundation	212,618
Hohenlohe, Paul	Morris Animal Foundation	84,639
Hohenlohe, Paul	National Science Foundation	868,041
Hunter, Samuel S.	Idaho Wheat Commission	37,578
Kennedy, Brian P.	Bonneville Power Administration	137,518
Kennedy, Brian P.	Bonneville Power Administration	127,750
Kennedy, Brian P.	National Science Foundation	3
Nuismer, Scott L.	National Science Foundation	89,398
Ridenhour, Benjamin	Washington State University	109,645
Robison, Barrie D	UI ORED	64,608
Stenkamp, Deborah L.	National Science Foundation	444,534
Tank, David C.	Amer. Soc. of Plant Taxonomists	1,500
	TOTAL	**7,235,260**

Appendix 6. Extramural Grants Awarded through IBEST in 2016

PI	**Sponsor**	**Award**
Sullivan, Jack M.	National Science Foundation	$275,372
Forney, Larry J.	University of Maryland	$38,213
Forney, Larry J.	FioTec -Foundation	$23,009.67
Forney, Larry J.	University of Florida	$38,120
Kennedy, Brian P.	Bonneville Power Administration	$152,390
Forney, Larry J.	Johnson & Johnson	$224,669
Forney, Larry J.	Indiana University	$131,135
Brown, Celeste J.	Texas Biomedical Research Institute	$85,539
Nuismer, Scott L.	National Science Foundation	$102,660
Harmon, Luke J.	National Science Foundation	$24,197
Hohenlohe, Paul	Washington State University	$154,310
Forney, Larry J.	Dept. Health and Human Services	$519,360.26
Forney, Larry J.	Dept. Health and Human Services	$158,960.64
Forney, Larry J.	Dept. Health and Human Services	$370,307.08
Forney, Larry J.	Dept. Health and Human Services	$117,351.87
Forney, Larry J.	Dept. Health and Human Services	$93,028.71
Tank, David C.	Botonical Society & ASPT	$1,500
	Total	**$2,510,123.23**

Appendix 7. IBEST/BCB Seminar Series - Spring 2016



Appendix 7. IBEST/BCB Seminar Series - Fall 2016

Seminar Series
Fall 2016

Co-Sponsored by IBEST and CMCI
All seminars are at 12:30 in Engineering Physics 122

September 08	Dr. Matthew Scott, University of Waterloo Intrinsic coupling between pathogen virulence and antibiotic efficacy
September 15	Dr. Samarth Swarup, Biocomplexity Institute of Virginia Tech Behavior Modeling for Social Simulation
September 22	Dr. Amber Smith, St. Jude Children's Research Hospital Integrative Analysis of the Immune Response to Influenza-Pneumococcal Coinfection
October 20	Dr. Jeff Leek, Johns Hopkins What can we learn about human transcription from analyzing every RNA-seq data set ever generated?
November 03	Dr. Spencer Barrett, University of Toronto Evolutionary & demographic genetics of polymorphic sexual systems in plants
November 10	Dr. Claus Wilke, University of Texas at Austin Structural and functional constraints on protein evolution
November 17	Dr. Arun Sethuraman, California State University San Marcos Genomic Islands and Castaways - Model-based assessments of differential introgression during divergence and speciation
December 08	Dr. Ellie Graeden, Talus Analytics Systems Analysis of Information Flow: Network Mapping for Data

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

The Center for Modeling Complex Interactions
cmciuidaho.org

ibest

CENTER FOR MODELING COMPLEX INTERACTIONS

Appendix 8. The Inland Northwest Genomics Research Symposium - Registration

Inland Northwest Genomics Research Symposium, MAY 19, 2016

Speakers topics and institutions

Oral presentations	Total	Genomics	Computation	Vendors	Keynote
Number presentations	**10**	4	1	4	1

Speaker Institution	U Idaho	Washington State U	University of California - Davis	University of Montana	USDA	Industry
Number speakers	1	1	1	1	1	4

Posters	31

Institutions/Vendors Represented

MPG Ranch	1	Qiagen	2
University of California Davis	1	Roche Molecular Diagnostics	3
USDA	6	Idaho Wheat Commission	1
University of Nebraska Medical Center	1	Illumina	2
PNNL	1	Bio-Rad Laboratories	3
Washington State University	46		
University of Idaho	76	**Subtotal**	**11**
Subtotal	**132**	**TOTAL ATTENDEES**	**143**

Funding

	COBRE	BEST F&A	Vendors	Total cost
Source of funds	$8,713	$2,964	$1,500	$13,177

Vendors: Illumina, Roche Molecular Diagnostics, Bio-Rad Laboratories, Qiagen

Appendix 8. The Inland Northwest Genomics Research Symposium - Schedule

Schedule

8:00 – 8:50	Continental Breakfast and Registration
8:50 – 9:00	Welcome Remarks Dr. Larry Forney, University of Idaho
9:00 – 10:45	Session One - Moderator: Dr. Sam Hunter
9:00 –9:25	Dr. Kendra Stisser, Illumina, Inc
9:25 – 9:50	Dr. Hector Macias-Saldivar, Bio-Rad Laboratories
9:50 – 10:15	Dr. Neha Jalan, Qiagen
10:15 –10:40	Shelly Thompson, Roche Diagnostics
10:45 –12:30	Poster Session and Lunch
11:45	Lunch served
12:30 – 1:30	Keynote Address - Introduction by Dr. Barrie Robison (poster award announcement) Dr. Megan Dennis, University of California Davis *Searching within the dark matter of primate genomes to better understand human brain evolution and disease*
1:45 – 3:05	Session Two - Moderator: Dr. Benji Oswald (poster award announcement)
1:45 – 2:25	Dr. Ylva Lekberg, University of Montana *Using next-generation sequencing to open the black box of soil microbial communities*
2:25 – 3:05	Dr. Phil Bregitzer, USDA Agricultural Research Service *Transposons, RNAi, and Selection: Bioinformatics and the Quest for Better Beer and Oatmeal*
3:05 – 3:20	Break
3:20 – 4:40	Session Three - Moderator: Dr. Alida Gerritsen (poster award announcement)
3:20 – 4:00	Dr. Christine Parent, University of Idaho *Ecological Opportunity and Diversification on Islands*
4:00 – 4:40	Dr. Michael Varnum, Washington State University *Going Blind: CRISPR/Cas9 genome editing to generate zebrafish models of cone dystrophy*
4:40 – 5:00	Closing Remarks (poster award announcement) Dr. Jack Sullivan, University of Idaho

Appendix 9 - IBEST Publications

2016

Agashe, D., Sane, M., Phalnikar, K., Diwan, G. D., Habibullah, A., Martinez-Gomez, N. C., . . . Marx, C. J. (2016). Large-Effect Beneficial Synonymous Mutations Mediate Rapid and Parallel Adaptation in a Bacterium. *Molecular Biology and Evolution, 33*(6), 1542-1553. doi:10.1093/molbev/msw035

Ahrabi, A. F., Handa, D., Codipilly, C. N., Shah, S., Williams, J. E., McGuire, M. A., . . . Schanler, R. J. (2016). Effects of Extended Freezer Storage on the Integrity of Human Milk. *J Pediatr*. doi:10.1016/j.jpeds.2016.06.024

Andrews, K. R., Good, J. M., Miller, M. R., Luikart, G., & Hohenlohe, P. A. (2016). Harnessing the power of RADseq for ecological and evolutionary genomics. *Nature Reviews Genetics, 17*(2), 81-92. doi:10.1038/nrg.2015.28

Baker, C. W., Miller, C. R., Thaweethai, T., Yuan, J., Baker, M. H., Joyce, P., & Weinreich, D. M. (2016). Genetically Determined Variation in Lysis Time Variance in the Bacteriophage phi X174. *G3-Genes Genomes Genetics, 6*(4), 939-955. doi:10.1534/g3.115.024075

Banzhaf, W., Baumgaertner, B., Beslon, G., Doursat, R., Foster, J. A., McMullin, B., . . . White, R. (2016). Defining and simulating open-ended novelty: requirements, guidelines, and challenges. *Theory in Biosciences, 135*(3), 131-161. doi:10.1007/s12064-016-0229-7

Baumgaertner, B., & Holthuijzen, W. (2016). On nonepistemic values in conservation biology. *Conserv Biol*. doi:10.1111/cobi.12756

Baumgaertner, B. O., Tyson, R. T., & Krone, S. M. (2016). Opinion strength influences the spatial dynamics of opinion formation. *The Journal of Mathematical Sociology*, 1-12. doi:10.1080/0022250X.2016.1205049

Benestan, L. M., Ferchaud, A. L., Hohenlohe, P. A., Garner, B. A., Naylor, G. J., Baums, I. B., . . . Luikart, G. (2016). Conservation genomics of natural and managed populations: building a conceptual and practical framework. *Mol Ecol, 25*(13), 2967-2977. doi:10.1111/mec.13647

Borgogna, T. R., Borgogna, J. L., Mielke, J. A., Brown, C. J., Top, E. M., Botts, R. T., & Cummings, D. E. (2016). High Diversity of CTX-M Extended-Spectrum beta-Lactamases in Municipal Wastewater and Urban Wetlands. *Microbial Drug Resistance, 22*(4), 312-320. doi:10.1089/mdr.2015.0197

Brown, C. J., Quates, C. J., Mirabzadeh, C. A., Miller, C. R., Wichman, H. A., Miura, T. A., & Ytreberg, F. M. (2016). New Perspectives on Ebola Virus Evolution. *PLoS One, 11*(8). doi:ARTN e0160410

Chikh-Ali, M., Alruwaili, H., Pol, D. V., & Karasev, A. V. (2016). Molecular Characterization of Recombinant Strains of Potato virus Y From Saudi Arabia. *Plant Disease, 100*(2), 292-297. doi:10.1094/Pdis-05-15-0562-Re

Chikh-Ali, M., & Karasev, A. V. (2015). Immunocapture-Multiplex RT-PCR for the Simultaneous Detection and Identification of Plant Viruses and Their Strains: Study Case, Potato Virus Y (PVY). In C. Lacomme (Ed.), *Plant Pathology: Techniques and Protocols* (pp. 177-186). New York, NY: Springer New York.

Chikh-Ali, M., Naidu, R. A., & Karasev, A. V. (2015). First Report of Potato virus Y (PVY) Strain PVYC Associated with a Tomato Disease in Kenya. *Plant Disease, 100*(4), 864. doi:10.1094/PDIS-08-15-0890-PDN

Douglas, S. M., Chubiz, L. M., Harcombe, W. R., Ytreberg, F. M., & Marx, C. J. (2016). Parallel Mutations Result in a Wide Range of Cooperation and Community Consequences in a Two-Species Bacterial Consortium. *PLoS One, 11*(9), e0161837. doi:10.1371/journal.pone.0161837

Epstein, B., Jones, M., Hamede, R., Hendricks, S., McCallum, H., Murchison, E. P., . . . Storfer, A. (2016). Rapid evolutionary response to a transmissible cancer in Tasmanian devils. *Nature Communications, 7*, 12684. doi:10.1038/ncomms12684

Funk, W. C., Lovich, R. E., Hohenlohe, P. A., Hofman, C. A., Morrison, S. A., Sillett, T. S., . . . Andelt, W. F. (2016). Adaptive divergence despite strong genetic drift: genomic analysis of the evolutionary mechanisms causing genetic differentiation in the island fox (*Urocyon littoralis*). *Mol Ecol, 25*(10), 2176-2194. doi:10.1111/mec.13605

Hubbs, G. (2016). Teaching Philosophy by Designing a Wikipedia Page. In J. Oxley & R. Ilea (Eds.), *Experiential Learning in Philosophy*: Taylor & Francis.

Garrett, A. M., Tadenev, A. L., Hammond, Y. T., Fuerst, P. G., & Burgess, R. W. (2016). Replacing the PDZ-interacting C-termini of DSCAM and DSCAML1 with epitope tags causes different phenotypic severity in different cell populations. *Elife, 5*. doi:10.7554/eLife.16144

Gerritsen, A. T., New, D. D., Robison, B. D., Rashed, A., Hohenlohe, P., Forney, L., . . . Settles, M. L. (2016). Full Mitochondrial Genome Sequence of the Sugar Beet Wireworm *Limonius californicus* (Coleoptera: Elateridae), a Common Agricultural Pest. *Genome Announc, 4*(1). doi:10.1128/genomeA.01628-15

Gillies, K., Krone, S. M., Nagler, J. J., & Schultz, I. R. (2016). A Computational Model of the Rainbow Trout Hypothalamus-Pituitary-Ovary-Liver Axis. *PLoS Comput Biol, 12*(4), e1004874. doi:10.1371/journal.pcbi.1004874

Greene, C. S., Foster, J. A., Stanton, B. A., Hogan, D. A., & Bromberg, Y. (2016). Computational Approaches to Study Microbes and Microbiomes. *Pac Symp Biocomput, 21*, 557-567.

Hagey, T. J., Puthoff, J. B., Crandell, K. E., Autumn, K., & Harmon, L. J. (2016). Modeling observed animal performance using the Weibull distribution. *Journal of Experimental Biology, 219*(11), 1603-1607. doi:10.1242/jeb.129940

Harcombe, W. R., Betts, A., Shapiro, J. W., & Marx, C. J. (2016). Adding biotic complexity alters the metabolic benefits of mutualism. *Evolution, 70*(8). doi:10.1111/evo.12973

Hickey, R., & Forney, L. (2016). Gardnerella vaginalis does not always cause bacterial vaginosis. *Journal of Infectious Diseases*.

Hunter, S. S., Settles, M. L., New, D. D., Parent, C. E., & Gerritsen, A. T. (2016). Mitochondrial Genome Sequence of the Galapagos Endemic Land Snail *Naesiotus nux*. *Genome Announc, 4*(1). doi:10.1128/genomeA.01362-15

Jayaram, A., Witkin, S. S., Zhou, X., Brown, C. J., Rey, G. E., Linhares, I. M., . . . Forney, L. J. (2016). The bacterial microbiome in paired vaginal and vestibular samples from women with vulvar vestibulitis syndrome. *Pathog Dis, 72*(3), 161-166. doi:10.1111/2049-632X.12197

Jensen, P. K., Wujcik, C. E., McGuire, M. K., & McGuire, M. A. (2016a). Validation of reliable and selective methods for direct determination of glyphosate and aminomethylphosphonic acid in milk and urine using LC-MS/MS. *J Environ Sci Health B, 51*(4), 254-259. doi:10.1080/03601234.2015.1120619

Jensen, P. K., Wujcik, C. E., McGuire, M. K., & McGuire, M. A. (2016b). Validation of reliable and selective methods for direct determination of glyphosate and aminomethylphosphonic acid in milk and urine using LC-MS/MS. *Journal of Environmental Science and Health Part B-Pesticides Food Contaminants and Agricultural Wastes, 51*(4), 254-259. doi:10.1080/03601234.2015.1120619

Kim, M. S., Hohenlohe, P. A., Kim, K. H., Seo, S. T., & Klopfenstein, N. B. (2016). Genetic diversity and population structure of *Raffaelea quercus-mongolicae*, a fungus associated with oak mortality in South Korea. *Forest Pathology, 46*(2), 164-167. doi:10.1111/efp.12263

Li, H., Xu, Z., Yang, S., Li, X., Top, E. M., Wang, R., . . . Jiang, Y. (2016). Responses of Soil Bacterial Communities to Nitrogen Deposition and Precipitation Increment Are Closely Linked with Aboveground Community Variation. *Microb Ecol, 71*(4), 974-989. doi:10.1007/s00248-016-0730-z

Li, S., Mitchell, J., Briggs, D. J., Young, J. K., Long, S. S., & Fuerst, P. G. (2016). Morphological Diversity of the Rod Spherule: A Study of Serially Reconstructed Electron Micrographs. *PLoS One, 11*(3), e0150024. doi:10.1371/journal.pone.0150024

Li, S., Woodfin, M., Long, S. S., & Fuerst, P. G. (2016). IPLaminator: an ImageJ plugin for automated binning and quantification of retinal lamination. *BMC Bioinformatics, 17*, 36. doi:10.1186/s12859-016-0876-1

Li, X., Wang, Y., Brown, C. J., Yao, F., Jiang, Y., Top, E. M., & Li, H. (2016). Diversification of broad host range plasmids correlates with the presence of antibiotic resistance genes. *FEMS Microbiology Ecology, 92*(1). doi:10.1093/femsec/fiv151

Loftie-Eaton, W., Yano, H., Burleigh, S., Simmons, R. S., Hughes, J. M., Rogers, L. M., . . . Top, E. M. (2015). Evolutionary paths that expand plasmid host-range: implications for spread of antibiotic resistance. *Molecular Biology and Evolution*. doi:10.1093/molbev/msv339

Loftie-Eaton, W., Yano, H., Burleigh, S., Simmons, R. S., Hughes, J. M., Rogers, L. M., . . . Top, E. M. (2016). Evolutionary Paths That Expand Plasmid Host-Range: Implications for Spread of Antibiotic Resistance. *Molecular Biology and Evolution, 33*(4), 885-897. doi:10.1093/molbev/msv339

Magalhaes, I. S., D'Agostino, D., Hohenlohe, P. A., & MacColl, A. D. (2016). The ecology of an adaptive radiation of three-spined stickleback from North Uist, Scotland. *Mol Ecol, 25*(17), 4319-4336. doi:10.1111/mec.13746

Marx, H. E., Giblin, D. E., Dunwiddie, P. W., & Tank, D. C. (2016). Deconstructing Darwin's Naturalization Conundrum in the San Juan Islands using community phylogenetics and functional traits. *Diversity and Distributions, 22*(3), 318-331. doi:10.1111/ddi.12401

Mendes-Soares, H., Suzuki, H., Hickey, R. J., & Forney, L. J. (2016). Comparative Functional Genomics of Lactobacillus spp. Reveals Possible Mechanisms for Specialization of Vaginal Lactobacilli to Their Environment. *Journal of Bacteriology, 196*(7), 1458-1470. doi:10.1128/Jb.01439-13

Michelle K McGuire, M. A. M., William J Price,Bahman Shafii,Janae M Carrothers,Kimberly A Lackey,Daniel A Goldstein,Pamela K Jensen,John L Vicini. (2016). Glyphosate and aminomethylphosphonic acid are not detectable in human milk. *The American journal of clinical nutrition, 103*, 1285-1290.

Michener, J. K., Vuilleumier, S., Bringel, F., & Marx, C. J. (2016). Transfer of a Catabolic Pathway for Chloromethane in Methylobacterium Strains Highlights Different Limitations for Growth with Chloromethane or with Dichloromethane. *Frontiers in Microbiology, 7*. doi:ARTN 1116

Miler, C. R., Johnson, E. L., Burke, A. Z., Martin, K. P., Miura, T. A., Wichma, H. A., . . . Ytreberg, F. M. (2016). Initiating a watch list for Ebola virus antibody escape mutations. *Peerj, 4*. doi:ARTN e1674

Miller, C. R., Nagel, A. C., Scott, L., Settles, M., Joyce, P., & Wichman, H. A. (2016). Love the one you're with: replicate viral adaptations converge on the same phenotypic change. *Peerj, 4*. doi:ARTN e2227

Murdoch, B. M., & Murdoch, G. K. (2016). Genetics of Prion Disease in Cattle. *Bioinformatics and Biology Insights, 9*, 1-10. doi:10.4137/BBi.s29678

Nayak, D. D., Agashe, D., Lee, M. C., & Marx, C. J. (2016). Selection Maintains Apparently Degenerate Metabolic Pathways due to Tradeoffs in Using Methylamine for Carbon versus Nitrogen. *Current Biology, 26*(11), 1416-1426. doi:10.1016/j.cub.2016.04.029

Nuismer, S. L., & Dybdahl, M. F. (2016). Quantifying the coevolutionary potential of multistep immune defenses. *Evolution, 70*(2), 282-295. doi:10.1111/evo.12863

Paff, M. L., Nuismer, S. L., Ellington, A., Molineux, I. J., & Bull, J. J. (2016). Virus wars: using one us to block the spread of another. *Peerj, 4*. doi:ARTN e2166

Ravel, J., Brotman, R. M., Gajer, P., Ma, B., Nandy, M., Fadrosh, D. W., . . . Forney, L. J. (2016). Daily temporal dynamics of vaginal microbiota before, during and after episodes of bacterial vaginosis. *Microbiome, 1*(1), 29. doi:10.1186/2049-2618-1-29

Rezamand, P., Hatch, B. P., Carnahan, K. G., & McGuire, M. A. (2016). Effects of alpha-linolenic acid-enriched diets on gene expression of key inflammatory mediators in immune and milk cells obtained from Holstein dairy cows. *Journal of Dairy Research, 83*(1), 20-27. doi:10.1017/S0022029915000709

Ridenhour, B. J., and E.M. Top. (2016). Plasmid driven evolution of Bacteria. In R. M. Kliman (Ed.), *The Encyclopedia of Evolutionary Biology:* Elsevier.

Robison, B. D., Soule, T., Streett, D., Mirabzadeh, C. A., & Wood, N. (2016). *Implementing evolution in video games*. Paper presented at the Games Learning Society, Madison, WI.

Rondon, S. I., Roster, M. S., Hamlin, L. L., Green, K. J., Karasev, A. V., & Crosslin, J. M. (2016). Characterization of Beet curly top virus Strains Circulating in Beet Leafhoppers (Hemiptera: Cicadellidae) in Northeastern Oregon. *Plant Disease, 100*(8), 1586-1590. doi:10.1094/Pdis-10-15-1189-Re

Rutledge, L. Y., Devillard, S., Hohenlohe, P. A., & White, B. N. (2016). Considering all the evidence: a reply to Sefc and Koblmüller (2016). *Biology Letters, 12*(2). doi:10.1098/rsbl.2015.1009

Shen, J., Song, N., Williams, C. J., Brown, C. J., Yan, Z., Xu, C., & Forney, L. J. (2016). Effects of low dose estrogen therapy on the vaginal microbiomes of women with atrophic vaginitis. *Scientific Reports, 6*. doi:ARTN 24380

Shen, J., Song, N., Williams, C. J., Brown, C. J., Yan, Z., Xu, C., & Forney, L. J. (2016). Effects of low dose estrogen therapy on the vaginal microbiomes of women with atrophic vaginitis. *Scientific Reports, 6*, 24380. doi:10.1038/srep24380

Simmons, A. B., Bloomsburg, S. J., Billingslea, S. A., Merrill, M. M., Li, S., Thomas, M. W., & Fuerst, P. G. (2016). Pou4f2 knock-in Cre mouse: A multifaceted genetic tool for vision researchers. *Mol Vis, 22*, 705-717.

Singer, M. L., Oreschak, K., Rhinehart, Z., & Robison, B. D. (2016). Anxiolytic effects of fluoxetine and nicotine exposure on exploratory behavior in zebrafish. *PeerJ Preprints, 4*, e1718v1712.

Soule, T., Robison, B. D., & Heckendorn, R. B. (2016). *Co-evolution of Sensor Morphology and Behavior*. Paper presented at the Proceedings of the 2016 on Genetic and Evolutionary Computation Conference Companion, Denver, Colorado, USA.

Trumbo, D. R., Epstein, B., Hohenlohe, P. A., Alford, R. A., Schwarzkopf, L., & Storfer, A. (2016). Mixed population genomics support for the central marginal hypothesis across the invasive range of the cane toad (*Rhinella marina*) in Australia. *Mol Ecol, 25*(17), 4161-4176. doi:10.1111/mec.13754

Uribe-Convers, S., Settles, M. L., & Tank, D. C. (2016). A Phylogenomic Approach Based on PCR Target Enrichment and High Throughput Sequencing: Resolving the Diversity within the South American Species of *Bartsia* L. (Orobanchaceae). *PLoS One, 11*(2), e0148203. doi:10.1371/journal.pone.0148203

Uribe-Convers, S., & Tank, D. C. (2016). Phylogenetic Revision of the Genus *Bartsia* (Orobanchaceae): Disjunct Distributions Correlate to Independent Lineages. *Systematic Botany, 41*(3). doi:10.1600/036364416X692299

Villasante, A., Powell, M. S., Murdoch, G. K., Overturf, K., Cain, K., Wacyk, J., & Hardy, R. W. (2016). Effect of anthocyanidins on myogenic differentiation in induced and non-induced primary myoblasts from rainbow trout (*Oncorhynchus mykiss*). *Comp Biochem Physiol B Biochem Mol Biol, 196-197*, 102-108. doi:10.1016/j.cbpb.2016.03.004

Yano, H., Wegrzyn, K., Loftie-Eaton, W., Johnson, J., Deckert, G. E., Rogers, L. M., . . . Top, E. M. (2016). Evolved plasmid-host interactions reduce plasmid interference cost. *Mol Microbiol, 101*(5), 743-756. doi:10.1111/mmi.13407

2015

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

Ausband D, Stansbury CR, Stenglein JL, Struthers JL, & Waits LP. Recruitment in a social carnivore before and after harvest. Animal Conservation. (in press).

Bao X, Johnson JL, & Rao H. Rad25 protein is targeted for degradation by the Ubc4-Ufd4 pathway. Journal of Biological Chemistry. 2015; 290:8606-8612.

Beck D, Dennis C, & Foster JA. Seed: a user-friendly tool for exploring and visualizing microbial community data. Bioinformatics. 2015; 31:602-603.

Bohling JH, Beyer A, & Waits LP. Factors influencing red wolf-coyote hybridization in eastern North Carolina. Biological Conservation. 2015; 184:108-116.

Bull JJ, Crandall C, Rodriguez A, & Krone SM. Models for the directed evolution of bacterial allelopathy: bacteriophage lysins. PeerJ. 2015; 3, e879.

Buzbas EO, & Rosenberg NA. AABC: Approximate approximate Bayesian computation for inference in population-genetic models. Theoretical Population Biology. 2015; 99:31-42.

Carroll SM, Chubiz LM, Agashe D, & Marx CJ. Parallel and divergent evolutionary solutions for the optimization of an engineered central metabolism in *Methylobacterium extorquens* AM1. Microorganisms. 2015; 3:52-174.

Carrothers JM, York MA, Brooker SL, Lackey KA, Williams JE, Shafii B, ... & McGuire MK. Fecal microbial community structure is stable over time and related to variation in macronutrient and micronutrient intake in lactating women. The Journal of Nutrition. 2015; jn211110.

Chou HH, Marx CJ, & Sauer U. Transhydrogenase promotes the robustness and evolvability of e. coli deficient in nadph production. PLoS Genetics. 2015; 11:e1005007-e1005007.

DeBlasio SL, Johnson R, Sweeney MM, Karasev A, Gray SM, MacCoss MJ, & Cilia M. Potato leafroll virus structural proteins manipulate overlapping, yet distinct protein interaction networks during infection. Proteomics. 2015.

Chapalamadugu KC, Murdoch BM, Robison BD, Hill RA, & Murdoch GK. *Oncorhynchus mykiss* pax7 sequence variations with comparative analyses against other teleost species. SpringerPlus.

DeMay SM, Rachlow JL, Waits LP, & Becker PA. Comparing telemetry and fecal DNA sampling methods to quantify survival and dispersal of juvenile pygmy rabbits. Wildlife Society Bulletin. 2015; 39:413-421.
Dhakal S, Stevens CB, Sebbagh M, Weiss O, Frey RA, Adamson S, ... & Stenkamp DL. Abnormal retinal development in Cloche mutant zebrafish. Developmental Dynamics. 2015.

Domer MC, Beerman KA, Ahmadzadeh A, Dasgupta N, Williams JE, McGuire, MA, & McGuire MK. Loss of body fat and associated decrease in leptin in early lactation are related to shorter duration of postpartum anovulation in healthy US women. Journal of Human Lactation. 2015; 0890334414565794.

Escalante-Chong R, Savir Y, Carroll SM, Ingraham JB, Wang J, Marx CJ, & Springer M. Galactose metabolic genes in yeast respond to a ratio of galactose and glucose. Proceedings of the National Academy of Sciences. 2015; 112:1636-1641.

Fortenberry JD, Hickey R, & Forney L. Reply to “Accuracy of Self-Report of Sexual Activity among Adolescent Girls: Implications for Interpretation of Vaginal Flora Patterns”. mBio. 2015; 6.

Gese EM, Knowlton FF, Adams JR, Beck K, Fuller TK, Murray DL, Steury T, Stoskopf MK, Waddell W, & Waits LP. Managing hybridization in endangered species recovery: The case of the red wolf. Current Zoology 2015; 61:191-205.

Hagey, TJ, Cole N, Davidson D, Henricks A, Harmon LL, & Harmon LJ. Temporal variation in structural microhabitat use of *Phelsuma* geckos in mauritius. Journal of Herpetology. 2015.

Hand BK Hether TD, Kovach RP, Muhlfeld CC, Amish SJ, Boyer MC, O'Rourke SM, Miller MR, Lowe WH, Hohenlohe PA, & Luikart G. Genomics and introgression: Discovery and mapping of thousands of species-diagnostic SNPs using RAD sequencing. Current Zoology 2015; 61:146-154.

Hardwick KM, Harmon LJ, Hardwick SD, & Rosenblum EB. When field experiments yield unexpected results: lessons learned from measuring selection in white sands lizards. PloS One. 2015; 10.

Harmon LJ, & Harrison S. Species diversity is dynamic and unbounded at local and continental scales. The American Naturalist. 2015; 185:584-593.

Hickey RJ, Zhou X, Settles ML, Erb J, Malone K, Hansmann MA, ... & Forney LJ. Vaginal microbiota of adolescent girls prior to the onset of menarche resemble those of reproductive- age women. mBio. 2015; 6:e00097-15.

Garud NR, Messer PW, Buzbas EO, & Petrov DA. Recent selective sweeps in North American *Drosophila melanogaster* show signatures of soft sweeps. PLoS Genetics. 2015; 11:e1005004.

Hunter SS, Lyon RT, Sarver BA, Hardwick K, Forney LJ, & Settles ML. Assembly by Reduced Complexity (ARC): a hybrid approach for targeted assembly of homologous sequences. bioRxiv. 2015; 014662.

Kebaabetswe LP, Haick AK, Gritsenko MA, Fillmore TL, Chu RK, Purvine SO., ... & Miura TA. Proteomic analysis reveals down-regulation of surfactant protein B in murine type II pneumocytes infected with influenza A virus. Virology. 2015; 483:96-107.

Liang S, Gliniewicz K, Mendes-Soares H, Settles ML, Forney LJ, Coats ER, & McDonald AG. Comparative analysis of microbial community of novel lactic acid fermentation inoculated with different undefined mixed cultures. Bioresource Technology. 2015; 179:268-274.

Lonsinger RC, Gese EM, Dempsey SJ, Kluever M, Johnson TR, & Waits LP. Balancing sample accumulation and DNA degradation rates to optimize noninvasive genetic sampling of sympatric carnivores. Molecular Ecology Resources. 2015.

Lonsinger RC, Gese, EM, & Waits LP. Evaluating the reliability of field identification and morphometric classifications for carnivore scats confirmed with genetic analysis. Wildlife Society Bulletin. (in press).

Ma ZS, Guan Q, Ye C, Zhang C, Foster JA, & Forney LJ. Network analysis suggests a potentially/evil/'alliance of opportunistic pathogens inhibited by a cooperative network in human milk bacterial communities. Scientific Reports. 2015; 5.

MacPherson A, Hohenlohe PA, & Nuismer SL. Trait dimensionality explains widespread variation in local adaptation. Proceedings of the Royal Society of London B: Biological Sciences. 015; 282(1802):20141570.

Marx HE, Giblin DE, Dunwiddie PW, Tank. DC. Deconstructing Darwin's Naturalization Conundrum in the San Juan Islands using community phylogenetics and functional traits. Diversity and Distributions. 2015. (in press).

McGuire MK, & McGuire MA. (Human milk: Mother nature's prototypical probiotic food?. Advances in Nutrition: An International Review Journal. 2015; 6:112-123.

Mendes-Soares H, Krishnan V, Settles ML, Ravel J, Brown CJ, & Forney LJ. Fine-scale analysis of 16S rRNA sequences reveals a high level of taxonomic diversity among vaginal Atopobium spp. Pathogens and Disease. 2015; 73.

Loftie-Eaton W, Suzuki H, Bashford K, Heuer H, Stragier P, De Vos P, ... & Top EM. Draft genome sequence of *Pseudomonas* sp. nov. H2. Genome Announcements. 2015; 3:e00241-15.

Metzger G, Espíndola A, Waits LP, & Sullivan J. Genetic structure across broad spatial and temporal scales: Rocky Mountain tailed frogs (*Ascaphus montanus*; Anura: Ascaphidae) in the inland temperate rainforest. Journal of Heredity. doi:10.1093/jhered/esv061

Michener JK & Marx CJ. After horizontal gene transfers, metabolic pathways may need further optimization. Microbe. 2015; 10:61–67.

Mitchell DM, Stevens CB, Frey RA, Hunter SS, Ashino R, Kawamura S, & Stenkamp, DL. Retinoic acid signaling regulates differential expression of the tandemly-duplicated long wavelength- sensitive cone opsin genes in zebrafish. PLoS Genetics. 2015; 11:e1005483.

Mumma MA, Zieminski C, Fuller T, Mahoney SP, & Waits LP. Evaluating noninvasive genetic sampling techniques to estimate large carnivore abundance. Molecular Ecology Resources. 2015; 15:1133–1144.

Murray DL, Bastille-Rousseau G, Adams JR, & Waits LP. The challenges of red wolf conservation and the fate of an endangered species recovery program. Conservation Letters. 2015.

Nayak DD, & Marx CJ. Experimental horizontal gene transfer of methylamine dehydrogenase mimics prevalent exchange in nature and overcomes the methylamine growth constraints posed by the sub-optimal n-methylglutamate pathway. Microorganisms. 2015; 3:60-79.

Neuendorf E, Gajer P, Bowlin AK, Marques PX, Ma B, Yang H, ... & Ravel J. Chlamydia caviae infection alters

abundance but not composition of the guinea pig vaginal microbiota. Pathogens and Disease. 2015; 73.

Nuismer SL, & Harmon LJ. Predicting rates of interspecific interaction from phylogenetic trees. Ecology Letters. 2015; 18:17-27.

Nürk NM, Uribe-Convers S, Gehrke B, Tank DC, & Blattner FR. Oligocene niche shift, Miocene diversification–cold tolerance and accelerated speciation rates in the St. John's Worts (Hypericum, Hypericaceae). BMC Evolutionary Biology. 2015; 15:80.

Roches S, Harmon LJ, & Rosenblum EB. Colonization of a novel depauperate habitat leads to trophic niche shifts in three desert lizard species. Oikos. 2015.

Rosindell J, Harmon LJ, & Etienne RS. Unifying ecology and macroevolution with individual-based theory. Ecology Letters. 2015; 18:472-482.

Rowley JS, Gray SM, & Karasev, AV. Screening potato cultivars for new sources of resistance to Potato virus Y. American Journal of Potato Research. 2015; 92:38-48.

Rutledge LY, Devillard S, Boone JQ, Hohenlohe PA, & White, BN. RAD sequencing and genomic simulations resolve hybrid origins within North American *Canis*. Biology Letters. 2015; 11: 20150303.

Shaver I, Chain-Guadarrama A, Cleary K, Sanfiorenzo A, Santiago-Garcia R, Finegan B, Hormel L, Sibelet N, Vierling LA, Bosque-Perez N, Fagan ME, DeClerck F, & Waits LP. Coupled social and ecological outcomes of agricultural intensification in Costa Rica and the future of biodiversity conservation in tropical agricultural regions. Global Environmental Change. 2015.

Spear SF, Groves JD, Williams LA, & Waits LP. Using environmental DNA methods to improve detectability in a hellbender (Cryptobranchus alleganiensis) monitoring program. Biological Conservation. 2015; 183:38-45.

Stenkamp-Strahm CM, Nyavor YE, Kappmeyer AJ, Horton S, Gericke M, & Balemba OB. Prolonged high fat diet ingestion, obesity, and type 2 diabetes symptoms correlate with phenotypic plasticity in myenteric neurons and nerve damage in the mouse duodenum. Cell and Tissue Research. 2015; 1-16.

Tank DC, Eastman JM, Pennell MW, Soltis PS, Soltis DE, Hinchliff CE, ... & Harmon LJ. Nested radiations and the pulse of angiosperm diversification: increased diversification rates often follow whole genome duplications. New Phytologist. 2015; 207:454-467.

Tenge VR, Zuehlke AD, Shrestha N, & Johnson,JL. The Hsp90 cochaperones Cpr6, Cpr7, and Cns1 interact with the intact ribosome. Eukaryotic Cell. 2015; 14:55-63.

Wojtowicz AJ, Miller CR, & Joyce P. Inference for one-step beneficial mutations using next generation sequencing. Statistical Applications in Genetics and Molecular Biology; 2015; 14:65- 81.

Woodruff S, Johnson T, & Waits LP. Evaluating the interaction of faecal pellet deposition rates and DNA degradation rates to optimize sampling design for DNA-based mark-recapture analysis of Sonoran pronghorn. Molecular Ecology Resources. 2015.

Yahvah KM, Brooker S L, Williams JE, Settles ML, McGuire MA, & McGuire MK. Elevated dairy fat intake in lactating women alters milk lipid and fatty acids without detectible changes in expression of genes related to lipid uptake or synthesis. Nutrition Research. 2015; 35:221-228.

Uribe-Convers S, & Tank DC. Shifts in diversification rates linked to biogeographic movement into new areas, an example of disparate continental distributions and a recent radiation in the Andes. bioRxiv. 2015; 019554.

Uribe-Convers S, Settles ML, & Tank DC. A targeted subgenomic approach for phylogenomics based on microfluidic PCR and high throughput sequencing. bioRxiv. 2015; 021246.

Zanne AE, Tank DC, Cornwell WK, Eastman JM, Smith SA, FitzJohn RG ... & Beaulieu JM. (2015). Zanne et al. reply. Nature. 2015; 521(7552):E6-E7.

Zhan YA, & Ytreberg FM. The cis conformation of proline leads to weaker binding of a p53 peptide to MDM2 compared to trans. Archives of Biochemistry and Biophysics. 2015; 575:22- 29.

Zhbannikov IY, & Foster JA. MetAmp: combining amplicon data from multiple markers for OTU analysis. Bioinformatics. 2015; 31:1830-1832.

Appendix 10. BEACON Awards for FY 2016

FY 2016 IBEST Beacon Awards				
Awardee	**Title**	**Direct**	**F&A**	**Total**
Dr. James Foster	Idaho Administrative Support Yr 6	$64,996	$29,443	$94,439
Dr. Holly Wichman	Evolution of Cultured Stem Cells	$33,902	$15,357	$49,259
Dr. Robert Heckendorn	Using Evolution to Manage Real-time Evacuation Planning	$34,700	$15,719	$50,419
Dr. Deb Stenkamp	Evolution of sensory systems in response to loss of visual information	$16,081	$7,285	$23,366
Dr. Eva Top	Identifying the reservoirs of antibiotic resistance	$25,930	$10,489	$36,419
Dr. Holly Wichman	Rapid analysis of parasite dynamics and evolution in arthropod populations	$51,474	$23,318	$74,792
Dr. Holly Wichman	Predicting non-functional mutations in protein complexes	$65,977	$29,888	$95,865
Dr. Chris Marx	What Does The Flux Say: Empirical Validation of Flux Balance Analysis	$16,657	$7,545	$24,202
Dr. Terry Soule	Teaching Evolution Through Game Based Simulation	$38,580	$17,477	$56,057
	Totals	**$348,297**	**$156,521**	**$504,818**

Appendix 11. Review Criteria and Policies Governing Clinical Faculty

1. ANNUAL REVIEW

All clinical IBEST faculty will undergo an annual review by the Director in January of each year, based on his/her *Position Description* (see below) and *Accomplishments Form* (see below) from the previous year. Evaluations from any courses taught the previous year will be considered in this review as will any input provided by collaborating regular faculty. This review will use the current UI *Annual Performance Evaluation Form* and include a narrative consisting of evaluative comments.

2. THIRD-YEAR REVIEW

All IBEST clinical faculty will undergo an in-depth review to begin 24 months after beginning UI employment. This will be conducted by the Institute or Academic Unit in which he or she is appointed. The purpose of this review shall be to inform the person of her/his progress toward attainment promotion.

The candidate is responsible for compiling the following information: current UI standard format curriculum vitae (CV), the most recent syllabus from any courses or workshops taught, a professional portfolio, and selected publications. The Institute will provide: all position descriptions, all annual performance evaluations, all mentoring reports, and all course/workshop evaluations. The combined materials provided by the candidate and department will form the review packet.

The Third Year Review Committee committee shall be composed of three tenured faculty from the Institute, and all members must be in attendance to conduct a meeting. The committee will study the information within the candidate's review file to determine compliance with the *Promotion Criteria* (described below). At its discretion, the Committee may require the candidate to meet in person and address questions about his or her record. At the conclusion of their review, the Committee will submit a written evaluation containing a recommendation (satisfactory/unsatisfactory progress) to the Institute Director or Department Chair, who will forward the Committee's written review and her/his written evaluation to the Dean of CoS; copies will also be sent to the candidate. In the event of a jointly-appointed person being reviewed (i.e., other academic program) the Committee's written review will be sent to the appropriate program administrator.

2. REVIEW FOR PROMOTION

a) Timing and Purpose: All clinical assistant professors will be reviewed after their fifth full year of UI employment. This will be conducted by the Institute or Academic Unit in which he or she is appointed. Consideration for promotion can be postponed with provost approval (see *FSH 3520 F9*). The purpose of this review shall be to consider promotion to the rank of clinical associate professor.

The candidate is responsible for compiling the following information: current UI standard format curriculum vitae (CV), the most recent syllabus from any workshops, a professional portfolio, and

selected publication reprints. The Institute will provide: all position descriptions, all annual performance evaluations, all mentoring reports, all workshop teaching evaluations (if not provided by the candidate), external review letters, and third year review evaluation. The combined materials provided by the candidate and Institute will form the review packet.

All clinical associate professors will be reviewed six years after being promoted from clinical assistant professor. With provost approval, these tenure/promotion reviews may be postponed (see *FSH 3520 F9*). The purpose of this review shall be to determine the awarding of promotion to the rank of clinical professor. All other aspects of this review will be similar to those described above for clinical assistant professors.

b) Promotion Review Committee Composition: The Promotion Review Committee will consist of three (3) tenured faculty selected as described above for the Third Year review. This committee will also contain one additional individual, an untenured faculty member that holds a position similar to the candidate. The Institute Director, in consultation with the candidate, will choose this person. The committee will choose among the three tenured faculty one member to serve as the committee chairperson.

c) Promotion Review Committee Procedures: This committee must have at least three (3) members in attendance to conduct a meeting. The Promotion Review Committee will study the information within the candidate's review packet to determine compliance with the *Promotion Criteria* described below. All procedures will be similar to those described above for the Third Year Review, the only difference being that the Committee's written evaluation will contain a recommendation for/against promotion to the next higher rank and will be included in the candidate's packet for review by all faculty in advance of a vote.

d) Promotion Vote: An IBEST faculty meeting will be held after the Promotion Review Committee evaluation is complete at which time the candidate will be excused and all faculty invited to provide comments. At the conclusion of this discussion, a vote will be conducted by all faculty at or above the proposed rank via paper ballot.

e) Institute Reporting: The Institute Director, in consultation with the Associate Director, will prepare her/his evaluation containing the vote results and submit this report the evaluation of Promotion Review Committee to the College of Science Dean (i.e., submit two written evaluations), with copies to the candidate.

3. PROMOTION CRITERIA

The criteria for promotion of clinical faculty are, to a large extent, unique to each position. As such, position-specific criteria will be appended to hiring documents on a case-by-case basis, and will be structured following individual position descriptions. However, in general, the following guidelines will apply.

Teaching and Advising

There should be clear evidence that:

- The content and organization of each workshop or course is appropriate.

- Each workshop/course represents a comprehensive and up-to-date distillation of the subject area.

- Each workshop/course is rigorous and challenging.

Evaluation of workshop performance or teaching shall be based on:

i) Evidence from the course or workshop: including, as appropriate, the syllabus, assignments, examinations, or literature used.
ii) Peer-evaluation of teaching: a written report(s) by the peer evaluators based upon attendance in two (or more) lectures.
iii) Course or workshop assessment.

Scholarship

There should be clear evidence that the candidate has established a strong, independent research program. The requirement for independence is not intended to exclude collaborative and/or interdisciplinary research. There should also be clear evidence that the candidate has contributed effectively to the Department's graduate program.

The first line of evidence is the record of peer-reviewed publications and other research products (e.g. other publications, software, data sets, biological resources, other citable products) based upon work performed at UI. No specific number of research products is required. Rather, the quality of the venue in which they are published will be weighted by the percentage research effort indicated in the candidate's position description. The candidate should describe his/her specific contribution to each multi-author product.

The second line of evidence will be the reports of the external reviewers. This evidence is to indicate whether the external academic community views the candidate's reputation as solid and the candidate's research as significant.

The third line of evidence will be the quality of undergraduate, graduate or post-doctoral mentoring.

The fourth line of evidence will be the candidate's record pursuing extramural research funding.

Service and Citizenship

The Institute expects that the candidate will have honored reasonable requests to participate on committees as deemed appropriate by the Director. Service to the scientific community such as review of manuscripts or grant proposals, panel service for granting agencies, professional societies (e.g., executive committee service), and other outreach activities is expected. In addition, the Director and Associate Director will assess the management and financial strength of the GRC.

Adminstration

The Director and Associate Director will assess the performance of administrative duties for candidates with administrative responsibilities, relative to the candidate's position description.

4. POSITION DESCRIPTION POLICY

During each year, each clinical faculty member will be required to update his or her annual *Position Description* for the next year. The *Position Description* will reflect courses to be taught (if any), students to be advised, scholarship activities planned, outreach, administrative, and university service and leadership commitments.

The Institute Director will review each clinical faculty member's *Position Description* and, when required, in consultation with the faculty member revise this document as necessary to meet the Institute's teaching, administrative, research and service obligations. To be valid, the *Position Description* must be signed by the faculty member, Director, and any joint appointment administrator (if applicable), and the Dean of CoS.

5. ANNUAL ACCOMPLISHMENTS POLICY

In December of each year, every clinical faculty member will be required to complete his or her *Accomplishments Form* for that calendar year. The completed *Accomplishments Form* will be due by the end of that fall semester. This document is an important component used for the Annual Review.