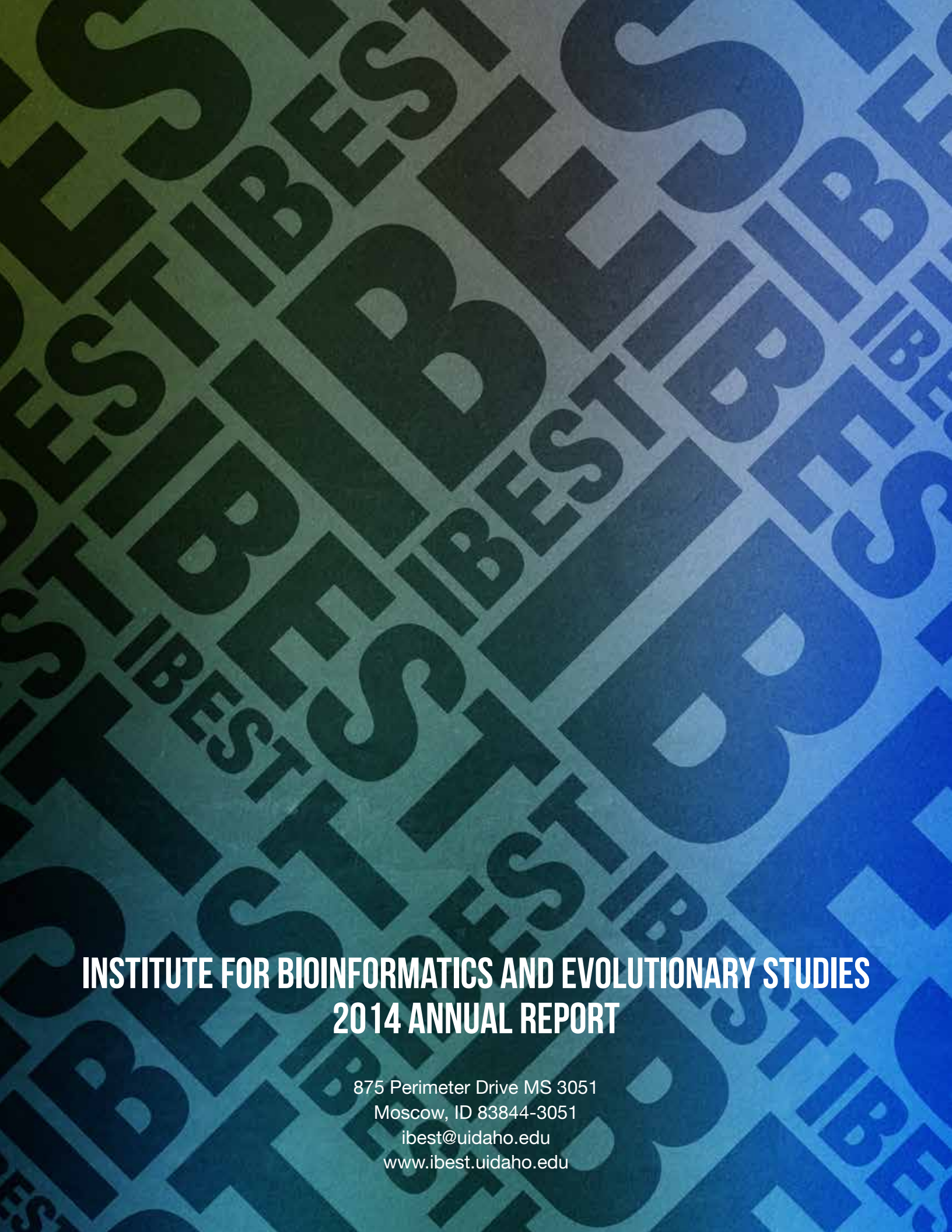

INSTITUTE FOR BIOINFORMATICS AND EVOLUTIONARY STUDIES
2014 ANNUAL REPORT

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IBEST OVERVIEW

Here we report the accomplishments of the Institute for Bioinformatics and Evolutionary Studies (IBEST) for fiscal year 2013-14 (for financial information) and the calendar year 2014 for programmatic activities. The report is organized according to the four elements of IBEST's mission, namely:

- Facilitate interdisciplinary research on evolutionary processes at different levels of biological complexity ranging from studies on the molecular processes of evolutionary change to the adaptation of organisms on a landscape level.
- Establish and nurture strategic collaborations or partnerships with research groups across the United States and abroad.
- Maintain and enhance the capabilities of core facilities for DNA sequence analysis, bioinformatics, and optical imaging and facilitate their use by investigators across campus.
- Promote graduate and undergraduate education in bioinformatics and computational biology at the University of Idaho.

I B E S T

FACILITATE INTERDISCIPLINARY RESEARCH

STRATEGIC REINVESTMENTS

During the past year a total of $488,928 was strategically reinvested in research related to the IBEST theme of 'real-time' evolution. The investments fell into a handful of categories including (a) the recruitment and retention of faculty; (b) creation of new research opportunities (pilot grants, technology access grants, and travel and collaboration grants); and (c) professional development workshops and seminars.

FUNDING SOURCES

In accordance with the institute charter, 50% of the F&A (indirect costs) earned from grants related to 'real-time' evolution and administered by IBEST was returned to the institute. The majority of these funds were reinvested in people and programs to enable and stimulate interdisciplinary research activities, faculty development, and graduate student education as described elsewhere in this report. As in years past a small portion of the earned F&A was passed through to principal investigators, co-principal investigators and their academic departments. The amounts returned to investigators and their departments were based on the amount of F&A earned from their grants.

The UI Office of Research and Economic Development (ORED) provided direct support of IBEST in FY13-14. These funds have been used to subsidize the salaries of administrative and core facility staff. The remainder was used to support the BCB graduate program, mostly in the form of graduate student stipends and travel grants. Separately ORED also paid the salaries and fringe benefits of the directors of the Mass Spectrometry Core and the Optical Imaging Core as well as the service contract costs on instruments in these facilities.

Funds from the NIH COBRE grant were used to fund three sorts of grant opportunities: (a) pilot grants, (b) technology access grants, and (c) travel and collaboration grants.

EXPENDITURES OF FUNDS

Our largest investments have been made in the recruitment and retention of faculty. This is based on the premise that investments in talented new investigators will yield high returns in the future. These funds have mostly been used for the salaries and research program start-up funds provided to new faculty members.

TARGETED AND CLUSTER HIRES

In an effort to bolster systems biology research at the UI, the College of Science conducted a targeted search for an established, mid-career scientist with expertise in systems biology and coordinated a cluster hire of three new faculty in the Departments of Mathematics, Statistics, and Physics. IBEST played a prominent role in the recruitment of these individuals.

Dr. Chris Marx

Dr. Marx was a targeted hire by the Department of Biological Sciences. His research program is focused on

evolutionary systems biology wherein new functional genomics approaches are used to investigate the physiology of adaptation of bacteria. This allows his research team to pursue a top-down approach to understanding the physiological changes that have occurred in bacterial strains with increased fitness, as well as a bottom-up approach in which genomic data are used to identify and understand how mutations affect fitness.

The intellectual environment and core facilities of IBEST provide fertile ground for Dr. Marx's research and this played a large role in attracting him to the University of Idaho. Prior to joining the UI faculty Dr. Marx was an Associate Professor of Biology at Harvard University. His doctoral degree was earned under the mentorship of Dr. Mary Lidstrom at the University of Washington and he worked with Dr. Richard Lenski as a postdoctoral scientist from 2003-2005.

To build expertise in evolutionary and computational biology of complex systems the College of Science conducted a cluster hire of three faculty in the Departments of Mathematics, Statistics, and Physics faculty who have demonstrated that they can work across disciplines and collaborate broadly. The candidates were drawn to the interdisciplinary research environment of IBEST and the core facilities for high-level genomics, computing, imaging, and mass spectrometry that are administered by IBEST to support research in these areas. In addition IBEST helped facilitate the searches by providing funds to advertise the positions in *Science* and organize and fund "meet and greets" for the candidates and University faculty and administration. Successful hires were made for each position:

Dr. Andreas Vasdekis, Physics

Dr. Vasdekis received his PhD for his work in polymer photophysics and applications. Following a short spell at Caltech, he spent three years as a postdoctoral scholar at the Ecole Polytechnique Federale de Lausanne, Switzerland. Prior to joining the University of Idaho in October 2014, he was at the Pacific Northwest National Laboratory investigating metabolism at the single cell level.

Dr. Chris Remien, Mathematics

Dr. Remien received his PhD from the University of Utah and for two years was appointed as a postdoctoral scientist at the National Institute for Mathematical and Biological Synthesis at the University of Tennessee. His research is focused on the use of mathematical methods to analyze how animals process nutrients and toxins with applications in medicine and ecology.

Dr. Audrey Fu, Statistics

Dr. Fu uses statistics to develop a framework for systematically extracting signals from large amounts of high-throughput data, which are often the outcome of multiple, complex biological processes. Much of her research aims to understand the mechanisms underlying gene regulation and their implications in human diseases. She has training in statistical genetics and experience in genomics and is actively involved in experimental design, data preprocessing and the development of statistical methodologies and algorithms. She completed her PhD at the University of Washington, is now completing postdoctoral training in the Department of Human Genetics at the University of Chicago, and will join the UI faculty in 2015.

RESEARCH FUNDING

EXTRAMURAL RESEARCH FUNDING

Research grant proposals related to the University strategic theme of 'real time evolution' can be submitted through IBEST. In these instances the IBEST Business Manager assists principal investigators to prepare and submit their grant applications to the UI Office of Sponsored Programs (OSP) who in turn review and submit the application to the granting agency. The level of support provided investigators varies depending on their level of experience and the agency requirements. At a minimum, the Business Manager works with the PI to prepare the budget and budget justification in accordance with UI policies and those of the granting agency. Once a grant is awarded the IBEST administrative staff help the PI recruit personnel, handle all purchasing and travel expenditures, and help the PI manage their budget.

Grant applications requesting a total of $15.7 million were submitted to various agencies in FY13-14 and a total of $2.7 million in grants were awarded. Total grant expenditures during this period totaled $3.8 million. (See Appendix 3 for a detailed accounting of grant awards.) Faculty reported publishing 67 peer-reviewed publications during the last year and presenting their results in a total of 56 conference presentations and department seminars.

IBEST GRANTS

IBEST PILOT GRANT

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

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

2014 Pilot Grant Award

The call for IBEST Research Pilot Project proposals was advertised campus wide, and four proposals were received. Four external peer reviewers that had no conflict of interest with the applicants were selected. Three reviewers were selected for each proposal; one of the three was an expert in the subject of the proposal. The review criteria were identical to those used by NIH with a couple of additional items, including the relevance of the proposed work to the 'evolution theme' of our COBRE grant and whether the investigator would use IBEST core facilities. Members of the IBEST Research Oversight Team read the reviews and met to discuss the scores. The proposal with the lowest (best) score was "Directed evolution of the molecular chaperone Hsp90 and its clients" (see description on following page) that was submitted by Dr. Jill Johnson from the Department of Biological Sciences.

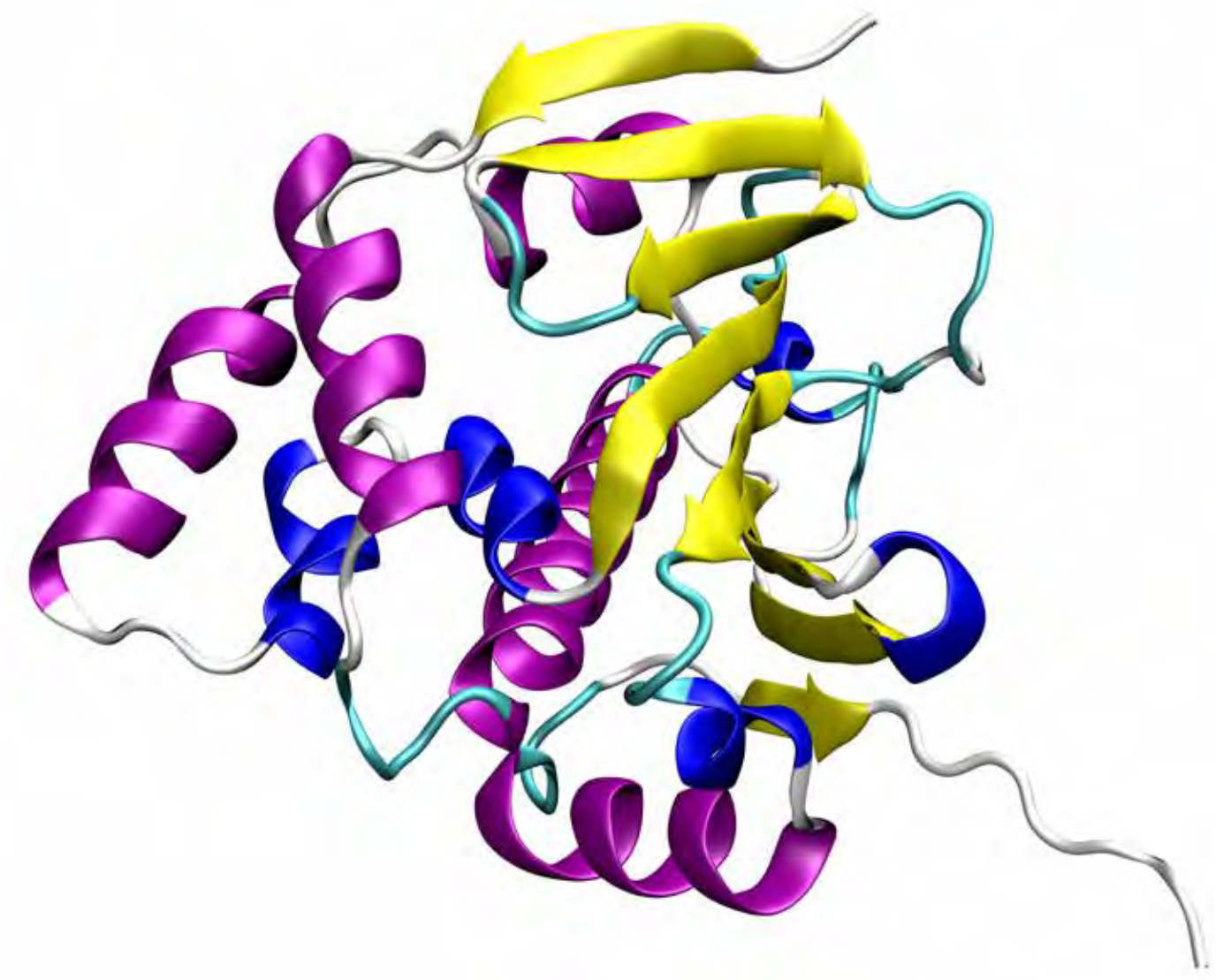
Dr. Johnson's proposal was then distributed to the IBEST External Advisory Committee (EAC) who endorsed the recommendation before it was forwarded to NIH for final approval. In June 2014 Dr. Johnson was awarded the IBEST Pilot Research Grant for year one, which can be renewed for a second year if progress is satisfactory.

DIRECTED EVOLUTION OF THE MOLECULAR HSP90 AND ITS CLIENTS

Dr. Jill Johnson

In this project we will use a directed evolution to identify ways to optimize the folding and activation of proteins by Hsp90. Hsp90 inhibitors are in Phase II/III trials for a range of cancers that are driven by oncogenic kinases that require Hsp90. My goal is to use the Pilot Research Grant to establish and validate genetic screens in Saccharomyces cerevisiae that will be used to identify Hsp90 variants that selectively enhance activity of two specific clients, including one that is mutated in human diseases. This represents a novel approach to altering Hsp90 function and has potential to increase the folding and activity of multiple Hsp90 clients that are associated with disease.

The projected use of IBEST Core Facilities will be minimal in the first year during the initial isolation and characterization of plasmid-borne Hsp90 variants. Since Hsp90 modulates the function of multiple transcription factors, we expect that Hsp90 variants with altered client ranges will result in distinct transcriptional patterns. We will use IBEST Core facilities in the second year to conduct RNAseq analysis to compare the genome-wide transcriptome in yeast expressing wild-type Hsp90 versus two or three Hsp90 variants. This will provide us an idea of how many clients are affected by Hsp90 variants and will also indicate genetic markers to help distinguish activities of Hsp90 modulators during future small molecule screens. Characterization of the Hsp90 variants obtained in these studies will provide new mechanistic details about Hsp90-client interaction and will justify a subsequent NIH proposal that will include screens for small molecules that mimic the Hsp90 variants.



IBEST TECHNOLOGY ACCESS GRANTS

IBEST has partnered with the Idaho-INBRE to administer and fund the Technology Access Grant Program. This is essentially a pilot grant program that provides funding to investigators so they can conduct exploratory studies using the technologies and technical support of the IBEST Genomics Resources Core, Computational Resources Core, and Optical Imaging Core. These grants are intended to help investigators produce preliminary or proof-of-concept data needed for competitive external proposals.

Proposals related to the IBEST theme of 'real time' evolution or the INBRE theme of 'cell-cell signaling' are accepted at anytime during the year and the review process is simplified and expedited; requiring only the review by members of the Research Oversight Team, the INBRE leadership, and one external reviewer. The amount of each award depends on the analyses done, but typically range from $5,000 to $10,000. Amounts up to $15,000 may be awarded if the need is justified based on project requirements. IBEST and INBRE require all recipients of a Technology Access Grant to cite this support in publications that emanate from this funding. For reporting purposes, IBEST and INBRE will also require information about all publications, presentations, and grant submissions that result from this funding.

So far in 2014 three Technology Access Grants totaling $15,457 have been awarded.

1. "High-Fat Diet- Induced Gastrointestinal Neuropathy", Dr. Onesmo Balemba, Department of Biological Sciences
2. "The Rod Photoreceptor Transcriptome" Deborah L. Stenkamp, Department of Biological Sciences
3. "Cell Signaling Within the Vertebrate Retina" Peter G. Fuerst, Department of Biological Sciences

The progress reports from these Technology Access grants can be found in Appendix 5.

IBEST TRAVEL AND COLLABORATIVE GRANTS

The Travel and Collaborations Grant Program allows investigators to explore new collaborative research opportunities, spur the productivity of an existing collaboration, or facilitate the preparation of research grant proposals. These awards can also be used by IBEST faculty to attend scientific conferences that focus on topics outside of their area of research; this will add breadth to their expertise. The individuals who wish to avail themselves of this opportunity can request these funds in a brief letter to the Director that explains why the proposed travel would be beneficial. Following the conference the attendee will be required to make an oral presentation as a "science update" at an IBEST Lunch. These small grants will typically not exceed $2,000.

In 2014 two such grants were awarded. One was awarded to Dr. Riley in order for him to send his postdoc, Dr. Travis Hagey, to further their collaboration with reserachers at the Argonne National Laboratory in the collection of data on the surface interactions and dynamics of the gecko adhesive system. The other grant was awarded to Dr. Haruo Suzuki of Yamaguchi University in Japan to further his collaboration with Dr. Eva Top (see description on next page).

TRAVEL AND COLLABORATION GRANT TO DR. HARUO SUZUKI

Dr. Haruo Suzuki, Yamaguchi University, Yamaguchi, Japan

While microorganisms play important roles in environmental and human health, they are also the cause of many infectious diseases. Moreover, the rapid rise of multi-drug resistant bacterial pathogens is an ever-increasing threat to human health. Plasmids play an important role in this health crisis as exemplified by the rapid spread of plasmids that encode ESBL (extended spectrum β-lactamases) or other new β-lactamases together with other resistance traits. To slow the alarmingly rapid spread of these unwanted traits in human pathogens we first need to understand the reservoirs of the corresponding genes and plasmids and how the latter are exchanged so rapidly in bacterial communities of natural and clinical habitats. While plasmid host range has until recently only been assessed empirically, Dr. Suzuki and others have begun to predict candidate hosts and the putative host range of a plasmid based on its genome sequence alone (1-3). Dr. Suzuki did this work while he was a postdoctoral scientist in Dr. Top's lab from 2006 till 2009 at the University of Idaho. Funding provided through a Travel and Collaboration grant were used to continue previous work on predicting plasmid hosts and host range research, and to explore ways to collaborate on new projects focused on plasmid-chromosome gene exchange and bacterial genome sequence analysis. Orogree was made in three socific areas described below.

First, we predicted the historical hosts of various plasmids encoding New Delhi metallo-β-lactamase-1 (NDM-1) by comparing their oligonucleotide composition with those of various bacterial chromosomes. Our results suggest that most NDM-1 plasmids belong to typical narrow-host-range plasmid groups (IncF, IncI, and IncX) that have evolved in a limited range of hosts (Enterobacteriales), while some NDM-1 plasmid belonging to the IncA/C group of broad-host-range plasmids evolved in a wider range of hosts. These findings were reported in a poster at the 20th Annual International Meeting on Microbial Genomics held at Lake Arrowhead, CA on September 14-18.

Second, the role of plasmids in chromosome evolution and the signatures of plasmid and chromosome signatures are poorly understood. During his visit Dr. Suzuki detected the presence of IncP-1 plasmid replication initiator gene sequences (trfA) in bacterial chromosomes, suggesting plasmid-chromosome exchange of essential plasmid backbone genes. We will further examine the horizontal transfer of genes between plasmids and chromosomes.

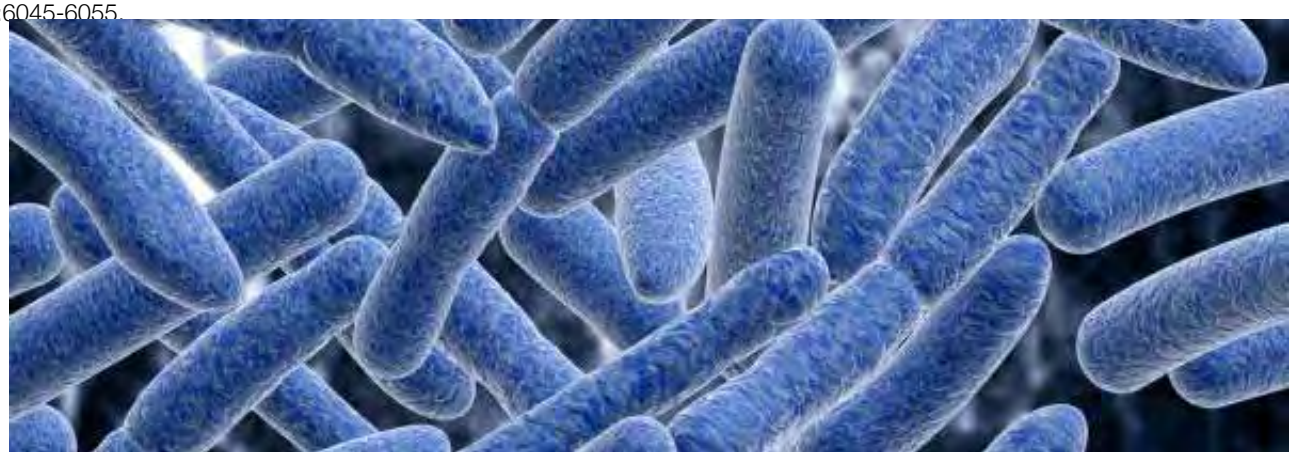
Third, in studies of plasmid-host coevolution Dr. Suzuki helped to annotate the evolved genomes of *Pseudomonas putida* H2. We will continue to compare experimentally evolved and ancestral genomes of strain H2 to understand differences in phenotypes, in particular the ability of the prototype IncP-1 plasmid RP4 to maintain itself in these hosts in the absence of selection.

References:

1. Norberg, P., M. Bergstrom, V. Jethava, D. Dubhashi, and M. Hermansson. 2011. The IncP-1 plasmid backbone adapts to different host bacterial species and evolves through homologous recombination. Nat Commun 2:268.

2. Suzuki, H., M. Sota, C. J. Brown, and E. M. Top. 2008. Using Mahalanobis distance to compare genomic signatures between bacterial plasmids and chromosomes. Nucleic Acids Res 36:e147.

3. Suzuki, H., H. Yano, C. J. Brown, and E. M. Top. 2010. Predicting plasmid promiscuity based on genomic signature. J Bacteriol 192:6045-6055.



DISSEMINATION OF INFORMATION

IBEST SEMINAR PROGRAM

The IBEST Seminar Series attracts top scientists from across the nation and world to the campus of the University of Idaho. These formal seminars and informal interactions expose IBEST personnel to the research interests, ideas, and expertise of leaders in the field. Over the years we have realized an indirect benefit of our seminar series in that invited speakers return to their home institutions and spread the word about the impressive research done at the University of Idaho and the collegial and collaborative atmosphere within IBEST. This has bolstered our reputation in the scientific community and helped us recruit students. See Appendix 6 for a listing of seminar speakers and topics in 2014.

These seminars (about four per semester) are used as a core element of a graduate seminar course (BCB 501) and are open to the public. Often more than 50 people attend them. The persons invited typically spend two days on campus meeting one-on-one with faculty members or small groups of students and postdocs. The graduate students of the Bioinformatics and Computational Biology program choose and invite speakers for the seminar series and organize their itinerary.

IBEST LUNCH

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

IBEST NEWSLETTER

This year marked the distribution of our first newsletter (Appendix 7). The newsletter targets a lay audience and had a "did you know" theme that made heavy use of graphics to convey interesting facts related to IBEST core facilities and nontechnical articles about research done by students and faculty of IBEST. The printed newsletter was distributed to over 70 people nationwide, including IBEST collaborators, University administration, friends and colleagues of IBEST investigators. A digital version was also distributed to the greater University of Idaho community.

INLAND NORTHWEST GENOMICS RESEARCH SYMPOSIUM (INWGRS)

The second annual Inland Northwest Genomics Research Symposium was held in May 2014. The symposium was a one-day event used a lecture format and included presentations by IBEST core facility directors, vendors, regional and national researchers. The symposium keynote address was given by Dr. Elhanan Borenstein, a prominent scientist in computational research in Evolutionary Systems Biology – an emerging field that examines the interplay between the evolutionary process and the organization of complex biological systems. Dr. Borenstein is in the Department of Genome Sciences at the University of Washington.

The objectives of the Symposium were to provide the University of Idaho research community an opportunity to learn more about IBEST GRC and CRC core facilities, potential uses of newly introduced technologies and approaches to data analysis, increase awareness of leading edge research projects at both the local and national level, and to provide insights into emerging technologies. It provided opportunities for local researchers to interact with invited nationally renowned scholars and interact with technology representatives. The Symposium provided benefit to IBEST cores by increasing awareness of their capabilities and highlighting local research programs that utilize core services.

The symposium had 135 attendees. Of those 69 were from the University of Idaho, 32 were from Washington State University, with the remainder coming from further away (Appendix 8 for more details).

INNOVATION

BUSINESS FOR SCIENTISTS

Developing a successful and productive research program requires skills that are not part of the traditional graduate school educational experience. Skills such as project management, budget development, human resource administration, strategic planning, risk assessment, team building, and communicating with 'stakeholders' and lay audiences are critical building blocks for a successful career as a scientific investigator. While some principal investigators are able to acquire these skills 'on the job', most struggle with the business and management side of research administration. To help hone these skills, IBEST and the University of Idaho College of Business and Economics developed a short course entitled "Leading and Sustaining Your Research Program" as part of a Business for Scientists educational initiative. The specific aim of the initiative is to teach the basics of business to researchers so they can more effectively develop and oversee their research programs. The course was advertised across the Moscow UI campus. Faculty of all ranks who oversee a funded research program were encouraged to attend at no cost.

"As much as I like science, the reality is I run a business. The course has been key to helping me frame what I do as a business program and see it with a fresh perspective." Chris Caudill

"The course was very beneficial and allowed me to think about my research and pitching my work in a different way. It was helpful for me to understand human behavior and team dynamics." John Crepeau

The first pilot course was team-taught by leading faculty in the College of Business and Economics June 2-6, 2014 to 21 faculty enrolled from five different colleges. (See Appendix 9 for attendee information.) The course was taught in the mornings for a one-week period (20 contact hours). Course content was specifically developed to meet the needs of research faculty in the fields of science and engineering. (See Appendix 10 for the course schedule.) At the end of the course an assessment was done to obtain feedback from participants and the course reviews were quite positive. Participants provided excellent suggestions on ways the course could be improved and recommended that more in-depth specialized courses be offered in the future on topics such as team building and 'elevator talks'. These are being considered. Meanwhile we have already made plans to offer the course again in June 2015, taking into account the suggestions made by participants in this year's course.

PHILOSOPHY OF SCIENCE CONFERENCE

This year the 18th Annual Inland Northwest Philosophy of Science Conference was held on the Washington State University (WSU) campus and organized through collaborative efforts of WSU and University of Idaho faculty and staff. Set up as a two-day workshop, this conference facilitated discussion about issues at the disciplines boundaries by bringing together researchers from fields in science and philosophy. There were 36 people from 14 different institutions that participated in the conference. The 10 presentations made at the conference were by people from eight institutions.

IBEST provided administrative support and funding for the conference by developing and posting conference flyers and providing funds for participant travel and food.

SPEAKERS

Name	Institution
Michael O'Rourke	Michigan State University
Graham Hubbs	University of Idaho
Tyrus Fisher	University of California-Davis
Ted Shear	University of California-Davis
Hayley Clatterbuck	University of Wisconsin-Madison
Matthew Kopec	Northwestern University
Matt Barker	Concordia University
Trevor Pearce	University of North Carolina-Charlotte
Josh Filler	Ripon College
Larry Forney	University of Idaho

SESSION CHAIRS

Name	Institution
Ron Wilburn	University of Nevada-Las Vegas
Brian Henning	Gonzaga University
Michael Myers	Washington State
Ann Levey	University of Calgary
Ian O'Laughlin	University of Iowa

I B E S T

STRATEGIC COLLABORATIONS AND PARTNERSHIP

BEACON

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 5 years with a possible renewal to 10 years at $5M per year. BEACON is a consortium of universities led by Michigan State University, and including IBEST at the University of Idaho along with the University of Texas at Austin, the University of Washington, and North Carolina A&T State University. BEACON unites biologists, computer scientists and engineers in joint study of natural and artificial evolutionary processes and in harnessing them to solve real-world problems.

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

We are currently in year 5 of the BEACON award and have received a total of $2,768,478 over the five year grant period. Thirty projects have been funded over the course of the five year grant, providing financial support for six postdoctoral scientists, 17 graduate students, and 16 undergraduate students. A complete listing of the projects funded can be found in Appendix 11.

CORE FACILITIES

COBRE PHASE III

TRANSITIONAL CENTER FOR RESEARCH ON PROCESSES IN EVOLUTION

The Center of Biomedical Research Excellence (COBRE) for Research on Processes in Evolution at the University of Idaho has received $21,649,028 in funding over 10 years from the NIH IDeA program. This funding has been critical to the growth and success of IBEST and enabled us to conduct leading-edge interdisciplinary research in computational and evolutionary biology and to mentor early career faculty to develop nationally competitive, independently funded research programs. Under COBRE, we also established and expanded the Computational Resources and Genomics Resources Core facilities at the University. These facilities provide a diverse array of advanced instrumentation and computational resources as well as technical support to investigators that are well beyond what could be supported by single investigators or small groups. The capabilities and services of the cores have come to be integral parts and essential resources for on-going and proposed research programs. We are completing year 2 of this five year third phase of COBRE funding that began in February 2013 and brings an additional $5,096,846 in funding to the university. This final phase of COBRE funding, along with institutional investments in IBEST as a strategic institute, will help the core facilities become self-sustaining and maintain the momentum of the highly competitive research programs built during the first ten years of COBRE funding.

IBEST COMPUTATIONAL RESOURCES CORE

VISION

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

INFRASTRUCTURE

The CRC contains a mix of advanced high performance computing clusters, powerful servers and reliable data storage components and is staffed by personnel with the knowledge and technical skills required to compress years of analysis into days. Our data center is a 1400 square foot facility in Room 124 in McClure Hall on the University of Idaho campus that has been specifically designed and renovated for our core. This room has a dedicated Uninterruptable Power Supply (UPS) with three-phase power and four-forced air handlers attached to redundant university chilled water systems. Optical fiber and copper interconnects provide high-speed data transfer for server and storage intercommunication and communication to the University backbone that is connected to the high-speed Internet 2 network. The features of our primary systems are described below.

High Performance Computing

CRC has one main computer cluster for research and genomic data analyses. The main cluster provides 512 processor cores and over 2 terabytes of system memory. Cluster nodes are connected with 40Gb/s QDR Infiniband connections, providing fast, low latency data transmission for increased performance of HPC bioinformatics applications. Our previously maintained overflow cluster is now retired due to maintenance associated with the

older equipment. The CRC also maintains nine servers (272 total cores and 2.4 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 heavily for hybrid sequence assembly of next-generation sequencing data.

Data Storage

The CRC maintains two kinds of data storage systems. The first of these include computational storage (198 TB gross, 91 TB realized) comprised of fast but more expensive disk arrays, and commodity storage on several control systems that are linked together through a special type of file system. The second is for long-term data archiving and backup storage (284 TB gross). This storage group comprises fast disk arrays for quick access to shared data, as well as commodity storage and tape robots for offsite storage of important data. In addition the core provides solutions to maintain data integrity and restoration.

Support Systems

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

Education and Training Support

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

NEW INFRASTRUCTURE

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

- Upgraded the network connection between GRC sequencers (and most GRC/CRC researchers) from 1 to 10 gigabits per second, by upgrading switches and installing fiber optic cables. These new resources connect the CRC server room directly to the GRC and to the campus backbone.
- Increased data storage and archiving capacity by installing new data storage and networking hardware, and upgraded the storage backbone networking to Infiniband for the main cluster.
- Improved our ability to gather information about how customers are using our services by installing the Robinhood monitoring software. This will also improve the accuracy and timeliness with which we can monitor trends in usage, allowing us to better anticipate future needs.
- Reduced the time for recovering data from backups while increasing our backup capacity. We accomplished this by replacing our tape-based backup system with a fully disk based backup system.

PLANNED INFRASTRUCTURE

- We will improve system redundancy, which will increase the availability to our customers and reduce downtime due to system failures, by adding a second core network switch.
- We are moving services to ITS where possible in order to reduce the administrative burden on CRC staff. For example, we will use ITS LDAP services so that our UI customers can use their UI system IDs rather than having to maintain a separate CRC IDs.

UNDER CONSIDERATION

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

- Repurposing older systems from research to the support of non-CRC account holders, such as students in classes that need computing support and UI faculty members who need resources for experimental purposes. This has the potential disadvantage of increasing the complexity of our systems administration,

but has the potential advantage of increasing CRC visibility and thereby broadening our customer base.

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

INNOVATION

Continuing Innovation in Technology and Services

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

Examples of our innovative use of existing technology include:

- We use configuration management systems (the modules environment) to provide customized software services, including versioning. Most cores provide only one version of software, which makes it difficult to replicate prior work or to test new user-developed software. This mechanism is uniform across 70 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.

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.

IMPACT ON RESEARCH

The CRC seeks to facilitate innovative research across a wide array of research disciplines. As examples of research that is facilitated by the CRC we offer summaries from Dr. Brendan Epstein and Tyler Hether on the following page.

DISEASE TRANSMISSION IN TASMANIAN DEVILS

Dr. Brendan Epstein, Postdoctoral Researcher, Biological Sciences, Washington State University

I am working for Paul Hohenlohe (University of Idaho, IBEST subaward from WSU) and Andrew Storfer (Washington State University) on disease transmission in Tasmanian Devils.

In the mid 1990's, Tasmanian Devils in the NE part of Tasmania started showing signs of a facial tumour that could be transmitted from one individual to another. Since then, the cancer has spread west through most of the country and will probably have completely swept through in the near future. Although the disease has not completely eliminated devils, it has greatly reduced the population size.

Because Tasmanian Devils live only in Tasmania, and we have detailed information on the origin and spread of the cancer, this is an excellent model system to study the spread of disease in general. Currently I'm using the IBEST CRC to analyze a RAD-seq dataset from three populations, with samples of Devils from the years before and after the disease reached these populations. I'm looking for loci (genes) that have experienced large changes since the beginning of the disease, which may be associated with differences in susceptibility. We will also be using the genetic data to look at how landscape features influence the movement of individuals around Tasmania. Eventually, we are going to combine the genetic information with field studies on contact networks to develop predictive models of disease spread that can take into account both genetics and behavior. Our collaborators in Tasmania are working to get data from a population that is not currently infected, but will be soon, so we'll have a real-world test of our predictions.

This project is funded by the US National Science Foundation's Ecology and Evolution of Infectious Disease program in the Division of Environmental Biology. The principal investigator is Andrew Storfer, with Paul Hohenlohe, Menna Jones, Elizabeth Murchison and Hamish McCallum as co-principal investigators.

THE ROLE OF GENETIC INTERACTIONS IN ADAPTATION

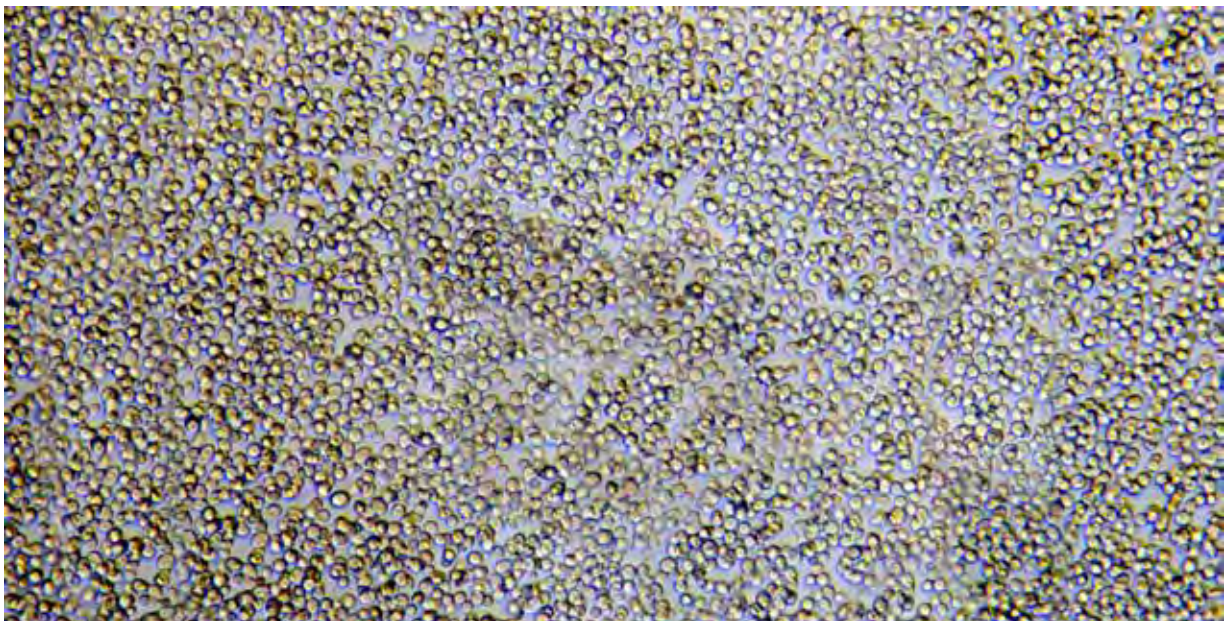
Tyler Hether, Postdoctoral Candidate, Bioinformatics and Evolutionary Studies, University of Idaho

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

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

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

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



SUSTAINABILITY

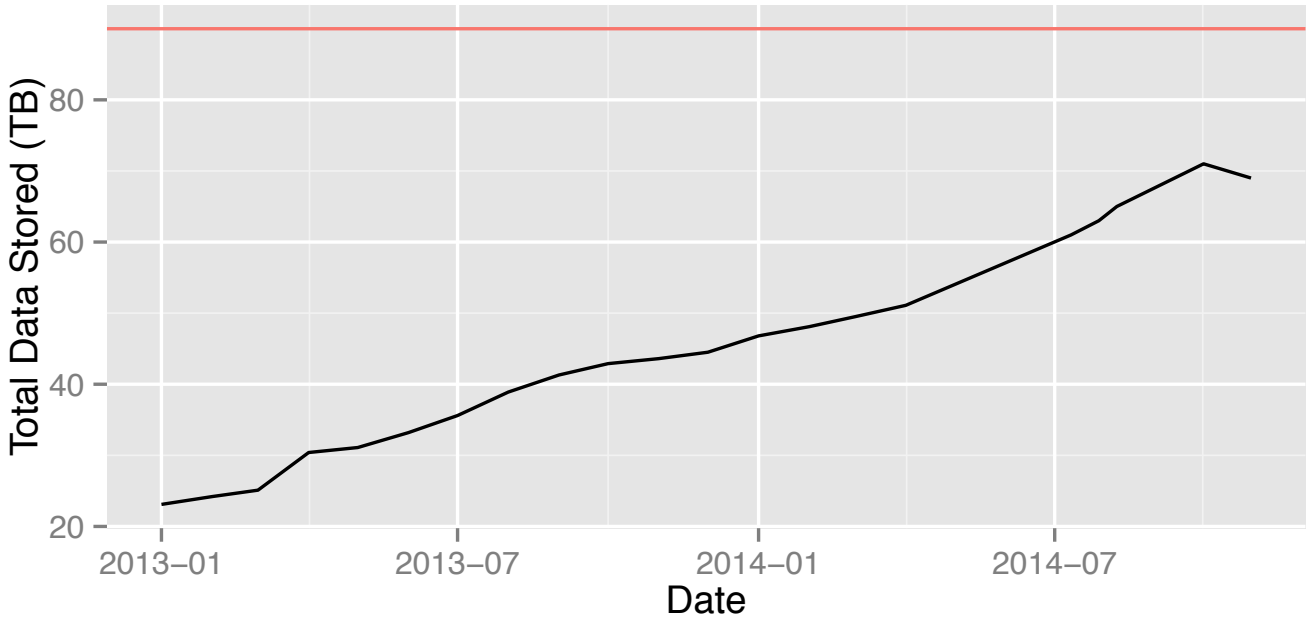
To sustain the level of service required by investigators we must continually update hardware and software to remain an attractive option for researchers. There are two dimensions to sustainability in the CRC: maintaining our current services and updating services to remain on the cutting edge.

MAINTAINING CURRENT STATUS

In June 2014, we implemented a fee for service model with a single user fee for access to all systems, and hourly charges for custom services. A single user subscription currently costs $1880 per year, and can be acquired on a quarterly basis. There are currently 23 paid users, of which 18 are individual researchers and 5 are associated with the GRC. Pursuant to federal guidelines, user fees fund personnel costs associated with administering the CRC, not hardware. The CRC is currently heavily subsidized by the COBRE and ORED.

Customers have changed how they use the CRC as we have made new options available. As DNA sequencing technology has advanced the amount of data stored by researchers using the CRC has increased. We project it will continue to do so (Figure 1). We have seen dramatic increases in the use of large memory standalone servers, while fewer jobs are running on the high performance computing clusters.

Figure 1. Temporal pattern of data storage in the CRC. The red line indicates our maximum storage capacity.



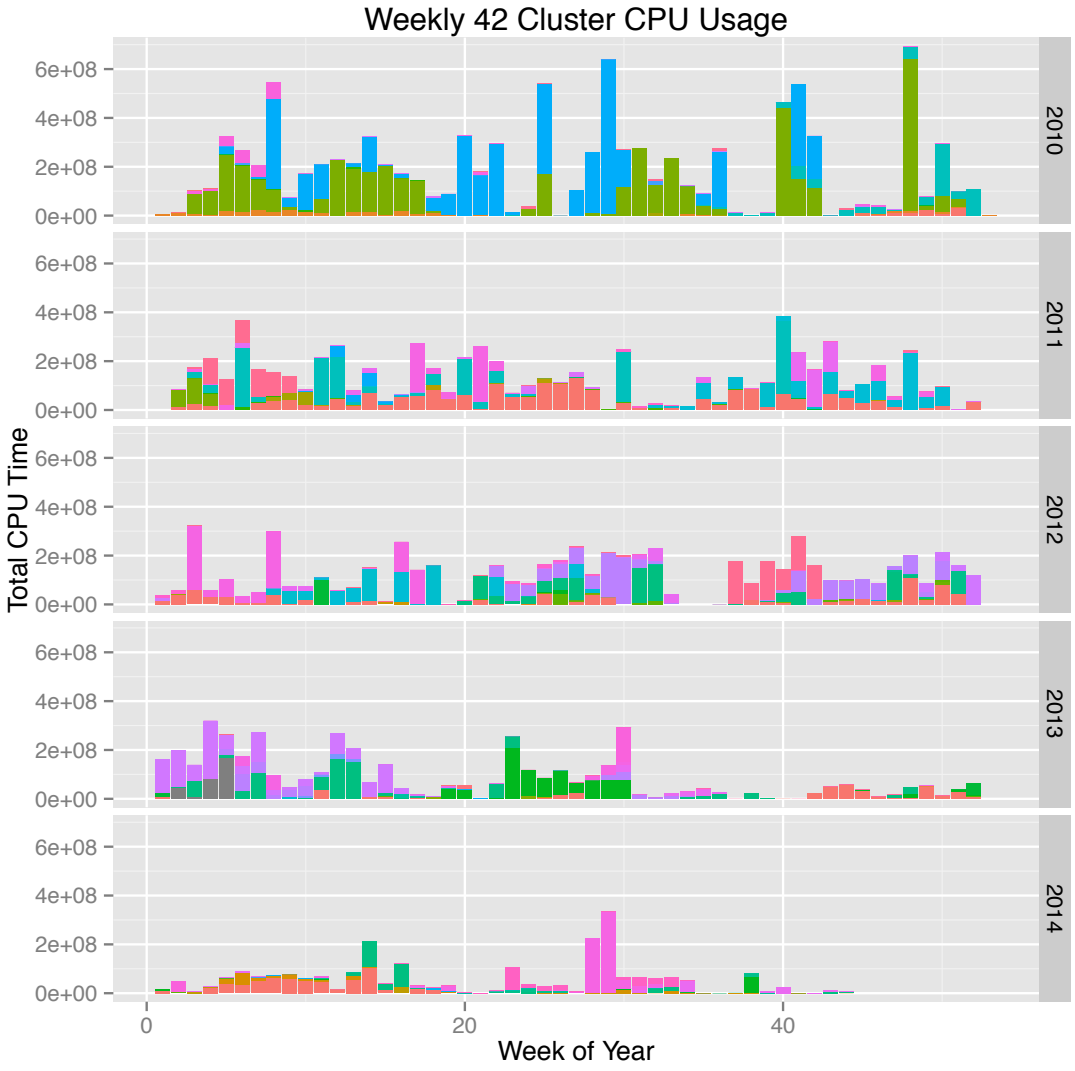
Contingency Fund

One important component of sustainability is the ability to respond to hardware failures. For example, the CRC currently uses hundreds of hard drives, and despite the low overall failure rate, we replace failed hard drives on a monthly basis. Other components that also fail somewhat less regularly include system memory sticks, power supplies, and motherboards. Unfortunately, these failures are more likely to occur during periods of intense usage, so system outages tend to occur at the worst possible time for researchers. We are therefore considering strategies to create a contingency fund that would allow us to have spare components readily available or purchase them quickly.

USAGE PATTERN TRENDS AND PROSPECTUS

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

Figure 2. Temporal patterns of cluster usage. Each color represents an individual user.



KEEPING CURRENT

Maintaining current hardware is a continuous challenge. Academic and corporate data centers assume a half-life of about two years for high end equipment like ours. Thus, after approximately four years, the equipment is fully depreciated. HPC equipment depreciates much faster than laptops, for example, because it often runs at high load in unusually hot environments 24/7. So, even though an individual user may find a four year old or older laptop adequate for basic computational needs, the equipment in the CRC is effectively at or near end of life after four years. Our two newest systems were purchased 2 years ago (Nov 2012) and our primary cluster nodes are 5 years old. (purchased Nov 2009).

In 2012, we upgraded the system memory in each of the main cluster nodes from 8GB to 32GB to cope with the increased memory demand from current bioinformatics applications. These cluster nodes are now at the maximum supported memory, and future upgrades to these systems are not possible. It will thus be necessary to replace these cluster nodes to realize increased performance. The comparatively low amount of system memory available on the cluster nodes is the primary reason cited by our users for switching to the higher memory standalone servers.

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 4,000% and are in the process of installing that equipment.

PLANS

The sustainability of the CRC over the long term will require that we increase self-generated revenue and retain institutional financial support. User fees alone cannot maintain centers such as the CRC given their high capitalization and maintenance costs. Therefore, institutional support will always be part of the core's revenue. Our goal is to support 50% of personnel expenses with self-generated revenue. With our current cost structure this will require approximately 48-50 active user accounts. We currently have 23 such accounts.

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

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

OUTREACH

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

OPPORTUNITIES

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

- Potential synergies with program projects or infrastructure efforts, which are part of the University's strategic plan. For example:
    - INBRE is developing undergraduate bioinformatics summer projects. To pursue these, the CRC could engage with the INBRE Bioinformatics Core.
    - The likely new COBRE includes a modeling collaboratorium and several potentially computationally intensive projects that may lead to additional user accounts.
    - The Northwest Knowledge Network may be able to provide offsite archival services, if pricing could be negotiated.
- Potential synergies with program projects or infrastructure efforts, which are part of the University's strategic plan. For example:

- Strategic integration with ITS. For example, using the university authentication services would benefit users (who could log into CRC resources with their university accounts) and remove the need for administering authentication services and some systems security responsibilities.
- UI media services may be able to help with teleconferencing (such as the BEACON conference room) and the IBEST classroom.

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

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

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

CHALLENGES

User Accounts

The CRC strives to provide quality, cutting edge research computing to researchers within the UI and beyond. However, sustaining this effort is a constant challenge. We have begun charging for services using a user account model, but these fees cannot currently be used to charge for hardware. Adding additional user accounts is not a catchall solution, as additional users will eventually require additional staff. Nevertheless, we are striving to minimize and recover costs when possible. Our goal is to reach 50 user accounts, a number that can be sustained at our current staffing level. This should recover ~50% of the personnel costs of the CRC.

Data Storage

As the cost of DNA sequencing has fallen, the amount of data available to researchers from both on campus resources such as the GRC, and from public databases such as NCBI has increased dramatically. This readily available sequence data has found its way to our servers en masse, enabling CRC users to study previously intractable evolutionary processes. However, our data storage capacity has not increased sufficiently to accommodate the rate at which users are uploading data, and our current primary storage system will be at capacity in approximately six months (see Figure 1, pg.18). Additionally, as our primary data capacity increases, backups of that data have become increasingly difficult to manage using open source backup solutions. We are currently evaluating potential solutions including: cloud backup systems, large hard disk arrays, and reducing number of backup copies currently being maintained.

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. But this system was purchased in 2012 and the batteries will be reaching end of life in 2016.

IBEST GENOMICS RESOURCES CORE

VISION

The mission of the IBEST Genomics Resources Core 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. Our vision is to stay current in genomics technology and bioinformatics while remaining agile in our ability to build partnerships with research groups and other regional core facilities.

INFRASTRUCTURE AND PERSONNEL

The IBEST Genomics Resources Core (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. We provide the molecular expertise and equipment needed for most high-throughput sequencing studies, and develop partnerships with other service facilities when additional capacity or other specialized equipment is warranted. The real benefit of the IBEST Genomics Resources Core facility however, has been our integration of bioinformatics, or data analysis, with data generation. We offer consultations on experimental design, appropriate and best use of technologies, as well as bioinformatic 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 as a team to discuss the goals and objectives for a project. This strategy helps improve the success rate of the project, and reduces costs by generating truly informative data and reducing failures.

As part of the Genomics Resources Core facility, we also maintain equipment that is accessible to both staff and students of University of Idaho investigators. The equipment, in what we call the "GRC USER CORE", is primarily associated with high-throughput sample preparation and quality assurance. Users are first trained by GRC laboratory staff and then can book time to use the equipment. Users are responsible for any reagents needed to run their samples and fees are associated with training and maintaining equipment maintenance agreements. When needed, core laboratory staff are available to help troubleshoot issues with the equipment's use.

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 sq. feet of laboratory space in Gibb Hall 242, 775 sq. feet of laboratory space in the GRC USER CORE, Gibb Hall 116, and approximately 300 sq. feet of office space in Life Sciences South at the University of Idaho main campus in Moscow, Idaho. The Core facility infrastructure is described in more detail below.

GRC DNA Sequencing Laboratory

DNA sequencing has become an indispensible tool for basic biological research, biomedical research, diagnostics, and molecular systematics. Current applications using DNA sequencing include whole genome shotgun sequencing, including de novo sequencing of previously unknown genomes; transcriptome sequencing; targeted re-sequencing; single nucleotide polymorphism (SNP) discovery; 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 upstream DNA sequencing library preparation. Importantly, this eliminates the need to hire additional staff, thereby reducing the costs of operating the core. Presently the core has the following equipment in its DNA Sequencing Laboratory.

- Illumina MiSeq High Throughput DNA Sequencing Platform: The MiSeq is the only fully integrated DNA sequencer that executes DNA sequencing – from sample preparation to data analysis – in less than 55 hours. The MiSeq performs paired-end sequencing (600bp total per DNA fragment) and 15Gb of DNA sequence per run.
- Fluidigm Access Array Target Enrichment System: The Access Array System is the first high-throughput, target-enrichment system designed to work with all of the major next-generation sequencing instruments. The Access Array System enables the GRC to enrich multiple unique targets (such as exons) from a large number of samples, all at one time using micro-fluidics and PCR. It allows the GRC to obtain quality results while minimizing the time, cost, and labor required for targeted re-sequencing projects.

- Wafergen Apollo 324 for NGS Library Preparation: The Apollo 324 is a bench top system that automates next-generation sequence library preparation workflows (Illumina libraries) by using bead technology to execute high-performance DNA isolation and purification.
- Life Technologies StepOnePlus Real Time PCR System for Library Quantification: The StepOnePlus Real-Time PCR System is a 96-well Real-Time PCR instrument that uses robust LED based 4-color optical recording.
- Sage Biosciences Pippen Prep for DNA Fragment Size Selection: The Pippen prep features the ability to collect narrow and even fragment distributions from DNA samples, this enables the lab to select specific size range DNA sequence libraries depending on experiment needs
- Agilent 2100 Bioanalyzer for Quality Assessment of DNA and RNA Samples: A microfluidics-based platform for sizing, quantification and quality control of DNA, RNA, proteins and cells.
- Fluorometry for Accurate DNA Quantification: The DNA or RNA in samples can be quantified using fluorescent assays. For multiple samples in a 96-well plate format these assays can be done using the Gemini XPS microplate reader from Molecular Devices, smaller numbers of samples can be assayed using the TBS-380 from Turner Biosystems.

GRC User Core

By acquiring new instruments in the GRC User Core for high-throughput sample preparation and quality assurance, we provide 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 that provides for high sample throughput and quality assurance includes the following equipment.

- Qiagen QIASymphony SP for DNA/RNA Isolation and Purification: The QIASymphony SP saves time by processing 1-96 samples in batches of 24 for purification of DNA, RNA, and protein from a wide range of sample types.
- Qiagen QIAgility for Automated Assay Setup: A compact bench top instrument that enables automated PCR setup in a wide range of formats. The high precision of the QIAgility delivers reproducible results in your end-point and real-time PCR assays. Automated PCR setup is rapid and reliable, and eliminates manual pipetting steps that can be prone to human error.
- Qiagen QIACube for automation of Qiagen Spin-Column Kits: The QIACube uses an advanced technology to process QIAGEN spin columns for nucleic acid and protein purification, enabling integration of automated, low-throughput sample preparation.
- Qiagen QIAxcel for DNA and RNA Analysis: The QIAxcel system is a multi-capillary electrophoresis system designed to overcome the bottlenecks of gel electrophoresis. The fully automated system can process up to 96 samples per run.
- Boreal Genomics Aurora System for DNA Extraction of Challenging Samples: The Aurora system employs Boreal's electrophoretic extraction technology to purify DNA and RNA from samples with low amounts of DNA or those that have materials that co-purify with DNA when other methods are used.
- Molecular Devices SpectraMax Paradigm Microplate Reader: The SpectraMax Paradigm is a multimode microplate detection platform. It is the only user upgradeable microplate reader on the market that allows for real-time system configuration. Our current capabilities include the absorbance (ABS) detection and the tunable wavelength (TUNE) detection cartridges.
- Diagenode Bioruptor Plus (UCD-300) Sonication platform for DNA Shearing: The Diagenode Bioruptor is a sonication device for DNA and chromatin shearing as well as for cell and tissue disruption.
- BioRad T100 PCR instrument: The T100 thermal cycler is a small thermal cycler with an intuitive touch-screen user interface for PCR in a 96-well format.

GRC staff continuously monitor current technologies 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. Each of these features are considered from the perspective of our mission – to facilitate cutting edge research in "real time evolution".

RECENTLY PURCHASED

The GRC has added three new pieces of equipment to the DNA Sequencing Laboratory in the past year:

- Life Technologies Qubit 2.0 Fluorometer for DNA Quantification: The Qubit 2.0 is an upgrade to the Turner Biosystems TBS-38 Fluorometry offering faster and more accurate DNA quantification of single samples for the same price per sample. The Qubit 2.0 Fluorometer utilizes specifically designed fluorometric technology using Molecular Probes dyes to quantify biomolecules of interest (DNA, RNA, or protein). These fluorescent dyes emit signals ONLY when bound to specific target molecules. Benefits: Faster throughput, more reliable quality assessment, higher quality genomic data.
- Advanced Analytical Technologies Fragment Analyzer for Quality Assessment of DNA/RNA Samples: The Fragment Analyzer increases the throughput and accuracy and reduces costs associated with DNA/RNA quality assessment relative to the Applied Biosystems Bioanalyzer. It accepts 96-well plates containing samples and balances speed and resolution for sizing, quantification and quality control of DNA, RNA, proteins and cells by altering capillary length. Benefits: Faster throughput, lower per-sample cost.
- Covaris S220 Focused Ultrasonicator for DNA Shearing: The Covaris S220 upgrades our previous method of shearing, nebulization, which was a very manual process that also required a significant amount of input DNA sample. The addition of the Covaris S220 allows the GRC to expand its service offering to those projects that require large insert library sizes, such as Illumina synthetic long-reads, improve quality associated with more accurate shearing and increasing throughput by replacing a time consuming manual process. It is an ultrasonication device for DNA and chromatin shearing as well as for cell and tissue disruption. Benefits: Higher quality data, lower personnel costs.

PLANNED

The GRC is currently evaluating the purchase of the following equipment for addition to the GRC User Core:

- Life Technologies MagMAX Sample Preparation System for DNA/RNA Isolation and Purification: The MagMAX Sample Preparation System differentiates itself from the other DNA/RNA isolation and purification equipment in the GRC User Core by its use of silica-magnetic particle technology. Magnetic beads bind to DNA/RNA more efficiently increasing sample DNA yields and reduces processing time by eliminating the need for centrifugation or vacuum processing.

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 laboratories, the “wet” lab and the “dry” lab and the GRC Director oversees 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 bioinformatic data scientists and is where data generated in the “wet” lab is analyzed, summarized and interpreted. A significant amount of communication and coordination occurs between the “wet” and “dry” laboratories.

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

Genomics Resources Core Director

Dr. Matthew Settles received his PhD in Bioinformatics and Computational Biology from the University of Idaho. He also holds a M.S. in computer science also from the University of Idaho and B.S. degree in electrical engineering from the University of Portland. Prior to joining IBEST in 2009, Dr. Settles was manager of the Bioinformatics Core facility at Washington State University. His experience and background involve the computational manipulation and interpretation of very large datasets, often by innovative uses development of new bioinformatics tools.

Bioinformatic Data Scientist

The position is currently vacant. Until very recently Dr. Samuel Hunter held this position for two previous years and was responsible for bioinformatic and analysis of genomics data. Dr. Hunter accepted a position with the Dana-Farber Cancer Institute in Boston, MA. We anticipate filling this vacant position in 2015.

Genomics Laboratory Manager

Mr. Daniel New earned a B.S. degree in Microbiology, Molecular Biology and Biochemistry from the University of Idaho. 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 extensive experience with various molecular biological assays and high throughput technologies. Mr. New is responsible for the day-to-day operation of the GRC "wet" laboratory.

Genomics Laboratory Scientist

Dr. Alida Gerritsen earned her PhD in Biology from the University of Oregon. In addition she also has a B.S. degree in Biology from the St. Lawrence University. Dr. Gerritsen joined the GRC in 2014 and currently in a hybrid role in both the "wet" and "dry" labs. Her duties emphasize molecular biology in times of high demand, and bioinformatic analyses of GRC produced data sets, when activity in the wet lab can be handled by Mr. New alone.

Undergraduate Research Assistant

David Streett is an undergraduate researcher with the GRC. He is on schedule to receive his B.S. in Biochemistry in May of 2015 and is working on a software project in the GRC to track sequence quality over time.

Bioinformatics Analysis Resources

The GRC does not maintain any specialized equipment for data management or bioinformatic analysis, but rather 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 us from other more "traditional" genomics core facilities around the US and the world.

SERVICES AND INNOVATION

The Genomics Resources Core offers "*genomics project management*" to our customers by integrating services in all three phases of genomics research: project planning and consultation, genomic data generation, and bioinformatic 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.

Project Consultation

Core facility staff members consult with investigators to discuss project aims and expectations, experimental design, appropriate and best use of technology, sample quantity and quality issues, and data analysis needs. During consultation, a project timeline is typically formed and expected costs are discussed. Having these discussions early in a project provides an opportunity for Core personnel to offer their expertise, advice, and assistance to enhance the proposed project and sidestep potential problems. Consultation is a service that the GRC currently provides free of charge. 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. This approach helps keeps overall costs low by minimizing costly problems in the later stages of a project.

Genomic Data Generation

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

Bioinformatics and Data Analysis

The GRC offers bioinformatics services through staff bioinformaticians and can perform a full range of analysis tasks to address biological questions in areas such as population genetics, genomics, microbial community dynamics,

functional genomics and systems biology. GRC bioinformaticians begin with raw 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 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 projects 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. Core staff members are often included as co-authors on publications resulting from significant intellectual contributions to research projects.

INNOVATIVE NEW METHODS

The innovative core product described above allows for the Core facility to participate in the design and development of new methods and techniques for genomics research. Two such projects are briefly described below.

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 consists of three steps: 1) reads are compared to a set of reference targets; 2) reads are then split into bins based on the results of these comparisons and 3) assemblies are performed using sequences from each bin. This process is iterated using the newly assembled contigs as comparison targets for the next iteration. ARC works effectively with divergent references, functions well with short low quality sequence reads and compares favorably to de novo assembly in terms of CPU and memory requirements.

A Modular, Highly Multiplexed Design for Illumina Amplicon Sequencing

Dr. Matthew Settles, in collaboration with Mr. New, 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 and significantly reduce experimental costs.

As an example of research that is facilitated by the GRC, see excerpt from Dave Tank and Simon Uribe-Convers on the following page.

PHYLOGENETIC INSIGHTS INTO THE RADIATION OF AN ANDEAN GROUP OF PLANTS

Dr. Simon Uribe-Convers and Dr. Dave Tank, University of Idaho

Advances in high-throughput sequencing (HTS) have allowed researchers to obtain large amounts of biological sequence information at speeds and costs unimaginable only a decade ago. Phylogenetics, and the study of evolution in general, is quickly migrating towards using HTS in order to obtain larger and more complex molecular datasets. In collaboration with the University of Idaho IBEST GRC, we developed a method that utilizes microfluidic PCR and HTS to generating large amounts of sequence data suitable for phylogenetic analysis. The approach uses a Fluidigm microfluidic PCR array and two sets of PCR primers to simultaneously amplify 48 target regions across 48 samples, incorporating sample-specific barcodes and HTS adapters (2,304 unique amplicons per microfluidic array). The final product is a pooled set of amplicons ready to be sequenced, and thus, there is no need to construct costly genomic libraries for each sample. Further, we developed a bioinformatics pipeline to process the raw HTS reads to either generate consensus sequences (with or without ambiguities) for every locus in every sample or – more importantly – recover the separate alleles from heterozygous target regions in each sample. This is important not only because it adds allelic information that is well suited for coalescent-based phylogenetic analyses, and the detection of allopolyploids, but also because it allows for the possibility of estimating minimum ploidy levels. We tested our genomic method and our bioinformatics pipeline, by sequencing 576 samples across 96 target regions belonging to the South American clade of the genus Bartsia in the plant family Orobanchaceae.

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 in FY2014. Even so the number of users and projects in the GRC increased by ~20%.

PLANS

Long-term sustainability will require that the GRC continue to increase its user base for genomics data generation next year (FY 2014-2015) and increase charges associated with bioinformatic analysis. The GRC has continued to gain ~20% new users and projects each year and has earned a positive reputation nationwide. We expect that these channels will continue to generate new customers. Further, the University of Idaho hired a number of new faculty in the past year who will also need GRC services and the Core will reach out to them to learn more about their needs. There are also several developing opportunities to grow the user base of the GRC in the next fiscal year (listed under "opportunities", below). In addition, the development of efficient workflows and automation of procedures in the "wet" lab have brought us to a point were two full time molecular biologists are no longer needed. We will therefore be able to shift more of Dr. Alida Gerritsen's effort to data analysis in the "dry" lab, while she will still provide backup in the "wet" lab during busy times.

Charging for bioinformatics services has increased steadily over the past 5 years, but remains a challenge because there is a tendency to underestimate the effort actually expended. We are currently developing plans to more accurately account for the "billable hours" of our bioinformatics staff, which will allow us to recover more of the personnel costs in the "dry" lab. In addition, we will continue to work with investigators to incorporate bioinformatics time into their grant proposal budgets.

Finally, the GRC implemented iLabs project management and billing system in late FY2014. Using the resources available in iLabs, we will be able to use the finer granularity of usage data that is now available to facilitate the efforts of high-volume users. In addition, iLabs should help us more effectively bill for bioinformatics time.

OUTREACH

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

- Genomics technology partnerships with the University of Oregon, University of California-Berkeley and University of California-Irvine.
- The Core Director served in the program organizing committee for the Western Association of Core Directors (WACD) in 2013 and 2014. Including giving a talk at the 2014 annual WACD meeting in Davis, CA on the Genomic Resources Core's innovative and unique structure.
- The Core Director is also a member of the National Association for Biomolecular Resource Facilities (ABRF) Metagenomics Research Group (MGRG)

OPPORTUNITIES

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

- The Idaho INBRE is developing bioinformatics projects for undergraduate researchers. The GRC has been collaborating with the INBRE Bioinformatics Core to develop these projects at institutions across the state.
- The UI anticipates that a new NIH Center of Biomedical Research Excellence (COBRE) will be funded in early 2015. This center includes projects that will require genomics technologies and a systems biology modeling collaboratorium that will engage both the GRC's "wet" and "dry" labs.
- There are two other potential COBRE grants in the state of Idaho (at BSU and the VA hospital) that may be in a position to collaborate with the GRC. We plan to reach out to these entities in 2015 to develop these collaborations.

We are also exploring collaborations and partnerships with regional entities to provide genomics support in the form of data generation and bioinformatics expertise. These Include:

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

FUTURE OBJECTIVES

Challenges

Maintaining a balance between accessibility and financial sustainability continues to be the biggest challenge for the GRC. The GRC operates under a unique structure that integrates all three phases of genomics project management - combining data generation and bioinformatics like few other facilities in the United States. This is our greatest strength, and our greatest ongoing challenge. Because we are 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. We work with a wide variety of data types, many 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 our ability to develop high volume standardized workflows. Despite these challenges, our integrated approach remains our signature characteristic, and a key component to continued success.

Perhaps the most significant threat to the Genomics Resources Core continues to be its ability to hire new staff and retain them. The Genomics Resources Core facility was able to hire one new Genomics Laboratory Scientist (Dr. Alida Gerritsen) in FY2015. Dr. Gerritsen is an excellent addition to the GRC and she will be able to significantly contribute to our data analysis efforts after she is fully trained. Existing classification and pay scales at the UI significantly hinder our efforts to hire well-qualified people with experience because we cannot offer competitive salaries. This is of immediate concern because in October 2014 the Genomics Resources Core lost its only full time bioinformatic data scientist (Dr. Sam Hunter) to the Dana Farber Cancer Institute in Boston, MA and we will be conducting a search for a replacement.

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. Our goal is to continue to provide integrated services to IBEST researchers – facilitating cutting edge research in real time evolution.

We are constantly evaluating our portfolio of services, a critical activity because the field of genomics changes remarkably fast. New technologies emerge every year, and the capacity for data generation is now out pacing the capacity to store, analyze, and interpret these data. Our most important strength is our intellectual capital and expertise. It may therefore be necessary to shift efforts away from "data generation" and into consultation and analysis - areas that have less capital costs and more personnel costs. We are therefore analyzing strategies that will facilitate cost recovery associated with personnel time.

The University of Idaho has begun construction of the new Integrated Research and Innovation Center (IRIC) on the Moscow campus. The Genomics Resources Core has worked with the architects and designers of NBBJ Architects of Seattle to design space in the new building that the GRC will occupy once the construction of IRIC is completed in mid-2016. This new building presents numerous exciting opportunities for the GRC to reach more customers and facilitate the research of investigators within and beyond IBEST.

IBEST OPTICAL IMAGING CORE

The IBEST Optical Imaging Core (OIC) provides expertise and instrumentation in optical imaging, flow cytometry and associated analysis. Investigators can choose to work independently or use the full services of the director of the Optical Imaging Core, Ann Norton, for experimental design, data acquisition and analysis, to producing publication ready results. Sharing the expenses of these services across campus and throughout the region provides an increase in applications available to everyone, appropriate technical expertise for experimental design and maintenance of instrumentation, and significant assistance in securing funds for new instrumentation.

INFRASTRUCTURE

Existing

Instruments from a number of locations across campus have been consolidated in one location. This provides the following advantages:

- Cost sharing among many investigators allows more options in cameras and detectors for imaging and additional choices in fluorescent biomarkers to be maintained and available.
- Multiple microscope platforms in one location provides imaging options for a wide range of sample sizes, resolution needs, and improved training and instrument maintenance.
- As part of the consolidation, the OIC now has the only fluorescence activated cell sorter on campus. This is a high maintenance tool that was not being actively maintained in a small group setting on campus.

New

A spinning disk confocal microscope has been purchased and will come on line in November 2014.

- Two grants were awarded to purchase a spinning disk confocal microscope with multiple cameras, environmental control and a separate image analysis computer with multiple analysis modules. These grants are from the National Science Foundation and the Murdoch Trust.
- Instrument demonstrations on UI investigators' samples informed the purchasing decision and created preliminary data for individual grant proposals.
- The spinning disk confocal microscope will allow for time-lapse imaging of live samples over long periods of time and is kinder to live samples than the laser scanning confocal microscope that we currently own. Environmental controls will increase the types of samples that can be imaged in the OIC.
- The increased sensitivity and speed of the newer cameras creates the only opportunity for some investigators to answer critical questions in their research.

Potential

The OIC now provides services to a broad base of users, but some of the instruments used are inefficient and have more limited capabilities than systems now available. This is especially true for the confocal laser scanning microscope and the fluorescence activated cell sorter. Newer flow cytometry instruments have increased sensitivity, decreased laser costs, smaller footprints and software improvements that simplify use.

- The OIC director will explore replacement options and survey the faculty to determine the priorities for instrument replacement.
- The success of securing funds for the spinning disk confocal microscope has reinforced the pivotal role of shared instrumentation grants in providing improved and increased services in our shared resources facilities. The recent increase in plant research projects at the OIC may open some opportunities for funding from non-biomedical agencies as well.

INNOVATION

New ideas and new applications often require new instrumentation. New instrumentation and experienced personnel help bring new ideas to fruition and strengthen an investigator's chances for extramural funding. Centralization of these services is an efficient use of resources, provides a place to learn from others who are using the core facility, and provides assistance in overcoming technical difficulties that often curtail innovation.

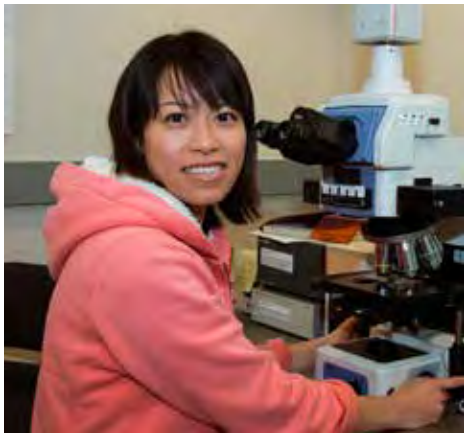
Grand Scale

- Cells and tissues change during development, disease process, as a result of genetic or environmental changes. These dynamic processes can be better understood by characterizing and visualizing these changes. Expertise and appropriate instrumentation are necessary to effectively and efficiently characterize and capture these critical dynamic events.
- The recent success in securing funds for new instrumentation in the OIC required a clear vision and collaborative effort. Contributing investigators appreciated the efforts of the OIC Director in setting up multiple instrument demonstrations, focusing on the technical details and preparing purchasing documentation.
- Many faculty candidates met with the OIC director and toured the Optical Imaging Core during the interview process. Some of those candidates are now new faculty and are already using the services of the OIC.

Person Scale

Though it is the role of the OIC director to become embedded in the tools and techniques available in imaging and flow cytometry, the personal service to researchers from the undergraduate level to the experienced principal investigator is a key component of the OIC services. The main goal of the director is to facilitate the research process by assisting researchers. At times this simply requires some basic training until the user is able to work independently. Other times, the OIC director provides personal service from experimental design to publication ready results.

- It is critical to provide services and instrumentation that are specific to UI researchers' needs and create quality results in an efficient and cost-effective way. This requires attention to new applications, instrumentation and funding opportunities that may be useful for researchers on our campus. To that end, the OIC director attends at least one meeting annually to learn of new techniques and instrumentation that may apply to the goals of UI researchers. Additional insight is gained by watching webinars, pushing vendors for answers and ideas and reading appropriate literature.
- The College of Science is supporting a graduate Research Assistant (RA) as a part-time staff member in the Optical Imaging Core this year. The NSF response to our recent grant proposal saw this as a 'novel opportunity for a graduate student'. Mandy Kuan, the OIC RA, is already providing back up support for the OIC director and gaining new skills.
- The OIC director recently began offering services outside of the core facility. These include consultations on new instrumentation, assistant in the procurement process and maintenance of existing systems. These much appreciated services also introduce potential customers to the quality and personal service available at the OIC.



Mandy Kuan

SUSTAINABILITY

Historically, optical imaging services were provided at no charge to the user. We began to charge fees for service in November 2012.

Current Status

- The sustainability of services such as the Optical Imaging Core depends on the sustainability of research dollars on our campus. At the OIC, we aim to provide quality expertise and instrumentation to assist UI researchers in their quest to advance their research goals and secure funding, yet, those standards are expensive to maintain.
- To keep expenses under control the OIC director works closely with principal investigators to actively pursue funding opportunities that provide new instrumentation at minimal cost to the researcher and the university. The fees for services remained the same throughout FY2013 and FY2014. They rose slightly for FY2015.

PLANS

- Critical review of the overall expenses of the OIC is an on going activity. That review includes considering the retirement and/or replacement of existing instruments. Efforts to replace instruments will be focused on improved efficiency, increased service options specific to UI research goals and overall cost to maintain.
- New users come to the OIC in a variety of ways. New instrumentation provides new applications for researchers and new faculty come to get preliminary data and training for their staff and students. New funding sources, such as the strongly anticipated NIH-COBRE program grant (PI, Dr. Holly Wichman), provide opportunities for existing and new users.
- Salary, fringe benefits and service contracts make up the majority of OIC expenses. Self-insurance of older instruments is being considered to potentially reduce annual maintenance costs and provide intentional review for each repair cost.

OUTREACH

- The OIC director presents separate workshops on optical microscopy and flow cytometry each semester. The workshops, available to everyone on campus, broadens the user's knowledge of what additional applications are available in the OIC and deepens their understanding of what is happening inside the instruments.
- The summer INBRE fellows program of undergraduate researchers come from UI and other academic institutions in and outside the state. Individuals receive specific training on instruments and the OIC director presents an overview of the shared resources available in the OIC to the full group of young scientists.
- The OIC director is a member of the Microscopy Society of America and the Association of Biomolecular Resource Facilities (ABRF), an organization of shared facility managers and directors. ABRF is focused on assisting efficient management and financial compliance of core facilities, provides networking opportunities and insight on biotechnology advances. The OIC director is a board member of the regional chapter of ABRF, Western Association of Core Directors (WACD) and organized a session on single cell analysis for the regional meeting. The regional meeting also provided opportunities for discussions on future collaborations with Boise State University researchers.

OPPORTUNITIES

The IBEST Optical Imaging Core creates many opportunities for investigators to move forward with new ideas and advance their individual research programs. Whether an investigator is working with single cells in solution, plant or animal tissue or even small embryos, they can gain additional insight into how their model system moves and morphs over time.

- The existing laser scanning confocal microscope has created wonderful high-resolution imaging on stable samples, yet, to really answer the question of what happened when and where in a biological system requires something that is much faster. With the new spinning disk confocal microscope and the opportunity for live, dynamic imaging an investigator can answer questions concerning what happened when and where on one sample. In addition to new insights, this will save the investigator time, animals and resources.
- Once dynamic imaging has provided new insight about a biological process, in depth, high-resolution imaging technology available on the existing laser scanning system can elucidate some details about stages in the process that are deemed important. Therefore, the existing imaging opportunities in the OIC are complimented, not replaced, by the addition of the spinning disk system.
- The University of Idaho research faculty are very generous in opening their laboratories to undergraduate researchers. Many of these undergraduate students have had opportunities to use the Optical Imaging Core services and are grateful for the extra skills they gain.
- A Research Assistant in the OIC provides improved service for the users and a very unique learning opportunity for a graduate student.
- New faculty, the new instrument and the very likely funding of a new COBRE program grant on campus (PI, Dr. Holly Wichman) will provide new research avenues for the OIC and some insight into new directions

to consider.

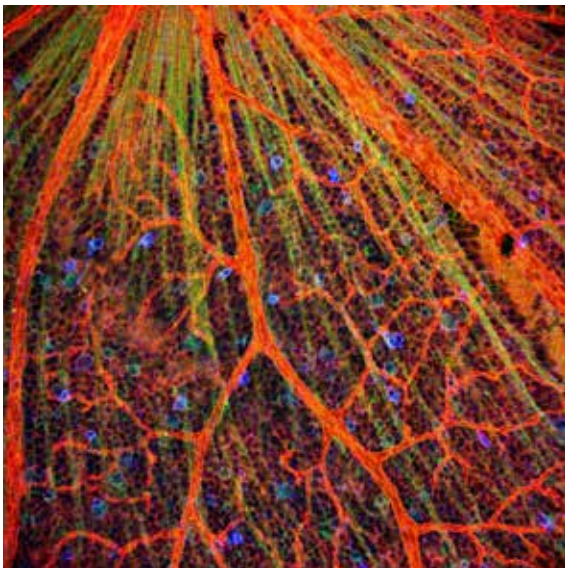
FUTURE OBJECTIVES

Challenges

- The reduction in research funds available directly affects how many users will have the monies for projects that use the services of the OIC and reduces the chances for the OIC to stay current with new instrumentation and application offerings.
- The RA position is only funded for one year, leaving the OIC with only one trained person. The lack of cross trained professionals reduces the chance of offering the full range of services and efficient assistance that are needed to keep our research programs moving forward.
- Cost increases, especially for maintenance of these complex instruments, are a major challenge. A recent survey of core facility directors shows that generating revenue and meeting budgets is their top challenge and raising customer usage to fill the gaps has not very successful in the recent years. User fees will never be able to fully cover the costs here at the University of Idaho OIC and that is always a major concern.

VISION

- Cytometry will continue to be a vital tool in many research pursuits. The knowledge gained from visualization of biological events and changes that occur within biological processes is crucial to a better understanding of development, evolution and disease process. The basic infrastructure of a supported Optical Imaging Core, the spirit of service to quality results, and the innovative pursuits of the talented faculty will keep these research avenues active and successful at the University of Idaho.



Confocal Image

MASS SPECTROMETRY CORE

In the summer of 2014 administrative responsibilities for the Mass Spectroscopy Core (MSC) were transferred to the Department of Chemistry in the College of Science. This decision was made because the services of the MSC were not widely used by IBEST investigators, while investigators in the Department of Chemistry have a vested interest in the financial viability of the MSC and insuring that MSC resources and services continue to be available. This new arrangement was agree to by all the stakeholders in various academic units and the Vice-President for Research and Economic Development. This change will have no adverse consequences to IBEST investigators because the MSC will continue to operate as a service center and provide campus-wide benefits by conducting mass spectral analyses on a fee basis for investigators.

ADMINISTRATIVE CORE

INSTITUTE LEADERSHIP

Dr. Larry Forney is the Director of IBEST and has overall responsibility for strategic planning, IBEST finances, oversight of IBEST Core facilities, supervision of administrative and core facility staff, coordination of research and education programs affiliated with IBEST, and responsibility for compliance with federal, state, and university policies and regulations. Dr. Forney devotes 35% of his effort to being Director of IBEST and in this capacity he reports directly to the Vice-President for Research and Economic Development.

The Research Oversight Team (ROT) serves as the executive board of IBEST and provides advice to the Director on the development of strategic plans and implementation of IBEST policies and procedures. Drs. Foster, Sullivan and Wichman are currently members of the Research Oversight Team. These individuals meet with the Director and Associate Director on a weekly basis and devote 5% of their effort to service on ROT.

Appointment of Associate Director

The leadership of IBEST has identified three objectives that must be met to insure the sustainablility IBEST. First, strategic plans for the sustainable operation of Core Facilities must be developed and successfully implemented. Second, to ensure the continued growth and high quality of IBEST research programs, we need to develop training programs for graduate students and postdoctoral scientists. Third, we need to reach out to companies, government agencies, and foundations to identify interesting opportunities for research and funding that are viable alternatives to federal agencies. This will also help faculty and students contribute to solving real world problems, develop and deploy new technologies, and create opportunities for economic development. We have named Dr. Barrie Robison to be Associate Director of IBEST and charged him with leading efforts to achieve these objectives. 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. He has already begun his work in these areas and led efforts to prepare and submit a proposal to obtain funding through the NSF Research Traineeship (NRT) program (as described below). Dr. Robison will contribute 25% of his annual effort to this position.

Key Administrative Staff

IBEST operates with a very modest administrative staff of three people. This is possible because they are consummate professionals who play a positive and critical role in the work of IBEST; demonstrate creativity, collegiality, and commitment to excellence; and work above and beyond normal job responsibilities. These individuals continue to work as an 'up tempo' team with a 'can do, will do' attitude. They couple teamwork, dedication, professionalism, and collaborative problem solving to enable the IBEST community to make significant progress." However, they now work at full capacity and with the continued growth from additional extramural grants and other activities such as the *Business for Scientists* program, we may face the need to add additional staff. The administrative team is led by Rose Poulin, the IBEST Business Manager and includes Lisha Abendroth, the IBEST Program Coordinator, and Whitney Schroeder, the IBEST Marketing and Communications Administrator.

IBEST Administrative Staff at the Inland Northwest Genomics Research Symposium. L-R: Whitney Schroeder, Lisha Abendroth, Rose Poulin

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.

After about a decade of service Dr. Warren Ewens stepped down from the EAC this past year. To fill this vacancy we invited two individuals to join the EAC and bring new expertise to group. In addition to her expertise in comparative yeast genomics, Dr. Maggie Washburn-Werner brings years of experience and advocacy for diversity in the workplace, mentoring individuals in under-represented groups, and innovation in STEM education. These issues reflect the core values of IBEST faculty and our desire accomplish more in these areas in the future. Dr. Owen White has been an prominent leader in genomics and bioinformatics for many years in a career that began with the Institute for Genome Research (TIGR) and continued at the Institute for Genome Sciences at the University of Maryland School of Medicine where he is now Associate Director for Bioinformatics in the Institute for Genome Sciences, Co-Director of the Center for Health-related Informatics and Bioimaging, and Director of Bioinformatics for the School of Medicine. Dr. White led the Human Microbiome Project Data Analysis and Coordination Center, and has worked to synergize protocols for data acquisition, analysis, archiving across research centers around the globe in the realm of big data and human health. 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

Typically IBEST meets with the EAC each fall semester. Despite heroic efforts we were unable to find a three day window of dates in which a quorum of the EAC members could assemble. In lieu of this we will distribute this report to the EAC, arrange for a videoconference so that IBEST leadership can answer questions and discuss topic of interest. The EAC members will then submit written comments to the chair of the EAC, Dr. John Roth. He will then assemble these into a single report that will be sent to the IBEST Director.

Internal Advisory Committee

The Internal Advisory Committee (IAC) consists of four Deans or their designees who are selected by the Vice-President for Research and Economic Development. The following individuals are the current members of the IAC:

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

I B E S T

GRADUATE AND UNDERGRADUATE EDUCATION

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY PROGRAM

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

To address this challenge investigators will need to be fluent in more than one disciplinary 'language' so they can communicate about research goals, discuss experimental design, data analysis options and technical limitations, and interpret the end result of a large data analysis exercise with all caveats in mind. Our unique contribution to this exciting area of science is to provide BCB students with a strong shared educational foundation and a required rotation in a research group outside their area of expertise. In combination with in-depth training in one specific area (Biological Sciences or Computer Sciences/Mathematics/Statistics) 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 **19 students in the BCB program** (18 PhD, 1 MS). Currently there are only five BCB student fellowships so most students are funded by extramural grants and other sources. IBEST provided $105,000 toward these fellowships and the University provided $34,000, thus most institutional support for BCB students was 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 funding. 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, but vacant, positions on extramural grants. Since fellowship support is limited to 4 semesters, the faculty must find alternative means to support their students, which releases the funding for future recruitment. Secondly, students supported by BCB fellowships can work on 'not yet

funded' research and collect preliminary data to support future grant applications. Thus student support 'primes the pump' for extramural grant funding. IBEST faculty derive large benefits from the BCB program – mostly through the recruitment and training of truly exceptional students – so we will continue to pursue ways to grow and sustain the program. One such effort is through the NSF Research Traineeship (NRT) program described below.

BCB Certificate Program

At the suggestion of the external review committee the leadership of the BCB graduate program developed plans for a BCB certificate program. It will provide students who are getting their graduate degrees in other areas with recognition for taking core course of the BCB curriculum. Graduate with this certificate will 1) have improved their understanding in bioinformatics, mathematics and computational sciences, and 2) have the capability to participate in interdisciplinary research and in academia, industry, or government agencies. They will learn a common 'language' that allows those with a background in one of the BCB disciplines to communicate and collaborate in interdisciplinary projects with colleagues from other disciplines. They will be able to explain BCB concepts to people with widely carrying backgrounds, from professionals in other fields to lay people. Various curriculum committees in the University easily approved our plan for the BCB certificate program and it has been forwarded to the Idaho State Board of Education for final approval. If it is approved we will commence the recruitment of students and launch the program in the fall of 2015.

BCB Students, Spring 2014

NSF INTERDISCIPLINARY TRAINING FOR UNDERGRADUATES IN BIOLOGICAL AND MATHEMATICAL SCIENCES

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

The goal of the Undergraduate Biology and Mathematics (UBM) program is to enhance undergraduate education and training at the intersection of the biological and mathematical sciences, and to better prepare undergraduate biology or mathematics students to pursue graduate study and careers in fields that integrate the mathematical and biological sciences. The central activity is mentoring teams of undergraduate students (usually two individuals)

in long-term interdisciplinary research projects that expose students to contemporary mathematics and biology and address research questions with modern research tools and methods. Projects are therefore designed to be genuine research experiences rather than rehearsals of research methods. Projects also involve students from both mathematical and biological sciences and include joint mentorship by faculty in both fields. It is expected that projects will strengthen the research and education capacity, infrastructure, and culture of the partner institutions, the University of Idaho and Washington State University. To this end, projects should create models for education in the mathematical and biological sciences and influence the direction of academic programs for a broad range of students.

The UBM program has completed its fourth year. To date, UBM has funded 20 students (14 women and six men), and many of these students were enrolled in the program for two full years. This long-term research experience is designed to facilitate the realization of research objectives, and emphasis is placed on the publication and presentation of results at scientific meetings. Students have presented their work at institutional (UI and WSU), regional (Pacific Northwest), and national scientific meetings, and in one case published a peer reviewed journal article. Other article submissions are currently in preparation.

Several students who have completed the program have enrolled in graduate programs in mathematical biology. Recruitment of students has been broad, particularly from the biological sciences. The program now includes mentors and students from four colleges at the UI (Agriculture, Science, Letters Arts and Social Sciences, and Engineering).

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

HOWARD HUGHES MEDICAL INSTITUTE UNDERGRADUATE SCIENCE EDUCATION

The demand for college students with expertise in the Science, Technology, Engineering and Math (STEM) fields is increasing while fewer US students are choosing or persisting in these fields. To address this issue, Dr. Patricia Hartzell (University of Idaho) proposed and received funding for a program that takes a collaborative, problem-solving approach to encourage undergraduate and high school students to embrace science. Several IBEST faculty are participating in this program and the IBEST Director is a co-principal investigator on the grant.

The program will 1) employ interdisciplinary learning to increase STEM retention, 2) involve topics relevant to the health of people in Idaho and elsewhere, 3) encourage student to be innovative by inviting them to engineer solutions to real problems, 4) engage college students as mentors for high school students, 5) expose students to funded research programs at the university, 6) train high school teachers throughout the state to teach dual credit science laboratory courses, 7) introduces educators to active learning and intervention techniques that significantly reduce the failure rate and education gap between advantaged and disadvantaged students, 8) involve communities in the scientific process, 9) reaches rural communities with increasing populations of Hispanic students, and 10) builds on the University of Idaho's tripartite land grant mission of teaching, research and outreach.

NATIONAL SCIENCE FOUNDATION RESEARCH TRAINEESHIP PROGRAM

The NSF Research Traineeship (NRT) program is designed to encourage the development of bold, new, potentially transformative, and scalable models for STEM graduate training that ensure that graduate students develop the skills, knowledge, and competencies needed to pursue a range of STEM careers. NRT programs should develop evidence-based, sustainable approaches and practices that substantially improve STEM graduate education for NRT trainees and for STEM graduate students broadly at an institution. NRT emphasizes the development of competencies for both research and research-related careers. Strategic collaborations with the private sector, non-governmental organizations (NGOs), government agencies, museums, and academic partners that enhance research quality and impacts and that facilitate development of technical and transferrable professional skills are encouraged. Creation of sustainable programmatic capacity at institutions is an expected outcome.[1]

This past year Dr. Barrie Robison developed and submitted a proposal for an NSF Research Traineeship Program at the University of Idaho. The proposal outlined an innovative graduate training program that responds to the emerging needs in the STEM workforce by closing two key gaps in the current model of STEM graduate student training: lack of awareness of the diversity of research related careers and lack of preparation to compete for and thrive in these careers. The program will have a scientific focus on the analysis of complex, interacting biological systems and build enduring partnerships with local, regional and national research-related entities that will continuously shape the training activities. Modular, intensive, and focused training activities will also be offered to train students in transferrable professional skills and offer a venue to apply them to train students as versatile researchers who are adaptable and able to embrace today's research opportunities.

The NRT program will be administered through the Bioinformatics and Computational Biology graduate program; which is part of the interdisciplinary portfolio within IBEST. Significant administrative advantages of established infrastructure and lines of communication to key University officials are enabled through IBEST. Over the last ten years IBEST has instituted successful mechanisms to increase awareness and to promote collegial interactions and support among IBEST faculty and students, including the IBEST lunch and seminar programs. These will be continued in the years ahead, incorporating and welcoming all who interact with the NRT program.

PROCTOR & GAMBLE CAREER OPTIONS IN INDUSTRY

Many students enter graduate school with aspirations of a tenure track position in an academic research institution, and faculty cater this in mentoring the students and postdoctoral scientists under their supervision. This is a comfortable arrangement that allows faculty to draw on their own experiences and knowledge. However, it is inconsistent with the reality that fewer then half the students who earn PhD's actually go on to hold tenure track positions. Students are becoming increasingly aware that there is stiff competition for the shrinking number of tenure-track positions available in academia and it is increasingly difficult to secure extramural funding to support academic research. Consequently there is growing interest in learning more about career opportunities in industry and government agencies. In response to this IBEST has launched an effort to provide students with a variety of means to learn more about alternative career paths. One way is through formal training programs such as the NSF Research Traineeship program described above. In addition we are creating opportunities for students to meet face-to-face with scientists from industry and government agencies.

Earlier in 2014 we hosted Drs. Yuli Song and Bruce Keswick from Proctor & Gamble who graciously agreed to give a presentation about careers paths for research scientists in industry. They also participated in an extended Q&A session with the more than 30 graduate students and postdoctoral scientists in attendance. The students reported that they learned a lot and very much appreciated the opportunity. A second such meeting is schedule for January 2015 when the graduate students and postdoctoral scientists will meet with Drs. Chris Henry and Folker Meyer who work at the Argonne Laboratory of the Department of Energy. We propose to host about four such events in the coming year.

1 http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=505015

Dr. Bruce Keswick from P&G presenting to students and postdoctoral researchers at the University of Idaho.

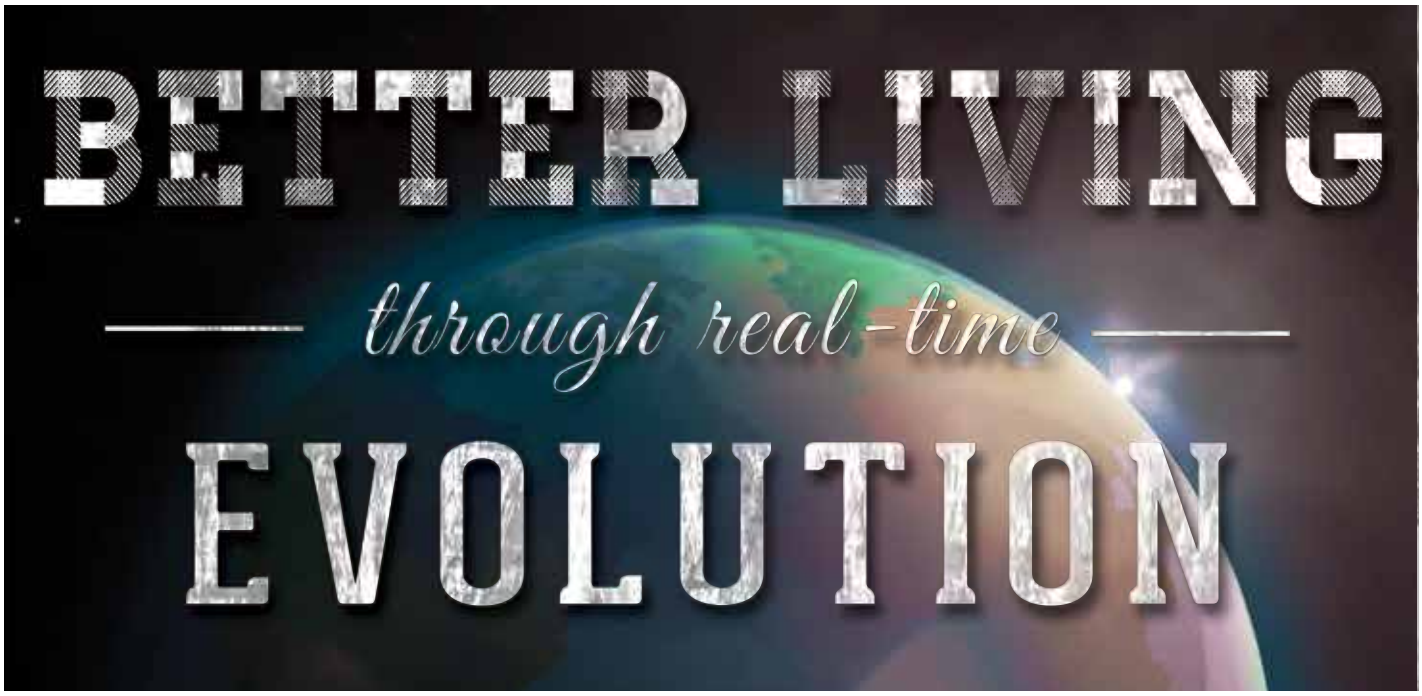
APPENDIX

APPENDIX 1 - OVERVIEW

HISTORY OF IBEST

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

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



APPENDIX 2 - PUBLICATIONS

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APPENDIX 3 - AWARDS RECEIVED

IBEST AWARDS RECEIVED IN FY2014					
Sponsor	PI	CO-PI1	CO-PI2	Award Title	Award Amount
National Institutes of Health	Top, Eva M.	None	None	Plasmid Host-Range	$346,108
National Institutes of Health	Joyce, Paul	Wichman, Holly	Miller, Craig	Patterns Adaptive Evolution	$276,070
National Institutes of Health	Forney, Larry	None	None	Vaginal Microbial Communities	$30,271
National Institutes of Health	Forney, Larry	None	None	Vaginal Microbial Communities	$30,271
National Institutes of Health	Forney, Larry	None	None	U19 ECO-PATHOGENOMICS	$107,808
National Institutes of Health	Forney, Larry	None	None	COBRE III Admin Yr 2	$38,087
National Institutes of Health	Forney, Larry	None	None	COBRE III Admin Yr 2	$399,777
National Institutes of Health	Forney, Larry	None	None	COBRE III CRC Yr 2	$21,246
National Institutes of Health	Forney, Larry	None	None	COBRE III CRC Yr 2	$150,428
National Institutes of Health	Forney, Larry	None	None	COBRE III GRC Yr 2	$40,522
National Institutes of Health	Forney, Larry	None	None	COBRE III GRC Yr 2	$348,492
National Science Foundation	Foster, James	Hagey, Travis	None	MichSU BEACON	$45,313
National Science Foundation	Foster, James	Hagey, Travis	None	MichSU BEACON	$52,690
National Science Foundation	Foster, James	None	None	MichSU BEACON	$49,759
National Science Foundation	Foster, James	None	None	MichSU BEACON Yr2	$57,884
National Science Foundation	Foster, James	None	None	MichSU BEACON	$1,453
National Science Foundation	Foster, James	None	None	WSU NSF Inspire Milk Project	$171,092
National Science Foundation	Fuerst, Peter	Foster, James	None	MichSU BEACON	$31,878
National Science Foundation	Harmon, Luke	Foster, James	None	MichSU BEACON	$17,770
National Science Foundation	Harmon, Luke	Foster, James	None	MichSU BEACON	$727
National Science Foundation	Heckendorn, Robert	Foster, James	None	MichSU BEACON Diversity	$2,501
National Science Foundation	Heckendorn, Robert	Foster, James	None	MichSU BEACON Diversity	$363
National Science Foundation	Hohenlohe, Paul	None	None	NSF Genetic Interaction Adaptation	$18,823
National Science Foundation	Hohenlohe, Paul	None	None	WSU Tasmanian Facial Tumor	$99,879
National Science Foundation	Marx, Christopher	Foster, James	None	MichSU BEACON	$31,240
National Science Foundation	McGowan, Craig	Foster, James	None	MichSU BEACON	$46,337
National Science Foundation	McGowan, Craig	Foster, James	None	MichSU BEACON	$19,624
National Science Foundation	Nuismer, Scott	Foster, James	None	MichSU BEACON	$6,974
National Science Foundation	Settles, Matthew	None	None	NSF FUNGAL PATHOGEN VERTEBRATE HOST	$10,000
National Science Foundation	Soule, Terence	Foster, James	None	MichSU BEACON	$26,994
National Science Foundation	Soule, Terence	Foster, James	None	MichSU BEACON	$21,959
National Science Foundation	Tank, David	None	None	NSF GRFP Marx	$1,667
National Science Foundation	Tank, David	None	None	NSF GRFP Marx	$3,333
National Science Foundation	Wichman, Holly	None	None	MichSU BEACON Yr2-Wichman	$65,799
National Science Foundation	Wichman, Holly	None	None	MichSU BEACON Yr2-Wichman	$62,431
USDA USFS	Settles, Matthew	None	None	USFS Soil Metagenomic Study	$30,000
Smithsonian Institution	Tank, David C.		None	Multiple - Marx Student Awards	$4,250
Floragenex Inc	Hohenlohe, Paul			Floragenex Population Genetics	$25,000.00
# OF AWARDS RECEIVED: 38				**TOTAL AMOUNT OF AWARDS RECEIVED:**	**$2,694,820.00**

APPENDIX 4 - PILOT GRANT PROPOSAL CRITERIA

IBEST PILOT RESEARCH GRANT PROGRAM

Applications due: xxx, 2015
Start date: xxx, 2015
Number of proposals to be funded: 1 to 2

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

ELIGABILITY CRITERIA

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 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 COBRE – processes of evolution – and have clear relevance to human health. Proposals outside this field will be deemed unacceptable and will be returned to the applicant without being sent out for review. To better determine if your project might be NIH-fundable and to place it in the context of other funded NIH grants, search the NIH RePORT site of grant abstracts at http://projectreporter.nih.gov/reporter.cfm.

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

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

INSTRUCTIONS

1. All applications should be accompanied by a cover letter that contains:
    - A brief statement of how their research is relevant to the thematic focus of the COBRE;
    - A description of the projected use of COBRE subsidized Core Facilities;
    - A statement of the plan for developing and submitting a proposal for external funding; 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

APPENDIX 4 (CONT'D) - PILOT GRANT PROPOSAL CRITERIA

- 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 which includes the cover letter and all forms in the appropriate order. Send to IBEST via email ibest@uidaho.edu before xxx, 2015. 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 Research Oversight Team will identify potential reviewers for the applications based on the subject matter of the proposals. Two referees from outside the University of Idaho will review each application, and each reviewer will be asked to evaluate multiple proposals. The reviewers will be asked to prepare an anonymous written review that will subsequently be provided to the applicant. The proposals will be scored based on NIH guidelines (see section 6 in PHS 398):

APPENDIX 4 (CONT'D) - PILOT GRANT PROPOSAL CRITERIA

- 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 Research Oversight Team will discuss the reviews and choose the most meritorious proposal.

APPENDIX 5 - TECHNOLOGY ACCESS GRANT PROGRESS REPORTS

HIGH-FAT DIET- INDUCED GASTROINTESTINAL NEUROPATHY

Onesmo B. Balemba, Department of Biological Sciences,
IBEST-INBRE Technology Access Grant Award Recipient ($8,735.00)

The overall goal of the technology access grant is to support the analysis of gut samples collected from mice with high fat (HF) diet-induced type two diabetes (T2D). Our specific aims are to characterize the nature of injuries in the enteric nervous system (ENS) occurring during T2D using a mouse model of diet induced T2D; define the role of gut microbiota in the development of this diabetic nerve damage; and identify whether anti-oxidative/anti-inflammatory biflavanones isolated from Garcinia buchananii stem bark (GBB) mitigate such nerve damages.

Nerve injuries have been extensively analyzed in the duodenums and colons diabetic mice, non-diabetic mice and diabetic treated with (2R,3S,2”R,3”R)-manniflavanone, GBB, and alpha-lipoic acid (positive control) using the Optical Imaging Center. In brief, we have found that damages caused by HF in ENS neurons are in many ways similar to injuries seen in pre-diabetic and T2D humans. Like in diabetic humans, ENS neurons, which signal relaxation of the gut are the most vulnerable class of gut nerve cells to HF diet-induce diabetic injury. However, prolonged ingestion of HF causes damage to neurons, which signal contractions of gut muscle. Preliminary data show that (2R,3S,2”R,3”R)-manniflavanone and GBB might alleviate nerve cell injuries and accompanying disrupted bowel motility.

We collected 1,262 samples from 86 mice consisting of feces and contents from stomach, small bowel and large bowel. We have used the Genomics resources core equipment to extract genomic DNA from 300 samples and sequence 200 samples from the GI tract. Data obtained is being used to determine if microbial community shifts are involved in the development of diabetic nerve damage in the gut.

Data and publications obtained from this work are helping to advance our research record of accomplishment and the competitiveness for external funding. We have published two papers (Stenkamp-Strahm et al. Cell and Tissue Research 2013; 354(2):381-94; and Stenkamp-Strahm et al. Auton Neurosci 2013; 177(2):199-210). A third manuscript will be re-submitted to Cell and Tissue Research after two weeks. We have submitted an R03 proposal to NIH, which is pending. We plan to submit three new applications to NIH, the American Heart Association, and American Diabetes Association.

APPENDIX 5 (CONT'D) - TECHNOLOGY ACCESS GRANT PROGRESS REPORTS

THE ROD PHOTORECEPTOR TRANSCRIPTOME

Deb Stenkamp, Department of Biological Sciences,
IBEST-INBRE Technology Access Grant Award Recipient ($7,682)

Our research program focuses on the factors that regulate the development, survival, and regeneration of the neurons of the retina, the neural tissue that carries out visual processing. Our major interest is in the differentiation of rod and cone photoreceptors, the cells that detect light.

The majority of inherited retinal disorders that result in blindness are the consequence of mutations in genes expressed in rod photoreceptors. The presence of defective proteins, or the absence of specific proteins, causes the death of rod photoreceptors, and therefore the loss of scotopic vision (i.e. "night blindness") in patients with these disorders. Due to the loss of supportive factors derived from the rod cell population, cone photoreceptors are lost secondarily, and patients progressively lose photopic vision as well, resulting in complete blindness. In humans, photoreceptors that are lost due to genetic or environmental damage are not replaced, and treatment options for protecting photoreceptors from death are virtually nonexistent.

We pursue our studies in a model organism, the zebrafish, which has the capacity to continuously generate new rod photoreceptors throughout life, and to respond to retinal damage by generating new retinal neurons that replace those lost to damage.

With support from an IBEST/INBRE Technology Access Grant, we discovered the set of genes uniquely or predominantly expressed in zebrafish rod photoreceptors – genes that allow rods to develop and maintain their distinctive morphology and function. This set of genes includes many that were previously not known to be rod-specific. The function of specific gene products will be pursued through approaches already in place in the laboratory. The results of the Technology Access Grant-supported studies are also likely to provide us with novel markers for rod photoreceptors, and potentially for cells that generate new rods, and therefore important tools for tracking rod neurogenesis. These studies will support proposals aimed at understanding the mechanisms underlying the ongoing neurogenesis of rod photoreceptors in the zebrafish, in order to apply this information in the field of regenerative medicine and treatments for human rod degenerations that result in blindness.

APPENDIX 5 (CONT'D) - TECHNOLOGY ACCESS GRANT PROGRESS REPORTS

THE ROD PHOTORECEPTOR TRANSCRIPTOME

Peter Fuerst, Department of Biological Sciences,
IBEST-INBRE Technology Access Grant Award Recipient ($8,800)

I would like to update you on progress that has been made possible by the grant our group received last year. This grant focused on giving Idaho students access to the IBEST Optical Imaging Core (OIC), including training by the director, Ann Norton.

Publications utilizing and citing these grants to date :

DSCAM localization and function at the mouse cone synapse. Gabriel Belem de Andrade, Samuel S. Long, Harrison Fleming, Wei Li and Peter G. Fuerst. J Comp Neurol. 2014 Aug 1;522(11):2609-33 PMID: 24477985

Developmental Localization of Adhesion and Scaffolding Proteins at the Cone Synapse. John S. Nuhn and Peter G. Fuerst. Gene expression patterns, in press

Developmentally Dynamic Colocalization Patterns of DSCAM with Adhesion and Synaptic Proteins in the Mouse Retina. Gabriel Belem de Andrade, Morgan Merrill, Landon Kunzelman and Peter G. Fuerst. Molecular Vision, Accepted Pending Minor Revisions

Two additional publications are under review or in revision. I would like to draw attention to the authors of these papers. All first authors are undergraduate students supported by the technology access grant including:

Gabriel de Andrade: Gabriel was an exchange student working through the Brazilian CAPES program.

Harrison Fleming: Harrison was a BYUI-intern.

John Nuhn: John was an INBRE summer fellow.

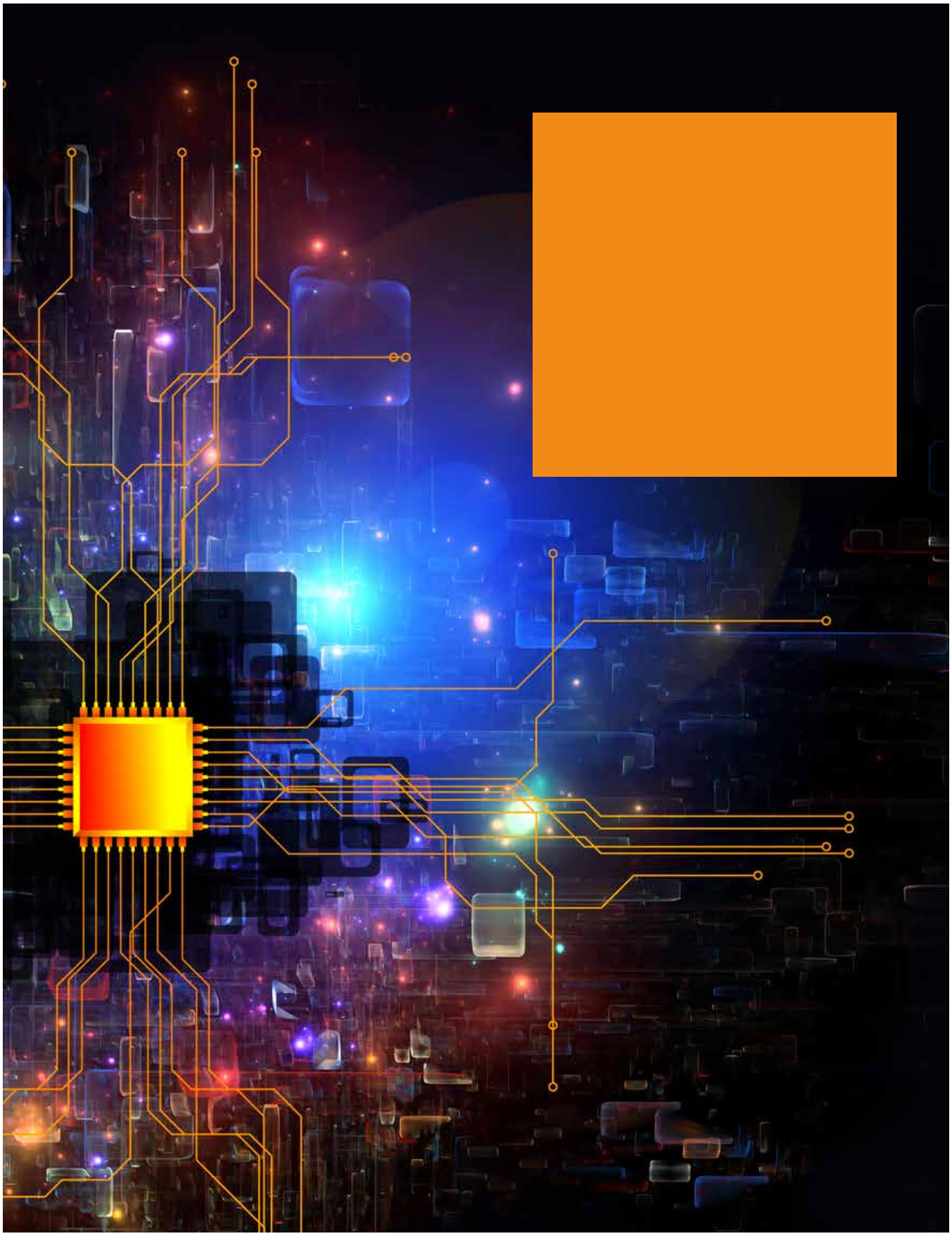
Landon Kunzelman: Landon was a BYUI-intern.

As you can see giving students access to the imaging core through this grant has resulted in outstanding research experiences for undergraduate students working in my lab group.

APPENDIX 6 - SPRING 2014 SEMINAR SERIES

APPENDIX 6 (CONT'D) - FALL 2014 SEMINAR SERIES

APPENDIX 7 - IBEST NEWSLETTER



APPENDIX 7 (CONT'D) - NEWSLETTER

Did you know.....

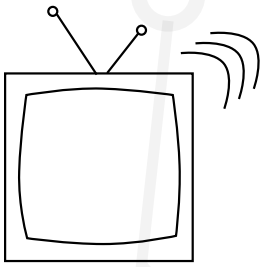
The IBEST Computational Resources Core (CRC) provides world class computing facilities for storing and analyzing biological data, and for sophisticated mathematical simulations.

The state of the art computational and data storage systems rival that of larger institutions such as Virginia Tech and UC Davis, and have computational power equivalent to over 800 standard desktop computers. A single computer would require over 250 years to perform the analysis that the CRC system performs in just one year.

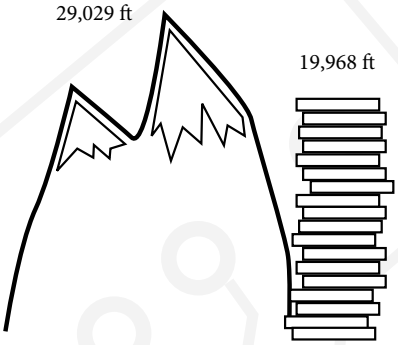
The CRC has the capacity to store vast amounts of data, the equivalent of over 1 trillion large documents or over 320 million high quality photos. It also provides computing and educational support to all Idaho universities and colleges.

The CRC facility has been funded by the National Science Foundation and the National Institutes of Health. It is an essential part of projects that have brought tens of millions of dollars into Idaho, and it is recognized nationally for its excellence.

APPENDIX 7 (CONT'D) - NEWSLETTER



TV running continuously for 60 years

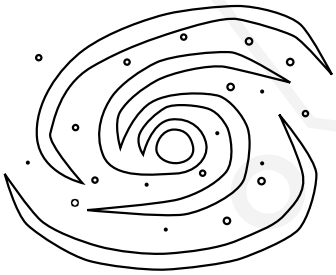


768,000 CD roms full of data put in cases and stacked equal nearly the height of Everest.

The BEST CRC has .5 PETABYTES of storage

512 TERABYTES

1,024 laptops with average storage size of 512 GB.

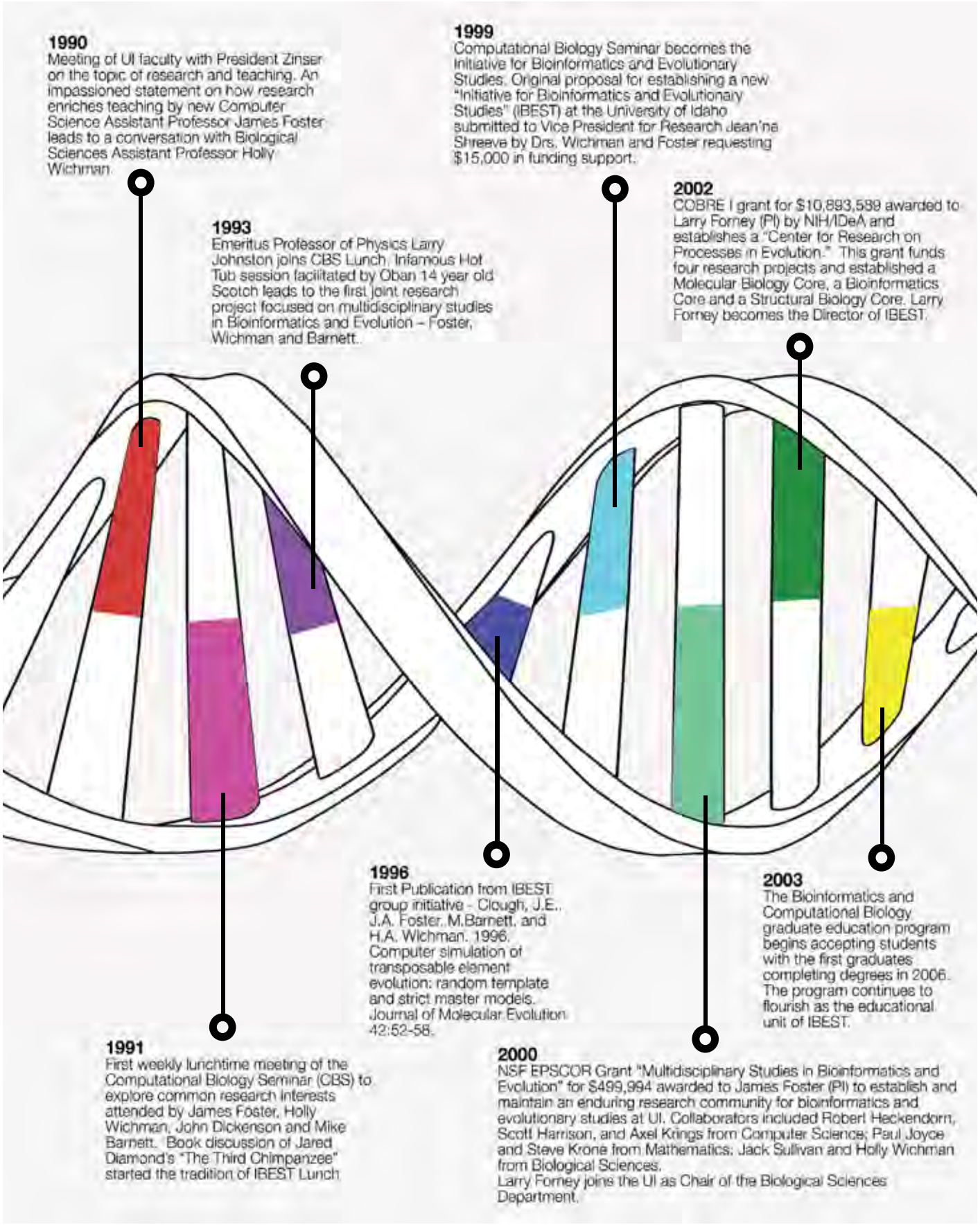


If each star represents a byte, that is 7, 500 Milky Way Galaxies.

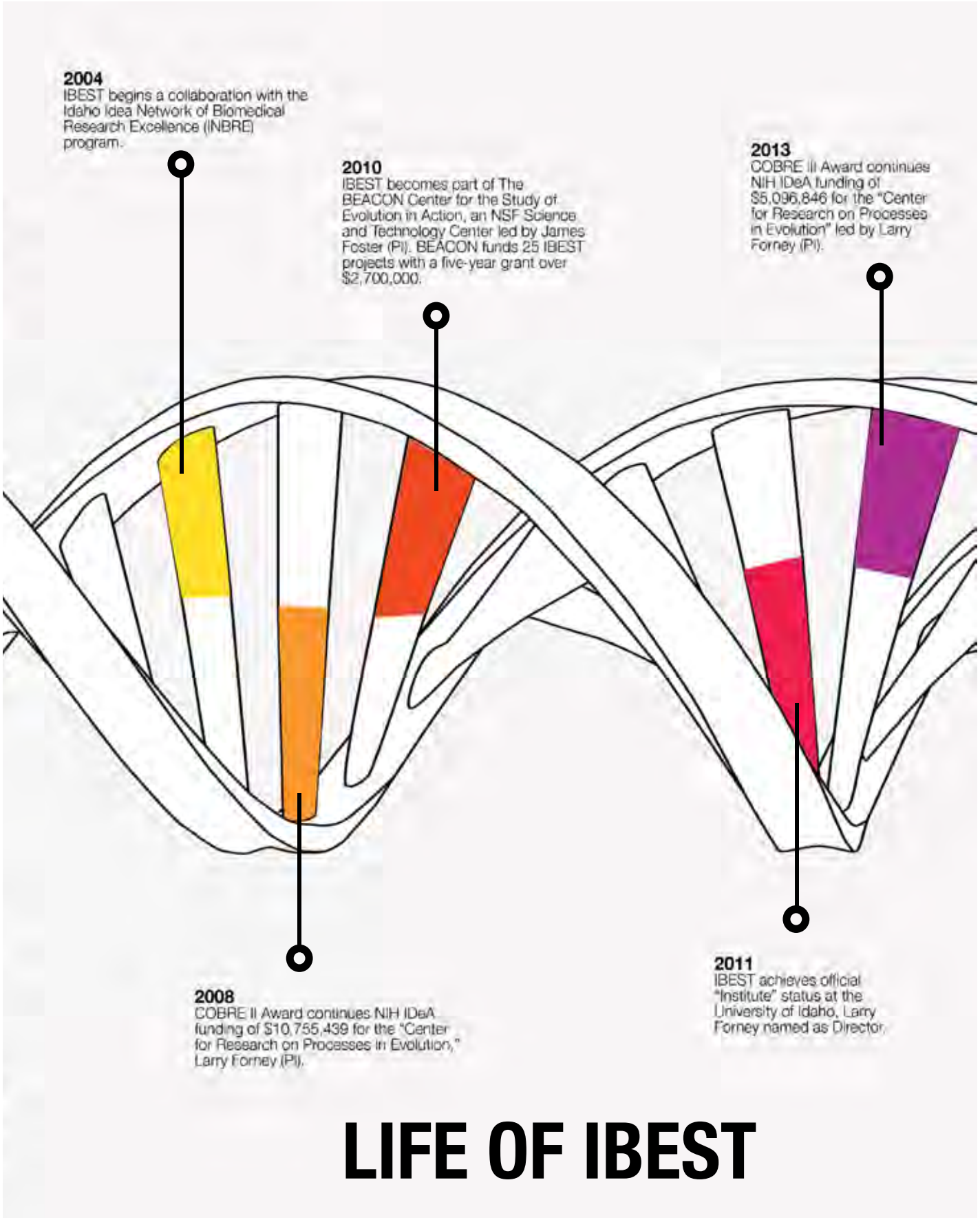
Fun Fact

All servers are named after characters from "The Hitchhiker's Guide to the Galaxy."

APPENDIX 7 (CONT'D) - NEWSLETTER



APPENDIX 7 (CONT'D) - NEWSLETTER



COMPUTING For Cutthroat

By Whitney Schroeder

Cutthroat trout play a fundamental role in their habitat and are used by many scientists as an indicator species for the health of larger ecosystems. The growing recreational fishing industry has been a primary motivator of introducing a popular sportsman fish, the rainbow trout, to many lakes, streams, and reservoirs it is not native to. This introduction has placed pressure on the native cutthroat species of trout, causing a noticeable decline in population trends and resulting in its classification as a threatened species. The replacement of cutthroat trout with non-native trout species is not only about the possibility of endangerment and extinction of a species, it also affects whole ecosystems by changing the energy and nutrient flow, causing a potentially negative ripple effect of influence on the health and balance of the larger system the cutthroat trout is a part of.

Dr. Paul Hohenlohe studies the fitness of cutthroat trout in the waterways of Montana, where rainbow trout have been introduced. Over the years, rainbow and cutthroat trout have been crossbreeding, producing a hybrid called a cutbow trout. Past studies have shown these hybrids have a lower fitness level. The fitness of a species is measured by the number of surviving offspring it has and how well it contributes its genes to the next generation, or in other words, a species

PAUL A. HOHENLOHE

Research in the Hohenlohe Lab addresses basic questions in evolutionary genetics and genomics from both theoretical and empirical perspectives, and also applies genomic tools to conservation of threatened species.

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APPENDIX 7 (CONT'D) - NEWSLETTER

survivability. Past studies infer that cutbow hybrids are not a real threat to the cutthroat population. However, it has been discovered that despite hybrids lower fitness, there are some parts of the rainbow trout's genetic information that is being favored in the selection process and continues to spread throughout the native cutthroat population, resulting in a decline in native cutthroat numbers.

"What are these genes and why are they behaving like that?"

"It's an interesting question," Dr. Hohenlohe says, "what are these genes and why are they behaving like that?"

These are the questions that form the foundation of his research. By searching for answers, he hopes to learn what it means for the population fitness and dynamics of the native cutthroat trout and their increasingly threatened status.

How does one go about tracking specific genomic material? Dr. Hohenlohe relies on RAD Sequencing and massive computational power. RAD stands for "Restriction site Association DNA". RAD sequencing allows researchers to sample the genomes of multiple individuals in a population. Massive amounts of data are produced, which

Dr. Hohenlohe then analyzes. Since the data sets can be large (easily hundreds of gigabytes), high-powered computing is necessary to navigate the information.

"When I was in graduate school I ran a bunch of computer simulations and it was just a single, big computer," Dr. Hohenlohe says, "I would have to start it running and come back a week later, then start a new one running." Repeating this process over and over again, Dr. Hohenlohe would process his data, often waiting months for it all to be completed before he could even begin the analysis portion.

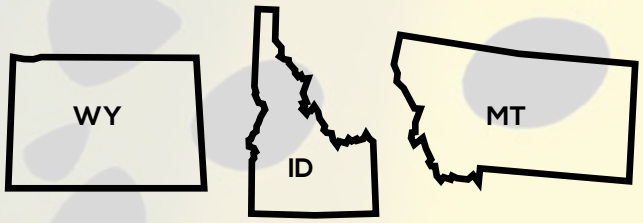
Today, with the availability of the IBEST Computational Resources Core, he is able to run many simulations at once, greatly diminishing the time it takes to get his data. After running all his simulations, Dr. Hohenlohe then sorts through the data produced, analyzing and summarizing it for the publication of papers in scientific journals, presentations and advancement of research

"With genomic technology, people are actually uncovering the structure of real genetic networks in actual organisms, in humans, and other creatures," he says. "They are understanding how different genes affect each other and how they are interconnected."

With this information, Dr. Hohenlohe seeks to better understand genetic variation in natural populations, specifically those of the cutthroat trout. In evolutionary terms, this means he can gain a better understanding of how the trout populations adapt and evolve and how genetic variation is structured in these populations and as a result, aid in preserving the populations of native cutthroat trout that are threatened.

DID YOU KNOW?

Cutthroat are the state fish of:

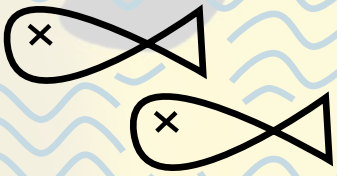


bonneville

yellowstone

There are 13 species of Cutthroat trout. Most are named for the body of water they live in.

Most species of Cutthroat trout are either threatened or endangered.



Unlike Salmon, Cutthroat trout can spawn multiple times before they die.

It is a common misconception that Cutbow are sterile.

CRAZY Multi-Variant Vector Space

By Whitney Schroeder

Tyler Hether scrolls rapidly through the various items open on his computer screen, stopping at the document he wants as he describes his work running quantitative genetics simulations.

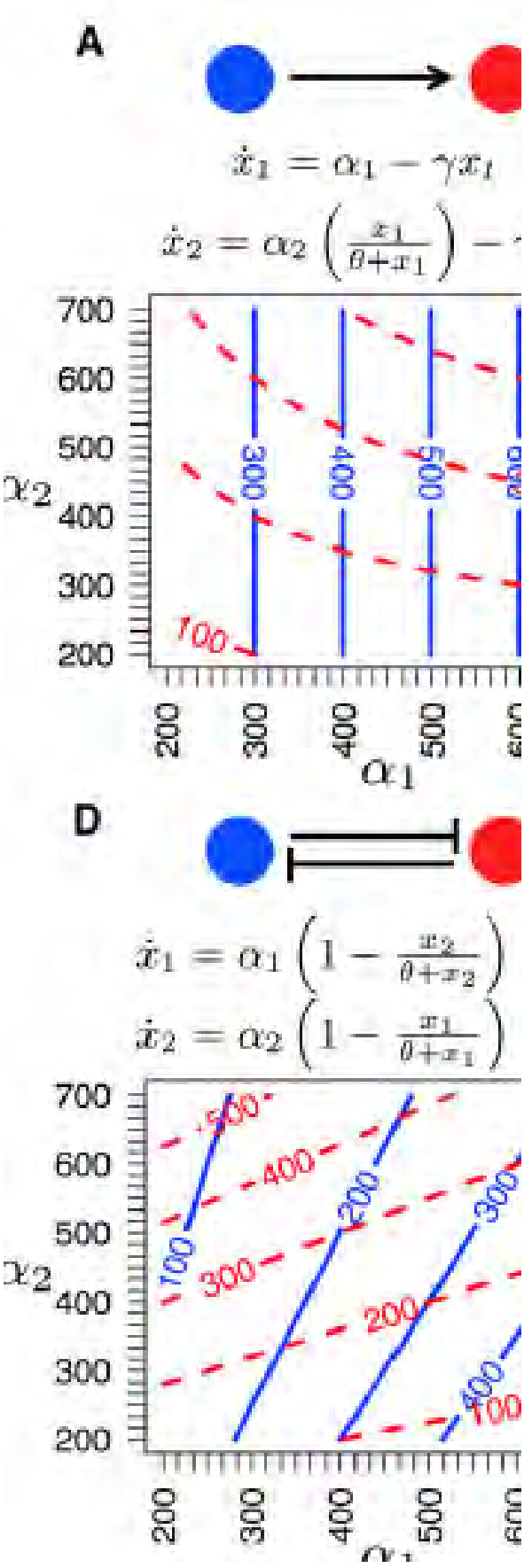
"If you know something about the genetic make up of the population and something about the strength of selection," he says, "then you can predict the next generation."

On his screen, pairs of red and blue dots rest above graphs, different types of lines run between them, representing their associations. With each graph a complex mathematical equation explains it all. I sigh. This is going to be a tough conversation to follow.

Tyler is a graduate student studying to be an evolutionary biologist under Dr. Paul Hohenlohe at the University of Idaho. The word biologist conjures mental images of Charles Darwin's bird studies or high school frog dissections, but Tyler spends much of his time in front of a computer screen dealing with complex mathematical equations and analyzing data in a multi-planar, multi-axis theoretical universe. Sounds complicated because it is. Being exposed to the work of biologists on a day-to-day basis has made me realize that often the center of their research world is technology.

"We are interested in how genetic networks in general can effect phenotypic variation," Tyler says. I give him a blank look.

Lets back up a bit here. Genetic networks? Phenotypes? I was digging deep for any sort of information gleaned from freshman biology years ago, coming up mostly empty handed and grateful for Tyler's patience in explaining "the basics" to me. A genetic network, or gene regulatory network (GRN), is a collection of DNA (our genetic information) segments in a cell that interact with each other or other substances in the cell. These interactions distribute genetic information and



determine how and to what level this information is expressed. The outcomes of the interactions and expressions are called phenotypes or more broadly, traits (such as blue eyes or red hair). Some genes in the network have more of an effect on certain outcomes then others.

Lets say we have gene 1 and gene 2. They interact, creating a phenotype. Simple right? In theory, yes, but not in reality. In reality it is more then just two genes contributing to create a phenotype. Some genes may contribute a lot, while others may only contribute a little, but it still takes them all to make a phenotype. Along with the variety of genes contributing, you also have environmental factors affecting the selection and expression of these traits. All these things come together to create a complicated and multi-faceted realm in which to navigate.

"There's this idea," says Tyler, "that you can predict the response to some selection, whether it be natural or artificial. For example, if a breeder wants to get higher percent milk fat in a cow they might do something similar to this."

Tyler's simulations model interactions between genes, allowing him to see different results that occur depending on how he manipulates the network. He explores how wiring the networks differently causes changes in the gene interactions. In a simulation, populations are formed, they mate and produce offspring, and they die, all in the computer. In order to get good information from these types of simulations, he has to run lots of replicates where he applies different parameters to the networks. This makes it computationally intense because Tyler ends up doing iteration upon iteration of these simulations, each producing different variations – such as migration between populations, rate of evolution and other factors – to be studied and analyzed.

> "If you had knowledge of the networks, then you could form decisions on management for an endangered species."

"So the result is essentially that genetic regulatory networks, even really simple ones," says Dr. Hohenlohe, who oversees Tyler's research, "can have interesting effects on patterns of variation in populations and you can see those effects on how populations adapt through natural selection."

Of course, when Dr. Hohenlohe was in school, the computational resources Tyler now accesses did not exist. The computing resources

TYLER HETHER

A Ph.D. student in the Hohenlohe Lab, Tyler's research focuses on merging concepts from ecology, physiology, mathematics, computer science and molecular biology in an attempt to elucidate how diversity arises.

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available at the University of Idaho influenced his decision to enroll.

"I did my undergrad and my masters at University of Central Florida in Orlando," he says. "It's a huge University but it's a space grant institute. The math was really solid but as far as the biology part, as far as genomics is concerned or computational biology, there was no equivalent service (there)."

Tyler has four processors in his laptop. Each simulation requires at least one processor, meaning he can do four simulations at one time. At the moment, he is running 3600 simulations for an upcoming conference. Each of the simulations take roughly 6 hours time to complete. If he were to run these simulations on his laptop, it would take him around 225 days to complete. He would definitely not have them completed, nor their analysis, in time for the conference. (Not to mention he would be unable to use his laptop for much else in the mean time.) Instead, Tyler is utilizing the IBEST Computational Resources Core. Showing me complex script on his computer screen, he explains how he sends his information to the core, runs the simulations and receives large quantities of data back for his analysis. All this is completed in roughly 3.5 days, and he is not even using the full capability of the core.

With the information from these simulations, Tyler is able to explore and test common assumptions about quantitative genetics that have been generally accepted over the last decade. He must have noticed my pained expression while trying to connect the dots, because he explains that he is also contributing to the growing need for biologists to understand genetic networks and their interactions. Despite being theoretical in nature, Tyler contributes to work that is used often in important applications, especially in the agriculture realm, people wanting to increase the yield in their wheat or produce cattle to a certain level of meat quality.

"If you had knowledge of the networks then you could form decisions on management for an endangered species," Tyler says, "or populations changing from different land use, such as larger, regional and global climate change."

Even within these simplified networks, Tyler Hether's work demonstrates the important role of genetic networks when it comes to adaptation. The wiring of certain networks makes it difficult for a population to adapt and change to a new environment, while others aid in the change. As more and more people pay attention to and comprehend how genes are networked together, profound impacts on how populations adapt and our role in that adaptation will continue to be understood.

APPENDIX 7 (CONT'D) - NEWSLETTER

DOES **SIZE** MATTER?

WHAT IT TAKES TO BEGIN TO DECODE THE HUMAN GENOME?

There are roughly 2.9 billion base pairs in the human genome.

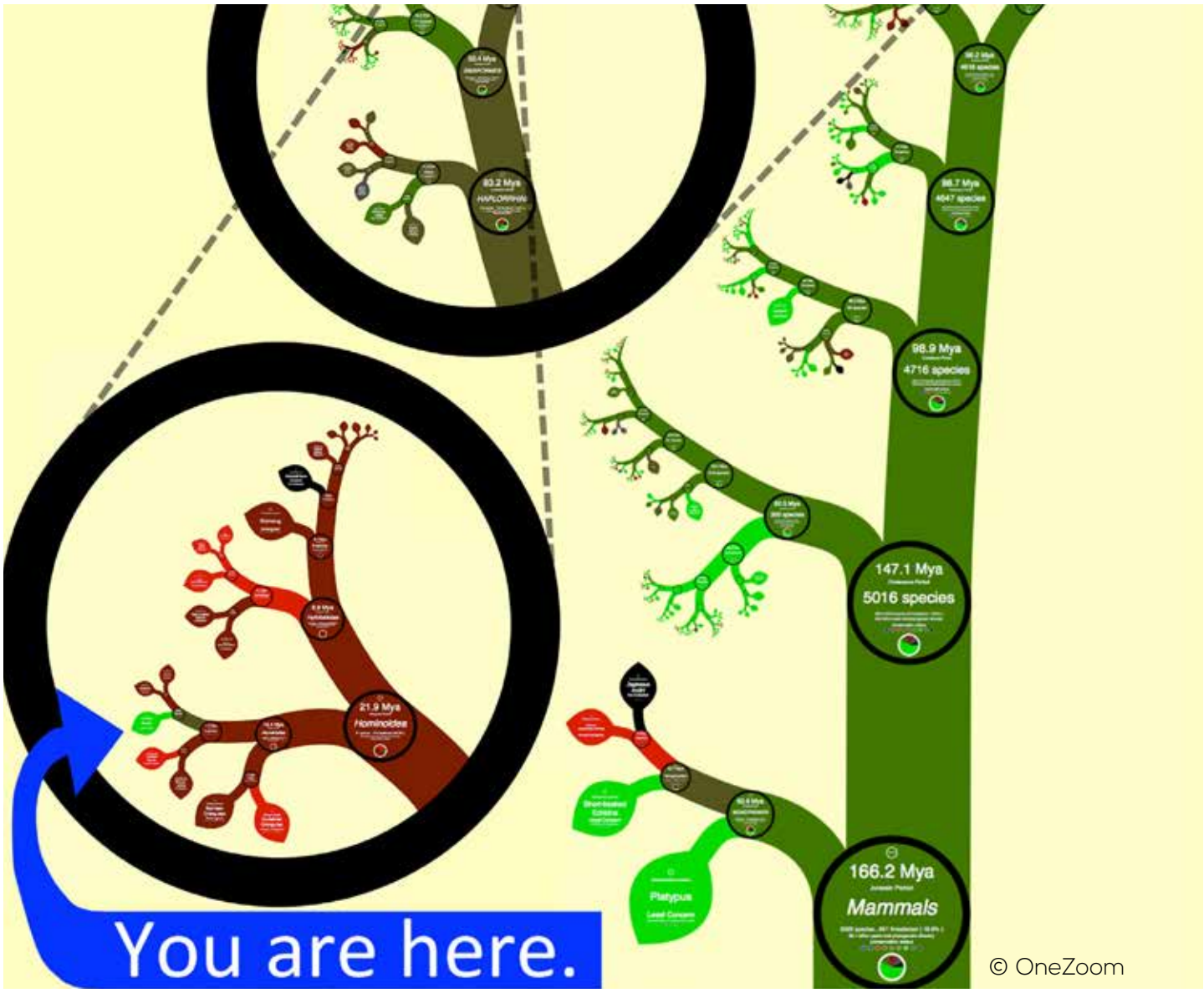
Sequencing (decoded) is typically done with 30X coverage. This means 30 copies of the human genome are made, meaning 87 billion base pairs are generated for the human genome.

The whole genome can't be sequenced all at once because available methods of DNA sequencing can only handle short stretches of DNA at a time. Scientists break the genome into small pieces, sequence the pieces, and then reassemble them in the proper order to arrive at the sequence of the whole genome.

Imagine buying a 1,000 piece jigsaw puzzle and then 29 more exactly like it. Open each box and dump all the pices into a large bag. Then start sampling pieces from the bag to build the puzzle. That is 30X coverage.

The IBEST Genomics Resources Core produces 20 million reads per full cycle. Each read contains 600 base pairs. A full cycle takes 36 hours to complete, generating 12 billion base pairs. It takes roughly 11 days to do 30X coverage of the human genome.

Massive computing power is needed to handle all the data generated by sequencing and enables researchers to put together the puzzle of the human genome.



MAPPING The Tree Of Life

By Whitney Schroeder

Hundreds of years ago people looked to their genealogical lines to see if they were related to nobility. Today it has become an over 1.6 billion dollar industry of curiosity and history. Now scientist Dr. James Rosindell has taken genealogy to a whole new level, asking not whom you are related to, but what. While working for Dr. Harmon as a postdoctoral student, Dr. Rosindell decided to apply his love of fractals to create One Zoom, an online, interactive map allowing anyone to navigate the complex and extensive phylogenetic tree of life. Phylogenetics refers to the study of branching diagrams called trees that represent the relationships among various biological species or entities. One Zoom compiles all these trees into one giant tree, the tree of life.

"One Zoom took some serious programming," Says Dr. Harmon, "When James would come in and

tell me what he was doing, I thought whoa, keep doing that."

The goal of One Zoom is to the raise awareness about the diversity of life, its history and threats of extinction. Every living organism on planet earth, from bacteria to humans, chimps, fish, reptiles, and amphibians – over 2 million known species are mapped on the One Zoom tree. Most of the tree represents things we cannot see with the naked eye. Visible creatures and organisms only make up a small twig.

"It is important to understand where we came from, our history, the history of species on the earth, how we are all related to each other," says Dr. Harmon, "Its the story of life on earth, which I think is important to know."

There are many practical implications to understanding relationships among species. For example, Dr. Harmon uses the tree to figure out how often new species form. This is important because if we are wiping species out at a rapid rate, knowing how often new species form will tell us just how dire the consequences our human caused extinctions might be. If it takes a million years for an extinct species to be replaced by others, then we can gain a sense of how devastating our actions will be for future life on earth.

"The tree (One Zoom) is overwhelmingly large, there are so many species and we don't know that much about a lot of them," says Dr. Harmon.

> "It is important to understand where we came from."

Having One Zoom as a map allows scientists to focus on really interesting or little known parts of the tree. It can guide research to species that have been studied very little or to explore strange parts of the tree, such as fish known as cichlids in east African lakes. These cichlids are showing some of the fastest vertebrate speciation rates in the whole tree of life. This pattern may have gone unnoticed without viewing the cichlids in the broader context of the tree. Now researchers are investigating why there is such rapid forming of new species in cichlids and what that might mean in regards to other parts of the tree.

"All of these things require really heavy-duty computational tools that we wouldn't be able to do without the cluster here at Idaho," says Dr. Harmon, "These trees are actually too big to print out, they are too big for the human brain to comprehend, so we use the computational cluster to do the processing and statistical analysis that tells us what parts of the tree are interesting and unusual, to characterize their general properties and to measure them."

LUKE HARMON

Research in the Harmon Lab investigates ecological and evolutionary aspects of adaptive radiations. They explore the causes and effects of both speciation and trait change and how species interactions shape macroevolution.

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APPENDIX 7 (CONT'D) - NEWSLETTER

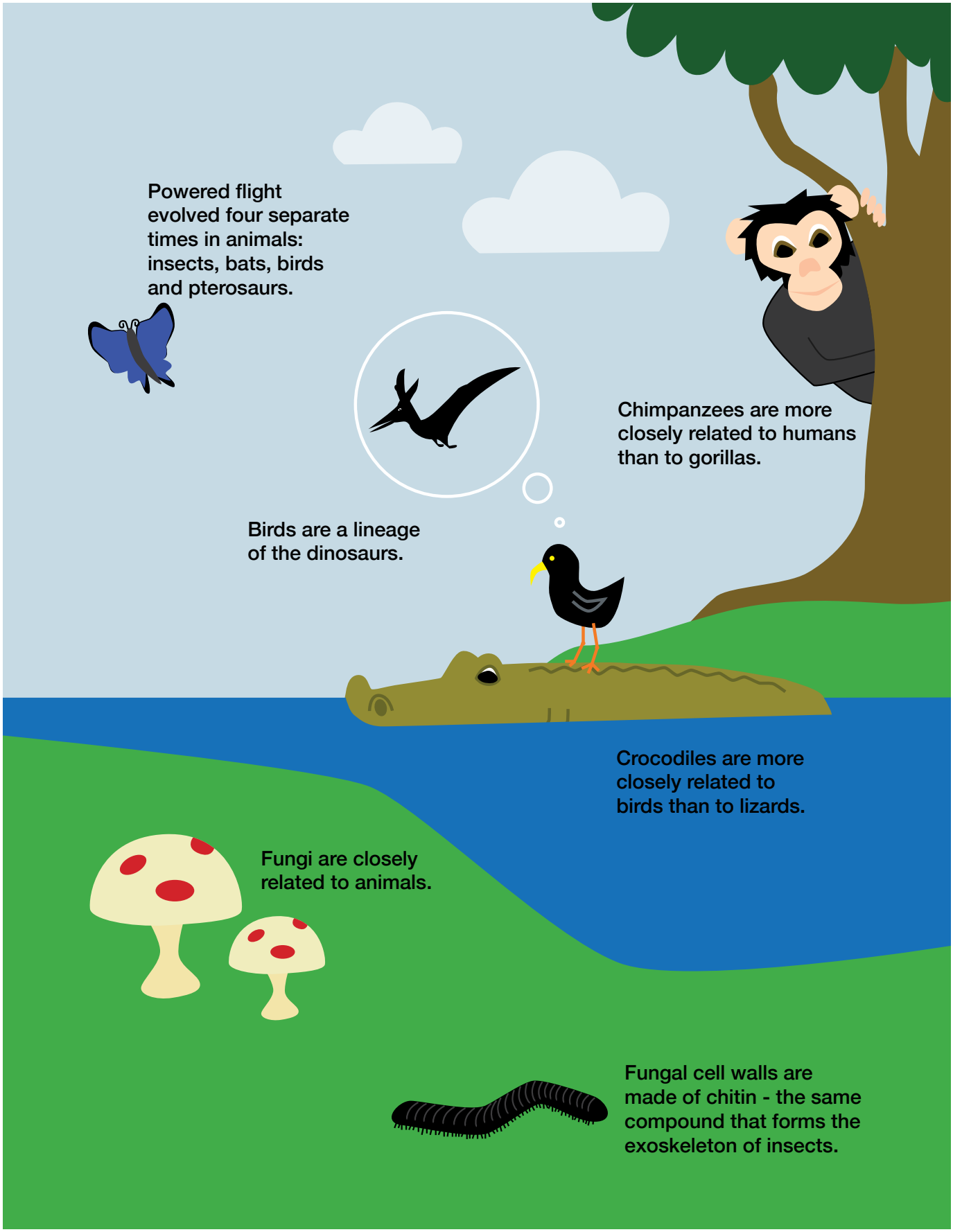
Each species' information is obtained primarily through genetic sequencing. If you have a tree with 50,000 species on it, each with a large amount of genetic data, the files for these trees become massive. They would easily crash your laptop or desktop computer, a problem Drs. Rosindell and Harmon had to wrestle with before utilizing the IBEST Computational Resources Core.

In the Inland Northwest there is a species called the tailed frog. It has its own branch on the tree of life. Only males of the species have tails, which they use to internally fertilize the females. This is really unique in amphibians, which typically fertilize eggs externally, after females have expelled them. When researchers started looking at the tailed frog in the context of the whole tree of life, they discovered there are only two species of this frog in the whole world, one in the Inland Northwest and the other on the west coast around Seattle. These two species are connected to the rest of the frogs on a branch that spans 200 million years or so. Not having any other relatives anywhere near them on the tree of life makes them absolutely and completely unique and relatively unchanged over millions of years.

"I think we've learned over the last 20 years in biology that it matters species are related to one another," says Dr. Harmon.

As a rough guide, the One Zoom comprehensive tree of life helps Dr. Harmon and other researchers like him navigate the complicated realm of how species form and evolve, how we are all interconnected and what that might mean for future generations.

APPENDIX 7 (CONT'D) - NEWSLETTER



CRC
Then and Now

The IBEST Computational Resources Core came from humble beginnings. Drs. James Foster and Robert Heckendorn built the first computers with a class of Computer Science students in the basement of the Janssen Engineering Building for a total of $35,000 . Funding was provided by NSF-EPSCoR. They jokingly called the computer cluster LOBOS, "Lots of boxes on shelves" and later, The Cube. (In the words of the Borg, "You will be assimilated!")

After burning out two window AC units and suffering several system failures due to overheating while housed in the Janssen Engineering Buildings, Beowulf was moved to the basement of the McClure building. The University paid for a comprehensive renovation to accomodate the needs of such a large computer system, creating a state of the art facility. Here it began its transition into the large computing cluster it is today supported by funding from Idaho INBRE and the IBEST COBRE.

2000

The Cube

Computer Science students building Beowulf

Drs Robert Heckendorn and James Foster

2002

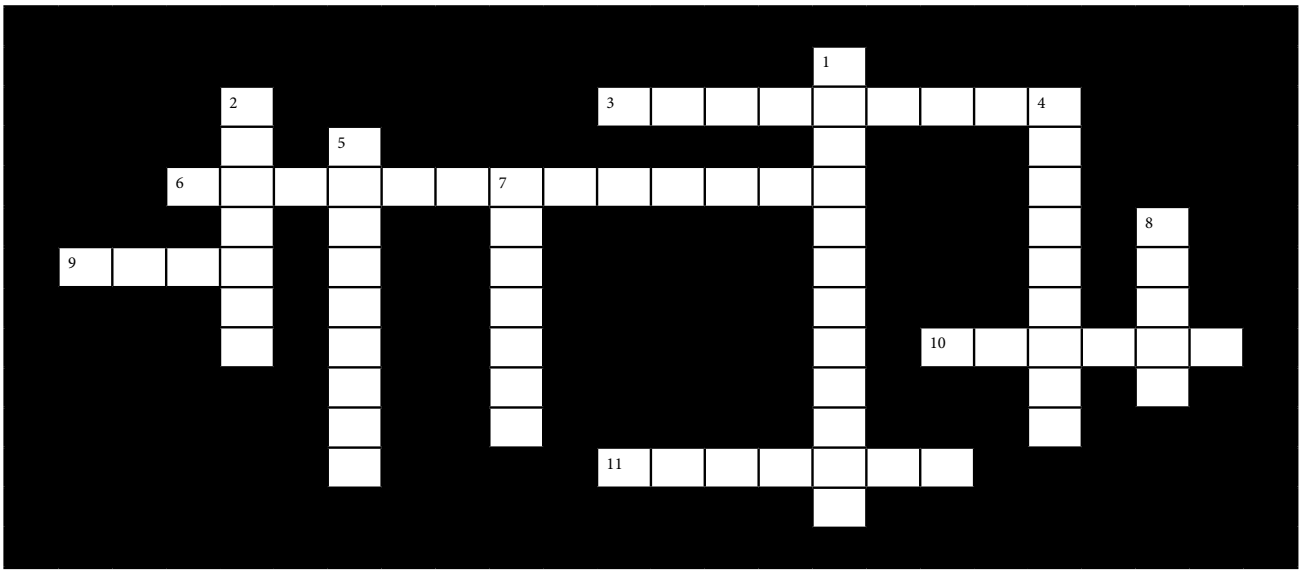
Beowulf moved to the basement of McClure

2014

IBEST Computational Resources Core

APPENDIX 7 (CONT'D) - NEWSLETTER

Now You Know!



Across

3. Dr. Paul Hohenlohe studies the fitness of _____ trout.
6. Along with gene contribution, _____ factors affect the selection and expression of traits.
9. One _____ is an interactive map allowing anyone to navigate the phylogenetic tree of life.
10. The hybrid of a rainbow trout and cutthroat trout is called a _____.
11. The IBEST Genomics Resources Core produces twenty _____ reads per full sequencing cycle.

Down

1. _____ trees represent the relationships among various biological species or entities.
2. RAD Sequencing allows researchers to sample the _____ of multiple individuals in a population.
4. The IBEST Computational Resources Core has 512 _____ of storage.
5. Birds are a lineage of the _____.
7. A genetic _____, is a collection of DNA segments in a cell which interact with each other indirectly and with other substances in the cell.
8. _____, or "lots of boxes on shelves," was the nickname of the NSF EPSCOR computer cluster that grew into the now IBEST Computational Resources Core.

APPENDIX 8 - 2014 INLAND NORTHWEST GENOMICS RESEARCH SYMPOSIUM

Inland Northwest Genomics Research Symposium, MAY 22, 2014

Speakers topics and institutions

		Topics						
Oral presentations	**Total**	**Genomics**	**Computation**	**Vendors**	**Keynote**			
Number presentations	**10**	7	1	1	1			
Speaker Institution	U Idaho	Washington State U	University of California - San Francisco	University of Oregon	University of Montana	Univeristy of Washington	USDA-ARS	Industry
Number speakers	3	1	1	1	1	1	1	1
Posters	39							

Institutions represented

Central Washington University	2	Thermo Fisher	2
Rocky Mountain Laboratory, NIH	1	Wafergen Biosystems	2
University of Oregon	2	HTG	1
University of Alberta	1	Qiagen Inc.	3
University of California - San Francisco	1	Illumina	2
Lanzhou Veterinary Research Institute - CAAS	1		
Washington State University	32	**Subtotal**	**10**
Northwest Nazarene University	1		
University of Idaho	69	**Agency**	
University of Montana	4	USDA	8
University of Washington	1	**Subtotal**	**8**
Moscow High School	2		
Subtotal	**117**	**TOTAL ATTENDEES**	**135**

Funding

	COBRE	IBEST F&A	Vendors	Total cost
Source of funds	$10,314	$5,682	$2,900	$18,896

Vendors: Fluidigm, Qiagen, Bio-Rad, Illumina

APPENDIX 9 - BUSINESS FOR SCIENTIST ATTENDEE INFORMATION

Business for Scientists 2014

Tanya Miura	tmiura@uidaho.edu	Biology	COS
Elizabeth Cassel	ecassel@uidaho.edu	Geology	COS
Ling-Ling Tsao	ltsao@uidaho.edu	Family and Consumer Sciences	CALS
Chris Caudill	caudill@uidaho.edu	Fish and Wildlife	CNR
Kurt Schroeder	kschroeder@uidaho.edu	Plant, Soil & Entomology	CALS
Robert Heinse	rheinse@uidaho.edu	Soil Sciences	CALS
Dave Tank	dtank@uidaho.edu	Biology	COS
Barrie Robison	brobison@uidaho.edu	Biology	COS
Luke Harmon	lukeh@uidaho.edu	Biology	COS
Matt Settles	msettles@uidaho.edu	IBEST	ORED
Sarah Koerber	skoerber@uidaho.edu	Proposal Development Specialist	ORED
Celeste Brown	celesteb@uidaho.edu	Biology	COS
Armando McDonald	armandm@uidaho.edu	Dept. Forest, Rangeland and Fire Sciences	CNR
Frank Wilhelm	fwilhelm@uidaho.edu	Fish and Wildlife	CNR
Nancy Deringer	deringer@uidaho.edu	Family and Consumer Sciences	CALS
James Frenzel	jfrenzel@uidaho.edu	Electrical and Computer Engineering	COEngineering
Yong Zhang	yzhang@uidaho.edu	Office of Technology Transfer	
Helen Joyner	hjoyner@uidaho.edu	Food Sciences	CALS
Jocelyn Aycrigg	aycrigg@uidaho.edu	Fish and Wildlife	CNR
John Crepeau	crepeau@uidaho.edu	Mechanical Engineering	COEngineering
James Foster	foster@uidaho.edu	Biology	COS

APPENDIX 10 - BUSINESS FOR SCIENTIST COURSE SCHEDULE

Business for Scientists			
	Day 1	Day 2	Day 3
8:00 - 9:00	An Overview of Business: The Pillars of Feasibility	What is a Business Plan?	Budget/Cash Management
9:00 - 10:00	Overview of Marketing (as it relates to Market Feasibility)		
10:00 - 11:00		Economic Impact Analysis	Managing a Team
11:00 - 12:00	Business Model		

Business for Scientists		
	Day 4	Day 5
8:00 - 9:00	Behavioral Aspects of Decision Making	Panel Disccusion: (1) Trends in University Research, (2) The Role of Open Innovation, (3) Challenges of R&D
9:00 - 10:00		
10:00 - 11:00		
11:00 - 12:00		

APPENDIX 11 - BEACON FUNDED PROJECTS

BUDGET #	UI PI	Co Pis with UI member in bold	PROJECT TITLE
KGK001	**Soule 1**		*Evolutionary Games K - 6*
	Soule 2	Getty	*Evolution curriculum for elementary classrooms: implementation and assessment of LadyBug and supporting activities*
	Soule 3	**Heckendorn,** McKinley, Zhan, Harrison, Espinosa	*Distributed, Onboard Evolution in a Robotic Cloud*
	Soule 4	Dozier**, Heckendorn, Stenkamp, Fuerst**	*Genetic and Evolutionary Feature Extraction for Evolutionary robotics*
KGK002	**Harmon 1**	Boughman, Lenski, Williams	*Mystery of Mysteries*
	Harmon 2	Eisthen, Zakon, Liebeskind	*Evolution of mechanisms enabling the use of a neurotoxin as a pheromone*
	Harmon3	Felsenstein	*Long-term consequences of evolution in action examined over a phylogeny*
KGK003	**Sullivan**	Hillis	*An integrated approach to testing divergence with gene flow model of speciation; empirical genomics: simulation, and in silico evolution*
KGK004	**Wichman 1**	Ellington	*Evolution of synthetic genomes*
	Wichman 2	**Miura**, Bull	*A tractable animal model for experimental viral evolution*
	Wichman 2	**Miura**, Bull	*A tractable animal model for experimental viral evolution Year 2*
KGK005	**Harmon**	**Hohenlohe, Rosenblum,** Boughman	*The Genetic Architecture of Multidimensional Adaptation and Speciation*
KGK006	**McGowan**	**Gutmann,** McKinley, Moore	*Why hop? Understanding morphology, mechanics, and natural selection in the evolution of bipedal hopping*
	McGowan 2	McKinley, Moore	*Watch Your Step! Exploring the Evolution of Robust Joint-Level Control*
KGK007	**Hohenlohe**	Williams	*An experimental evolution model for genomic islands of speciation*
KGK008	**Top**	**Forney**, Kerr, Ofria, Pennock, Wilke	*Slow and steady wins the race? Adaptation in structured worlds*
KGK009	**Tank**	**Foster**, Conner	*The genetic basis of weediness: rapid evolution of flowering time in wild radish,*
KGK010	**Heckendorn**	Dworkin, Lenski	*Cross-fertilization of techniques for epistasis from evolutionary computation and biology*
KGK011	**Foster**	**Day, Soule**, Dozier, Ofria	*Teaching evolution through action: the Avida challenge*
	Foster	**Soule**, Pennock, Ofria, Graves, Smith,Swalla, Wilke	*Avida-ED Infrastructure Maintenance and Development*
	Foster	**Soule**, Pennock, Mead, Graves, Kerr, Wilke, Smith, Lark, Johnson	*Avida-ED Curriculum Development and Assessment Pilot Study*
KGK312	**Heckendorn**	Clarke	*BEACON Summit to Catalyze Diversity*
	Heckendorn	Clarke	*BEACON'S Disability Action Plan*
KGK313	**Foster**	**Harmon,** Eisthen, Vaelli, Theis	*The role of symbiotic bacteria in a predator-prey coevolutionary arms race*
KGK314	**Hagey**	Riley, Soroushian	*Optimization of the Gecko Adhesive System*
	Hagey	Riley, Soroushian	*Optimization of the Gecko Adhesive System Year 2*
KGK315	**Marx**	Barrick	*Mechanistic Basis of Mutations Potentiating the Evolution of Citrate Utilization in the LTEE*
KGK316	**Fuerst**	**Stenkamp**, Boughman, **Robison**	*Genome Duplication as a Source of Variability in Evolution of the Fish Visual System*
KGK317	**Nuismer**	Bull	*Predicting the evolution of synthentic genomes: transmissible viral defense*
ABK919	**Heckendorn**		*Sabbatical Support*
N/A	**O'Rourke**	Pennock	*Developing a virtue-based approach to RCR training*
ABK918	**Foster**	**Heckendorn, Soule**	*Idaho Administrative Budget*
ABK917	**Foster**		*Idaho Administrative Budget*

Post docs funded: 6 Sean Carroll with Chris Marx has not yet started.	Martina Ederer, Thibault Stalder, Travis Hagey Ann Gutmann Josef Uyeda Jonathan Eastman
Grad Students : 17	Tyler Hether, Dan Norris, Matt Pennell, Josh Rubini, Brice Sarver, Simon Uribe Convers, Max McKinnon, Travis DeVault, Kayla Hardwick, Thomas Poorten, Timothy Meekhof, Julie Hughes, Sam Hunter, Josh Sukeena, Tim McGuin, Janet Williams, Jayandra Pokharel
Undergrads funded: 16	Raish Marissa, Katie Slavens, Sasha Solomon, Damien Tabis, Josh Rubini, Solomon Michael, Ryan Parks, Nicholas Forshee, Sam Billingslea, Erin McColly Rebecca McKenzie, Tracy Myron, Justin Anast, Brian Lohman, Ryan Simmons, Cody Wiench