It’s a sunny winter’s morning in Buffalo as I sit down with a Diet Dr. Pepper to pen the first “President’s Message” for our ABRF Communications newsletter. And I’ve just finished reading an article that Ron Nice, our Membership Committee chair, had forwarded along to the rest of us earlier today and it’s given me cause for a moment of reflection. It was a publication in The Scientist, written by Steven Wiley and entitled:

“To Join or Not to Join”: The benefits of membership to a scientific society are decreasing every year. Lately, I’m asking: Why bother?

Wiley discusses the increasing sense of indecision scientists have towards maintaining membership in scientific societies - member benefits, such as discounted journal subscriptions or opportunities to present abstracts at conferences, have become less exclusive. Freely accessible online journals are more ubiquitous and a plethora of scientific and technological meetings exist. In the current economic climate, it becomes progressively more difficult to choose which associations, societies and conferences will give you the most “bang for your buck”. Which ones will best advance your knowledge, your career and your future?

So, I considered today: how DOES the Association of Biomolecular Resource Facilities stand out in this crowded crowd of competitors? What makes our association so unique and distinctive? What do we offer that gives the most value to our membership and how can we do more?

These days, our membership faces a vastly different environment than folks did roughly twenty years ago when the ABRF first began as an offshoot of The Protein Society. Core consolidation, outsourcing and less financial institutional support have become a fact of life for many of our members. It’s no longer enough that we are the local institutional experts in a specialized technology or scientific application (the part that fascinates us most). We must also now be businesspeople (gasp or groan) - administrators, strategic planners with crystal balls, financial managers, counselors, grant writers; in certain instances we even play the roles of PIs on scientific projects. Our members must be jacks-of-all trades...and masters of all of them as well.

So how does the ABRF assist its members in tackling these widely diverse responsibilities?

Our Research Groups are arguably one of the greatest strengths of the ABRF and their impact is far-reaching. Our RGs are involved in a wide spectrum of technologies, ranging from DNA Sequencing to Proteomics to Light Microscopy. The studies they perform help us bring new methods into our labs, give us opportunities to benchmark our techniques, and provide knowledge and education to the scientific community at large. The Research Groups are indeed one of the hallmarks of our association.

The ABRF listserv, with over 1700 subscribers, is a worldwide discussion forum that provides an invaluable means for laboratory folks to share advice, compare notes and assist others in troubleshooting. Together, the RGs and the listserv serve as the “technological arm” of the ABRF.

There is also our highly anticipated ABRF Annual Conference where one can go to hear about the latest in cutting-edge technology and science; receive practical, take-home information about managing and operating shared facilities; visit exhibitors to see exciting new developments and products, and network in the collegial and inviting atmosphere for which the ABRF meetings are well-known.

This year’s meeting theme is “Translating Basic Research with Advances in Biomolecular Technology” and is proving to be one of the most innovative and exciting ABRF conferences yet. Enthusiastic thanks go out to the ABRF2010 Program Organizers - Jay Fox, Chris Turck and Susan Hardin, for the exceptional agenda they have assembled. As President, I often follow along peripherally with their activities preparing for the meeting – and I can
As I finish my first term as President, I can truly say this has been a most rewarding, energizing and challenging experience. While I am relatively new to the association, I’ve been so fortunate to have advisors and mentors to whom I’ve been able to turn — they’ve always been there to offer me wisdom, advice and to share their experiences. It is they who have helped further instill in me the core values of the ABRF — how we began, our continuing growth throughout the years, and our current missions and goals. I’d like to take this opportunity to say thank you to all of you who have helped me over this past year.

I’d also like to extend my sincerest appreciation to our two outgoing Executive Board members, Scottie Adams and Jeff Kowalak. Each of them has brought their own unique perspectives and strengths to the ABRF. As their terms end now, they can surely see the positive marks they have left behind on the society. They have been wonderful colleagues to work with, and we will miss them. Thank you so much, Scottie and Jeff. Enjoy some quiet time now ...smile.

We also welcome our two newest Executive Board members, Tom Neubert and David Friedman, whom we are confident will help propel the society into future positive directions! We’re very excited to have them on board with us and truly look forward to the time we will be able to work with them.

In conclusion - what I’ve ultimately come to appreciate, first-hand, is the one thing that makes this association so very special to so many - our membership! There is a true sense of community and camaraderie in our association. We have so many enthusiastic volunteers - and the commitment and dedication of these are what help maintain the vitality and growth of the ABRF. And we continually encourage members to actively participate - join an RG or Committee! It can be one of the most rewarding professional experiences you will have. If there is a need you might feel is missing in ABRF, let us know! We are always excited to see grassroots efforts spring from our membership — whether it be forming a new RG, or suggesting a new initiative or program that further strengthens the mission of the ABRF — your participation is always strongly encouraged!

The people of ABRF are not simply professional colleagues who share a similar scientific interest or research focus. The ABRF is, at its core, a group of friends. People who are there to share resources and knowledge, provide advice (and sometimes commiseration), and to just simply support each other. And that is a comforting thing to know...because working in a core facility can sometimes be a rocky road that is a difficult one to walk alone.

And to me, THIS is what makes the ABRF the worthiest of societies to join.

There is no compare.
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ABRF2010

Meeting highlights—Sacramento, CA
Interviews with Tom Neubert and David Friedman

By Seth Crosby

The who?” I croaked groggily by email.

“The newest members of the EB!!” sparkled back Michelle Detwiler, current president of the ABRF. “Could you interview them for our new Newsletter?”

Like many editors of brand new newsletters, Detwiler had clearly scraped through the bottom of the barrel and was still digging. The e-ink of my membership acceptance from the ABRF was still wet, and all I had done to prove my competence for this task was to smile wanly as Detwiler beat my behind like a drum at darts during the NERLSCD (I have to look that up every time) meeting.

“I was thinking,” she continued, “the article could be sort of humorous. Mark Twain, David Sedaris and Hunter Thompson walk into a bar sort of thing. Come on! You’re from Missouri!!”

“What does EB mean?” I managed.

A few days later an e-mail arrived formally introducing me to David Friedman and Tom Neubert. Detwiler had even had the foresight to include pictures of us, so we’d recognize each other over the phone. Tom and David’s portraits glittered with intelligence and good humor. Mine was the size of a postage stamp and looked like a Macon County mug shot. This wasn’t going well.

It didn’t get any better when I finally caught Tom by phone. He was relaxed, friendly and eloquent. I glanced at a long list of suggested questions Detwiler had crafted for me in the unlikely event that I didn’t know what I was doing.

“Tell me about some of the people you’ve met while working on ABRF”

“What was your first impression of ABRF?”

“What else can you tell me about ABRF?”

“Oh,” I began.

“Would you like me to tell you a little about myself?” Tom offered.

“Yes,” I answered.

Tom Neubert used to play college basketball and race bikes, but that all ended with the birth of his first of two children, now aged four and six. In 1998 he established the NYU Protein Analysis Facility. Even before starting his core, he attended his first ABRF meeting and was immediately struck by the attention that was paid to the frustrating but critical non-science issues we directors spent too much of our time worrying about. He remembers a talk given by Marjorie Tingle on the NIH Shared Instrumentation Grants program. Tom talked extensively with me about the economic impossibilities of running an academic core facility. He referred me to a 1999 paper written by ABRF EB members, Ruth Angeletti et al (FASEB J, 1999 13:595-601), which he keeps in his back pocket whenever he has a meeting with a Dean. One of the tenets of the paper is that it can be counterproductive to science to expect cores to break even...that by supplementing their cores, institutions attract talent and increase discovery and publication, thus essentially adding to their bottom line. To not invest in cores is like keeping your savings in a mattress.

After 12 years in the ABRF, Tom still appreciates the multiple challenges of the association – to keep its membership scientifically, economically and politically current; and to support its networking function, both electronic and face-to-face. “I get that with our limited time and resources we can not be perfect at all these jobs,” he said. “For example, at the annual meetings, time is our tightest resource and we have to prioritize session topics. A key, I hope, is to be able to leverage communication technologies to continue to increase what we can do.”

Tom still gets out for punishment on a bicycle once a year with Bill Lane, the guy who “convinced” him over several years to accept the Executive Board nomination. He did not mention if he forgoes training wheels.
David Friedman, who co-runs the Proteomics Laboratory within the Vanderbilt University Mass Spectrometry Research Center, upon learning of this interview, promptly left the country. A week later he was back, having, I suspect, run out of money.

“I met my wife while we were in grad school,” he began. He had also studied yeast genetics. This led to a post-doc involving protein phosphorylation, which, in turn, led to an interest in the intricacies of mass-spec. David decided to support his wife’s science career by using his knowledge and skill concerning mass spec to run a core. “See, that way I would be less busy and could pick up more of the slack at home with our [now] three kids,” he explained rather naively. He was, in the subsequent months and years, brought up to speed on how Margarita-ville-ish our lives as core directors are. In 2006 he was invited to give a talk at ABRF and was blown away by how a relatively small meeting could be so full of people who shared his interests. He kept coming back and was, of course, sucked into serving on various committees, co-organizing satellite workshops and ultimately...the ABRF Executive Board.

“What do you see as strengths of the ABRF?” I asked. Thanks, Michelle.

David remains amazed at how cool the Research Groups (RG) of the ABRF are. He has been on the Proteomics Research Group for the past three years, and is currently heading it up. RGs, for those who, like me, are new to the ABRF, are one of the aspects of the organization which sets it apart from other professional groups. These groups organize efforts to refine and improve operations and procedures in its member facilities. They do so by defining certain questions and then by providing test samples. Data are returned, members of the RG crunch the results and provide their conclusions to the membership.

In addition, David will do what he can to foster the relationship the ABRF has with its partner vendors. He sees this as reflective of the mutually beneficial relationships facilities have with the companies that provide our technology. “Our partner vendors provide some of the resources that allow us and our membership to succeed. They provide us with invaluable information of what is current and what is over the horizon. Our success as an association makes us more viable customers for them. It’s completely symbiotic!”

After ending the call with David and looking up the word ‘symbiotic’, I called Detwiler. “You sure you want this funny? These guys had some pretty serious stuff to discuss.”

Editor's note: Left - my initial attempt at virtually introducing our interviewees/interviewer via e-mail. While I had great high-resolution pictures of David and Tom from the recent EB elections page, the only photo I had of Seth was one quickly swiped off of his LinkedIn page. Seth suggested that it looked like something I fished out of an e-gutter. I have since apologized and tried to rectify in this newsletter.

M.D.
Metabolomics (MRG)

Expanding my –omics horizon: starting a new ABRF Research Group

By Chris Turck

New technologies that gain popularity in the life sciences and require experts to deliver meaningful results will eventually find their way into core laboratories.

This is particularly true for the -omics technologies where expensive equipment and reagents are used and expert operation is critical.

I was therefore not at all surprised when in 2009 we, the ABRF Executive Board members, were approached by Don Rose (then at Metabolon) inquiring about the possibility of creating a ‘Metabolomics Research Group’ (MRG). Metabolomics, the comprehensive profiling of metabolites and other small molecules uses equipment including NMR and mass spectrometry and is therefore predestined for implementation in a core environment.

From day one I was enthusiastic about the proposal to establish an MRG, and I was eventually charged to go ahead with coordinating the task. I was particularly keen on taking this on since my own research projects also moved in the direction of metabolite analysis as it relates to disease-related pathways.

An e-mail to the ABRF community and individuals known as experts in the field inquiring about the interest in metabolomics resulted in a number of responses that upon follow up led to the selection of several member candidates. After further discussions over the phone outlining the various duties/responsibilities I went ahead and selected eight members for the new MRG that were subsequently approved by the ABRF Executive Board.

This was the first time I had ever done something like this. I have been involved with the ‘Proteomics Research Group’ (PRG) for almost a decade starting as a member, then chair and now EB liaison, but that was an existing RG where everything was already set up and running. Furthermore, I was not really very familiar with the field of metabolomics. All this presented a great challenge, but I am very glad that I took over the responsibility of establishing the new MRG. Instrumental in this venture were of course the group’s members, who are very experienced and competent individuals from academic core and research laboratories, industrial analytical laboratories and providers of metabolomic services, analytical standards and instrumentation.

First order of business was to initiate conference calls and getting to know each other. Fortunately, everybody was present at the 2009 ASMS conference in Philadelphia where the group got together for a nice Italian dinner. It was at that point that we came up with our first survey project. The survey was meant to collect data on the current use of metabolomics technologies in core facilities and results will be presented at the ABRF2010 conference in Sacramento. I encourage you to come to the MRG session on Sunday to find out more. The other speakers at the session will all come from the MRG and will give you a flavour on what is involved in running a metabolomics core. Future activities of the group will include the organization of research studies, something similar to what the PRG and other RGs are doing each year.

For ABRF2010, Bill Wikoff, the incoming MRG chair, has organized a ‘Metabolomics Scientific Session’ with three outstanding speakers taking place on Tuesday. This should be a dynamite session that will deal with metabolomics applications and technologies alike. Some of our ABRF sponsors have already taken note and were interested in sponsoring the session. I am sure this interest will become even greater in the future as the technology matures.

The MRG mission states: “The immediate aim of the Metabolomics Research Group is a) to educate research scientists and resource facilities in the analytical approaches and management of data resulting from comprehensive metabolite studies and b) to promote the science and standardization of metabolomic analyses for a variety of applications.”

This certainly applies in my case. It did not take very long for me to realize how valuable metabolite information can be for life science projects, and I now have ongoing collaborations with 2 MRG members greatly benefiting my own research. In summary, I can say that taking the MRG off the ground continues to be a very rewarding activity and learning experience. New technologies will continue to emerge. I can only encourage the ABRF...
and its members to take these opportunities and further expand the society’s portfolio.

Finally I would like to thank all present and past MRG members for making this such a joyful experience: Pavel Aronov, Nathan Dodder, Brenda Kessler, Thomas O’Connell, Matt Pamuku, Don Rose, Vladimir Tolstikov and Bill Wikoff. I also want to welcome our incoming members John Asara, David Powell and Vladimir Shulaev and look forward to another exciting MRG year. If you are interested in learning more about metabolomics get in touch with an MRG member at ABRF2010. Maybe you can even arrange to get a tour of the ‘Metabolomics Core Lab’ at UC Davis that is run by MRG member Vladimir Tolstikov.

Quiz (answers to the questions will be given in the ‘Metabolomics Research Group’ and ‘Metabolomics Scientific’ sessions … and … in the next ABRF Communications)

1. What is the estimate for the number of primary human metabolites?
2. What are the biggest challenges in metabolomics analysis?
3. What are the major technology platforms used in metabolomics analysis?
4. What is the meaning of the Greek word “metabol”?

Light Microscopy (LMRG)

By Rich Cole

First a little history - Light microscopes (LM) have had a seminal influence on science for more than 300 years. The past three decades have seen a dramatic resurgence in the use of the light microscope, as well as very substantial technical advances. This has in turn led to an increase in the use of the LM as a research tool. The most important advance has been the development of the confocal microscope, which combines the detection efficiency of fluorescence with the high resolution of the LM.

As a result of improved performance and functionality of the systems, there has been a dramatic increase in costs of these types of instruments. The increase in cost coupled with decreasing grant support for research has resulted in many of these new instruments being placed in multi-user facilities, i.e. imaging “cores”.

Establishment of imaging cores has led to a shift in responsibility for instrument acquisition, maintenance and training, from an individual PI to the director of core and core personnel. Users need to be confident that data collected will be uniform over time and between specimens. There is a need to develop standard Good Operating Practice (GOP) procedures for the imaging instrumentation. Funding (NIH through SIGs) as well as regulating agencies (FDA) will soon require some form of “performance” testing to be conducted on a regular basis.

How we started - to the best of my recollection: Carol Bayles and I were talking at the first Northeast Regional Life Sciences Core Directors (NERLSCD) meeting bemoaning the loss of LM from the Microscopy Society of America when we ran into Ted Thannhauser. The rest gets a little fuzzy, but 30 minutes later, we had formed a RG, developed a project, and started the recruiting campaign. Thanks Ted, hum I think…

What are we doing?

Academic view - Our goal is to promote scientific exchange between researchers, specifically those in core facilities in order to increase our general knowledge and experience. We seek to provide a forum for multi-site experiments exploring “standards” for the field of LM.
Carbohydrate analysis used to be the purview of highly trained scientists working in very specialized labs at academic institutions. However, analysis of the glycan component of glycoproteins has become a quite common undertaking because of the renewed interest in understanding the role of glycosylation in various cellular processes, uncovering predictive disease glycoprotein biomarkers, and the prevalence of glycoprotein based human therapeutics.

Much of the growth in glycan analysis has also been fueled by the increased availability of easy to use mass spectrometers. Due to the exquisite complexity of glycosylation and glycans, analysis of these structures can be extremely complicated. Experimental methods for glycan analysis are plentiful in the literature but without the knowledge of which would be the best method to answer a particular scientific question a researcher can become overwhelmed with the wide variety of available methods.

This is exactly where the gPRG aims to help, providing ABRF members with a central source of “best practices” for glycan and glycoprotein analysis.

With ABRF members input, the gPRG aims to identify a set of dependable glycoprotein analysis tools that researchers can use to answer glycan and glycoprotein related questions. The gPRG is always looking for new members, so please contact Ron Orlando (Orlando@ccrc.uga.edu) if you are interested in joining this committee!
# ABRF Research Group Members 2009–2010

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**ABRF RESEARCH GROUP MEMBERS**

**2009–2010**
Membership Committee  By Ron Niece

It is a pleasure and an honor to be asked to provide a Committee Communiqué from the Membership Committee for this first issue of the new newsletter for ABRF. The original newsletter grew out of the concern for meeting the needs of ABRF members. That version was an enormous success and became our Journal of Biomolecular Technology, which is now on line for all to see. We are looking forward to the new newsletter becoming as useful as was the original.

What has the Membership Committee been doing during the past year? The year 2009 included several significant initiatives. Together with Genome Technology, the Membership Committee brought all core facilities access to the premium content of Genomeweb. This gave ABRF members access to daily blogs, instrument and company news usually costing $995 for each of the BioArray News, BioInform, InSequence, PGx Reporter, ProteoMonitor, and RNAi News. Another project started by the Membership Committee was to institute a Member-Get-a-Member rebate. To help the Membership Committee recruit members we are offering a bounty under certain conditions when a current member is recognized by a newly recruited member. Each current member can offset up to half of the next year’s membership fee using this mechanism. Try it and save some money for yourself or your institution.

Have you found the technical interests listed for each member in the white pages to be useful? The Membership Committee worked very hard to reorganize the listing and get it into a format where the data could be helpful in understanding what is available in core facilities. As technologies change over time we know that there will have to be revisions. Let us know when you think a category should be listed, moved or deleted.

What does the Membership Committee hope to do this next year? One of the activities that all members can help with is identifying other meetings where ABRF should have a presence to help educate researchers and to talk to research resource staff and administrators. Send us your suggestions for meetings and conventions where we should make it a point to have presence. As a recruiting tool, the Membership Committee is revising the membership brochure to make it more attractive. It is a tri-fold document that can be sent in response to inquiries about ABRF and can be distributed at meetings where ABRF sends a delegation.

The demographic of the membership in ABRF has always been predominantly North American. The Membership Committee thinks that ABRF has much to offer to other parts of the world. An important activity for 2010 is to pursue this idea and design ways to get ABRF recognized throughout the world where we can help resource facilities meet their mission and research scientists do the best science as productively as possible. Once again, the Membership Committee is looking to the membership of ABRF for ideas and help on this task. Please let us know what you think.

This is a brief summary of Membership Committee activities and plans. Let us know if you have some additional ideas about how we can help members of ABRF!

Ronald L. Niece (Chair)
Research Resources & Technologies

Stephen A Bobin
Norris Cotton Cancer Center,
Dartmouth Medical School

Sridar V Chittur
SUNY Albany

David B. Friedman
Vanderbilt University

George S. Grills
Cornell University

Leslie M. Hicks
Donald Danforth Plant Science Center

Kathryn Lilley
University of Cambridge

Kathleen M Schegg
University of Nevada, Reno

Peter A. Schweitzer
Cornell University

Derrick Swinton
Lincoln University

Theodore Thannhauser
USDA/Agricultural Research Service

Jack Simpson
(EB Liaison)
SAIC - Frederick

You Want Controls With That?
You Sure You Want to Know What It Is?

These fun mottos were recently submitted to a call from the Membership Committee for an ABRF motto/tag-line contest. Some more reasonable entries were also noted, such as:

ABRF:  Facilitating Science, Educating Scientists
ABRF:  People and Technology Advancing Research
ABRF:  Technology Benchmarking, Service, and Administration
ABRF:  One Helping Many - Many Helping One

Think you’ve got something better? Jot it down, and send an email to ABRFmotto@gmail.com. You can also hand in your submission during the ABRF2010 conference. Maybe we can find a motto that defines us with verve and panache—something we’ll be proud to be associated with for the next ten years or so!
Welcome New ABRF Members in Fall 2009!

Pamela Alexander, Morehouse School of Medicine
Eric Antoniou, The Jackson Laboratory
Matthew Berberich, Laboratory of Neurotoxicology
Kip Bodl, Tufts University School of Medicine
Roland Bucher, Bucher Biotec AG
Lisa Bukovnik, Duke University
Robert Carnahan, Vanderbilt University Medical Center
Barbara Carter, EcoArray, Inc.
Eli Casdin, Alliance Bernstein L P
Christopher Colangelo, Yale University
Seth Crosby, Washington University School of Medicine
Benjamin Cutak, Sigma-Aldrich
Carolyn Diaz, University of Florida
Shi-Jian Ding, University of Nebraska Medical Center
Melinda Fittje, University of Nebraska Medical Center
Natalia G.Reyero Vinas, Jackson State University
Anne-Marie Girard, Oregon State University
Weikuan Gu
Marjan Gucek
Muna Haddad, University of Nebraska Medical Center
Tim Harkins, Roche
Jason Harrington
Anthony High, St. Jude Children's Research Hospital
Rodney Keck, Genentech, Inc.
James Kenyon, University of Nevada, Reno
Brenda Kesler, Thermo Fisher Scientific
Zhen Tony Li, Pfizer
Terry McClean, University of Wyoming Nucleic Acid Exploration Facility
Lauren McNew, Battelle/US Army ECBC
Gordon Miller
Marc Moniatte, EPFL Proteomics Core Facility
Robert Moritz, Institute for Systems Biology
Ejvind Mortz, Alphalyse
Cheryl Nargang, University of Alberta
Aaron Noll, Stowers Institute for Medical Research
Amanda Nourse, St. Jude Children's Research Hospital
Thomas O'Connell, University of North Carolina
Cynthia Opansky, Blood Center of Wisconsin
Michael Powell, Morehouse School of Medicine
Xiao Hong Qian, Beijing Proteome Research Center, China
Jeanne Riley, ATCC
Eduardo Rosa-Molinar, University of Puerto Rico-Rio Piedras
William Roth, Morehouse School of Medicine
Caroline Safar, Agilent
Ralph Schlapbach, Functional Genomics Center, Zurich
Benno Schwikowski, Institut Pasteur
Valerie Scott, The Jackson Laboratory
Karen Staehling-Hampton, Stowers Institute for Medical Research
Erick Suh, Kapa Biosystems
Derrick Swinton, Lincoln University
Vladimir Tolstikov, UC Davis Genome Center
Lara Torien, Illumina
James Vincent, University of Vermont
Lee Weigt, Smithsonian Institute
Peter White, The Research Institute at Nationwide Children's Hospital
Lloyd Williams, Center For Study of Gene Structure and Function
Philip Wyatt, Wyatt Technology Corporation
Bosong Xiang, Monsanto Company
Ninglin Yin, USU Center for Integrated BioSystems
Ying Qing Yu, Waters Corporation
**American Society of Human Genetics**

October 20-24, 2009, Honolulu, HI

*by Tim Hunter and Katia Sol-Church*

The Annual American Society of Human Genetics (ASHG) meeting was held at the Honolulu Convention Center from October 20-24, 2009 and brought more than 5,000 attendees. An exciting and informative agenda was scheduled that included: exhibitor sponsored workshops, presentations on research studies who benefited by the work from the 1,000 genomes project to genome wide association studies now accelerated because of recent advancements in biotechnology.

The ABRF was represented at the annual meeting by members Katia Sol-Church from Nemours Biomedical Research at the A. I. duPont Hospital for Children, DE, and Tim Hunter from the University of Vermont. Together they presented a poster titled “Association of Biomolecular Resource Facilities: Advancing Human Genetics through Research, Communication, and Education”.

Representation at ASHG allowed them to promote the benefits of ABRF membership and research group studies by providing an overview of the ABRF goals and the results of current and past ABRF research group studies that illustrate the challenges and opportunities of implementing genetic technologies. ABRF flyers, pamphlets, and copies of past RG posters were handed out at the poster to educate attendee’s and encourage attendance at the upcoming ABRF 2010 meeting and promote new membership. A computer with 3G wireless connection was on site next to the poster allowing access to the ABRF website to demonstrate the activities supported through this society.

**Waters Core Facilities Technology Summit**

October 27-28, 2009 - Columbia, MD

*By Jack Simpson*

Executive Board members Jack Simpson and Tony Yeung attended the Waters Core Facilities Summit last October in Columbia, Maryland. As Waters stated in its invitation, “Since the early 1990s, Waters Technology Forums have provided a venue for frank and open dialog on the prevailing challenges and trends facing senior managers and executives in laboratory-dependent organizations around the world.”

The October meeting brought together approximately 15 Director and Principal Scientist delegates from East Coast government and university core facilities for discussions on how advances and applications in separation science, sample preparation, informatics, mass spectrometry and industry trends impacted these businesses.

As part of the agenda, Dr. Simpson was an invited speaker and asked to provide an overview of the ABRF and its role in supporting core facilities as well as the results from the recent ABRF survey on laboratory funding. The presentation was well received and several scientists were introduced to the ABRF for the first time. Betsy Baer, Roy Williams, Ann Gray and the many other Waters representatives provided wonderful hospitality and an open and engaging environment for productive discussions. The presentations from all the speakers can be found on the Waters website: [http://www.waters.com/waters/promotionDetail.htm?id=10135744](http://www.waters.com/waters/promotionDetail.htm?id=10135744)
Communications - March 2010

Northeast Regional Life Sciences Core Directors
November 9-11, 2009, Ithaca, NY

by Bic Scripto (my pen name—aka Ted Thannhauser)

The fourth annual Northeast Regional Life Sciences Core Directors (NERLSCD) meeting was held November 9-11, 2009, at Cornell University in Ithaca, NY. This meeting was sponsored, in part, by the ABRF which participated in the meeting activities by providing an informational booth to enlighten meeting attendees concerning recent ABRF activities and the many benefits of ABRF membership. The booth was ably manned by a contingent from the ABRF Membership Committee (Bobbin, Grills, Chittur, Schweitzer and Thannhauser).

For those unfamiliar with the NERLSCD meeting, it is a regional forum for core facility directors and managers to network with colleagues, to learn about biotechnology advances and applications, and to discuss the challenges of implementing shared research resources. The 2009 meeting featured presentations and discussion forums on operational issues facing biotechnology core laboratories and technical workshops on genomics, proteomics, imaging, and other technologies, including next generation sequencing, microarrays, proteomics, metabolomics, optical imaging, flow cytometry, stem cells, nanobiotechnology, and bioinformatics. Additional information concerning the 2009 NERLSCD meeting can be found at the meeting website (www.nerlscd.org/).

The next NERLSCD meeting will be held October 27-29, 2010 at the University of Massachusetts Medical School in Worcester, MA. Please contact Susanna Perkins (Susanna.Perkins@umassmed.edu) for more information.

Annual Biomedical Research Conference for Minority Students
November 7, 2009, Phoenix, AZ.

By Mike Zianni

This exciting conference for minority students has been held for over 10 years and is sponsored by the National Institute of General Medical Sciences. The ABRCMS meeting was an amazing collection of very motivated and talented students where almost everyone presented a poster or a talk, and most of the speakers made science and education seem like one of the best things you could ever do with your life.

Michael Zianni and Caprice Rosato attended the conference as representatives of ABRF and were sponsored by FASEB which has a large presence there to promote professional societies to the students. Mike and Caprice talked to many students about the mission of core facilities, use of the core as clients, career opportunities in the core, and how ABRF can help in all of these areas. In addition, they promoted the MARC program and minority travel awards available to attend ABRF2010. In the tradition of service at ABRF, the two were also judges and reviewed over 25 posters with accompanying oral evaluations for the best research awards.

Coming Up!

National Institutes of Health Career Symposium
May 18, 2010, Bethesda, MD

As part of his role with the newly formed ABRF Career Development Committee, Executive Board member Jack Simpson has been asked to participate in the NIH Career Symposium in May, 2010 in Bethesda, MD. According to the invitation, the Symposium is “inviting a diverse group of outside experts to provide insights into different job paths in academia, the private sector, and government. This is not a job fair featuring employers, but an opportunity for NIH trainees to learn from experts about various career opportunities in the biomedical sciences and to explore factors that lead to career success. Last year over 1200 graduate students and postdoctoral fellows (basic scientists and physician-scientists) attended the symposium to hear from over 75 distinguished speakers.” Dr. Simpson along with ABRF members Tim Hunter and Chris Colangelo, have been asked to participate in a panel discussion focused on Non-tenure Track Bench Positions.
A word from our Communications sponsor:

AB SCIEX is pleased to sponsor this special inaugural issue of the ABRF newsletter, Communications.

AB SCIEX is a global leader in the development of life science analytical technologies that help answer complex scientific challenges. The company combines the two halves of the highly successful Applied Biosystems/MDS Analytical Technologies mass spectrometry joint venture into an integrated organization. AB SCIEX provides instrumentation, software and services that are used in a number of critical life science applications, including protein biomarker research, disease studies, drug discovery and development, and food and environmental safety. AB SCIEX is uniquely positioned to continue its global leadership in the mass spectrometry market, building on a more than 20-year history of innovation. More than 12,000 AB SCIEX mass spectrometry systems are currently deployed in virtually every major laboratory around the world. AB SCIEX has the industry’s broadest portfolio of mass spectrometry-based solutions. These include integrated platforms that combine liquid chromatography with mass spectrometry (LC/MS/MS), such as the AB SCIEX QTRAP 5500 System. The company also provides MALDI TOF-TOF systems for protein biomarker research that include the AB SCIEX TOF-TOF 5800 System. For more information about AB SCIEX, go to www.absciex.com.

The Journal of Biomolecular Techniques (JBT) is published online-only, five times per year. The JBT was established to promote the central role biotechnology plays in contemporary research activities, to disseminate information among biomolecular resource facilities, and to communicate the biotechnology research conducted by the Association’s Research Groups and members as well as other investigators. JBT Online contains original research communications, articles, news and events.

http://jbt.abrf.org
### ABRF COMMITTEE MEMBERS 2009–2010

**ABRF Award**
Chair: Jay Fox
Susan Hardin
Kathryn Lilley
Lloyd Smith
Keith Wadell

**Career Development**
Chair: Jack Simpson
Kate McNerny
Gabriela Grigorean
James Farmar

**Corporate Advisory**
Chair: Roy Martin
Anita Hong
Lara Torien
Keith Wadell

**Corporate Relations**
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George Grills
Susan Hardin
Paul Morrison
Ron Niece
Margaret Robertson

**Education**
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Elke Kuster-Schock
Roy Martin
Janet Murray
David Needleman
John Neveau
Caprice Rosato
Katia Sol-Church

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Kathryn Lilley
Lloyd Smith
Keith Wadell

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Steve Bobin
Srider Chittur
David Friedman
George Grills
Leslie Hicks
Kathy Schegg
Peter Schweitzer
Derek Swinton
Ted Thannhauser

**Publications**
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Clive Slaughter
Gregg Fields

**Survey**
Chair: Jack Simpson
James Atwood
Rachel Loo
Ron Niece

**Travel Award**
Chair: Michelle Detwiler
Debbie Adam
Richard Pon
Satya Yadav

**Website**
Chair: Scottie Adams
Michelle Detwiler
Bryan Fleming
Brian Hampton
David Mohr
James VanEe
Xialong Yang
Tony Yeung
Len Packman

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**What the heck are the ABRF Yellow and White Pages?**

-Scottie Adams

Trudeau Institute (voted #1 place to work by post-doctoral researchers in The Scientist)

Have you ever been trying to contact someone you met at a meeting and you didn’t get their contact info? You can only remember their first name, that they are an ABRF member and they live in New York.

**Search the ABRF white pages!** The white pages are a directory of all current ABRF members. A member may choose to make their contact information available to the public or only available to other ABRF members. If the ABRF member chooses to make their contact information public, then the name will always show up as a link to the contact information whether the viewer is logged in as a member or not. If the ABRF member chooses to not make his contact information public, then the contact information will only appear as a link if a viewer is logged in as an ABRF member. If you are searching, remember that you must be logged in as a member for the entire member database to be searched.

How do you change how your contact information is viewed? Log in, go to Member Tools and select “Edit your Member Profile”. Look for White Page listings and edit accordingly. We encourage all members of Committees and Research Groups to have public listings so interested scientists who are not ABRF member can contact them for information.

Do you need a reliable lab to perform a service for you? No one is more reliable than an ABRF member. The Yellow Pages are a directory of ABRF member laboratories that offer services to outside scientists. Being listed in the yellow pages is entirely voluntary and is intended to be a member benefit. The yellow pages are searchable by a variety of parameters to help the user find the service that he needs. How do you change how your Yellow Page Listing? Log in, go to Member Tools and select “Edit facility record” or create a Yellow Pages listing for “your facility”. Only the person listed as the facility administrator can edit the facility record. If you need assistance feel free to email abrf@abrf.org or webmaster@abrf.org.
The Jackson Laboratory (JAX): Scientific Services

By Valerie E. Scott

JAX HISTORY: Founded in 1929 as a basic non-profit biomedical research facility, The Jackson Laboratory, an NCI designated Cancer Center, operates two campuses; one located in the coastal woods of “Downeast” Maine and the other in Sacramento, CA. Currently employing 1300 staff, JAX supports 38 independent research programs, robust pre- and post-doctoral training programs, comprehensive Courses and Conferences, Genetic Resource Sciences group, and JAX Mice and Services (animal production and distribution and In Vivo Service). Each of these units seeks to extend the research community’s access to animal models of human disease, relevant husbandry information, bioinformatics tools and integrated phenotypic and genetic data sets on strains and models.

All of these efforts support the institutional mission “to discover the genetic basis for preventing, treating and curing human disease, and to enable research for the global biomedical community.” It is in this context that JAX operates a comprehensive suite of centralized core facilities: JAX Scientific Services.

JAX SERVICE HISTORY: Scientific Services were established in the early 1950’s when Faculty initially pooled resources to establish a common histology facility. Over time as paradigm-changing life science technologies emerged (at the speed

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<tr>
<th>SCIENTIFIC SERVICE</th>
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<td>Computational Sciences</td>
<td>Scientific Applications &amp; Laboratory Information Management Systems, Statistics &amp; Analysis, and High Performance Computing</td>
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<td>Genome Sciences</td>
<td>Allele Typing, Sequencing, SNP Genotyping, Array Capture Enrichment &amp; Sequencing Library Construction, Fine Genetic Mapping &amp; High Molecular Weight DNA Resource</td>
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<td>Histopathology Sciences</td>
<td>Necropsy, Histology, Electron Microscopy, and Clinical Assessment</td>
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<tr>
<td>Imaging Sciences</td>
<td>Light, Confocal &amp; 4-Pi Microscopy, Cytogenetic Services, Physiological &amp; Behavioral testing &amp; In Vivo Small Animal Imaging</td>
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<td>Molecular Phenotyping Sciences</td>
<td>Flow Cytometry, Gene Expression, Next Generation Sequencing, Molecular, Mass Spec. and Protein Services</td>
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<tr>
<td>Reproductive Sciences</td>
<td>Rederivation, Cryopreservation, Reconstitution, Cell Biology &amp; Microinjection</td>
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<td>Transgenic Genotyping Services</td>
<td>Transgenic &amp; Targeted Mutant Genotyping</td>
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Figure 1. Organizational Scientific Service units of Jackson Laboratories

Val Scott, Ph.D., is the Senior Director of Scientific Services at the Jackson Laboratory in Bar Harbor, ME http://www.jax.org. She is also a brand new ABRF member and a NERLSCD stalwart.
of Moore’s Law) the shared or core facility model was extended adding electron microscopy, glassware, and flow cytometry services among others, culminating in the current portfolio which includes 10 core units employing 155 full time employees (FTE). Organizational Scientific Service units are listed in Figure 1 (previous page).

**Organization:** Today each Scientific Service unit is led by a Director or Senior Manager with technical domain experience. These Scientific Services leads report to a single central Senior Director who provides operational planning and advocacy, delivers financial oversight, assures consistent cross-facility policy application and technical currency (staffing and instrumentation). Each Service unit has the support of a Faculty Advisor also with relevant domain expertise but with no responsibility for day-to-day operations. These Advisors, who are supported institutionally for their effort, constitute a Faculty Advisory Committee for the Services at large addressing Service review, technology planning and procurement, policy review and recommendation and contributing to the hiring process for key personnel.

**Ultimately, the institutional investment in core facility operations makes JAX a vested owner, operator, partner and not simply a landlord or subcontract coordinator.** The centralized operational model does provide core leadership with unique opportunities, which – especially in these challenging financial times – work to the benefit of all involved.

**Challenges:** As if research weren’t challenging in and of itself, the impact of presidential administrations on the National Institutes of Health budget and the 2008 global economic downturn have certainly been felt by academic and independent cores alike. All these factors were compounded by the need for prime time delivery of, for example, next generation sequencing and ultra-high resolution 3-D microscopy through core facilities. Of the many management challenges these factors prompted, managing staffing and delivering current technology rise to the top of this Director’s list.

**Staffing:** Faced with stuttering federal research awards, increasing healthcare costs, and declining endowment support JAX, like many institutions, eliminated a number of positions in March of 2009. The impact to the Scientific Services was limited to a 3.6% effort reduction in part because of the centralized nature of operations. Outsourcing was the other factor that worked to balancing the scales. JAX took on projects for academic and commercial entities who themselves scaled back on-site animal colonies and services.

In modeling the funding nadir, Scientific Services management took steps early enough to implement cross service labor sharing methods. Rather than totally eliminate positions in some areas only to recruit in others, Service Managers regularly reviewed capacity and demand across units identifying and moving labor where and when needed. Given that recruitment costs average $8,500 per employee including the cost of interview, relocation and on-boarding (employee physical, unrecovered policy and benefits training and department training costs etc.), the transition and training investment in existing personnel was well worth it. Employee satisfaction and security increased, services vacancy periods were minimal at best and as a result users felt no real change in turnaround times or work quality. Operating core facilities with common standards and funding ap-
proaches enabled the management team to exercise the cross services view and flexibly retain and leverage its 155 FTE workforce.

Technology (Feeding the Beast):

Here’s my long overdue “Thank You” to President Obama and Congress for Stimulus funding...

Despite the (likely one-time) uptick in NCRR’s budget for Shared and High End Instrumentation, ARRA funding will not sate the research community’s appetite for technology. These days instruments approach the end of their useful technological life-span before an institution is through depreciating the platform’s book value. Even if one successfully secures funding for capital instruments, installation, validation and training costs need to be supported. Further complicating the service provider’s dilemma is the fact that end-users have increasingly limited funds to pay for technology access and institutions have limited options for funding and supporting high-tech operations. How are core facilities to keep up with the changing pace of change? So what’s the answer? In part the “secret lies within” the Core Facility community at large.

Over the past two years JAX has had the benefit of community access to at least two critical technologies, which our Faculty would otherwise not have employed without great difficulty, uncertainty and the headache of long-distance project management. Because of ABRF and NERLSCD relationships and registries, JAX Scientific Services facilitated access to Next Gen Sequencing technology through colleagues at The Cornell University Life Sciences Core Laboratories Center (CLC) and The Vanderbilt Functional Genomics shared resource (FGSR) formerly known as the Vanderbilt Microarray shared resource. The Vermont Genetics Network - Proteomics Facility and Medical University of South Carolina Mass Spectrometry Facility also delivered great data to our local community.

All of these outsourcing efforts helped JAX evaluate and compare available platforms and come to conclusions about bringing systems in house as happy users spread the word about success and demand increased. Were these experiences care free? Nothing is easy the first time, especially long distance technology access - but kudos to our service provider colleagues who came through on all counts.

What it took on our end was a dedicated single point of contact to assure effective translation of need, materials movement, interpretation of data and transaction of financial processes that were essentially transparent to the end user. “Try before you buy” is a real option in the core facility world today because of the networks and registries in place.

What’s missing? The technical disciplines and their user’s need to settle on terms of engagement – establishing operational ontologies for systems, configurations and outputs as well as common measures of efficiency and effectiveness and customer experience metrics. In sum, even with the coffers open we will never sate the beast— but as long as we all contribute a dish we can certainly stave off hunger!
Metrics Smetrics – What Should Be on the Core Director’s Radar To Keep the Good Ship Off the Rocky Shoals of Finance?

By Jay Fox

Perhaps some of us can remember back to the good old days when all a core director had to worry about was simply bringing on-line to our cores new technologies, instruments and protocols. And if we were adventurous we might actually develop some of these in our cores for the support of our clientele as well as our peers at other institutions. Rarely did we worry too much about funding; it seemed just to “happen”, sometimes generously, more often begrudgingly offered by our institution’s administration in support of the science of its faculty.

For better or worse, institutional shared research resources have been forced to adopt a much more “business-like” approach to service delivery in a very cost-conscious manner. This trend appears to be accelerating due to the current national fiscal constraints impacting our clientele - investigators and our institutions. In general, cores are being pressured to become more cost-effective and efficient, recover more of their costs (lessening the need for support by the institution), and seek funds for the cores from external sources (primarily for instrumentation, but not exclusively). In addition, as part of a new strategic approach to supporting institutional investigators, there is movement by some institutions to carefully look into the economic sense of outsourcing of services that was historically provided by institutional cores.

Thus, there are many reasons why the alert core director may desire to get ahead of some of these trends by carefully analyzing their business plan (in the next newsletter issue) for the core and developing a set of metrics, both long term metrics, and also short-term dashboard metrics, to evaluate and project the fiscal performance of the core just as one does to evaluation the service/science aspects of their core (to be discussed in the third article in this series).

What do you need to know for effective fiscal management?

There are many aspects of core operations (both service and fiscal) that you need to track to ensure your core is functioning according to its business plan and meeting established milestones. From the fiscal side you need to begin your fiscal year with budget expectations built on established past performance as well as new elements that might impact the upcoming year (loss of funding, new investigator arriving, etc.). You should minimally have assembled the following to build the budget:

1) carry over funds/deficit from past year
2) anticipated revenue/service units performed
3) anticipated major and minor costs (service contracts; reagents etc.)
4) encumbered salaries

At the beginning of each fiscal year, we plot the sum of the carryover funds/deficits from the past year, major anticipated charges (service contracts) and encumbered salaries. This generates a negative dollar amount (deficit) to begin our fiscal year with a defined goal of erasing the deficit by the end of the year. Each month we refresh the data taking into account the revenue (and non-encumbered expenses) which hopefully graphs to a...
trators so they can gain an appreciation of how your core fits into the overall research support enterprise.

Another interesting way to view your core within the context of the institutional research enterprise is to track your revenue over time alongside the total research budget for the institution (see Figure 2). In other words, as your institution’s research budget (in this context I am referring to all research funds such as grants, awards etc made to the institution) changes year to year, how does your revenue track with those changes? For example, if your institution has seen a steady increase in research funding has your core revenue paralleled that increase? Presumably it would if you maintain your “market share” of the research dollars flowing into the cores. If not then you must ask yourself “why not”? Conversely, trajectory taking the core to a net zero balance at the end of the year (see Figure 1 for an example). This representation of the fiscal profile of the core on a month to month basis allows for continual assessment, dashboard metric if you will, of the fiscal status of the core and whether the trajectory is as expected and if it is not, to determine whether steps can be taken to attempt to move it back on course to meet the expected outcome for the budget year.

A higher level view of your core’s performance requires a historical tracking of budget figures over the years of operation (see Figure 2). On a yearly basis it is also useful to compare the core’s revenue and expenses with previous years to track performance over time as well as to look for trends in terms of revenue, overall budget, salaries, reagents, service contracts etc. This itemized level of tracking allows you to better build future budgets and business plans as well as being of value to your institutional adminis-

![Figure 1](image1.png)

**Figure 1.** In this figure is an example of one tool for visualizing on a month to month basis the fiscal profile of a core. In this model a core’s main operating costs such as personnel and service contracts are encumbered at the onset of the fiscal year. On a monthly basis the revenues for the core along with monthly unencumbered expenses are tabulated to generate a trajectory toward a breakeven point at the end of the fiscal year. In this manner one can readily visual that this core is on a reasonable course to meet its fiscal monthly milestones and expected yearly outcome.

![Figure 2](image2.png)

**Figure 2.** In this figure is shown a single core’s yearly revenue and budget along with the total extramural funds for the institution. In 2007 there was a significant influx of funding to the institution which for this particular core there was no significant near term effect. As it turns out the bulk of the funding spike was due to the recruitment of a single particularly well-funded investigator who unfortunately had no business activity for that core. Otherwise, one would expect an increase in the core’s revenue and budget albeit with a lag.
As an administration, another interesting set of data one may wish to track is the institutional investment in the core research enterprise on a yearly basis (perhaps a future topic for discussion). There are many approaches to this that provide useful information but one simple way is to simply track institutional research funds vs aggregate core support. This can provide some basis for formulating an institutional policy and support metrics for an appropriate level of infrastructural support in line with the external research support for the institution. One could then develop arguments for greater or lesser institutional support of the cores depending on the strategic view of institutional research.

In summary, as a core director you, along with your administrators, need to keep constant vigilance over the fiscal performance of your core just as you do with the scientific, QA, and QC aspects. Tracking your budget on a monthly basis in a graphic format can readily allow for a visual inspection of your core’s budget trajectory for the year in more or less real time. Key economic indicators such as changes in expenses (broken down into appropriate categories), revenues, and overall budget must be monitored. These data can allow you to objectively review performance and strategically plan for the future. These data when mapped onto the institutions fiscal landscape, particularly its extramural funding, may allow some sense as to your core’s performance in terms of the “market”, i.e. the funds available as well as other “players” (aka cores) in the market. Having these fiscal data on your radar can help you avoid fiscal problems and better plan for the future and thus allow you to better focus on the scientific aspects of providing outstanding service to your colleagues.

Figure 3. In this example one can observe that in the early part of the decade the aggregate core budget increased in parallel with the overall institutional research funding. However as the institutional funding flattened in the latter part of the decade, the core budget’s trajectory continued to rise suggesting the need for a correction.

if your revenues remain constant or increase during a downturn in your institution’s funding levels then you have “beat the system” and again you should consider why that is the case.

In a similar manner you can track the core’s budget over time in parallel with the institution’s extramural funding (Figure 2). For example, if there is an increase in institutional research funding resources you may expect that there will be increased demand for core services and your budget will likely expand. However if there is a decline in institutional research funds there may be a need for you to reduce your budget since it is likely your revenues will decline in parallel with the decline of institutional research funds. In certain scenarios, without insight gained by analysis of the fiscal trajectories, there can be lags in the response of the cores to the changing institutional funding reality. Therefore, some form of tracking and critical analysis of these parameters over time can place your core in a better position to be prepared for changes in the funding environment of your institution. Additionally, comparison of the aggregate budget of an institution’s core enterprises with institutional funding (Figure 3) can also give a core director some indication of how their core compares with other cores in the system.
Peptide (Fragmentation) Mass Spectral Libraries: Giving Proteomics Data Analysis a Memory

By Paul Rudnick

The practice of using mass spectral libraries as reference to interpret unknown mass spectra is not new to the GC/MS community but has only recently gained notice as a complementary data analysis method for proteomics. GC/MS is a technique widely used to identify small molecules whose chemical structures are often not simple polymers (as is the case for peptides) and may contain complicating substructures such as rings. Consequently, GC/MS users are limited to manual interpretation of unknown spectra by skilled professionals or computer-automated mass spectral library searches which rely on ‘spectrum-spectrum’ matching algorithms [1]. The reference libraries for these searches are built by laboriously analyzing purified compounds and manually curating ‘high-quality’ reference spectra from those sources (Fig. 1).

Mass spectra represent physical properties of molecules and are therefore reproducible. Moreover, replicate similarity has been shown to inversely correlate with noise [2]. Reference spectra are information-rich, enabling highly specific and highly sensitive interpretations using ‘spectrum-spectrum’ matching algorithms [3,4,5]. The major limitation of using mass spectral libraries is of course that compounds not found in the libraries cannot be identified, requiring the libraries to be regularly updated.

Anyone who works in a proteomics core facility and is familiar with the speed of modern mass spectrometers knows that these instruments are workhorses, generating many thousands of tandem mass spectra (MS/MS) in under an hour. This volume of data requires robust computer-automated analysis. In the early 1990’s, proteomics charged ahead with the development of computer programs to match unknown MS/MS spectra against theoretical mass spectra...
derived from in silico digestion of protein sequences [reviewed in 6]. Key to the success of this invention is the specificity constraints of the digestion enzyme (i.e., trypsin), limiting the possible number of candidate mass spectra within a given mass tolerance amenable to the computational power of a desktop computer. The success of these software packages (both open-source and commercial), and improvements in mass accuracy, have allowed proteomics data analysts to keep up with the high rate of data acquisition on these instruments. These algorithms, while relatively specific, have been shown to lack some of the sensitivity achieved by 'spectrum-spectrum' matching [7]. This is in large part due to an inability to accurately predict relative peak intensities for a given peptide fragmentation, although improvements in this area are being made [8 and references therein].

Due to the success of 'spectrum-sequence' matching algorithms, limited access to data, and the seemingly intractable scale of developing libraries for all biologically relevant peptides, there was little activity in this area until 2005 when the idea of developing such a library received a resurgence. Using the power of the sequence search engine(s) to provide the initial assignments followed by subsequent levels of quality control, drafts of 'best-replicate' and/or 'consensus' libraries (Fig. 2) were produced by several groups independently [7,9,10].

![Figure 2](image_url)

**Figure 2.** An annotated consensus peptide fragmentation mass spectrum from the NIST human library (Feb. 4, 2009 build). Labeling on most intense peaks is shown. A key quality control metric for compiling these spectra is the percentage of unexplained (i.e., unlabeled) intensity.

These libraries have grown almost exponentially (now numbering >250,000 consensus spectra for human) due in large part to the data-sharing efforts spearheaded by the proteomics data repositories and/or a willingness of investigators to allow their data to be "recycled." The production of these libraries has been accompanied by the development of several spectral library search engines. In practice, searching these libraries is gaining in popularity as the coverage increases, which for some species, may be reaching the theoretical limits based on current LC-MS workflows for common sample preparations. Searching these libraries has all of the same benefits of searching EI mass spectra (as for GC/MS), namely the use of empirical peak intensities during scoring (for an illustration of 'sequence-spectrum' and 'spectrum-spectrum' comparison see Fig. 3A and Fig. 3B, respectively). Searching spectral libraries can also be much faster (up to 500X) due to the restricted search space: only previously identified (i.e., "remembered") peptides become candidates during matching [7]. Additionally, the combination of sequence and spectral library searching has been shown to improve identifications by >150% at a fixed confidence level [11].

Currently, there are several options for adopting the use of peptide mass spectral libraries in your peptide sequencing work. The Institute for Systems Biology has added SpectraST [7], which includes functions to build your own libraries [12], to the Trans Proteomic Pipeline. Additionally, GPM developers have released XIHunter [9], the MacCoss lab at the University of Washington have released BiblioSpec [10] and NIST have released MS PepSearch and a peptide version of MS Search available for download on their website (http://peptide.nist.gov).
Figure 3A. Top spectrum depicts a theoretical mass spectrum, as might be generated by a sequence search algorithm, matching an actual peptide MS/MS spectrum (bottom).

Figure 3B. An actual mass spectrum (top) matching a reference mass spectrum from a peptide mass spectral library (bottom). The use of both m/z and relative intensity values during scoring can give higher sensitivity.

Another use for mass spectral libraries that is gaining popularity is as reference for designing selected reaction monitoring (SRM or MRM) assays for targeted proteomics. It has been shown that, for the majority of peptides, the top fragmentation peaks observed in a ion trap mass-produced spectrum are identical to those observed on a triple quadrupole instrument [13]. This feature, along with the generation of libraries based solely on data from triple quadrupole instruments, is providing reference for selecting the best transitions. Several software applications for this purpose have been developed, including MaRiMba [14] and Skyline [15], both of which can read NIST peptide mass spectral libraries. Additionally, the PeptideAtlas, GPM and NIST websites offer web-based browsing of peptide spectra.

While the number of publications that use these libraries as reference for discovery and targeted proteomics is increasing, the field of peptide mass spectral libraries remains open to new developments (both open source and commercial) for construction and searching. Currently, all NIST, ISB and GPM library resources remain open and free community projects. You can help out these projects by contributing your data (or asking your customers if they wish to make copies of their data available), which in turn will help build a stronger community resource for future work in proteomics. Contact paul.rudnick@nist.gov or visit http://peptide.nist.gov to find out more.
FUTURE SUBMISSIONS AND... THANK YOU

The regeneration of the "ABRF Newsletter" came about as a way to provide a means of communications (hence the choice of title) amongst the members of the ABRF community. A way to share member news and highlights, lab tips and protocols, address the issues involved in the business of running a biomolecular resource...in an in-depth, yet informal format. Our hope is that our newsletter will provide a useful forum for members to share their experiences!

I’d like to take a moment to say thank you to everyone who has contributed to the making of this inaugural Newsletter. To AB SCIEX, whose generous financial support made it possible to cover costs and print this letter for the meeting. To David Friedman, Editor’s Assistant, who contributed content, thoughtfully critiqued and stayed up late hours to do so sometimes. To my son, Jeremy Detwiler, who helped with layout design and graphics, and acted as a creative sounding board for me (with great patience).

But most especially to all of our Communications contributors - those who so willingly and enthusiastically provided outstanding articles and content when I came knocking on their "email doors"!

We welcome future submissions to this newsletter as well - do you know of an ABRF member who was recently honored or recognized? Let us know! Do you have a fantastic protocol or method that you could share? Send it along! We’re also looking for scientific images from member laboratories that will be highlighted on the front cover of each issue. And in the next Communications, we hope to have a “Letters to the Editor” section where readers can provide commentary to articles printed in this issue. All future submissions or questions can be sent to abrf@abrf.org or michelle.detwiler@roswellpark.org.

We hope you enjoy the ABRF Communications - By the Members, For the Members!
Editor, Michelle Detwiler
Implementing Next-Generation Sequencing in a Core Facility

By Deborah Grove

The advent of massively parallel sequencing over the past five years has added a complex and costly service to the core facility service list. Even so, there are several reasons that a next-generation sequencer may be added. First, researchers may demand it. Second, there is an advantage in having the service on campus and having one-on-one discussions between the researcher and the core. And, sending the samples to other institutions may delay processing if they are lower priority. Costs can be higher as well.

The cost of the instrument is the most critical consideration in deciding whether to send samples out or to provide the service in your core. Currently, the price of the instruments range from $400 to $600K for the present long and short read instruments, to over $700K for the upcoming single molecule sequencers. Purchase of additional years of a service contract at a reduced rate can be a prudent option at the time of purchase.

Accessory equipment costing between $5 and $50K must be budgeted for. Some of the necessary equipment are the Covaris sonicator, the Hydroshear, the Coulter counter, and the TissueLyser, as well as additional thermal cyclers and centrifuges which can hold special plates or flow cells. Less expensive items are pipettors, microfuges, minifuges, and vortex mixers. There are a myriad of electrophoresis equipment, but buy what is recommended as well as pre-cast gels. With the expense and time required to prepare these samples, the cost is trivial compared to modifying existing protocols and making gels. More equipment equals more breakdowns and more time spent troubleshooting or waiting for a service engineer.

Education

Education of the customers, from PIs to techs to students, has always been in the job description of the core director. However, discussion of the next-gen technologies is much more complex and time-consuming than traditional technologies. Besides the shock of the higher costs, the core director must be able to explain the application, and details such as the expected number of reads and coverage. The customer will also suggest variations of the recommended procedures. Make it clear that diverging from the standard protocol is not recommended and emphasize that there will still be a charge for any samples handled differently than the supported protocol that fail to produce good quality data.

Schedule seminars or workshops. Start with an introductory seminar and perhaps have the company present an overview and then focus on applications. If you have done some test runs, ask researchers to present their data. Free pizza is always a good option.

Sample Integrity

The most important criterion for success is sample integrity, i.e., the submitted samples must be double-stranded DNA. The NanoDrop-derived concentrations do not differentiate dsDNA from other nucleic acids. Using the Qubit (~$900) gives true dsDNA concentrations and allows for the adjustment of protocols for successful library preparation. The Qubit has shown that, in reality, some samples only had 10% to 40% actual dsDNA. RNA integrity is important as well. Determination of RNA quality using the Bioanalyzer and Qubit was already in place in our facility.
for Microarray applications.

Training and Protocols

For this cutting-edge technology, training by the company is an absolute requirement. On-site as well as continuing training is invaluable. However, eventually the core still has to deal with problems. These can be anything from bad reagents in kits to errors in provided protocols. Always run the control in the kit, especially the first time it is being used—this eliminates the possibility that you may just have a bad sample. If the control fails, there is a better starting point for troubleshooting. Then—Good Luck!

The most common applications requested for the short-read instruments (in our case, an AB SOLiD system) are Transcriptome, ChIP-SEQ, small RNA, and bacterial whole genome sequencing with a few non-traditional requests of RNA Immunoprecipitation (RIP) and degradome sequencing. Our facility also supports a Roche 454 platform, and the 454 Titanium applications have included whole genome sequencing, as well as transcriptome libraries using recommended procedures, as kits are not yet available.

The companies frequently update protocols that may require new equipment and/or reagents. Purchase extra reagents to avoid being caught short when what you need might be back-ordered (this seems to happen more often for these new technologies than you would expect!) However, be careful not to overbuy, as new protocols requiring different reagents are constantly being released.

Sample Tracking and Data Delivery

A barcoding system is being implemented in our facility. The system designed by Anton Nekrutenko of Penn State’s Biochemistry and Molecular Biology Department provides a barcode to samples at the time of submission. The sample bar code will be scanned at several stations during processing, allowing the researchers to know the status of their samples at any time. When the sequencing run is finished, data is transferred to GALAXY (http://galaxy.psu.edu), a Penn State site where researchers can access data and use various tools to assemble and annotate the large data files.

Analysis

Analysis is still the greatest challenge. There are labs that have the personnel to handle this. There are some that are able to educate themselves or find a collaborator. Then there are labs who do a small amount of sequencing and may never need analysis support again. The latter will always be a problem. We do not provide analysis in the core and repeatedly tell the researcher this when a project is being set up—but it never really sinks in until they get the GB of data! In addition to data storage, analysis tools also reside on GALAXY. Third-party software is also available at a work station in our lab.

Conclusion

Next-generation technology is exciting and is transforming biological research. It is very interesting to see how protocols are being made easier and more cheaply already, as other companies scramble to get a share of the market. If you are considering adding this technology to your core, spend time discussing it with those who may have it already and visiting those sites.

Acknowledgements: Dr. Craig Praul, Director of Gene Expression; Technical Assistants, Candice Price and Greg Grove; and Anton Nekrutenko and lab (http://galaxy.psu.edu/).
Optimizing Techniques for Limited Sample Sizes for Microarray... Getting the Most Out of a Little...

By Scott Tighe
Vermont Genetics Network, Microarray Core Lab, University of Vermont

As many core laboratories face the challenges of working with smaller sample sizes or with limited number of cells (such as with laser capture micro-dissection), the ability to recover sufficient quantities of high-quality RNA is essential. In these circumstances, there are several steps that can be adopted to increase both the recovery of RNA and the amount of amplified product that can be used in microarray or other gene expression studies. These focus on methods to optimize column-based RNA extractions and a simple method to increase the amount of amplified product from the NuGEN Technologies Ribo-SPIA reaction. Although other high recovery extraction methods and reagents are available, they are not discussed here.

During column-based RNA extractions there are several technical tips to help maximize the quantity and quality of RNA recovered. These include the following five points:

1) Do not store cells or tissue in extraction buffer at any temperature because low concentrations of RNA will degrade,
2) The use of a “carrier” RNA is not recommended because, although it assists in the recovery of RNA, it significantly interferes with quantification,
3) The use of on-column DNase treatment is avoided (when appropriate) because this aqueous procedure can cause some “release” of RNA from the silica matrix and a consequential loss,
4) The use of micro-columns (Qiagen MinElute, Invitrogen Micro-column, or Ambion’s RNAqueous) in place of mini columns are advantageous because the smaller elution volume results in a higher sample concentration
5) The final elution of RNA off the column is done with a single ~12 ul aliquot of pre-warmed water that is passed over the column twice.

Quantification and assessment of RNA samples below 3 ng/ul can easily be performed using the Agilent 2100 Bioanalyzer PicoLab chip as an alternative to ribogreen by including two known RNA samples at known concentrations in neighboring wells to help estimate the actual concentration.

It should come as no surprise when RNA is limited, that a robust amplification method is required to generate enough product for microarray hybridization. Even with well established methods, limited RNA input can be problematic. For labs that are using the NuGEN Technologies reagents, either the Ovation V2 or Ovation Pico, increasing the yield of the Ribo-SPIA is as easy as using additional Ribo-SPIA master mix volume in each reaction, such as 1.5x or 2x volume. For instance, the required volume added for each sample for the Ovation V2 is 120ul, but if this is increased to 180ul, the yield also increases significantly. For samples that have extremely limited RNA (<2 ng), such as those recovered from a few hundred cells by laser capture micro-dissection, a 2x volume has been used successfully in our lab. However, validation and concordance data should be established for each individual lab performing the technique. It is not advisable to use a 1x, 1.5x or 2x interchangeability because each group of experimental samples should be processed using the same protocol. Any samples that do not meet the expected 5ug of amplified Ribo-SPIA product should be considered suspect as RNA degradation at some point in the procedure is a likely cause.
Imaging Collagen

By Carol Bayles
Microscopy and Imaging Facility, Life Sciences Core Laboratories Center, Cornell University

Collagen gels have become popular as a matrix for growing cells. One way to image the collagen matrix without staining is to use Single Harmonic Generation with a multiphoton microscope (MPM). However, if you don’t have one of those expensive toys, you can use confocal reflected light. Collagen is highly light scattering and thus is visible with this method.

You need a reflecting mirror in the beam splitter position, which may be designated RT 30/70 or RT 20/80 (for Reflected/Transmitted) in your system. If you have a spectral confocal put a narrow spectral region under a laser line. You can use any wavelength. (I am not sure if you can use a non-spectral system.) Focus beyond the cover slip, which may be very bright as it reflects light, too. You should see your collagen fibrils. You may have some artifacts, like a bright spot in the center, which may have dark diffraction rings around it. You can avoid the worst of this by zooming up and imaging off-center. A thicker gel is actually better as it will have more scattering and will overwhelm the artifacts. The image will be a confocal slice and you can take a z-series as usual. You may not get as deep as you can with MPM.

If you have labelled cells in the gel, you need to do the reflected light with a different laser line and collect sequentially. Since the beam splitter will have to change between images, you cannot do a fast sequential (line) method. Confocal reflected light also works with cartilage tissue but depth may be limited.

Bisulfite Sequencing on Capillary Sequencers—How to Keep Those G’s and T’s Going Strong

By Chris Borrelli
Biomolecular Resource Facility, DNA Sequencing Lab, Roswell Park Cancer Institute

Bisulfite treatment of DNA is a method used to help assess the methylation status of cytosine residues, particularly those located in CpG islands. Bisulfite functions to convert non-methylated cytosines to uracil, while methylated cytosines are left unaltered; sequencing of this treated DNA can then reveal these specific methylation patterns.

After bisulfite treatment, PCR is performed on genomic DNA and the resultant products are often inserted into cloning vectors for semi-quantitative sequencing. DNA sequencing of these templates can be accomplished using Applied Biosystems capillary sequencers and Big Dye terminator chemistry. However, it is frequently observed that when G-T rich regions of DNA are sequenced, fluorescent signal will fade prematurely. A trick to overcoming this? In the cycle sequencing reaction, simply lower the extension temperature from 60 degrees to 54 degrees. (See figure above). Presumably, the lower temperature provides the polymerase with a more stable attachment while amplifying these semi-repetitive G-T rich regions of DNA.
ABRF was ranked as the #1 meeting for Best Technology/Instrumentation by readers of Genome Technology!

Welcome to ABRF 2010: “Translating Basic Research with Advances in Biomolecular Technology”. This year’s annual meeting of the Association of Biomolecular Resource Facilities (ABRF) offers an exciting mix of cutting-edge science, novel technological developments, practical information on biomolecular analysis and facility operation, along with ample opportunities for networking and social interaction for which the ABRF and its members and vendors are well known.

Among these opportunities are:

- Scientific poster session receptions and evening social events
- An outstanding array of commercial exhibits representing all the cutting edge technologies and reagents critical for the operation of core facilities. This is particularly relevant in light of the Government’s American Recovery and Reinvestment Act (ARRA) Stimulus Package awards supporting biomedical research instrumentation
- The three plenary lectures that focus on the translational aspects of biomolecular research facilities:
  - Sunday March 21, 8:00am “Research Cores - Their Crucial Role in Translational Science”
    Lars Berglund University of California Davis
  - Monday March 22, 8:00am “Proteomic Applications to Translational Research”
    John Yates III The Scripps Research Institute
  - Tuesday March 23, 8:00am “Next-Generation Applications to Translational Research”
    Elaine Mardis Washington University
- The scientific sessions, with topics including:
  Proteomics  Genomics  micro RNA
  Metabolomics  Metagenomics  Interactomics
- Additional sessions that will provide practical information for research facilities, including:
  Proteomic and genomic pipelines  Data analysis/informatics
  Light microscopy  Protein expression
  Organization/operation models  The future of research cores
- New to the meeting this year are a series of three Experts' Tables for answering questions associated with the science, technology and operation of research facilities:
  Proteomics  Next-Gen Sequencing  Core Models and Management
- And don’t forget about the exciting presentations from this year’s ABRF Research Groups (RGs) throughout the meeting!

The distinguishing difference of ABRF 2010 is that the program has been developed by the membership and the Research Groups of the association, and most of the sessions are being organized by members.

SO REMEMBER -

this is YOUR meeting!
Why I Love Vendors

Talks and posters are about where biology has been—but the booths with the sales pitches and freebies tell you where science is going. By Steve Wiley

In December, I attended the annual meeting of the American Society for Cell Biology, as I have done regularly for the last several decades. It is always a good way to catch up with old friends and look for the latest trends in cell biology. I rarely attend the talks, having found that they more reflect the fashion of the moment (or the past) than the direction of the field. Poster sessions are more to my liking, since they provide a chance to talk to enthusiastic young scientists in the trenches. But my favorite stop has always been the vendor booths.

When I tell my friends that I love visiting vendor booths, most of them seem to think I am kidding. At meetings, many scientists seem to feel that vendors are necessary evils. They provide free candy and cheap pens in exchange for bombarding us with ads and scanning our badges. Like popup ads in Web browsers, we have learned to both ignore and accept them as part of the landscape. It is unfortunate that we have become so inured to their presence. Talks and posters capture exciting research from the last few years or months, but vendor booths capture the future, offering one of the clearest visions of where a field is going.

As a technology junkie, I always love to see the new instruments that are introduced at each meeting. When I got a faculty job, visiting the vendors became serious business, because they offered a fast way to compare features and prices of the stuff I needed. I soon became interested in learning about the odd variety of unfamiliar equipment I invariably saw at meetings. Not because I wanted to purchase it, but because I was interested in what other scientists were doing, and if a vendor had paid for a booth, odds are someone was using what they were selling.

Over the years, I started to see patterns. Microscopes have always been prominent at the cell biology meetings (go figure), but the numerous electron microscopes of 25 years ago have been replaced by increasingly complex confocal microscopes. Electrophoresis and centrifugal separation equipment has been replaced by kit vendors and PCR machines. Cell isolation and molecular biology supplies have been replaced by cell lines and clone libraries. The changing landscape of vendor booths shows, better than any talk or poster, that biology has become a prepackaged kit science. Do-it-yourselfers need not apply.

The most interesting booths are those that show the “Next Big Thing.” This year, ultra-resolution optical microscopes were on prominent display, whereas several years ago, variants of fluorescent proteins, gene-cloning supplies and PCR machines were everywhere. In a couple of years, the publication record will be filled with data from the tools introduced this year. Where else at a scientific meeting but on the vendor floor can you tap into dozens of impromptu presentations about where a field is going, rather than where it has been?

I became much more aware of the roles vendors play in creating new technologies when I agreed to write some software for a company in the early 1990s. They were introducing a new type of quantitative gel imager and I was writing the interface software for Macintosh computers. The project consumed my spare time for over a year, and I was rewriting and debugging code up until 10 minutes before the new software was introduced at the ASCB meeting. However, all the work felt worthwhile when I saw how excited biologists were to see what my software could do. The experience was as fulfilling as giving a talk—I found that creating a new, useful tool for scientists can be just as gratifying as discovering a new protein.

My experience in participating in the “vendor side” of meetings also made me realize that many vendors were trained as scientists, but did not wish to pursue an academic career. Instead, they decided to help drive scientific research by providing new tools and services that make research easier and enable new research directions. I have known some of the vendors at the ASCB meeting for over 20 years and they are as passionate about showing their new instruments as I am about showing my latest data. So the next time you go to a scientific meeting, stop by the vendor booths and ask about the future. And pick up some candy.
Why Be An ABRF Member?
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- Special Note! In 2009, Genome Technology made its Premium Content pages, including In Sequence, ProteoMonitor, BioInform and others, available free to ABRF academic members (a separate $995 dollar value for each publication!). While this amazing benefit has now been extended to all academicians, the Membership Committee and Executive Board of the ABRF are always looking for new and innovative benefits to membership!

ABRF is a unique membership association comprised of scientists working in resource and research biotechnology laboratories. Our members represent over 140 international core laboratories in government, academia, research, industry and commercial settings, and are involved in a broad spectrum of biomolecular technologies.

The ABRF website at http://www.abrf.org is a comprehensive resource for biotechnology news, information about discussion groups, research group studies, career and exclusive networking opportunities.
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Invitation for Corporate Membership

Since its founding more than 20 years ago, the ABRF has had the following goals:

♦ To promote and support resource facilities, research laboratories and individual researchers regarding operation, research and development in the areas of methods, techniques, and instrumentation relevant to the analysis and synthesis of biomolecules.

♦ To provide mechanisms for the self-evaluation and improvement of procedural and operational accuracy, precision and efficiency in resource facilities and research laboratories.

♦ To provide a mechanism for the education of resource facility and research laboratory staff, users, administrators and interested members of the scientific community.

To accomplish these goals, the ABRF works closely with leading corporations that develop and supply the technologies used by our members. The ABRF invites your partnership in our organization. The following sponsorship levels are available and are compatible with your company’s fiscal year:

**Silver Sponsors** receive the following benefits at the $2000 annual dues level:

1. Acknowledgment of your sponsorship on the ABRF and on the *Journal of Biomolecular Techniques* websites (www.abrf.org and jbt.abrf.org), including links to your company’s website;

2. An electronic copy of the Membership directory, updated quarterly and available upon request during your sponsorship term.

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1-2. As detailed for Silver Sponsors;

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4. Second priority in reserving exhibitor booth space at the annual ABRF meeting;

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1-3. As detailed for Gold Sponsors;

4. Priority in reserving exhibitor booth space at the ABRF annual meeting;

5. A 50% discount on the cost of one exhibitor’s booth at the annual meeting;

6. One full-page advertisement in the meeting program;

7. One free meeting registration.

Please contact Prof. Mark Lively, Chair of the Corporate Relations Committee of the ABRF (336-716-2969; mlively@wfubmc.edu) for additional information.

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