ABRF Microarray Research Group

Introduction: MARG activities and microRNA profiling

Chris Harrington
Oregon Health & Science University
MARG activities 2009/10

- Expansion of technology focus areas
- Mission review: genomic profiling
- New name to reflect changes
- New website for technology/application updates from member labs & community discussion
- Recruitment of new members
MARG 2009 & 2010
Research Projects

• miRNA profiling on microarray & next-gen sequencing platforms

• miRNA standards for validating methods and platforms
MARG members - 2010

- Herbert Auer – IRB Barcelona, Spain
- Don Baldwin – University of Pennsylvania
- Chris Harrington – Oregon Health & Science University
- Nadereh Jafari – Northwestern University
- Nalini Raghavachari – NHLBI Genomics Core Facility, NIH
- Natalia Reyero – Jackson State University
- Wei Wang – Cornell University

Contact any MARG member if you are interested in joining MARG or email Chris Harrington at harringc@ohsu.edu
MARG Session Outline

• MARG-sponsored online technology forum
  – Natalia Reyero
• Technology forum example
  – Nalini Raghavachari
• microRNA profiling: platform comparison
  – Don Baldwin
• microRNA synthetic reference project
  – Don Baldwin
ABRF Microarray Research Group

MARG discussion forum: Wiki Page

Natàlia G. Reyero Vinas
Jackson State University

Nalini Raghavachari
NHLBI Genomics Core-NIH
Purpose of the Wiki Page

The idea was to create a forum moderated by MARG that everybody can use to post/ask about tips and troubleshooting.

The Wiki page allows this type of discussion.

It is free and anybody can join.

The users need to create a user account, but it is free and common for all wikis.
How to Access:

1. Direct Link:
   http://abrf-marg.wikispaces.com/

2. Wikipedia:

3. ABRF Site:
   Under ‘Activities’: MARG wiki – technology discussion forum
   (also under links)
Association of Biomolecular Resource Facilities

From Wikipedia, the free encyclopedia

The Association of Biomolecular Resource Facilities (ABRF) is dedicated to advancing core and research biotechnology laboratories through research, communication, and education. ABRF members include over 700 scientists representing 267 different core laboratories, including those in industry, government, academic and research institutions.

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6 Journal of Biomolecular Techniques
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History

In 1985 a Research Resource Facility Satellite Meeting was held in conjunction with the Sixth International Conference on Methods in Protein Sequence Analysis. The next year protein sequencing and amino acid samples were sent to survey 103 core facilities. By 1989 the ABRF was formally organized and incorporated. Each year an annual meeting was held as a satellite meeting of the Protein Society until 1996 when separate meetings began.

ABRF Research Groups

Research Groups are established to fulfill two of the purposes of the Association of Biomolecular Resource Facilities: first, to provide mechanisms for the self-evaluation and improvement of procedural and operational accuracy, precision and efficiency in resource facilities and research laboratories. Second, to contribute to the education of resource facility and research laboratory staff, users, administrators, and interested members of the scientific community.

- DNA Sequencing Research Group (DSRG)
- Genomic Variation Research Group (GVRG)
- Glycoprotein Research Group (GPRG)
- Light Microscopy Research Group (LMRG)
- Metabolomics Research Group (MIGO)
- Microarray Research Group (MARG)
- Molecular Interactions Research Group (MIRG)
- Nuclear Acid Research Group (NARG)
- Protein Expression Research Group (PERG)
- Protein Sequencing Research Group (PMSG)
- Proteomics Research Group (PRG)
- Proteomic Informatics Research Group (PIRG)
- Proteomic Standards Research Group (PSRG)

Resource Technologies

Members of ABRF are involved in a broad spectrum of genomic and proteomic technologies such as:

- Automation: high throughput screening, LIMS, robotics.
- Biophysics: calorimetry, CD, fluorescence, light scattering, SPR, ultracentrifugation.
- Gene Expression and Profiling: gene arrays, real-time PCR.
- Nuclear Acid Chemistry: DNA sequencing, DNA synthesis, RNA synthesis, protein chemistry.
- Protein Expression, identification, and Profiling: differential fluorescence, conventional and gel electrophoresis, disease biomarker discovery.
ABRF Research Groups

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- Glycoprotein Research Group (gPRG)
- Light Microscopy Research Group (LMRG)
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- Microarray Research Group (MARG); MARG discussion forum [1]
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MicroArray Research Group (MARG)

Background
The goal of the Microarray Research Group is to provide both academic and industrial scientists useful information and guidance in the use of various microarray platforms and applications in their research. The main focus of the MARG is to promote communication and cooperation among core laboratories providing microarray and data analysis services. In addition, the MARG is charged with conducting studies to help assess technological advancements and provide information about these technologies to all interested parties. Information developed and communicated by the MARG should be used to help laboratories evaluate their performance and achieve the highest quality results possible from the use of microarray technologies. In order to accomplish these goals the MARG will also strive to provide ways for sharing information relevant to the administration of facility laboratories that provide microarray technologies as a shared resource.

Current Membership
- Herbert Auwer - RB Barcelona
- Dr Ben A. Ealeon (co-chair) - University of Pennsylvania
- Dr. Christine A. Hamptom (co-chair) - Oregon Health & Science University
- Nader K. Khan - Northwestern University
- Nazir Rehman - NIH
- Jack Simons - SA/IC - Frederick
- Dr. Wei Wang - Cornell University
- Natalia Vranes - Jackson State University

Studies
- MARG 2009 study
- MARG 2009 study 2
- MARG 2007 study
  - View document: FinalG9a talk.ppt

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MicroArray Research Group (MARG)\(^p\)

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- Harbert Auer - IRB Barcelona.
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- Dr. Christina A. Herrington\(^p\) (Co-chair) - Oregon Health & Science University.
- Naderah Jafari - Northwestern University.
- Nalini Raghavachari - NIH.
- Jack Simpson\(^p\) - SA/C - Frederick.
- Dr. Wei Wang\(^p\) - Cornell University.
- Natalia Vinas - Jackson State University.

Studies
- MARG 2009 study.
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<th>Author</th>
<th>Replies</th>
<th>Views</th>
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Welcome message

natalia_vinas Dec 10, 2009 10:46 am
Welcome to the new MARG wiki site. Please feel free to post your comments/questions.

re: Welcome message
natalia_vinas just now
This is a test

Subject: re: Welcome message

Reply

[Monitor this topic]

Need help formatting text?
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<th>Author</th>
<th>Comment</th>
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Discussion Forum
Illustration:
Example from MARG
member array projects
Technical Challenges
Sample type

- Which is the best sample type for a clinical trial project of blood expression profiles
- Whole blood vs fractionated cell types
- Lymphoblastoid Cell lines
## PROS & CONS of different sample types for GEP

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<tr>
<th>Sample type</th>
<th>PROS</th>
<th>CONS</th>
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</thead>
<tbody>
<tr>
<td>PAXgene</td>
<td>easily accessible&lt;br&gt;standardization of sample collection&lt;br&gt;Multi-center clinical trials&lt;br&gt;No complex procedure in sample collection&lt;br&gt;No artificial activation of cells during cell fractionation&lt;br&gt;cost effective</td>
<td>heterogeneous cell population&lt;br&gt;interference of globins</td>
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<tr>
<td>PBMC</td>
<td>Homogenous cell population</td>
<td>labor intensive, expensive&lt;br&gt;impractical at clinical sites&lt;br&gt;Sample handling artifacts&lt;br&gt;artificial induction of genes</td>
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<tr>
<td>Buffy Coat</td>
<td>easier to process than fractionating PBMCs</td>
<td>Sample handling artifacts&lt;br&gt;artificial induction of genes&lt;br&gt;impractical at clinical sites</td>
</tr>
<tr>
<td>Cell Lines</td>
<td>Homogenous cell population</td>
<td>Sample handling artifacts&lt;br&gt;artificial induction of genes&lt;br&gt;expensive&lt;br&gt;Cell transformation effects on expressed genes</td>
</tr>
</tbody>
</table>
Preparation of labeled targets

- Interference of Globins in whole blood samples
- Input RNA
- cDNA vs cRNA amplification
QC samples

• Use of MAQC A and B
  – for data normalization
  – to correct for batch to batch variation
  – correct for reagent lot to lot variation
Feedback

• Specifics from researchers can be posted

• Follow up discussions

• Possible conclusions