



**Integrative Cancer Research Special Interest Group Teleconference**

**Proteomics SIG Meeting Minutes**

<b>Date, Time &amp; Location:</b>	July12, 2004 10:00AM – 11:00AM EDT
<b>Attendees:</b>	David Fenstermacher - Penn Steve Eschrich - Moffitt Patrick McConnell - Duke University Simon Lin – Duke University Claire Zhu - BAH Juli Klemm - BAH
<b>Application Presentation:</b>	<p><b><u>SMOS/RProteomics</u></b></p> <p>Simon Lin (Duke) gave a presentation of SMOS, a statistical data model that will be implemented in RProteomics. The slides can be downloaded from <a href="http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/proteomics">http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/proteomics</a>.</p> <p><b><u>SMOS/RProteomics Q &amp; A</u></b></p> <p>What analyses been addressed with the RProteomics prototype? (Juli)</p> <ul style="list-style-type: none"> <li>- Baseline removal, normalization, peak finding, clustering, etc. It is a working system currently used by the internal lung cancer project.</li> </ul> <p>Is RProteomics implemented in SMOS? (Juli)</p> <ul style="list-style-type: none"> <li>- Not yet – this effort has been used to develop use cases for SMOS development.</li> </ul> <p>Is SMOS focused on MALDI-TOF data at the moment? (Juli)</p> <ul style="list-style-type: none"> <li>- Yes.</li> </ul> <p>Has SMOS been presented to larger groups such as MIAPE? (Juli)</p> <ul style="list-style-type: none"> <li>- Not yet, but this is the intent. SMOS is a very recent effort.</li> </ul> <p>What is the status of MIAPE? (Juli)</p> <ul style="list-style-type: none"> <li>- PSI is based on the PEDRo model and represents the MIAPE requirements. Currently focused on 2D gel-MS studies.</li> <li>- PSI-ML is the XML markup representation of MIAPE and is at draft version stage</li> <li>- PSI-DB is a more recent effort.</li> </ul> <p>Has anyone looked into exactly what needs to be done in order to compare data from different institutes or from different instruments? (David)</p> <ul style="list-style-type: none"> <li>- Up-front efforts in comparing data is extremely important, judging from the experience with MIAME.</li> </ul> <p>Is there possibility for funding within caBIG for generating data for the purpose of comparison across institutes or equipments? (Simon)</p> <ul style="list-style-type: none"> <li>- This could be a key use case for Adopters.</li> <li>- There may be other data sources that are available to caBIG.</li> <li>- This is certainly a very important subject, as having the right datasets can drive the requirements for developing standards for data exchange.</li> </ul> <p>Is comparing data from multiple institutes a fundamental use case? Or people are</p>



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	<p>mainly concerned with data analysis within the institute? (Juli)</p> <ul style="list-style-type: none"> <li>- It is probably true that people are still figuring out how to do data analysis with their own data at the moment. However, comparing data across institutes and platforms is an important issue in the long run.</li> <li>- It takes only a couple of small projects, say, a few stable cell lines run in 3 cancer centers. The investment is minimal and the potential benefit is great – a “low-hanging fruit” kind of a project.</li> </ul> <p>Is there any plan within caBIG to create a centralized repository for protein identification? A commercial-grade protein database that contains information such as diseases, treatments, tissues, types of instrument used, etc.? (David)</p> <ul style="list-style-type: none"> <li>- caBIG’s vision is to create a data grid – a virtual repository as opposed to a physical one. However, the usefulness of such a database is valid. This is an important issue that should be re-visited in the future.</li> </ul>			
<p><b>Other Items Discussed</b></p>	<ul style="list-style-type: none"> <li>- The EDRN group has done significant work in ontological representation of SELDI data. Tina Xiao, from the Data Management and System Technologies team at the Jet Propulsion Laboratory, has shared her group’s efforts toward creation of an ontology to describe SELDI-TOF experiments. This work can be downloaded from <a href="http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/proteomics">http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/proteomics</a>.</li> </ul>			
<p><b>Action Items:</b></p>	<p><b>Name Responsible</b></p>	<p><b>Action Item</b></p>	<p><b>Date Due</b></p>	<p><b>Notes</b></p>
	<p>Juli Klemm</p>	<p>Follow up with Dartmouth and Fox Chase for next meeting’s presentation</p>	<p>7/23/04</p>	
	<p>Juli Klemm</p>	<p>Follow up on funding for generating datasets for cross institutes/instruments comparison</p>	<p>8/9/04</p>	
	<p>Juli Klemm</p>	<p>Distribute information on EDRN’s and Jet Propulsion Lab’s works on proteomics ontology</p>	<p>7/19/04</p>	
	<p>Juli Klemm</p>	<p>Distribute meeting minutes</p>	<p>7/19/04</p>	