



**Translational (Clinical Integration) Meeting Minutes**

<b>Date, Time &amp; Location:</b>	May 3, 2004, 1:00pm – 2:00pm EDT
<b>Attendees:</b>	<p>Naveen Vinukanda - The Institute for Cancer Prevention (<i>unfunded adopter</i>)  Tom Casavant - Holden (<i>funded developer</i>)  Terry Braun – Holden (<i>funded developer</i>)  David Fenstermacher - Penn (<i>funded adopter</i>)  Rakesh Nagarajan- Wash U (<i>funded developer</i>)  Mark Watson – Wash U (<i>funded developer</i>)  Michael Ochs – Fox Chase (<i>funded developer</i>)  Judith Goldberg – NYU (<i>funded adopter</i>)  Gary Bader – Sloan (<i>funded developer, funded adopter</i>)  Tom Caldwell - Vanderbilt (<i>funded participant</i>)  Craig Beam - Moffitt (<i>funded adopter</i>)  Leslie Derr – NCI  Scott Oster – Ohio State  Claire Zhu – BAH  Juli Klemm - BAH</p>
<b>Goals and objectives of the SIG</b>	<p><b><u>Create tools to support the integration of laboratory and clinical data</u></b></p> <ul style="list-style-type: none"> <li>▪ Link genomics data (microarray, proteomics, genotyping) with clinical outcomes (survival, recurrence, quality of life etc.) <ul style="list-style-type: none"> <li>○ Important to integrate the appropriate data at the right time</li> </ul> </li> <li>▪ The group agreed a common framework to support experimental design specific to translational research would be of great use to the community <ul style="list-style-type: none"> <li>○ It may be difficult to develop software to guide this process - special problems need special solutions</li> <li>○ A written guideline/"points to consider" will be produced by this group to outline a standard way of approaching translational study design</li> </ul> </li> </ul> <p><b><u>When available, adhere to standards for:</u></b></p> <ul style="list-style-type: none"> <li>▪ Microarray data (e.g. MAGE)</li> <li>▪ Proteomics data (emerging)</li> <li>▪ Genotyping data</li> <li>▪ Metabolomic data</li> <li>▪ Clinical data =&gt; this can be very complicated – phenotypes, histology, pathology <ul style="list-style-type: none"> <li>○ Controlled vocabularies very useful and important here</li> <li>○ Important for this team to interface with the Tissue Banks and Pathology Tools WS as well as the Controlled Vocabulary WS</li> <li>○ This team will produce a list of concepts for which a controlled vocabulary will be important to share with the other Workspaces.</li> </ul> </li> </ul>
<b>Center-by-center</b>	<b><u>Developers</u></b>



## Integrative Cancer Research Special Interest Group Teleconference

### discussions of interests

- Holden
  - CED: Clinical Expression Database, focused on linking clinical data with expression data. Very interested in collaborating with Fox Chase to integrate FGDP.
  - TrAPSS: A mature tool for gene-based screening/management system, capable of integrating data from multiple sources; data protection mechanism needs to be worked out.
  - CDOCS: Allows clinicians to collaborate – phenotype classification tool (also appropriate to the Collaboration Tools SIG and possibly to Tissue Banks and Pathology WS)
- Fox Chase: Functional Genomics Data Pipeline. Project goal is to integrate with Holden's CED. Is available for download immediately.
- Wash U - Future developers of visualization tools that allow simultaneous analysis of different datasets; will develop interface between tissue data and genomics data.

### Adopters

- NYU: Interested in adopting the Iowa/Fox Chase CED/FGDP integration; can help define functionality requirements; have some data also
- Penn: Interested in integration of genomics data with clinical data; looking for tools to try out.
- Vanderbilt: Has web-based tools for integrating clinical data and microarray/proteomics data – The Metaclinic Database System. A demo is available at:  
[https://ccbiomed2.mc.vanderbilt.edu/metaclinic\\_demo/main\\_page.pl](https://ccbiomed2.mc.vanderbilt.edu/metaclinic_demo/main_page.pl)  
The username/password is demo/demo. A paper describing the system has been uploaded to:  
<http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/translational>
- Sloan: Interested in molecular profiling tools; also interested in prioritization tools for microarray data analysis and developing markers for clinical diagnosis.
- Institute for Cancer Research: Interested in adopting Holden/Fox Chase CED/FGDP integration

### Other discussion items:

- Iowa/Fox Chase will host a live demo of CED and FGDP to provide potential adopters with a better understanding of these tools.
  - The team discussed what technology to use for these demos. Possibilities include T120 protocol, commercial tools (Centra, WebEx) or Chicago's Access Grid.
- There is a discrepancy in the caBIG website calendar and the on-line forum calendar – NCI/BAH to follow-up.
- The team agreed that meetings should be no more frequent than monthly.



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<b>Action Items:</b>	<b>Name Responsible</b>	<b>Action Item</b>	<b>Date Due</b>	<b>Notes</b>
	David Fenstermacher	SIG mission statement	5/12/04	
	Michael Ochs	Guideline for standards/controlled vocabulary	5/7/04	Will provide a starting point for further inputs
	Judith Goldberg	Guideline for Experimental Design	6/8/04	Judy will provide an outline to which others on the team can add
	Tom Casavant	Investigate T120 protocol for live software demos	5/14/04	Might be tricky to get it work for everyone. May use commercial tools (Centra, WebEx) in the interim. Also may investigate Chicago's AccessGrid.
	Tom Caldwell	Send publication and link describing Vanderbilt's translational tools	(done)	
	Juli Klemm	Work with NCI to resolve calendar discrepancy	5/5/04	
	Juli Klemm	Write and distribute meeting minutes	5/7/04	