caBIG Program Update

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MESSAGE FROM NCICB

Welcome to the July / August edition of the caBIG Program Update. Since our last issue, caBIG activites have continued to move forward at a rapid pace. In just one month, we've had three face-to-face meetings for caBIG Workspaces (Vocabularies and Common Data Elements, Clinical Trial Management Systems, and Architecture) and the caBIG initiative is averaging about 20 teleconferences per week.

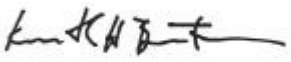
Additionally, since the final revised contracts basic agreement was sent out to Cancer Centers on June 24th, I am pleased to announce that we have received over 26 signed contracts with verbal agreement to sign from others. The caBIG Contracts staff has been very busy finalizing contracts basic agreements and communicating with each of the Cancer Centers on the status of their agreements. Task orders are now being issued and funding to Centers has commenced.

With all the success we've had, we've decided to dedicate the next several issues of the caBIG Program Update to more detailed introductions of each of the Workspaces and Working Groups to the caBIG community. The success of this initiative depends on effective collaboration among the Workspaces and Working Groups, therefore, each month we will profile a different Workspace or Working Group to highlight their activities and successes.

This issue, we will start with the Integrative Cancer Research (ICR) Workspace. With 20 tools/applications already identified to be part of the grid, 24 participating Cancer Centers, and 6 special interest groups; this Workspace has really gotten off to a fantastic start.

Once again, on behalf of NCI, I want to thank each and every one of you for your voluntary participation, enthusiasm and commitment to caBIG. We could not have come this far without you.

Sincerely,



Kenneth H. Buetow, Ph.D.
Director
NCI, Center for Bioinformatics

MEET THE DOMAIN WORKSPACES

This Issue– Integrative Cancer Research Workspace

The Integrative Cancer Research Workspace (ICR) is one of three Domain Workspaces that was established as part of the caBIG initiative to integrate and/or develop informatics products or solutions that address areas of need for the Cancer Center community. ICR will produce modular and interoperable tools and interfaces that provide for integration between biomedical informatics applications and data. This will ultimately enable translational and integrative research by providing for the integration of clinical and basic research data. The Workspace will develop a documented and validated software-engineered biomedical informatics toolset for use throughout the research community.

A major goal of this Workspace will be a demonstration of how a shared informatics platform can allow a comprehensive, federated grid of information to be made available to the cancer research community. Development of these systems will be based on key needs and priorities identified by the Cancer Center community and will be developed, tested and validated by Cancer Centers participating in the caBIG initiative.

To date, the ICR Workspace participants have focused their energies in creating and chartering special interest groups to address the ICR needs of the broader caBIG community. The remainder of this section will focus on key areas of activity for the ICR Workspace being undertaken by the Special Interest Groups and other highlights for this Workspace.

SPECIAL INTEREST GROUPS

Within the ICR Workspace, six special interest groups (SIGs) have been established to address specific activity areas identified for this Workspace and to consolidate efforts concerning shared areas of interest for Workspace members. Working under the umbrella of the ICR Workspace, these six SIGs represent the starting points for efforts to develop and extend existing integrative cancer research infrastructure for integration with caBIG.

Microarray Repositories SIG

The mission of the Microarray Repositories SIG is to identify and prioritize the needs of the larger cancer research community with respect to the capture, storage, and utilization of microarray data and related types of genetic data. Specifically, this SIG will address the needs for:

- A database for the storage and retrieval of microarray data and related data types that can be incorporated into the larger scheme of federated databases that store clinically relevant data and other relevant data types
- Software that facilitates the capture of important microarray experimental information and automatically loads it into a database
- Software that facilitates the querying of microarray databases and the retrieval of data
- Consumers and producers of microarray data to readily exchange data

In addressing these needs, this SIG is:

- Developing requirements that will drive subsequent development of microarray repositories

PARTICIPATING CANCER CENTERS

- Burnham Institute
- Cold Spring Harbor
- Columbia University—Herbert Irving
- Dartmouth—Norris Cotton
- Duke University
- Fox Chase
- Georgetown University—Lombardi
- Memorial Sloan Kettering
- Meyer L. Prentis-Karmanos
- MIT Center for Cancer Research
- New York University
- Northwestern University—Robert H. Lurie
- Oregon Health and Science University
- Thomas Jefferson University—Kimmel
- University of California San Francisco
- University of Chicago
- University of Iowa—Holden
- University of Michigan
- University of North Carolina—Lineberger
- University of Pennsylvania—Abramson
- University of South Florida—H. Lee Moffitt
- Vanderbilt University—Ingram
- Washington University—Siteman
- Wistar

- Evaluating existing repositories against the requirements defined by this SIG
- Developing guidelines for the adherence to MIAME (Minimum Information About a Microarray Experiment) standards and for supporting the capture of this information
- Working with the Data Analysis and Statistical Tools SIG and the Vocabularies and Common Data Elements Workspace to define standards for microarray data exchange

Principles and beliefs that guide the work of this SIG include:

- The association of microarray data with clinical sample details is key to supporting translational studies
- Integration with other experimental data and annotation information will increase the utility of microarry data
- Adherence to MIAME standards for the capture of microarray data is critical to the subsequent interpretation experiments, as there is a need to eliminate barriers to the capture of this information

The following projects are part of this SIG:

- caArray - NCICB is developing their next generation microarray data repository, termed caArray. Phase I of the system, to be released in September, will be caBIG-compliant and will contain the following key features: MIAME 1.1 compliant; support for MAGE-ML (Microarray Gene Expression - Markup Language) import and export; utilities for the submission and retrieval of Affymetrix and GenePix native file formats; use controlled vocabularies; accessiblity through a MAGE-OM API.
- Zebrafish Microarray Data Sharing - The Thomas Jefferson University Zebrafish Microarray Service provides microarray data generation services for the community of scientists using zebrafish as a model organism for the study of cancer. They have developed a custom microarray using the commercial Zebrafish oligo library (Compugen/ Sigma-Genosys). Through this project, Thomas Jefferson will make datasets from this repository available to the research community by identifying sharable datasets, creating a web application to select these datasets, and making these datasets available via a caBIG-defined exchange format.

Data Analysis and Statistical Methods SIG

The mission of the Data Analysis and Statistical Methods SIG of the ICR Workspace serves the needs of key categories of end users - experimentalists and data analysts - by provision of interoperable tools and associated standards, documentation, and training. Data analysis was identified as one of the most substantial needs across the Cancer Centers with much of the need stemming from the increased complexity and the volume of data sets resulting from high-throughput measurement technologies.

To address these needs, this SIG is:

- Working with end-users to ensure that efforts are appropriately aimed to satisfy their needs
- Designing, implementing, evaluating and extending new and existing software tools for data analysis and methods integration
- Identifying specific areas where training modules will need to be developed

- Investigating the possibility of involving commercial tool vendors in this SIG toward the goal of encouraging them to make their tools caBIG-compatible

- Working in conjunction with the other SIGs and Workspaces as appropriate

This SIG recognizes two distinct communities of end users: those whose roles are primarily in data analysis, and those whose roles are primarily in experimental biology and clinical research. Both groups will benefit from tools and standards designed to support and facilitate data integration, and linkage of data with the vast array of annotation information, which has become increasingly important in data interpretation. More specifically:

- Experimental scientists will benefit from tools for performing exploratory, interactive analyses of their own data, both to stimulate hypothesis generation and to offer methods for rigorous hypothesis testing. For this group, particular effort will be required for training, documentation, and for intuitive user interfaces with rich features for data and annotation import/export

- The data analysis group will benefit from having broad access to the statistical tools being developed across this community, and by methods and architectures to incorporate these tools into consistent workflows

The following projects are part of this SIG:

- JavaR – In this project, Duke Comprehensive Cancer Center will develop a toolkit, termed JavaR, to provide native code to connect a Java API with the R statistical package. R is a widely used open source language and environment for statistical computing (http://www.r-project.org/). JavaR will perform all of the necessary conversions to turn Java function calls and data types into R function calls and data types

- VISDA – To reveal all of the interesting patterns within a data set, a group working with the Lombardi Comprehensive Cancer Center has developed a VIsual and Statistical Data Analyzer (VISDA). The main application of VISDA is for multivariate cluster modeling, discovery, and visualization, particularly for data sets living in high dimensional space

- Distance-Weighted Discrimination– All large microarray datasets contain systematic biases that are due to different sources of RNA, different batches of microarrays, and especially different microarray platforms. To address this challenge, individuals at the Lineberger Comprehensive Cancer Center have developed a tool called Distance-Weighted Discrimination (DWD) that makes statistical corrections to reduce these biases

- GenePattern – Developed by MIT/ The Broad Institute, GenePattern is a flexible analysis platform developed to support multidisciplinary genomic research programs. Its architecture and environment are expressly designed to allow rapid prototyping and integration of new technologies

- Magellan – Developed by UC San Francisco Comprehensive Cancer Center, Magellan is a web-based system that allows biologists to perform complex analyses on heterogeneous data in an environment that does not require a background in computer programming or statistics. Stored data and annotations are treated as abstract entities such that arbitrary, user-defined types of information can be stored

Gene Annotation and Computational Genomics SIG

The mission of the Genome Annotation and Computational Genomics SIG is to provide data and tools that will greatly enhance the cancer research community's access to high quality, comprehensive gene annotations. Having standardized access to these data sources, this SIG will support a consistent view of all available gene information. This will be achieved by adapting existing software that meets the needs of the user community to comply with caBIG and by creating new software and tools.

The interests of this SIG are wide-ranging and include:

- Generation of automated, computed annotation
- Mapping annotations into ontologies
- Mapping objects between systems (matching indexes) and linking associated objects (genes, proteins, pathways, SNPs, etc) to each other
- Integration applications that combine caBIG experimental data with annotations
- Collection and exchange of externally curated annotations
- Collection and exchange of "active" annotation or feedback from user community

The Genome Annotation SIG software will be able to associate high throughput experimental data being stored and shared within caBIG with both computed and manually curated annotation of the genes/proteins being assayed. The annotation should be inter-operable between systems to allow for comparisons and exchange of annotations between applications.

To address these needs, this SIG is:

- Creating collaborations between developers and adopters so that development addresses needs of the user community
- Adapting annotation tools to use caBIG APIs, objects and standards to facilitate annotation exchange and incorporation into other caBIG compatible tools
- Addressing critical issues such as choice of identifiers; naming conventions and synonyms; overlap and redundancy of annotations from alternative sources; propagation of annotation errors; mapping between genomes, genes, transcripts and proteins; reliability scoring for annotations; etc.
- Keeping abreast of annotation efforts in the field, such as the ENCODE project, to ensure that key data sources and conventions are represented and to avoid duplication of efforts

The functionality covered by end-user software produced by this SIG will be based on the needs of the cancer research community in general. caBIG adopters will reflect and communicate this need to steer development towards un-met needs.

The following projects are part of this SIG:

- Cancer Molecular Pages - This system, being developed by The Burnham Institute, will adapt technology originally developed by the Joint Center for Structural Genomics, to aid cancer researchers in keeping up with all of the information being generated on a gene or gene set of interest. It is a fully functional database and automated annotation system, combining automated computer-based annotations and automated data collection from experimental stations, and web-based visualization tools

- GOMiner – Developed by NCI's Center for Cancer Research, GOMiner leverages the Gene Ontology (GO) to identify the biological processes, functions and components. Instead of analyzing microarray results with a gene-by-gene approach, GoMiner classifies the genes into biologically coherent categories and assesses these categories

- HapMap – Maintained by Cold Spring Harbor, the HapMap database is a repository of human SNPs (single nucleotide polymorphism), their genotypes, and the linkage disequilibrium relationships among them. The data is derived from the International Human HapMap Project, which seeks to map regions of common genetic variability in the human genome by genotyping three major world populations at a resolution of 1 marker per 5 kbp

- PIR – The Protein Information Resource (PIR), located at Georgetown University Medical Center, is an integrated public bioinformatics resource that supports genomic and proteomic research. PIR maintains the Protein Sequence Database (PSD), an annotated protein database containing over 283,000 sequences convering the entire taxonomic range. PIR is also a member of the UniProt consortium, the central international resource of protein sequence and function that unifies the PIR, Swiss-Prot, and TrEMBL databases

- SEED – Developed by The University of Chicago and Argonne National Laboratory, SEED is a framework that supports peer-to-peer annotation of genomes. Investigators can work independently on their own instances of the SEED database and synchronize their work when desired or update code versions quickly via the network. Several hundred microbial organisms are in SEED now and pipelines for high-throughput processing, e.g., BLAST, exist for new organisms

- FunctionExpress – Developed by Washington University Siteman Cancer Center, FunctionExpress is an environment for the integrated analysis and visualization of complementary data sets. The system provides a mechanism for regular updates of integrated annotation data that can be readily associated with probes on microarrays. The application allows for plotting of raw and transformed microarray data, for viewing orthologous probesets from other experiments, and for creating literature-based gene networks

Pathways SIG

This SIG will provide access, via the grid, to repositories of biological pathway information, with standardized tools for collection, storage, exchange and display of the associated data. The ability to analyze in the context of pathway models is an emerging need of the Cancer Centers and is critical to support basic research and ICR tool development. This SIG will help provide the cancer research community with easy access to pathway data and commonly used pathway analysis tools. Needs identified by this SIG include:

- A number of software development challenges are anticipated including:

- Making data and tools easy to use

- Representing pathway information from high to low level of detail (granularity)

- Integrating data from existing resources (http://www.cbio.mskcc.org/prl)

- A number of use cases are also anticipated, such as:

- User wants to find out more information about the context of a favorite gene/ protein in a pathway via a web-based database or via programmatic query (e.g. webservice)

- User wants to analyze gene lists from transcriptional profiling and other sources in the context of pathways (e.g. over-representation analysis)

- User wants to perform visualization of pathways and of cell state and molecular profile data in the context of pathways

- User wants to curate their own version of a pathway, based on their own experimental data in addition to publicly available information

- User wants to do qualitative pathway modeling

- User wants to do quantitative pathway modeling

In addressing these needs, this SIG had identified the following features as requirements to meet their goals:

- Common API and object model for pathway information to enable easy integration
- Common format for pathway information to enable easy sharing
- Shared curation or review of pathway data
- Data in a non-redundant format
- Pathway curation tools
- More signaling pathway and other cancer relevant data
- A reliability measure for pathway information

The principles and beliefs that guide this SIG's work include:

- Cellular and physiological process knowledge is vital for cancer research. Pathways define the molecular basis of these processes, and provide an organizing scaffold for integrating large amounts of genome-scale information with existing knowledge enabling biologists to link cohesive subsets of large, unmanageable datasets to concepts with which they are familiar
- A working definition of a pathway is a series of molecular interactions and reactions, often forming a network, the start and end points of which are often defined by observation of a detectable phenotype after stimulation or perturbation, such as observing gene expression after stimulating the cell with a peptide growth hormone

The following projects are part of this SIG:

- GKB Data - The Genome KnowledgeBase, developed at Cold Spring Harbor, is a curated database of fundamental biological pathways, which uses strict rules of assertion and evidence tracking to ensure a consistent high quality product
- Pathways Tool Development - Memorial Sloan-Kettering Cancer Center (MSKCC) has developed resources aimed at aiding life science researchers in visualizing and interacting with information in the context of biological pathways. These resources are:
- Biological Pathways Exchange (BioPAX), a common exchange format for pathways data
- cPath, a database focused on protein-protein interactions

- Cytoscape, a bioinformatics software platform for visualizing molecular interaction networks and integrating these interactions with gene expression profiles and other state data

MSKCC will leverage these existing resources to create a set of tools that will allow users to view pathway data in the context of caBIG annotation and expression data.

- QPACA – Quantitative Pathway Analysis in Cancer, developed by the University of California San Francisco Comprehensive Cancer Center, is a pathway modeling and analysis system that supports exploration of quantitative biological data in the context of a pathway description. At the center of the system is a pathway representation that enables visualization and computational analysis of pathway structure

Translational Tools SIG

This SIG will provide access to tools and technologies that are necessary for Cancer Centers to integrate clinical data with experimental data. Such tools are aimed at assuring that clinical data and studies enhance applied research technologies in order to more effectively utilize genomics and proteomics research data in cancer research and patient care.

Currently, the Translational Tools SIG is focused on:

- Tools and technologies which are necessary for Cancer Centers to integrate clinical data with experimental data, as well as experimental design tools that provide assistance to biomedical investigators embarking on translational research methodology
- Assuring that clinical data and studies more effectively utilize genomics and proteomics research data in cancer research and patient care
- Creating guidelines to aid in the design of experimental studies

In addressing these needs, this SIG is considering the following issues:

- Data integration and sharing are critical to translational studies and this group will focus on approaches to these issues to best address the end-users' needs
- The Translational Tools SIG will facilitate collaboration between developers and adopters in deploying current translational tools to facilitate data integration and provide platforms for iterative tools development
- The need for interoperability of translational tools with other caBIG ICR SIGs and Domain Workspaces requires developers and adopters to create or adopt metadata standards for SNPs (single nucleotide polymorphism), proteomics, expression profiling, and develop structured vocabularies to uniformly describe patients' or subjects' phenotypes, and the samples derived from them, across research organizations and institutions
- The Translational Tools SIG will work closely with the Strategic Level Working Groups and Cross Cutting Workspaces to incorporate common architectures, CDEs (common data elements) and structured vocabularies in order to assure translational tools are extendible across the caBIG community
- This SIG will explore various technologies and methodologies to enable the translational researcher to gain a greater understanding of study

design and that will allow consultations with biostatisticians and study designers to be more productive and interactive

The principles and beliefs that guide this SIG's work include:

- It is appreciated by the Translational Tools SIG that many of the experimental design factors cannot be automated using computer-based tools and that experts in biostatistics and experimental design need to be an integral part of creating new translational studies
- Issues that are common to undertaking a translational research study include having the correct numbers of patients, subjects, slides and biological samplings to assure that statistical measures have the power to explore the hypotheses being tested by the designed study
- Protection of patient confidentiality is a fundamental requirement for tools and data developed within this SIG

The following project is being undertaken as part of this SIG:

- TrAPSS – Developed by University of Iowa—Holden, TrAPSS is a system comprised of several tools that aid scientists who are searching for the genetic mutation or mutations that cause a defect or disease. The system offers support for almost all areas of a mutation discovery project, from the creation and prioritization of a large candidate gene list, to the selection, ordering, and managing of primer pairs, and even support for SSCP (Single Stranded Conformational Polymorphism) assay results

Informatics for Proteomics SIG

Tools for collecting and analyzing data from proteomics laboratory work are being developed to enable access according to caBIG standards, and will be deployed at Cancer Center sites for testing and validation. By using standard mechanisms for the collection and storage of proteomics information, future distribution of that information on the grid will be greatly facilitated.

The Informatics for Proteomics SIG is focused on:

- Tools and technologies which are necessary for cancer centers to store, annotate, and analyze the growing proteomics data sets
- Providing flexible tools for data and metadata storage, so that emerging technologies can be incorporated into developed systems
- Integrating proteomics data with other data through use of appropriate CDEs (common data elements) and architectures

To address these needs, this SIG is:

- Facilitating collaboration between developers and adopters to create laboratory information management systems (LIMS) linked to laboratory workflow, to store data and metadata
- Adapting existing analysis tools and integrating them through APIs to the developed databases in order to provide analysis capabilities linked to LIMS
- Working closely with Strategic Level Working Groups and Cross Cutting Workspaces to incorporate common architectures, CDEs and structured vocabularies to assure proteomics tools are extendible across the caBIG community

- Coordinating and collaborating with related proteomics standards efforts such as the EDRN (Early Detection Research Network) and the emerging caProteo efforts

The principles and beliefs that guide this SIG's work include:

- It is appreciated by the Informatics for Proteomics SIG that the field is rapidly evolving and that new technologies, data types, and analysis methods are likely to emerge in the next few years. As such, a design principle for all systems will be – flexibility - to allow additions to existing systems without significant reengineering
- Proteomics comprise only a part of the necessary data and methods for addressing the problems of understanding, treating, and controlling cancer, so integration of the tools created by this SIG with other SIGs is of paramount importance

The following projects are being undertaken as part of this SIG:

- Proteomics LIMS – Developed by Fox Chase Cancer Center, this project is focused on the creation of a proteomics Laboratory Information Management System (LIMS). The initial version will track the lab processes relevant to 2D gel electrophoresis but the schema will support the addition of new data types as they emerge. The availability of an open source proteomics LIMS will ultimately allow a distributed development model in which additional modules can be contributed by other centers
- RProteomics – Developed by Duke Comprehensive Cancer Center - In this project, R libraries will be developed to support the postprocessing of MALDI-TOF (Matrix Assisted Laser Desorption Ionization Time of Flight) and SELDI-TOF (Surface-Enhanced Laser Desorption/Ionization Time of Flight) data. These libraries will be incorporated into a caBIG-compliant, user-friendly system that will aid cancer researchers in the processing of their TOF data
- Q5 – Developed by Dartmouth--Norris Cotton, Probabilistic Disease Classification of Expression-Dependent Proteomic Data from Mass Spectrometry of Human Serum, the Q5 algorithm employs Principal Components Analysis (PCA) followed by Linear Discriminant Analysis (LDA) on whole spectrum SELDI-TOF (Surface-Enhanced Laser Desorption/Ionization Time of Flight) MS (Mass Spectrometry) data. Q5 is a closed-form, exact solution to the problem of classification of complete mass spectra of a complex protein mixture. Q5 employs a probabilistic classification algorithm built upon a dimension-reduced linear discriminant analysis

The functionality offered by these different tools is critical to facilitating the integration of clinical and basic research information between "bench and bedside" as well as from "bench to bench."

Other ICR Highlights

An important current issue within the ICR Workspace is that of common data representation and data exchange formats. A couple of interesting efforts are currently underway in ICR that are relevant to this issue:

BioPax

Gary Bader at Memorial Sloan-Kettering Cancer Center is involved in the BioPAX project, the goal of which is to develop a common exchange format for

biological pathways data. BioPAX 1.0 was just released in July and this "Level 1" functionality supports the capture of knowledge about known metabolic pathways. The availability of a pathways data exchange format will make it easier for database users to integrate data from multiple resources. This will promote creation of a centralized public pathway database, sharing of data between existing databases, as well as distribution of proprietary pathways data. As part of their caBIG development efforts, Memorial Sloan-Kettering will be converting an existing pathways data source to BioPAX format and adapting their pathways analysis tool, called Cytoscape, to read in BioPAX format.

SMOS, RProteomics

SMOS, RProteomics: Simon Lin is leading an effort at Duke University to create a standard for the representation of proteomics statistical data analysis, comparison and verification termed SMOS – Statistical Model of Spectra. SMOS is a proposed extension of the MIAPE (Minimum Information About a Proteomics Experiment) standard and associated PSI object model, both efforts of the HUPO (Human Proteome Organization) Proteomics Standards Initiative. As part of their work within caBIG, the Duke University team will implement SMOS in their RProteomics project, which will support the post-processing of MALDI-TOF data.

Next Steps

In the near term, the ICR Workspace is focusing initial efforts on adapting current tools and datasets to caBIG. By leveraging existing tools and data, the ICR Workspace will not only provide early access to these resources to interested Adopter sites, but also will provide early proof-of-concept activities for caBIG in general. Developers will work closely with adopters to train them on the current functionality of these tools. In addition, they will work closely with the Architecture and Vocabularies & Common Data Elements Workspaces to adapt their tools to the requirements set forth by these Cross Cutting Workspaces, and in turn inform them of the specific requirements of the ICR Workspace.

Future direction will be to continue momentum toward the ultimate vision of providing integrated access to research tools and data across the Cancer Center community. The Workspace will perform activities to address all previously identified, and any new needs raised by the community. These needs will be prioritized by Workspace discussions, clarified by white papers, and defined by formal analysis. These activities will ultimately lead to the development of additional new tools. Through this continued activity and prioritized development, the Workspace will provide a robust tool set to meet the entire range of Cancer Center ICR needs.

How to get involved with the ICR Workspace

Track activities on the website at http://caBIG.nci.nih.gov and the caBIG forums at http://ncicbforums.nci.nih.gov/cabigforum.

Watch the Calendar of Events (http://caBIG.nci.nih.gov/caBIG/calendar) on the website and What's BIG This Week for upcoming meetings, webcasts, and other events.

More specific questions or involvement should be directed to the Workspace Coordinator:

Juli Klemm (klemm_juli@bah.com)
(781) 890-4440, x 226

caBIG Information and Resources

There are many ways to access additional information and resources on the caBIG initiative and its activities. Following is a list of current resources:

- caBIG Website:

  http://caBIG.nci.nih.gov

- caBIG Workspaces:

  http://caBIG.nci.nih.gov/workspaces

- caBIG Strategic Level Working Groups:

  http://caBIG.nci.nih.gov/caBIG/working_groups

- caBIG Calendar of Events (includes Workspace and Working Group meetings)

  http://caBIG.nci.nih.gov/caBIG/calendar

- Inventory of caBIG infrastructure, applications and datasets:

  http://caBIG.nci.nih.gov/inventory

- caBIG Interactive Overview (multi-media presentation on caBIG):

  http://www.nci.nih.gov/directorscorner/caBIG

- National Cancer Institute Center for Bioinformatics (NCICB) homepage:

  http://ncicb.nci.nih.gov

In addition to these more general resources, a specific caBIG Forum has been established to provide a resource through which all of the caBIG participants can communicate and coordinate with other caBIG members. The forums are readable by anyone, but posting is limited to registered participants.

The caBIG forums can be reached at the following URL: http://ncicbforums.nci.nih.gov/cabigforum

If you do not yet have a login, and you are a registered participant in the caBIG project, you can get one by sending email to Leslie Derr at derrl@mail.nih.gov.

Raising Questions or Concerns

If you are a caBIG participant and you have any questions about caBIG Workspace and Working Group activities, please consider the following avenues to raise your questions:

- The caBIG Forum at http://ncicbforums.nci.nih.gov/cabigforum
- Workspace or Working Group Meetings

For specific, directed questions that you feel would be better addressed individually, please feel free to reach out to your respective Workspace/Working Group Coordinator from the caBIG Project Team, or Mark Adams at adams_mark@bah.com.