



caBIG[®] Innovation Platform: New Generation of Biomedicine

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21st Century Biomedicine and the Knowledge Economy



Quality

- **Quality care is delivered through ready access to care guidelines and practice plans accessible through decision support systems**



Comparative Effectiveness

- **Knowledge bases support ongoing assessment of effective interventions informed by individual characteristics including molecular information**



Pharmaco-Vigilance

- **Access to electronic health information at point of care permits ongoing assessment of safety of approved interventions in real world settings**



Biomedical Research

- **Biomedical research effectively leverages health observations and rapidly feeds back approved interventions into a care setting**

Knowledge Worker Ecosystem



Consumers

Personal Health Records



Commercial Innovators

Drug and Diagnostic Information



Healthcare Providers

Medical Records



Food and Drug Administration

Approval and Safety Information



Community Hospitals

Hospital Records



NIH

Research Results



Research Institutions

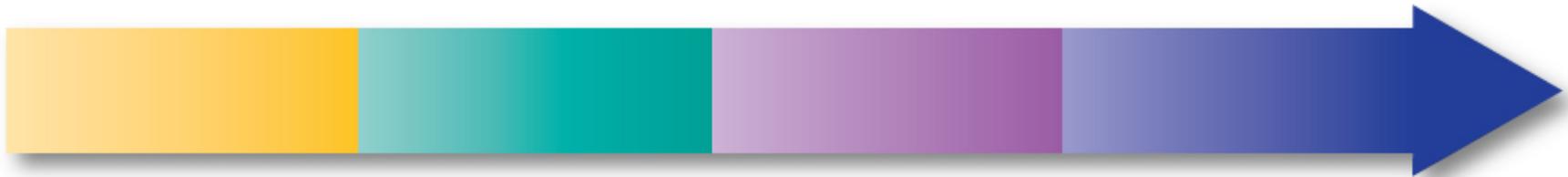
Clinical Trial Information



Medicaid and Medicare

Reimbursement Information

20th Century Research Biomedical Paradigm



Discovery

- Biological pathways
- Target identification and validation

Product Development

- Candidate selection and Optimization
- Pre-clinical testing
- Phase I, II, III
- New Drug application and Approval

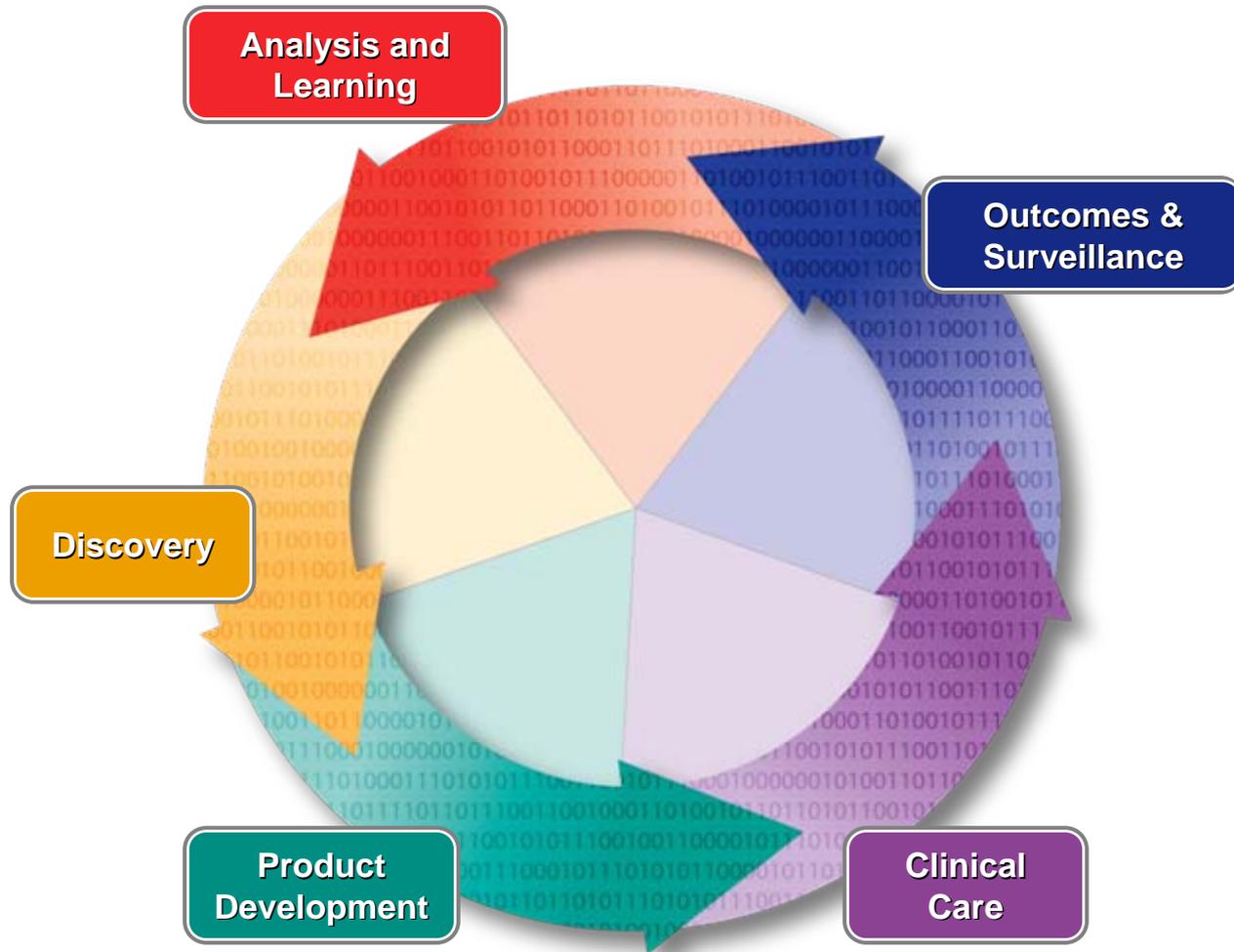
Clinical Care

- Product launch
- Clinical adoption

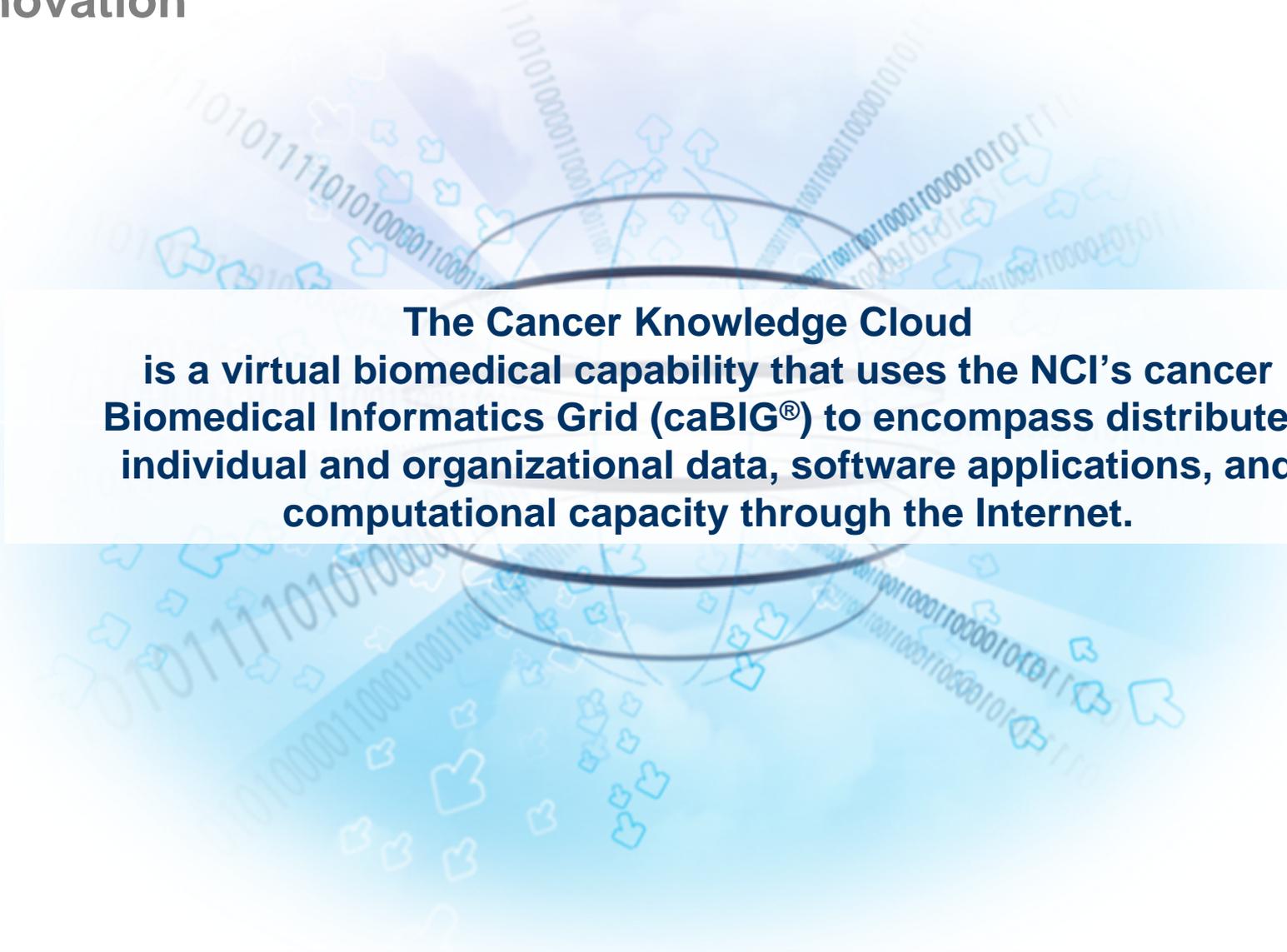
Outcomes & Surveillance

- Reporting of serious/fatal ADRs
- Re-labeling (or recall) as needed
- Additional indications as warranted

21st Century Research Biomedical Paradigm: a Learning Health System

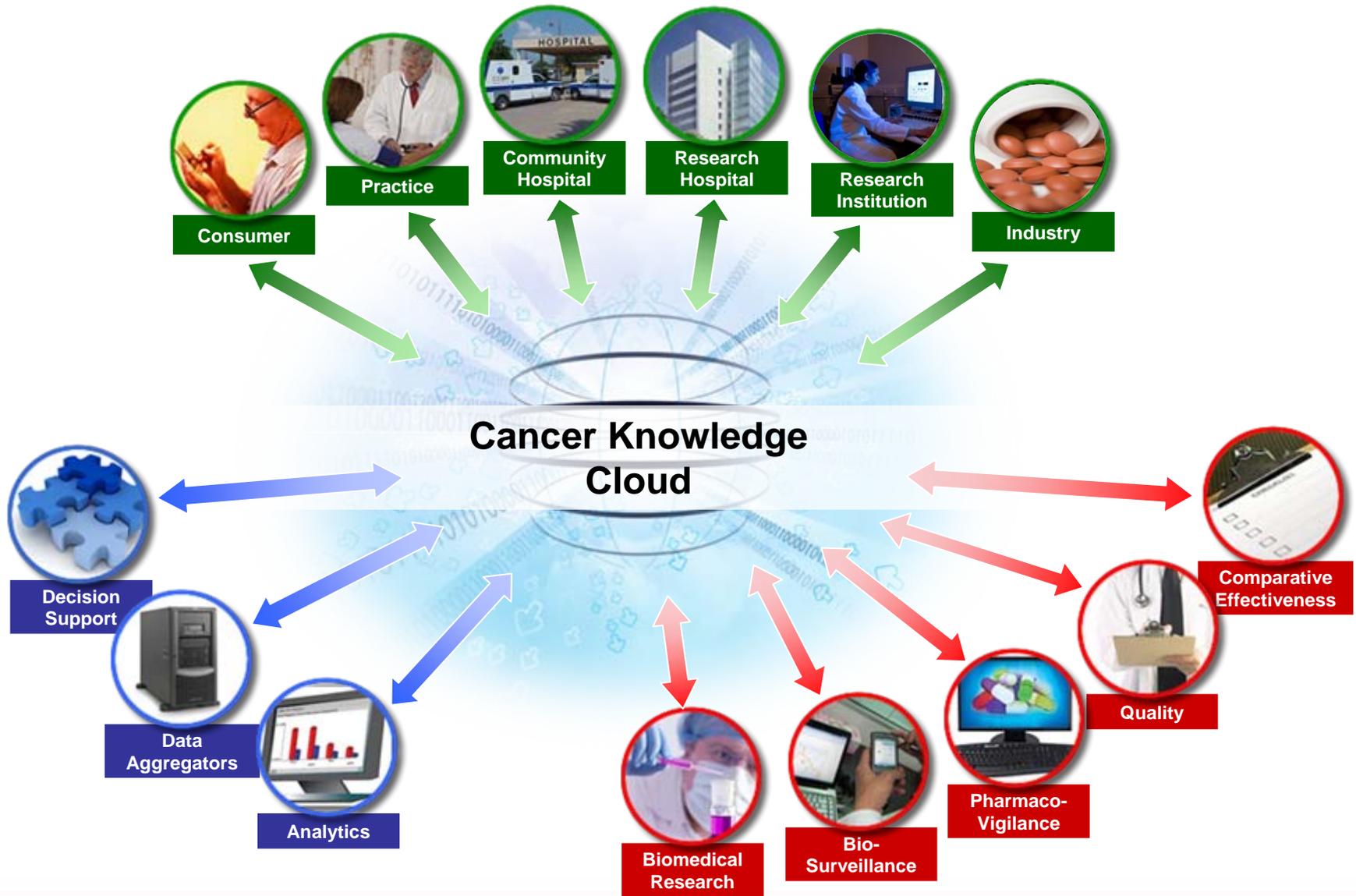


“Cancer Knowledge Cloud”: A Platform for Biomedical Innovation

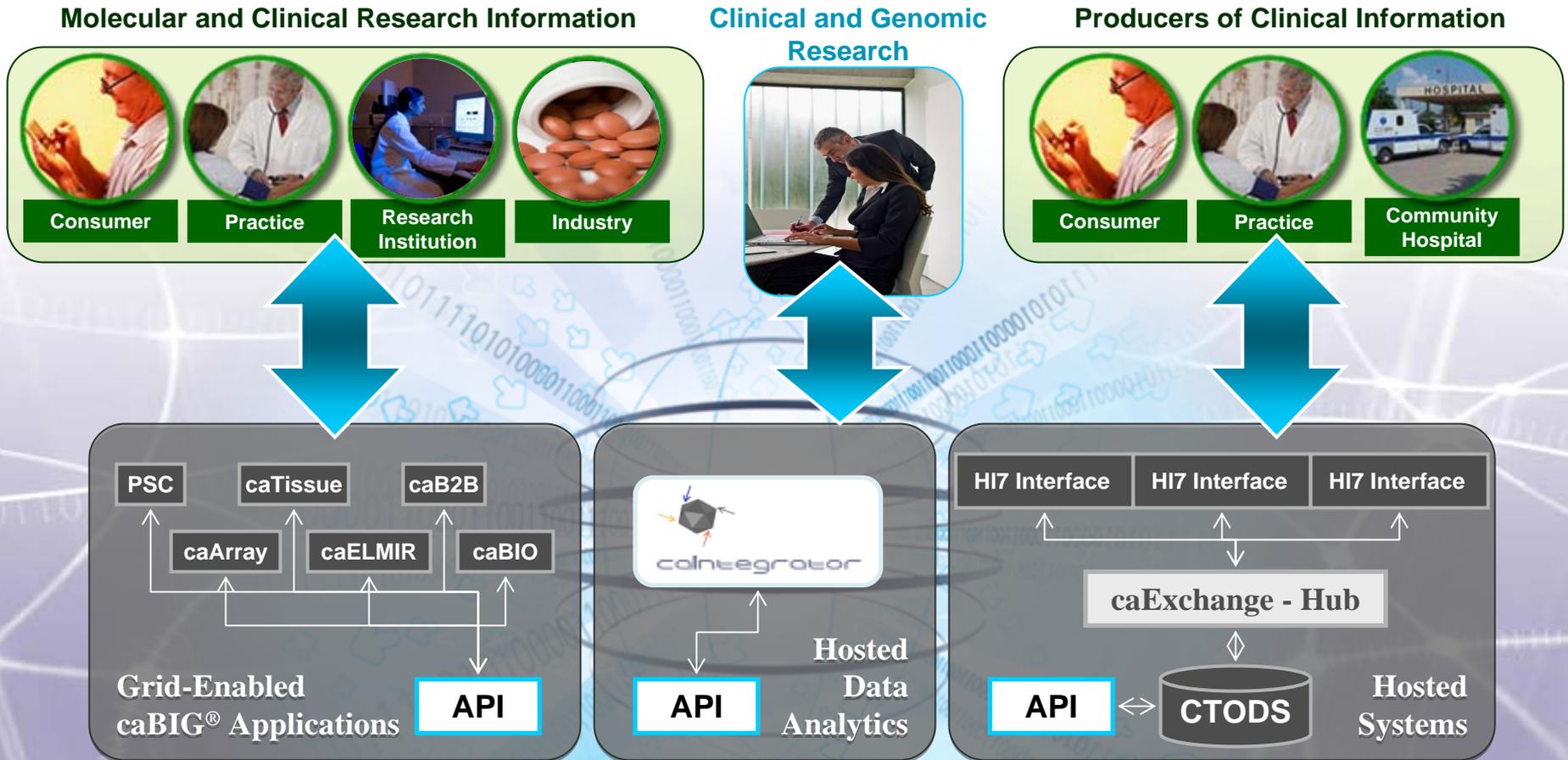


The Cancer Knowledge Cloud
is a virtual biomedical capability that uses the NCI’s cancer Biomedical Informatics Grid (caBIG[®]) to encompass distributed individual and organizational data, software applications, and computational capacity through the Internet.

“Cancer Knowledge Cloud”



caBIG[®] Underpins The Cancer Knowledge Cloud



caGRID

caBIG[®] Capabilities Are Relevant to Discovery, Clinical Research, and Clinical Care

- Track clinical trial registrations
- Facilitate automatic capture of clinical laboratory data
- Manage reports describing adverse events during clinical trials



Clinical Research

- Combine proteomics, gene expression, and other basic research data
- Submit and annotate microarray data
- Integrate microarray data from multiple manufacturers and permit analysis and visualization of data



Discovery Research



Clinical Care



Imaging

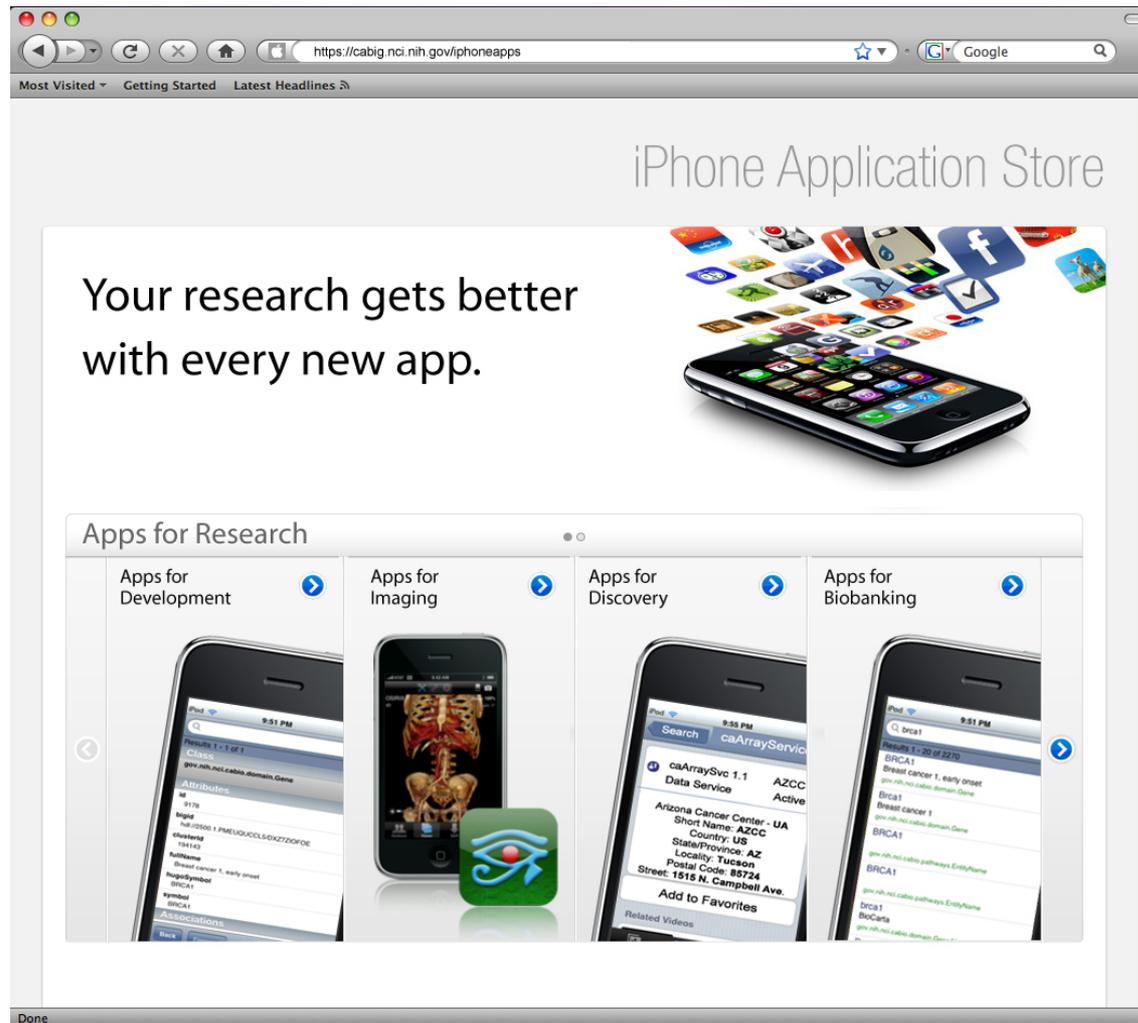
- Use NBIA repository for medical images including CAT scans and MRIs
- Visualize images using DICOM-compliant tools
- Annotated Images with distributed tools



Pathology

- Access library of well characterized and clinically annotated biospecimens
- Use tools to keep an inventory of a user's own samples
- Track storage, distribution, and quality assurance of specimens

caBIG[®] as a Platform for a Biomedical “App Store”



Biomedical
Information (caBIO)

Medical
Imaging (OsiriX)

Biomedical
Services (caGrid)

Biospecimens
(caTissue)

caBIG[®] In The Cloud...



**Clinical Trials Suite
(CCTS)**



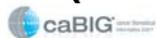
**Biospecimen
Repository (caTissue)**



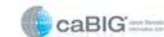
**Cancer
Knowledge Cloud**



**Health Information
Services (COPPA)**



**Biomedical
Information Services
(caBIO)**



Using caBIG[®] to Classify Lymphoma

• Scientific value

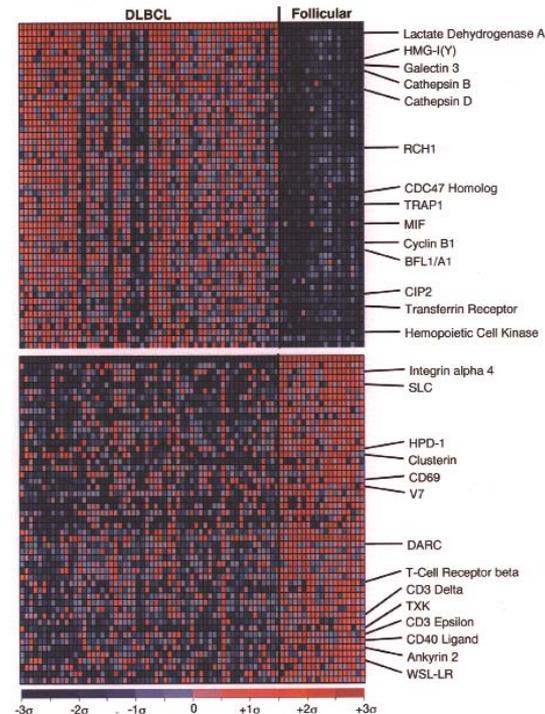
- Use **gene-expression** patterns associated with two lymphoma types to predict the type of an unknown sample.
- Connect caGrid data service (**caArray**) with analytical services (PreProcess, SVM and KNN from **GenePattern**).

• Major steps

- Querying training data from experiments stored in caArray.
- Preprocessing, i.e., normalizing the microarray data.
- **Predicting lymphoma type** using SVM & KNN services.

• Extension

- Generalized the workflow into a cancer type prediction routine that can be used on other caArray data sets.



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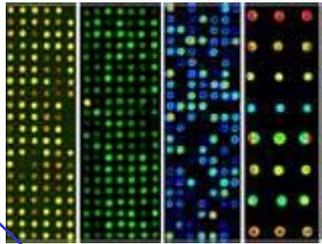
Stian Soiland-Reyes
U Manchester, UK



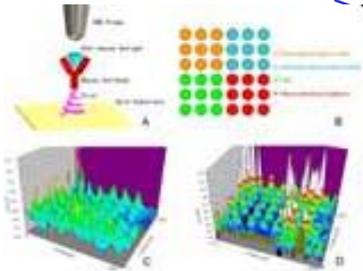
*Fig. from MA Shipp. Nature Medicine, 2002

Lymphoma Prediction Workflow

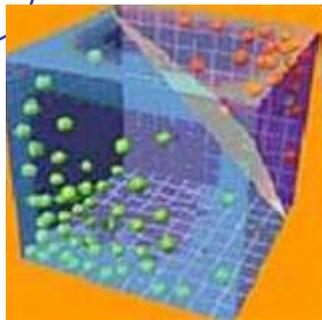
MicroArray from tumor tissue



Microarray preProcessing



Lymphoma classification



caGrid Portal

Home Data Sets People Tools Communities Institutions Catalog

Tools » Taverna Workflow

Lymphoma type prediction based on microarray data

Description: Scientific value Using gene-expression patterns associated with DLBCL and FL to predict the lymphoma type of an unknown sample. Using SVM (Support Vector Machine) to classify data, and predicting the tumor types of unknown examples. Steps Querying training data from experiments stored in caArray. Preprocessing, or normalize the microarray data. Adding training and testing data into SVM service to get classification result. The input to this workflow is an Experiment ID. Experiment ID identifies the experiment that caArray uses for data collection. For example, Experiment 95 contains microArray data regarding 77 tumor samples.

Scufl Path: /home/portal/portal-liferay/apache-tomcat-5.5.27/temp/3-taverna-new-portal/WEB-INF/classes/caArray_SVM-090710.t2flow

Number of Input Ports: 1

Author: Wei Tan

Select Workflow

caDSR metadata query in caGrid

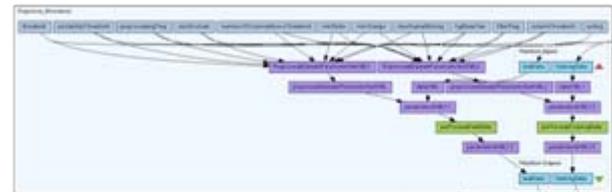
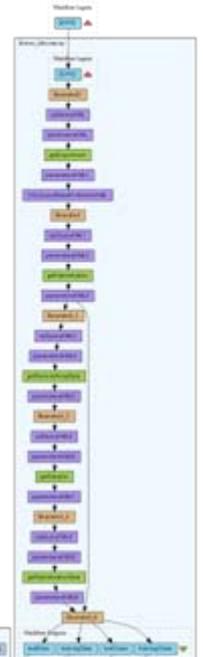
Description: This workflow uses caDSR (Cancer Data Standards Repository) service, which defines a comprehensive set of standardized metadata descriptors for cancer research terminology used in information collection and analysis. This Sample workflow is to find all the concepts related to a given context, for example caCore. The workflow uses context information to invoke findProjects in caDSR and get the project(s) information.

Scufl Path: /home/portal/portal-liferay/apache-tomcat-5.5.27/temp/3-taverna-new-portal/WEB-INF/classes/cadsr.t2flow

Number of Input Ports: 1

Author: Wei Tan

Select Workflow



Ack. Juli Klemm, Xiaopeng Bian, Rashmi Srinivasa (NCI)
Jared Nedzel (MIT)

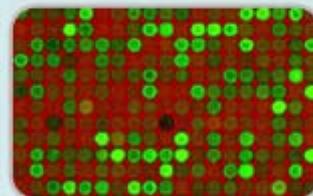


A New Model for Biomedicine

Using the Knowledge Cloud...



Research



BCM
Baylor College of Medicine

Participants

Patients join research networks, grant consent, agree to be "sought" and to enroll – "on-demand" participants

Biospecimen Collections

Researchers can access and query large collections of well-characterized, clinically annotated specimens

Discovery of Correlations

Biomarkers are identified and validated; disease sub-groups emerge

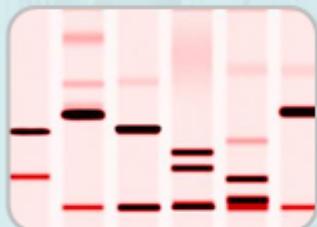
Individualization of Treatment

Patients are identified by sub-groups and treated appropriately

Using the Knowledge Cloud...



Consumer



My Genomic Profile

Consumers get their genetic and predisposition risk information



My Prevention Strategies

Consumers work with genetic counselors; coordinate with health care provider



My Clinical Record

Consumers link to their clinical histories with genetic profiles; access clinical research; participate in volunteer networks



Using the Knowledge Cloud...



Clinical Practice



Electronic Health Records

EHRs can connect to clinical trials in hospital settings



Research Finding Knowledgebases

Large-scale databases of latest research findings are connected to health delivery encounter



Learning Healthcare System

Local and national clinical encounter information is fed back to care providers to help inform clinical decision making

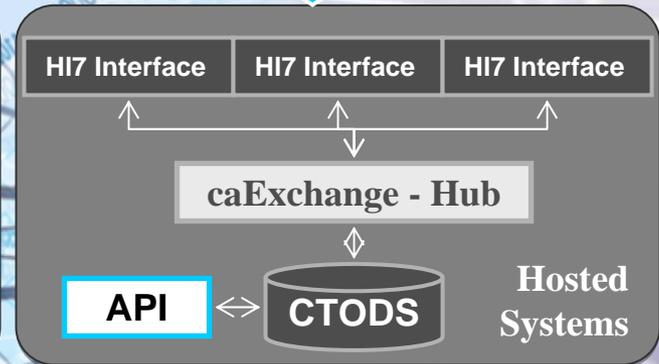
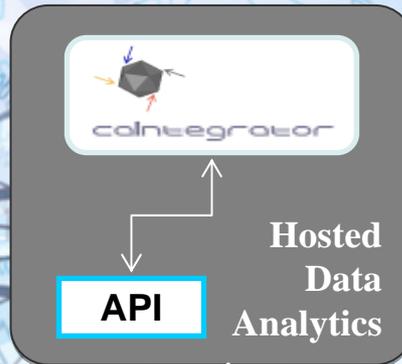
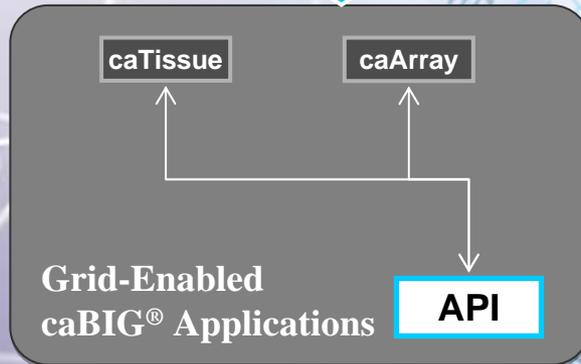


caBIG[®] Enables Comparative Effectiveness Research

Molecular and Clinical Research Information



Producers of Clinical Information



Comparative Effectiveness Research



caGRID

Our Distinguished Panel



- **Aneesh Chopra, M.P.P.**
United States Chief Technology Officer



- **Stephen Friend, M.D., Ph.D.**
President & CEO
Sage



- **Greg Simon, J.D.**
Senior Vice President, Worldwide Policy
Pfizer