caBIG™ cancer Biomedical Informatics Grid™

an initiative of the National Cancer Institute

The Impact of caBIG™ Products on the Cancer Patient's Experience

Clinical Researchers [Bedside]

Basic Science Researchers [Bench]

42 year old mother discovers symptoms that are abnormal

Visit PCP → Specialist → Radiologist

Electronic Health Records to Integrate patient data

Patient Work-up

Use electronic health record to integrate data from different doctors

Pathology
collection of specimens

caTISSUE Core
A core solution for biospecimen inventory, tracking, and basic annotation that may be used by biospecimen resource facilities. caTISSUE Core is enhanced for better integration with other Tissue banking tools and applications that will enable seamless integration within an institution

Tissue to Biorepository State of the art Biomarker assessment

Undergoes Biopsy

Scared and confused, so many different doctors and decisions to make. Where is the information?

Diagnosed with Cancer

The patient wants to know everything she can about cancer and how best to treat cancer.

Are there treatment options available?

Is there a clinical trial available?

caTIES
A text information extraction system automating the process of coding, storing and retrieving data from free-text pathology reports

Biopsy data entered into free text

Treatment in Clinical Trial

The patient's doctor explains the trial and a CRA answers all questions. A week later she decides to sign the informed consent and join the trial.

As individualized medicine evolves, patients will seek out clinical trials specific to their medical history and disease.

Treatment

Targeted personalized treatment based on the patient's tumor genotype / proteomics / expression and genotype.

caMatch
A system for matching eligible patients with clinical trials (currently in prototype for breast cancer)

I have found some clinical trials through caMatch which I would like to discuss with my doctor

Information in patient database

Response to Treatment

Information to influence future research

Information to influence future research

C3PR
A web-based application for managing participants across multiple cancer clinical trials

Data controlled in three views based on patient's consent:

1. Full access to limited number of medical personnel involved in clinical trial.
2. Limited subset of data accessible by scientists in same protocol.
3. De-identified data at aggregate level available to caBIG™ community.

Adverse Event

Patient data on adverse event can be easily communicated and explored at varying levels of granularity, by both clinical and basic science researchers. Information is seamlessly transported from bedside to bench and back to support personalized medicine.

C3D
A web-based application for managing clinical trial data across multiple cancer clinical trials

Successfully Treated

The patient feels hopeful and continues to improve. It seems she is responding to this treatment option!

caAERS (Adverse Events)
An open source software tool that is used to collect, process and report adverse events that occur during clinical trials

Monitored for Recurrence

FDA

Data Warehouse

No Recurrence

Recurrence

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Protein Expression | **DNA Genotyping** | **RNA Expression**

Proteomics Database | **Genomics Database** | **Gene expression Database**

RProteomics
For example, RProteomics will include R (a software language for statistical computing and graphics) libraries will be developed and incorporated into a caBIG™-compliant system that will aid cancer researchers in post-processing mass spectrometry data

HapMap
For example, a database that stores human SNPs, their genotypes, and the linkage disequilibrium relationships among them

caArray
For example, caARRAY is a microarray data repository that contains utilities for the submission and retrieval of Affymetrix and GenePix native file formats, and has accessibility through a MicroArray and Gene Expression Object Model Application Programming Interface (MAGE-OM API)

ANALYSIS TOOLS

caWorkbench | **GenePattern** | **VISDA**

Both caWorkbench and GenePattern provide the capability for visualizing and analyzing gene expression data and supports multidisciplinary genomic research and the integration of new technologies. VISDA is used for multivariate cluster-modeling, discovery, and visualization

Contributors:
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