

Abstract

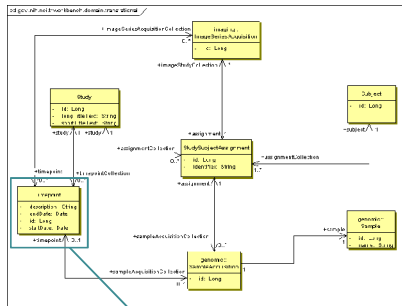
VASARI is the integration of Neuroimaging analysis with clinical and functional genomics data from clinical trials involving patients suffering from Gliomas in REpository for Molecular BRAin Neoplasia DaTa (REMBRANDT) repository. Vasari will provide researchers with the ability to perform ad hoc querying and reporting of Neuroimaging analysis across multiple data domains, such as Gene Expression, Chromosomal aberrations, and Clinical data. Via Rembrandt, researchers will also be able to view or download the annotated imaging data stored at the National Cancer Imaging Archive (NCIA) repository.

Description

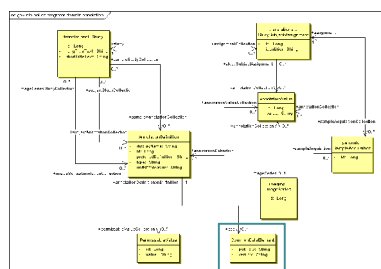
The caIntegrator2 framework will be used to implement VASARI. caIntegrator2 allows Study Managers to create new studies without any new software or database development. They can define the data sources, map the data to existing datatypes, and deploy the study using a web interface.

Research Investigators can then use the tool to browse the main study objects such as patients, image series and genes. They can also create, run, and save complex queries that can be made available to other users. Users can also integrate data with external tools such as GenePattern and GeWorkbench which can be used for performing classification and clustering analysis, among others.

Object Model

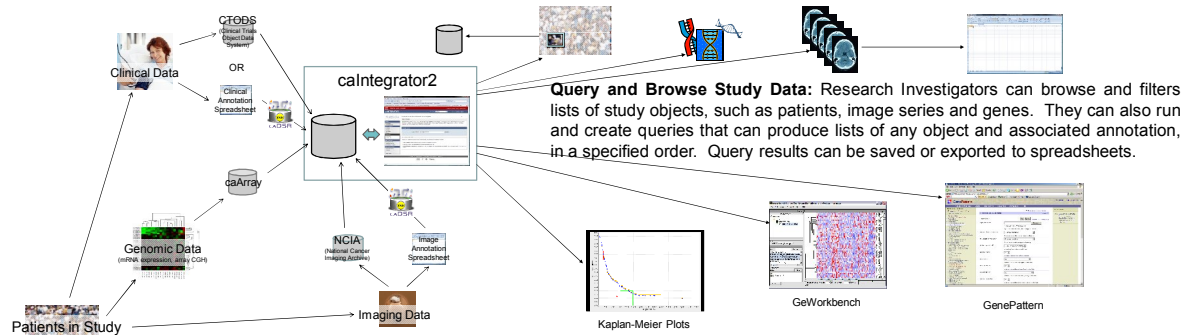


Translation Data Model: This object model shows the relationship between study subjects (patients) and the genomic and imaging data that is acquired from them. In addition, multiple timepoints can be defined for a study so that imaging and genomic data can be gathered multiple times. An example of timepoints would be 'At Diagnosis' and 'After Treatment'.



Annotation Data Model: This object model shows how annotations are stored. Annotations can be associated with patients, genomic samples and image series. The Common Data Element object defines a relationship with a caDSR datatype if an appropriate one can be found.

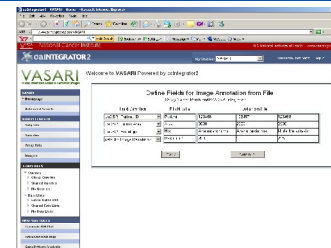
Use Cases



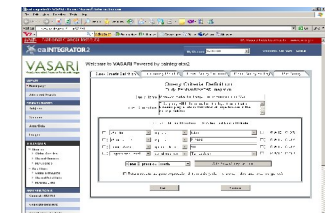
Deploy Study: The Study Manager defines the sources of data for a new study. The data is then accessed over the Grid or uploaded from files. The Study Manager defines relationships between patients and samples so that data can be compared properly across the data sources. The Study Manager also defines mapping of uploaded annotation fields to caDSR datatypes.

Perform Analysis: Data from caIntegrator2 can be sent to other software packages for more sophisticated analysis. GenePattern and GeWorkbench are available for clustering and classification analysis and several other analysis tools are built in, including Kaplan-Meier survival plots.

Web Interface



Deploy Study: This page allows the Study Manager to map each uploaded clinical data field to a caDSR datatype. The detailed datatype description, field type (number, date, yes/no, etc.) and allowable values can then be read from caDSR and used to validate the data.



Manage Queries: This page allows the Study Manager to create queries that can be shared with all researchers who have access to the study. These queries can access all fields from all data sources and complex queries can be built up from logical combinations of simpler queries. The queries can also look for correlation relationships such as genes that are up-regulated in a certain tumor type determined by imaging.

Future Directions

- Continued integration of images with other molecular technologies.
- Correlation of prospective and retrospective clinical data with image data for using images as surrogate markers to predict treatment responses.
- Coordinate with imaging communities to improve image analysis and feature prediction outcomes based on algorithms.