

# Molecular Analysis Tools Knowledge Center

## Solving Research Problems: Sharing Expression Data with Collaborators

Molecular analysis tools provide powerful analytic capabilities for genomic data interpretation. Four key tools will be supported by the Molecular Analysis Tools Knowledge Center: geWorkbench, which provides an innovative, open-source software platform for genomic data integration while bringing together analysis and visualization tools for gene expression, sequences, pathways and other biomedical data; GenePattern, which provides bioinformatics tools for gene expression, proteomic and SNP analysis; caArray, a system that supports the management and exchange of array data and annotations and caIntegrator, a novel translational informatics platform that allows researchers and bioinformaticians to access and analyze clinical and experimental data across multiple clinical trials and studies.

### The Problem: Sharing Expression Data with Collaborators

Before research results are published and related gene-expression data are deposited in GEO, researchers usually need to store their sample data and gene-expression data locally, preferably with access control. In a multi-lab collaboration, easy and selective data sharing is also desired. Excel and file-system-based data management are universal but inadequate.

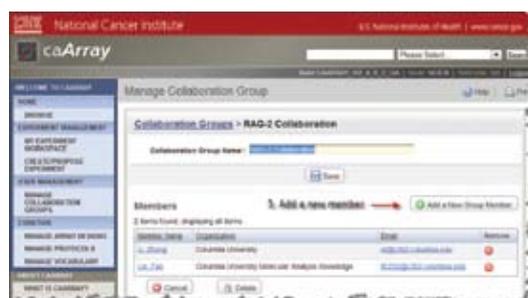
### The Solution: caArray

caArray is a web-based array data management system that among other innovative features, offers an easy-to-use and flexible data access control to manage data sharing. Once data are loaded into caArray, the following three steps are all a researcher needs to take to enable secure and selective data sharing:

#### Step 1: Create a collaboration group



#### Step 2: Add member(s) to the collaboration group



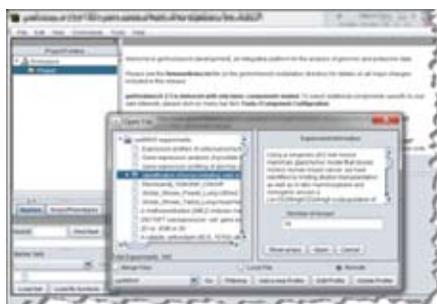
### Step 3: Assign selective data visibility to the collaboration group

At this step, the user can choose to give the selected collaboration group read or read/write access to the experiment or to a subset of the experiment data.



### Piping data from caArray into geWorkbench or GenePattern for data analysis

Once data are in caArray, a bioinformatician with access to the desired data set(s) can launch geWorkbench or GenePattern and retrieve data from caArray directly into geWorkbench or GenePattern. No need to worry about data formatting.



### The Benefits:

With caArray, cancer researchers now have total access control over their unpublished data and should find it convenient to share their data with their collaborators. Furthermore, they can easily access the data in two popular data analysis tools for analysis and result interpretation.

### Key Contributors:

caArray development team  
Molecular Analysis Tools Knowledge Center

### For More Information:

**Molecular Analysis Tools Knowledge Center:** [https://cabig-kc.nci.nih.gov/Molecular/KC/index.php/Main\\_Page](https://cabig-kc.nci.nih.gov/Molecular/KC/index.php/Main_Page)

