

## Implementing the National Cancer Institute's (NCI) Best Practices for Biospecimen Resources: Bioinformatics and caBIG™ - An Overview

### The Role of Bioinformatics for Biospecimen Resources

Several best practices in the “NCI Best Practices for Biospecimen Resources” speak to the importance of bioinformatics and effective software development practices. These practices reflect the importance of the data attached to each biospecimen managed by NCI-funded resources.

NCI's Cancer Biomedical Informatics Grid™ (caBIG™) helps biospecimen resources implement the NCI Best Practices in the areas of bioinformatics.

### What is caBIG™ and What Does It Offer?

Now in its fourth year, caBIG™ is an information technology (IT) initiative that has established both the infrastructure and tools required to share biospecimen-related data across a network of cancer researchers.

Two free, open source software tools released by caBIG™ directly relate to biospecimen management: caTissue Core, and caTIES. All caBIG™ tools are based on a shared set of common terms and data structures. Adopting caBIG™ tools not only provides valuable software, it also allows connections with other researchers and systems using the same common standards. If you already have a software tool, caBIG™ provides the tools and training to achieve this same connection – called “caBIG™ compatible.” The required effort depends on your existing tool.

### Strategic Considerations

The cost and complexity of becoming caBIG™ compatible may be less than you think, and the potential benefits of achieving compatibility are significant. Many features of NCI's informatics best practices are embedded within caBIG™ tools. Here are some options:

- If you are starting with a paper-based system or a tool that does not meet best practice standards, adopting caBIG™ software tools (already caBIG™ compatible) from scratch may be the best option.
- If you want to keep an existing basic tool, like Excel or Access, you can become caBIG™ compatible by mapping your tool to a caBIG™ tool, and then connecting to the caBIG™ network through it.
- If you have a bioinformatics system that is not caBIG™ compatible, you can become caBIG™ compatible by creating an interface that maps the existing tool's data structures to caBIG™ standards. You can do this for the entire database – or for just the existing tool's reporting function.

All of these options may require some temporary support from an IT programming/database specialist; however, you do not need full-time staff to achieve the benefits of caBIG™ compatibility.

*How caBIG™ benefits cancer patients and advocates:*

- caBIG™ establishes mechanisms that can increase the research potential associated with each patient's biospecimen donation – realizing maximum benefits across researchers.
- caBIG™ tools have built-in security needed to ensure regulatory compliance, and enhance patient trust with respect to privacy concerns.

*How caBIG™ benefits biospecimen resource researchers and directors:*

- Leveraging free, existing software tools available through caBIG™ reduces software development costs for those wishing to deploy tools at their sites.
- The shared standards governing caBIG™ allow even small repositories to advertise their presence and specimen/data availability AND learn what others have to offer. You need only share the data you want; your own research comes first.
- Increased data sharing increases the effectiveness and efficiency of cancer research, helping individual scientists, the cancer research community, and ultimately the cancer patient.

*The willingness of cancer patients to share tissue is fundamental to cancer research. Our willingness to share biospecimen-related data is critical to maintaining public trust.*