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by

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Integrating Clinical and Gene Expression Data

ABSTRACT

The existence of both clinical and expression databases has provided valuable information regarding disease pathways and genes. Until recently these two sets of data have primarily existed independent of one another. Currently, caBIG (Cancer Bioinformatics Grid) is creating a widely distributed infrastructure permitting the cancer research community to focus on innovation and integration in Cancer research. The caBIG is designed to produce quality shared tools and data repositories in support of cancer biology research. The present challenge is to develop a solution for integrating individual caBIG information systems such as caBIO, caCORE, caARRAY, and caTISSUE. These systems have separate APIs and are not fully linked. Additionally, no standard schema nor API for obtaining, storing, and querying a secure extended patient record exists, although partial ones seem to exist. This project builds a standard patient information repository, and an integrative API support complex to span caBIG repositories. Bridging these powerful information silos empowers integrative translational research and medical therapeutic interventions, thus furthering individualized patient care.