Computer Science

COLLABORATIVE TOOLS FOR COMPUTATIONAL BIOLOGY

Rico Carrell, Soon-Ok Park, Governors State University, University Park, IL 60466
Freddrick Logan, Jackson State University, Jackson, MS 39217
Edward Frank*, Michael Papka*
* Mathematics and Computer Science Division,
Argonne National Laboratory, Argonne, IL 60439

Research in genomic and biological science has the promise of benefiting society. One goal of bioinformatics is to mine biological databases to identify genes and their encoded products that govern biological reactions. Systems biology research uses computer models to help understand the behavior of the biological processes. Two main objectives in the project are; 1) Add the ability to connect to multiple databases simultaneously. 2) Add the ability to use multiple database technologies. We have achieved these goals during our research at Argonne National Laboratory. Previous ongoing research at Argonne National Laboratory has produced prototype tools to help build models. Kah is a framework for writing systems biology programs and the Model Editor is a graphical user interface (GUI), written in terms of Kah, that a scientist can use to build biochemical models. The previous KahDB was built with Oracle. This project we have worked on extending Kah to easily utilize any database such as Oracle, Postgres and MySQL. We have engaged in creation and modification of programming code to actually load the biological data into multiple databases. Our project focused on developing a collaborative tool which would allow scientists the ability to connect multiple databases of same or different type simultaneously. We have developed software to provided simultaneous access to multiple databases. Our research with building and collaboration of the project has created a foundation for the collaborative tools for computational biology.