



NSF Funds Petascale Algorithms for Genomic Relatedness Research

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NEW YORK (GenomeWeb News) – Scientists at three universities will use funding from the American Recovery and Reinvestment Act to develop computational biology tools that researchers will use with next-generation computers to study genomic evolution, according to Georgia Tech.

The \$1 million grant from the National Science Foundation's PetaApps program, which funds development of computer technologies for petascale machines that can conduct trillions of calculations per second, will include Georgia Tech, the University of South Carolina, and Pennsylvania State University.

These researchers will develop new algorithms in an open-source software framework that will use parallel, petascale computing to study ancestral genomics in an open source code called Genome Rearrangements Analysis under Parsimony and other Phylogenetic Algorithms (GRAPPA).

"GRAPPA is currently the most accurate method for determining genome rearrangement, but it has only been applied to small genomes with simple events because of the limitation of the algorithms and the lack of computational power," explained David Bader, a lead investigator on the grant and executive director of high-performance computing at Georgia Tech's College of Computing.

GRAPPA was recently used to determine the evolutionary relation of a dozen bellflower genomes one billion times faster than a method that did not use parallel processing or optimization.

The researchers in this program will use it to test their algorithms by analyzing a collection of fruit fly genomes. They expect their algorithms will provide "a relatively simple system to understand the mechanisms that underlie gene order diversity, which can later be extended to more complex mammalian genomes, such as primates," according to Georgia Tech.

They think that the algorithms will make genome rearrangement analysis reliable and efficient.

"Ultimately this information can be used to identify microorganisms, develop better vaccines, and help researchers better understand the dynamics of microbial communities and biochemical pathways," Bader said.

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