Article Withdrawn: GNARE: A Grid-based Server for the Analysis of User Submitted Genomes

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Nucleic Acids Res. doi: 10.1093/nar/gkm366

This article has been withdrawn by the Web Server Issue Editor. GNARE is a Web Server that allows users to submit their genome (fasta file with sequences) and it performs a detailed analysis of sequence data using HPC resources on the GRID. To access the Web Server, users have to register for a free account and then send their data to the website administrator for uploading and analysis. However, it is journal policy that all Web Servers featured in the issue must not limit access by a login requirement and usage must not be dependent on intervention by website developers. As this Web Server did not meet those criteria, the paper was withdrawn prior to publication in the 2007 Web Server issue.

The abstract, as originally published online as Advance Access, read as follows:

GeNome Analysis Research Environment (GNARE) is a bioinformatics server that supports both automated and interactive expert-driven analysis of user-submitted genomes and metagenomes. These analyses include gene function prediction and development of organism-specific metabolic reconstructions from sequence data. GNARE provides a framework for comparative and evolutionary analysis as well as annotation of genomes and metabolic networks in the context of phenotypic and taxonomic information. Results of analyses and metabolic models are visualized and extensively annotated with information from public databases. GNARE uses automated workflows and a Grid-based computational backend to perform high-throughput analysis of genomes. This use of distributed computing allows the analysis of an average-sized prokaryotic genome in less than 5h. GNARE is available at http://compbio.mcs.anl.gov/gnare/.

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