Resource Summary Report

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Genboree Discovery System

RRID:SCR_000747
Type: Tool

Proper Citation

Genboree Discovery System (RRID:SCR_000747)

Resource Information

URL: http://genboree.org

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Description: A software application and database viewing system for genomic research, more specifically formulti-genome comparison and pattern discovery via genome self-comparison. Data are available for a range of species including Human Chr3, Human Chr12, Sea Urchin, Tribolium, and cow. The Genboree Discovery System is the largest software system developed at the bioinformatics laboratory at Baylor in close collaboration with the Human Genome Sequencing Center. Genboree is a turnkey software system for genomic research. Genboree is hosted on the Internet and, as of early 2007, the number of registered users exceeds 600. While it can be configured to support almost any genome-centric discovery process, a number of configurations already exist for specific applications. Current focus is on enabling studies of genome variation, including array CGH studies, PCR-based resequencing, genome resequencing using comparative sequence assembly, genome remapping using paired-end tags and sequences, genome analysis and annotation, multi-genome comparison and pattern discovery via genome self-comparison. Genboree database and visualization settings, tools, and user roles are configurable to fit the needs of specific discovery processes. Private permanent project-specific databases can be accessed in a controlled way by collaborators via the Internet. Project-specific data is integrated with relevant data from public sources such as genome browsers and genomic databases. Data processing tools are integrated using a plug-in model. Genboree is extensible via flexible data-exchange formats to accommodate project specific tools and processing steps. Our Positional Hashing method, implemented in the Pash program, enables extremely fast and accurate sequence comparison and pattern discovery by employing low-level parallelism. Pash enables fast and sensitive detection of orthologous regions across mammalian genomes, and fast anchoring of hundreds of millions of short sequences produced by next-generation sequencing technologies. We are further developing the Pash program and employing it in the context of various discovery pipelines. Our laboratory participates in the

pilot stage of the TCGA (The Cancer Genome Atlas) project. We aim to develop comprehensive, rapid, and economical methods for detecting recurrent chromosomal aberrations in cancer using next-generation sequencing technologies. The methods will allow detection of recurrent chromosomal aberrations in hundreds of small (

Abbreviations: Genboree

Synonyms: Genboree Discovery System

Resource Type: data processing software, data or information resource, database, software resource, software application

Keywords: genome, genomic, next generation sequencing

Funding:

Resource Name: Genboree Discovery System

Resource ID: SCR_000747

Alternate IDs: nif-0000-08906

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250426T055424+0000

Ratings and Alerts

No rating or validation information has been found for Genboree Discovery System.

No alerts have been found for Genboree Discovery System.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Koupenova M, et al. (2018) Micro RNAs from DNA Viruses are Found Widely in Plasma in a Large Observational Human Population. Scientific reports, 8(1), 6397.

Mick E, et al. (2017) Stroke and Circulating Extracellular RNAs. Stroke, 48(4), 828.

Chen KG, et al. (2017) Mouse Genetic Analysis of Bone Marrow Stem Cell Niches: Technological Pitfalls, Challenges, and Translational Considerations. Stem cell reports, 9(5), 1343.

Freedman JE, et al. (2016) Diverse human extracellular RNAs are widely detected in human plasma. Nature communications, 7, 11106.

, et al. (2015) The Fourth International Meeting of ISEV, ISEV2015. Journal of extracellular vesicles, 4, 27783.

Subramanian SL, et al. (2015) Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. Journal of extracellular vesicles, 4, 27497.

, et al. (2015) Integrative analysis of 111 reference human epigenomes. Nature, 518(7539), 317.

Nilakanta H, et al. (2014) A review of software for analyzing molecular sequences. BMC research notes, 7, 830.

Dolled-Filhart MP, et al. (2013) Computational and bioinformatics frameworks for next-generation whole exome and genome sequencing. TheScientificWorldJournal, 2013, 730210.

Qin X, et al. (2012) Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. BMC microbiology, 12, 135.

Cejková D, et al. (2012) Whole genome sequences of three Treponema pallidum ssp. pertenue strains: yaws and syphilis treponemes differ in less than 0.2% of the genome sequence. PLoS neglected tropical diseases, 6(1), e1471.