Resource Summary Report

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GemTools

RRID:SCR_001259
Type: Tool

Proper Citation

GemTools (RRID:SCR_001259)

Resource Information

URL: http://www.wpic.pitt.edu/wpiccompgen/GemTools/GemTools.htm

Proper Citation: GemTools (RRID:SCR_001259)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software tools for modeling genetic ancestry based on the single nucleotide polymorphism (SNP) information. This package of functions helps the user account for genetic ancestry of a large number of individuals using spectral graph theory and projections to break a large problem into smaller pieces and calculate genetic ancestry information efficiently, i.e., a divide and conquer (dac) strategy. It is completely written in R and runs on any platform that supports R.

Abbreviations: GemTools

Synonyms: GemTools - A fast and efficient approach to estimating genetic ancestry

Resource Type: software resource

Keywords: genetic, ancestry, single nucleotide polymorphism, r

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GemTools

Resource ID: SCR_001259

Alternate IDs: OMICS_02079

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190136+0000

Ratings and Alerts

No rating or validation information has been found for GemTools.

No alerts have been found for GemTools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 45 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

García-Nieto E, et al. (2024) Clinical and molecular characterization of steatotic liver disease in the setting of immune-mediated inflammatory diseases. JHEP reports : innovation in hepatology, 6(10), 101167.

Fan L, et al. (2024) Chrom-seq identifies RNAs at chromatin marks. Science advances, 10(31), eadn1397.

Trastulla L, et al. (2024) Distinct genetic liability profiles define clinically relevant patient strata across common diseases. Nature communications, 15(1), 5534.

Gonen N, et al. (2023) In vitro cellular reprogramming to model gonad development and its disorders. Science advances, 9(1), eabn9793.

Kobayashi-Ishihara M, et al. (2023) Schlafen 12 restricts HIV-1 latency reversal by a codon-usage dependent post-transcriptional block in CD4+ T cells. Communications biology, 6(1), 487.

Brown AA, et al. (2023) Genetic analysis of blood molecular phenotypes reveals common properties in the regulatory networks affecting complex traits. Nature communications, 14(1), 5062.

Oriol-Tordera B, et al. (2022) Epigenetic landscape in the kick-and-kill therapeutic vaccine BCN02 clinical trial is associated with antiretroviral treatment interruption (ATI) outcome. EBioMedicine, 78, 103956.

Li J, et al. (2022) RecombineX: A generalized computational framework for automatic high-throughput gamete genotyping and tetrad-based recombination analysis. PLoS genetics, 18(5), e1010047.

Taub MA, et al. (2022) Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell genomics, 2(1).

Klei L, et al. (2021) How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular autism, 12(1), 66.

Gockley J, et al. (2021) Multi-tissue neocortical transcriptome-wide association study implicates 8 genes across 6 genomic loci in Alzheimer's disease. Genome medicine, 13(1), 76.

Arenas EJ, et al. (2021) Acquired cancer cell resistance to T cell bispecific antibodies and CAR T targeting HER2 through JAK2 down-modulation. Nature communications, 12(1), 1237.

Sararols P, et al. (2021) Specific Transcriptomic Signatures and Dual Regulation of Steroidogenesis Between Fetal and Adult Mouse Leydig Cells. Frontiers in cell and developmental biology, 9, 695546.

DeMichele-Sweet MAA, et al. (2021) Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular psychiatry, 26(10), 5797.

Smolander J, et al. (2021) Evaluation of tools for identifying large copy number variations from ultra-low-coverage whole-genome sequencing data. BMC genomics, 22(1), 357.

Sönmez Flitman R, et al. (2021) Untargeted Metabolome- and Transcriptome-Wide Association Study Suggests Causal Genes Modulating Metabolite Concentrations in Urine. Journal of proteome research, 20(11), 5103.

Vizán P, et al. (2020) The Polycomb-associated factor PHF19 controls hematopoietic stem cell state and differentiation. Science advances, 6(32), eabb2745.

Sieberts SK, et al. (2020) Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific data, 7(1), 340.

George L, et al. (2020) Blood eosinophil count and airway epithelial transcriptome relationships in COPD versus asthma. Allergy, 75(2), 370.

Chow NA, et al. (2020) Tracing the Evolutionary History and Global Expansion of Candida auris Using Population Genomic Analyses. mBio, 11(2).