Resource Summary Report

Generated by dkNET on Apr 17, 2025

TOMCAT

RRID:SCR_013120
Type: Tool

Proper Citation

TOMCAT (RRID:SCR_013120)

Resource Information

URL: https://www.dkfz.de/en/epidemiologie-krebserkrankungen/software/software.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May24,2023. Software program that implements the Mantel statistics as proposed by Beckmann et al. (2005) to test for association between genetic markers and phenotypes in case-control studies using haplotype information. The potential value of haplotypes has attracted widespread interest in the mapping of complex traits. Haplotype sharing methods take into account linkage disequilibrium information between multiple markers, and may have good power to detect predisposing genes. We present a new approach based on Mantel statistics for space time clustering, which we developed in order to improve the power of haplotype sharing analysis for gene mapping in complex disease. The new statistic correlates genetic similarity and phenotypic similarity across pairs of haplotypes for case-only and case-control studies. The genetic similarity is measured as the shared length between haplotypes around a putative disease locus. Alternative measures for the phenotypic similarity were implemented. (entry from Genetic Analysis Software)

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java, 5.0

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TOMCAT

Resource ID: SCR_013120

Alternate IDs: nlx_154681

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250416T063637+0000

Ratings and Alerts

No rating or validation information has been found for TOMCAT.

No alerts have been found for TOMCAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Harris SJ, et al. (2025) Methane emissions from the Nord Stream subsea pipeline leaks. Nature, 637(8048), 1124.

Paddo AR, et al. (2024) Development and validation of the DHIS2 platform for integrating sociomedical data to study wound care outcomes. PloS one, 19(12), e0308553.

Nóbrega JCD, et al. (2024) Symmetric dimethylarginine correlates with the urea, creatinine, potassium, and clinical scores in feline urethral obstructions. Journal of veterinary science, 25(2), e27.

Guo Q, et al. (2023) CellTracer: a comprehensive database to dissect the causative multilevel interplay contributing to cell development trajectories. Nucleic acids research, 51(D1), D861.

Leopardi S, et al. (2023) One health surveillance strategy for coronaviruses in Italian wildlife. Epidemiology and infection, 151, e96.

Freeman TF, et al. (2023) Ribosome biogenesis disruption mediated chromatin structure changes revealed by SRAtac, a customizable end to end analysis pipeline for ATAC-seq. BMC genomics, 24(1), 512.

Farag YM, et al. (2021) PeptideShaker Online: A User-Friendly Web-Based Framework for the Identification of Mass Spectrometry-Based Proteomics Data. Journal of proteome research, 20(12), 5419.

Schyman P, et al. (2021) TOXPANEL: A Gene-Set Analysis Tool to Assess Liver and Kidney Injuries. Frontiers in pharmacology, 12, 601511.

Gao Y, et al. (2021) LincSNP 3.0: an updated database for linking functional variants to human long non-coding RNAs, circular RNAs and their regulatory elements. Nucleic acids research, 49(D1), D1244.

Newham E, et al. (2021) A robust, semi-automated approach for counting cementum increments imaged with synchrotron X-ray computed tomography. PloS one, 16(11), e0249743.

Zhang L, et al. (2021) SAS: A Platform of Spike Antigenicity for SARS-CoV-2. Frontiers in cell and developmental biology, 9, 713188.

Barbone GE, et al. (2020) Establishing sample-preparation protocols for X-ray phase-contrast CT of rodent spinal cords: Aldehyde fixations and osmium impregnation. Journal of neuroscience methods, 339, 108744.

Cho M, et al. (2019) Prediction of cross-species infection propensities of viruses with receptor similarity. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 73, 71.

Xu L, et al. (2019) Chemometric Analysis of Elemental Fingerprints for GE Authentication of Multiple Geographical Origins. Journal of analytical methods in chemistry, 2019, 2796502.

Xie F, et al. (2017) Application of Text Information Extraction System for Real-Time Cancer Case Identification in an Integrated Healthcare Organization. Journal of pathology informatics, 8, 48.

Marone F, et al. (2017) Towards on-the-fly data post-processing for real-time tomographic imaging at TOMCAT. Advanced structural and chemical imaging, 3(1), 1.

Colangelo CM, et al. (2015) YPED: an integrated bioinformatics suite and database for mass spectrometry-based proteomics research. Genomics, proteomics & bioinformatics, 13(1), 25.

Floyd CN, et al. (2015) Expression of the PlA2 allele of glycoprotein IIIa and its impact on platelet function. JRSM cardiovascular disease, 4, 2048004015610252.