Resource Summary Report

Generated by dkNET on Apr 16, 2025

TREESCAN

RRID:SCR_007108
Type: Tool

Proper Citation

TREESCAN (RRID:SCR_007108)

Resource Information

URL: http://darwin.uvigo.es/software/treescan.html

Proper Citation: TREESCAN (RRID:SCR_007108)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11, 2023. Software application that is intended to provide p-values for the hypothesis of association between evolutionary clades and continuous traits, using haplotype trees. (entry from Genetic Analysis Software)

Abbreviations: TREESCAN

Resource Type: software resource, software application

Defining Citation: PMID:15681571

Keywords: gene, genetic, genomic, c, unix, ms-windows, ms-dos, macos, (x)

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TREESCAN

Resource ID: SCR_007108

Alternate IDs: nlx_154011

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250416T063455+0000

Ratings and Alerts

No rating or validation information has been found for TREESCAN.

No alerts have been found for TREESCAN.

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 dkNET.

Lin KJ, et al. (2023) Prospective validation of a dynamic prognostic model for identifying COVID-19 patients at high risk of rapid deterioration. Pharmacoepidemiology and drug safety, 32(5), 545.

Jeong NY, et al. (2023) Active surveillance for adverse events of influenza vaccine safety in elderly cancer patients using self-controlled tree-temporal scan statistic analysis. Scientific reports, 13(1), 13346.

Lorman V, et al. (2023) A machine learning-based phenotype for long COVID in children: An EHR-based study from the RECOVER program. PloS one, 18(8), e0289774.

Shiner B, et al. (2022) Mining Clinical Data for Novel Posttraumatic Stress Disorder Medications. Biological psychiatry, 91(7), 647.

Lorman V, et al. (2022) A machine learning-based phenotype for long COVID in children: an EHR-based study from the RECOVER program. medRxiv : the preprint server for health sciences.

Lee H, et al. (2022) Post-marketing surveillance study on influenza vaccine in South Korea using a nationwide spontaneous reporting database with multiple data mining methods. Scientific reports, 12(1), 20256.

Fralick M, et al. (2021) A novel data mining application to detect safety signals for newly approved medications in routine care of patients with diabetes. Endocrinology, diabetes & metabolism, 4(3), e00237.

Wintzell V, et al. (2020) Data Mining for Adverse Events of Tumor Necrosis Factor-Alpha Inhibitors in Pediatric Patients: Tree-Based Scan Statistic Analyses of Danish Nationwide Health Data. Clinical drug investigation, 40(12), 1147.

Park G, et al. (2020) Comparison of Data Mining Methods for the Signal Detection of

Adverse Drug Events with a Hierarchical Structure in Postmarketing Surveillance. Life (Basel, Switzerland), 10(8).

Duchemin SI, et al. (2016) Identification of QTL on Chromosome 18 Associated with Non-Coagulating Milk in Swedish Red Cows. Frontiers in genetics, 7, 57.

Auzanneau J, et al. (2011) Association study between the gibberellic acid insensitive gene and leaf length in a Lolium perenne L. synthetic variety. BMC plant biology, 11, 183.