

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

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)

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: 20260801T191040+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 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#).

Jeong NY, et al. (2025) A broad assessment of rotavirus vaccine safety in infants in Korea: Insights from a data-driven signal detection approach. *Human vaccines & immunotherapeutics*, 21(1), 2465161.

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.

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.

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*.

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.

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).

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.

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.