Resource Summary Report

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dndSCV

RRID:SCR_017093
Type: Tool

Proper Citation

dndSCV (RRID:SCR_017093)

Resource Information

URL: https://github.com/im3sanger/dndscv

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Description: Software R package as suite of dN/dS methods to quantify selection in cancer and somatic evolution. Contains functions to quantify dN/dS ratios for missense, nonsense and essential splice mutations, at level of individual genes, groups of genes or at whole genome level. Used to detect cancer driver genes on datasets.

Resource Type: data analysis software, software application, software resource, data processing software

Keywords: dN/dS, method, quantify, selection, cancer, somatic, evolution, missense, nonsense, essential, splice, mutation, gene, genome, dataset

Funding:

Availability: Free, Available for download, Freely available

Resource Name: dndSCV

Resource ID: SCR_017093

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250412T060053+0000

Ratings and Alerts

No rating or validation information has been found for dndSCV.

No alerts have been found for dndSCV.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. Cancer cell, 42(6), 1067.

Álvarez-Prado ÁF, et al. (2023) Immunogenomic analysis of human brain metastases reveals diverse immune landscapes across genetically distinct tumors. Cell reports. Medicine, 4(1), 100900.

Zapata L, et al. (2023) Immune selection determines tumor antigenicity and influences response to checkpoint inhibitors. Nature genetics, 55(3), 451.

Iranzo J, et al. (2023) Protocol for comparing gene-level selection on coding mutations between two groups of samples with Coselens. STAR protocols, 4(1), 102117.

Rouhani FJ, et al. (2022) Substantial somatic genomic variation and selection for BCOR mutations in human induced pluripotent stem cells. Nature genetics, 54(9), 1406.

Cosgrove N, et al. (2022) Mapping molecular subtype specific alterations in breast cancer brain metastases identifies clinically relevant vulnerabilities. Nature communications, 13(1), 514.

Parvandeh S, et al. (2022) EPIMUTESTR: a nearest neighbor machine learning approach to predict cancer driver genes from the evolutionary action of coding variants. Nucleic acids research, 50(12), e70.

Mitchell E, et al. (2022) Clonal dynamics of haematopoiesis across the human lifespan. Nature, 606(7913), 343.

Yu Y, et al. (2022) A recurrent somatic missense mutation in GNAS gene identified in familial thyroid follicular cell carcinomas in German longhaired pointer dogs. BMC genomics, 23(1), 669.

Lee SY, et al. (2022) The shaping of cancer genomes with the regional impact of mutation

processes. Experimental & molecular medicine, 54(7), 1049.

Song X, et al. (2022) Genomic and Single-Cell Landscape Reveals Novel Drivers and Therapeutic Vulnerabilities of Transformed Cutaneous T-cell Lymphoma. Cancer discovery, 12(5), 1294.

Iranzo J, et al. (2022) Pervasive conditional selection of driver mutations and modular epistasis networks in cancer. Cell reports, 40(8), 111272.

Chen K, et al. (2022) Spatiotemporal genomic analysis reveals distinct molecular features in recurrent stage I non-small cell lung cancers. Cell reports, 40(2), 111047.

de Kanter JK, et al. (2021) Antiviral treatment causes a unique mutational signature in cancers of transplantation recipients. Cell stem cell, 28(10), 1726.

Zhang M, et al. (2021) Clonal architecture in mesothelioma is prognostic and shapes the tumour microenvironment. Nature communications, 12(1), 1751.

Grossmann S, et al. (2021) Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell stem cell, 28(7), 1262.

Fujii Y, et al. (2021) Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer cell, 39(6), 793.

Hurst CD, et al. (2021) Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. Cell reports. Medicine, 2(12), 100472.

Bolton KL, et al. (2020) Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature genetics, 52(11), 1219.

Noorani A, et al. (2020) Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. Nature genetics, 52(1), 74.