

Resource Summary Report

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[dNdScv](#)

RRID:SCR_023123

Type: Tool

Proper Citation

dNdScv (RRID:SCR_023123)

Resource Information

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

Proper Citation: dNdScv (RRID:SCR_023123)

Description: Software R package is group of maximum likelihood dN/dS methods designed 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-exome level. Used to detect cancer driver genes on datasets ranging from few samples to thousands of samples, in whole-exome/genome or targeted sequencing studies.

Synonyms: dN/dScv

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

Keywords: quantify dN/dS ratios, missense, nonsense, essential splice mutations, detect cancer driver genes on datasets, whole-exome/genome, targeted sequencing studies,

Availability: Free, Freely available, Available for download

Resource Name: dNdScv

Resource ID: SCR_023123

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260813T055259+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 [RRID](#) .

Skrupskelyte G, et al. (2026) The dynamics of mutational selection in cutaneous squamous carcinogenesis. *Communications biology*, 9(1), 127.

Nicola PA, et al. (2026) Polyclonal selection of immune checkpoint mutations in thyroid autoimmunity. *Nature*, 654(8117), 131.

Keddar MR, et al. (2026) Pan-cancer analysis in the real-world setting uncovers immunogenomic drivers of acquired resistance post-immunotherapy. *Journal for immunotherapy of cancer*, 14(5).

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. *Nature medicine*, 32(3), 964.

Olafsson S, et al. (2026) A meta-analysis identifies driver genes and characterizes the molecular epidemiology of colorectal cancer. *Scientific reports*, 16(1).

Skoufou-Papoutsaki N, et al. (2026) Clonal biases dictate availability of colonic cancer driver mutations for transformation. *Nature communications*, 17(1).

Huang AY, et al. (2026) Somatic cancer variants enriched in Alzheimer's disease microglia-like cells drive inflammatory and proliferative states. *Cell*, 189(12), 3719.

Kapadia CD, et al. (2025) Clonal dynamics and somatic evolution of haematopoiesis in mouse. *Nature*, 641(8063), 681.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. *Cancer discovery*, 15(4), 717.

Brzozowska N, et al. (2025) Selection for somatic escape variants in SERPINA1 in the liver of patients with alpha-1 antitrypsin deficiency. *Nature genetics*, 57(4), 875.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. *Neoplasia (New York, N.Y.)*, 66, 101180.

Neville MDC, et al. (2025) Sperm sequencing reveals extensive positive selection in the male germline. *Nature*, 647(8089), 421.

Fusco C, et al. (2025) CD4+FOXP3Exon2+ regulatory T cell frequency predicts breast cancer prognosis and survival. *Science advances*, 11(3), eadr7934.

Lawson ARJ, et al. (2025) Somatic mutation and selection at population scale. *Nature*, 647(8089), 411.

Moutin EB, et al. (2025) Paired mutation calling and spatial transcriptomics identify cellular neighbourhoods dictating the neoplastic outcome of colitis. *Research square*.

Kershenbaum S, et al. (2025) Variation in phenotype, genotype, and somatic diversity among asexual *Schmidtea mediterranea* planarians. *iScience*, 28(8), 113035.

Han DJ, et al. (2024) Evolutionary dependency of cancer mutations in gene pairs inferred by nonsynonymous-synonymous mutation ratios. *Genome medicine*, 16(1), 103.

Nunes L, et al. (2024) Prognostic genome and transcriptome signatures in colorectal cancers. *Nature*, 633(8028), 137.

Gourmet L, et al. (2024) Immune evasion impacts the landscape of driver genes during cancer evolution. *Genome biology*, 25(1), 168.

Kapadia CD, et al. (2024) Clonal dynamics and somatic evolution of haematopoiesis in mouse. *bioRxiv : the preprint server for biology*.