

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

ExPANdS

RRID:SCR_005199

Type: Tool

Proper Citation

ExPANdS (RRID:SCR_005199)

Resource Information

URL: <http://cran.r-project.org/web/packages/expands/>

Proper Citation: ExPANdS (RRID:SCR_005199)

Description: Software that characterizes coexisting subpopulations (SPs) in a tumor using copy number and allele frequencies derived from exome- or whole genome sequencing input data. The model amplifies the statistical power to detect coexisting genotypes, by fully exploiting run-specific tradeoffs between depth of coverage and breadth of coverage. ExPANdS predicts the number of clonal expansions, the size of the resulting SPs in the tumor bulk, the mutations specific to each SP and tumor purity. The main function runExPANdS provides the complete functionality needed to predict coexisting SPs from single nucleotide variations (SNVs) and associated copy numbers. The robustness of the subpopulation predictions by ExPANdS increases with the number of mutations provided. It is recommended that at least 200 mutations are used as an input to obtain stable results.

Abbreviations: ExPANdS

Synonyms: Expanding Ploidy and Allele Frequency on Nested Subpopulations

Resource Type: software resource

Defining Citation: [PMID:24177718](#)

Keywords: copy number, allele, frequency, exome, whole genome, sequencing, ploidy, subpopulation, genotype, mutation, single nucleotide variation

Related Condition: Tumor

Availability: GNU General Public License, v2

Resource Name: ExPANdS

Resource ID: SCR_005199

Alternate IDs: OMICS_00218

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195622+0000

Ratings and Alerts

No rating or validation information has been found for ExPANdS.

No alerts have been found for ExPANdS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 907 mentions in open access literature.

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

Schmidt H, et al. (2024) A regression based approach to phylogenetic reconstruction from multi-sample bulk DNA sequencing of tumors. PLoS computational biology, 20(12), e1012631.

Pithan L, et al. (2023) Closing the loop: autonomous experiments enabled by machine-learning-based online data analysis in synchrotron beamline environments. Journal of synchrotron radiation, 30(Pt 6), 1064.

Zhang W, et al. (2021) The bone microenvironment invigorates metastatic seeds for further dissemination. Cell, 184(9), 2471.

Bado IL, et al. (2021) The bone microenvironment increases phenotypic plasticity of ER+ breast cancer cells. Developmental cell, 56(8), 1100.

Yun JW, et al. (2019) Biomarkers Associated with Tumor Heterogeneity in Prostate Cancer. Translational oncology, 12(1), 43.

Oh BY, et al. (2019) Intratumor heterogeneity inferred from targeted deep sequencing as a prognostic indicator. Scientific reports, 9(1), 4542.

Little P, et al. (2019) Associating somatic mutations to clinical outcomes: a pan-cancer study of survival time. Genome medicine, 11(1), 37.

Morrissy AS, et al. (2017) Spatial heterogeneity in medulloblastoma. Nature genetics, 49(5), 780.

Sveen A, et al. (2017) Multilevel genomics of colorectal cancers with microsatellite instability-clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome

medicine, 9(1), 46.

Akiyama K, et al. (2014) Systematic fine-mapping of association with BMI and type 2 diabetes at the FTO locus by integrating results from multiple ethnic groups. PloS one, 9(6), e101329.

Whiteson KL, et al. (2014) Breath gas metabolites and bacterial metagenomes from cystic fibrosis airways indicate active pH neutral 2,3-butanedione fermentation. The ISME journal, 8(6), 1247.

Gass K, et al. (2014) Exploring the relationship between access to water, sanitation and hygiene and soil-transmitted helminth infection: a demonstration of two recursive partitioning tools. PLoS neglected tropical diseases, 8(6), e2945.

Vaumourin E, et al. (2014) To be or not to be associated: power study of four statistical modeling approaches to identify parasite associations in cross-sectional studies. Frontiers in cellular and infection microbiology, 4, 62.

Zuo F, et al. (2014) Exploring population pharmacokinetic modeling with resampling visualization. BioMed research international, 2014, 585687.

Gibbons SM, et al. (2014) Human and environmental impacts on river sediment microbial communities. PloS one, 9(5), e97435.

De Meulder B, et al. (2014) Meta-analysis and gene set analysis of archived microarrays suggest implication of the spliceosome in metastatic and hypoxic phenotypes. PloS one, 9(1), e86699.

Italiani P, et al. (2014) Transcriptomic profiling of the development of the inflammatory response in human monocytes in vitro. PloS one, 9(2), e87680.

Rylander C, et al. (2014) Consumption of lean fish reduces the risk of type 2 diabetes mellitus: a prospective population based cohort study of Norwegian women. PloS one, 9(2), e89845.

Dugas M, et al. (2014) Integrated data management for clinical studies: automatic transformation of data models with semantic annotations for principal investigators, data managers and statisticians. PloS one, 9(2), e90492.

Minamoto T, et al. (2014) Extrapunitive and intropunitive individuals activate different parts of the prefrontal cortex under an ego-blocking frustration. PloS one, 9(1), e86036.