

Resource Summary Report

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

ExPANdS

RRID:SCR_005199

Type: Tool

Proper Citation

ExPANdS (RRID:SCR_005199)

Resource Information

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

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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: 20260801T190257+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 [ASWG](#) .

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.

Khaenam P, et al. (2014) A transcriptomic reporter assay employing neutrophils to measure immunogenic activity of septic patients' plasma. *Journal of translational medicine*, 12, 65.

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

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.

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.

Leroux D, et al. (2014) Clusthaplo: a plug-in for MCQTL to enhance QTL detection using ancestral alleles in multi-cross design. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 127(4), 921.

Meysman P, et al. (2014) COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia. *Nucleic acids research*, 42(Database issue), D649.

Schmidtke J, et al. (2014) Second language experience modulates word retrieval effort in bilinguals: evidence from pupillometry. *Frontiers in psychology*, 5, 137.

Hammerling D, et al. (2014) Completing the results of the 2013 Boston marathon. *PloS one*, 9(4), e93800.

Wurzbacher C, et al. (2014) Importance of saprotrophic freshwater fungi for pollen degradation. *PloS one*, 9(4), e94643.

Frost HR, et al. (2014) Optimization of gene set annotations via entropy minimization over variable clusters (EMVC). *Bioinformatics (Oxford, England)*, 30(12), 1698.