Resource Summary Report

Generated by NIF on Apr 30, 2025

SLIDE

RRID:SCR_005137
Type: Tool

Proper Citation

SLIDE (RRID:SCR_005137)

Resource Information

URL: https://sites.google.com/site/jingyijli/SLIDE.zip

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Description: Software package that takes exon boundaries and RNA-Seq data as input to discern the set of mRNA isoforms that are most likely to present in an RNA-Seq sample. It is based on a linear model with a design matrix that models the sampling probability of RNA-Seq reads from different mRNA isoforms. To tackle the model unidentifiability issue, SLIDE uses a modified Lasso procedure for parameter estimation. Compared with deterministic isoform assembly algorithms (e.g., Cufflinks), SLIDE considers the stochastic aspects of RNA-Seq reads in exons from different isoforms and thus has increased power in detecting more novel isoforms. Another advantage of SLIDE is its flexibility of incorporating other transcriptomic data such as RACE, CAGE, and EST into its model to further increase isoform discovery accuracy. SLIDE can also work downstream of other RNA-Seq assembly algorithms to integrate newly discovered genes and exons. Besides isoform discovery, SLIDE sequentially uses the same linear model to estimate the abundance of discovered isoforms.

Abbreviations: SLIDE

Synonyms: sparse linear modeling of RNA-Seq data for isoform discovery and abundance estimation

Resource Type: software resource

Defining Citation: PMID:22135461

Funding: NIH ;
NHGRI HG004695;

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Resource Name: SLIDE

Resource ID: SCR_005137

Alternate IDs: OMICS_01291

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014244+0000

Ratings and Alerts

No rating or validation information has been found for SLIDE.

No alerts have been found for SLIDE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Alemayehu E, et al. (2025) Optimizing design and stability of open pit slopes in Tolay coal mine, Ethiopia. Scientific reports, 15(1), 1570.

Sui J, et al. (2024) Interpretable machine learning uncovers epithelial transcriptional rewiring and a role for Gelsolin in COPD. JCI insight, 9(21).

Mukhametzyanova L, et al. (2024) Activation of recombinases at specific DNA loci by zinc-finger domain insertions. Nature biotechnology.

Park HE, et al. (2023) Spatial Transcriptomics: Technical Aspects of Recent Developments and Their Applications in Neuroscience and Cancer Research. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(16), e2206939.

Lansing F, et al. (2022) Correction of a Factor VIII genomic inversion with designer-recombinases. Nature communications, 13(1), 422.

Sundström M, et al. (2021) "I'm Never Going to Be in Phantom of the Opera": Relational and Emotional Wellbeing of Parkinson's Carers and Their Partners in and Beyond Dancing.

Frontiers in psychology, 12, 636135.

Asif H, et al. (2021) GWAS significance thresholds for deep phenotyping studies can depend upon minor allele frequencies and sample size. Molecular psychiatry, 26(6), 2048.

Xie G, et al. (2021) Characterization of HIV-induced remodeling reveals differences in infection susceptibility of memory CD4+ T cell subsets in vivo. Cell reports, 35(4), 109038.

Mandil R, et al. (2020) In vitro and in vivo effects of flubendiamide and copper on cyto-genotoxicity, oxidative stress and spleen histology of rats and its modulation by resveratrol, catechin, curcumin and ?-tocopherol. BMC pharmacology & toxicology, 21(1), 29.

Ma T, et al. (2020) HIV efficiently infects T cells from the endometrium and remodels them to promote systemic viral spread. eLife, 9.

Li WV, et al. (2019) AIDE: annotation-assisted isoform discovery with high precision. Genome research, 29(12), 2056.

Hess AL, et al. (2018) Analysis of circulating angiopoietin-like protein 3 and genetic variants in lipid metabolism and liver health: the DiOGenes study. Genes & nutrition, 13, 7.

Canzar S, et al. (2016) CIDANE: comprehensive isoform discovery and abundance estimation. Genome biology, 17, 16.

Ye Y, et al. (2016) NMFP: a non-negative matrix factorization based preselection method to increase accuracy of identifying mRNA isoforms from RNA-seq data. BMC genomics, 17 Suppl 1(Suppl 1), 11.

Schehr JL, et al. (2016) High Specificity in Circulating Tumor Cell Identification Is Required for Accurate Evaluation of Programmed Death-Ligand 1. PloS one, 11(7), e0159397.

Sun Y, et al. (2015) Using the gravitational energy of water to generate power by separation of charge at interfaces. Chemical science, 6(6), 3347.

Angelini C, et al. (2014) Computational approaches for isoform detection and estimation: good and bad news. BMC bioinformatics, 15, 135.

Casavant BP, et al. (2014) Efficient sample preparation from complex biological samples using a sliding lid for immobilized droplet extractions. Analytical chemistry, 86(13), 6355.

Aydin ÖZ, et al. (2014) Human ISWI complexes are targeted by SMARCA5 ATPase and SLIDE domains to help resolve lesion-stalled transcription. Nucleic acids research, 42(13), 8473.

Bernard E, et al. (2014) Efficient RNA isoform identification and quantification from RNA-Seq data with network flows. Bioinformatics (Oxford, England), 30(17), 2447.