

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 31, 2026

iReckon

RRID:SCR_005232

Type: Tool

Proper Citation

iReckon (RRID:SCR_005232)

Resource Information

URL: <http://compbio.cs.toronto.edu/ireckon/>

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Description: An algorithm for the simultaneous isoform reconstruction and abundance estimation. In addition to modelling novel isoforms, multi-mapped reads and read duplicates, this method takes into account the possible presence of unspliced pre-mRNA and intron retention. iReckon only requires a set of transcription start and end sites, but can use known full isoforms to improve sensitivity. Starting from the set of nearly all possible isoforms, iReckon uses a regularized EM algorithm to determine those actually present in the sequenced sample, together with their abundances. iReckon is multi-threaded to increase efficiency in all its time consuming steps.

Abbreviations: iReckon

Resource Type: software resource

Defining Citation: [PMID:23204306](#)

Resource Name: iReckon

Resource ID: SCR_005232

Alternate IDs: OMICS_01277

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260725T190603+0000

Ratings and Alerts

No rating or validation information has been found for iReckon.

No alerts have been found for iReckon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Newman JRB, et al. (2018) Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. G3 (Bethesda, Md.), 8(9), 2923.

Hayer KE, et al. (2015) Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. Bioinformatics (Oxford, England), 31(24), 3938.

Merico D, et al. (2015) Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. Nature communications, 6, 8718.