Resource Summary Report

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Parseq

RRID:SCR_003464
Type: Tool

Proper Citation

Parseq (RRID:SCR_003464)

Resource Information

URL: http://www.lgm.upmc.fr/parseq/

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Description: Statistical software for transcription landscape reconstruction at a basepair resolution from RNA Seq read counts. It is based on a state-space model which describes, in terms of abrupt shifts and more progressive drifts, the transcription level dynamics along the genome. Alongside variations of transcription level, it incorporates a component of short-range variation to pull apart local artifacts causing correlated dispersion. Reconstruction of the transcription level relies on a conditional sequential Monte Carlo approach that is combined with parameter estimation in a Markov chain Monte Carlo algorithm known as particle Gibbs. The method allows to estimate the local transcription level, to call transcribed regions, and to identify the transcript borders.

Abbreviations: Parseq

Resource Type: software resource

Defining Citation: PMID:24470570

Keywords: rna-seq, genome, transcription, bio.tools

Funding:

Resource Name: Parseq

Resource ID: SCR_003464

Alternate IDs: biotools:parseq, OMICS_02302

Alternate URLs: https://bio.tools/parseq

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250410T065009+0000

Ratings and Alerts

No rating or validation information has been found for Parseq.

No alerts have been found for Parseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Palyanova NV, et al. (2023) The Development of the SARS-CoV-2 Epidemic in Different Regions of Siberia in the 2020-2022 Period. Viruses, 15(10).

Oliveira PH, et al. (2020) Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature microbiology, 5(1), 166.