eXpress

RRID:SCR_006873
Type: Tool

Proper Citation

eXpress (RRID:SCR_006873)

Resource Information

URL: http://bio.math.berkeley.edu/eXpress/index.html

Description: A streaming software tool for quantifying the abundances of a set of target sequences from sampled subsequences. Example applications include transcript-level RNA-Seq quantification, allele-specific/haplotype expression analysis (from RNA-Seq), transcription factor binding quantification in ChIP-Seq, and analysis of metagenomic data. It is based on an online-EM algorithm (doi:10.1111/j.1467-9868.2009.00698.x) that results in space (memory) requirements proportional to the total size of the target sequences and time requirements that are proportional to the number of sampled fragments. Thus, in applications such as RNA-Seq, eXpress can accurately quantify much larger samples than other currently available tools greatly reducing computing infrastructure requirements. eXpress can be used to build lightweight high-throughput sequencing processing pipelines when coupled with a streaming aligner (such as Bowtie), as output can be piped directly into eXpress, effectively eliminating the need to store read alignments in memory or on disk.

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Resource Type: Resource, software resource

Resource ID: SCR_006873

Parent Organization: University of California; Berkeley; USA

Funding Agency: NHGRI, NSF

Website Status: Last checked up
Ratings and Alerts

No rating or validation information has been found for eXpress.

No alerts have been found for eXpress.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 336 mentions in open access literature.

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


