Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 25, 2025

BinPacker

RRID:SCR_017038
Type: Tool

Proper Citation

BinPacker (RRID:SCR_017038)

Resource Information

URL: https://github.com/macmanes-lab/BinPacker/blob/master/README

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Description: Software tool as de novo trascriptome assembler for RNA-Seq data. Used to assemble full length transcripts by remodeling problem as tracking set of trajectories of items over splicing graph. Input RNA-Seq reads in fasta or fastq format, and ouput all assembled candidate transcripts in fasta format. Operating system Unix/Linux.

Resource Type: data analysis software, data processing software, software resource, software application

Defining Citation: PMID:26894997

Keywords: de novo, transcriptome, assembler, RNAseq, data, full, length, transcript, bio.tools

Funding: National Natural Science Foundation of China ;
NSF 1553680;
NCRR P20 RR01 6460;
NIGMS P20 GM103429

Availability: Free, Available for download, Freely available

Resource Name: BinPacker

Resource ID: SCR_017038

Alternate IDs: OMICS_11199, biotools:binpacker

Alternate URLs:
http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker_1.0.tar.gz/download,
http://sourceforge.net/projects/transcriptomeassembly/files/BinPacker_binary.tar.gz/download,
https://bio.tools/binpacker

License: GNU GPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250423T060941+0000

Ratings and Alerts

No rating or validation information has been found for BinPacker.

No alerts have been found for BinPacker.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Xie B, et al. (2022) Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. BMC biology, 20(1), 4.

Sharma A, et al. (2021) Transcriptome profiling reveal key hub genes in co-expression networks involved in Iridoid glycosides biosynthetic machinery in Picrorhiza kurroa. Genomics, 113(5), 3381.

Karmeinski D, et al. (2021) Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of the enigmatic genus Embletonia. BMC ecology and evolution, 21(1), 226.

Niu J, et al. (2020) Multi-omic approach provides insights into osmoregulation and osmoconformation of the crab Scylla paramamosain. Scientific reports, 10(1), 21771.

Kashyap A, et al. (2020) Pan-tissue transcriptome analysis of long noncoding RNAs in the American beaver Castor canadensis. BMC genomics, 21(1), 153.

Soorni A, et al. (2019) Transcriptome Landscape Variation in the Genus Thymus. Genes,

10(8).

Söllner JF, et al. (2019) Exploiting orthology and de novo transcriptome assembly to refine target sequence information. BMC medical genomics, 12(1), 69.

Bushmanova E, et al. (2019) rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 8(9).

Oliphant A, et al. (2018) Transcriptomic analysis of crustacean neuropeptide signaling during the moult cycle in the green shore crab, Carcinus maenas. BMC genomics, 19(1), 711.

Jarett JK, et al. (2017) Comparative Genomics of Color Morphs In the Coral Montastraea cavernosa. Scientific reports, 7(1), 16039.