Jun 29, 2021

A bioinformatics pipeline for processing and analysis of whole transcriptome sequence data

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dx.doi.org/10.17504/protocols.io.brz8m79w

Systems Genomics

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ABSTRACT

Recent advances in next generation sequencing (NGS) technologies have paved the way for augmented genomic research. From the conventional microarray analysis to the current NGS-based whole transcriptome pipelines, there have been significant advances on how differentially expressed genes (DEGs) are identified. With several bioinformatics pipelines in use, inferring the candidate DEGs prove to be a cumbersome approach as one may have to reach consensus in analysing the results from various pipelines. To ensure this, we have benchmarked the well-known Cufflinks-Cuffdiff pipeline on a set of datasets and present it in the form of a protocol for the research community interested in performing downstream analysis of whole transcriptome shotgun sequencing.
Keywords: RNA-Seq, Transcriptome analysis, bioinformatics pipeline, differentially expressed genes

ATTACHMENTS

RNA-seq Pipeline.pdf

DOI

dx.doi.org/10.17504/protocols.io.brz8m79w

PROTOCOL CITATION

Ayam Gupta, Shalin Rajagopal, Sonal Gupta, Ashwani Kumar Mishra, Prashanth Suravajhala 2021. A bioinformatics pipeline for processing and analysis of whole transcriptome sequence data. **protocols.io** https://dx.doi.org/10.17504/protocols.io.brz8m79w

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CREATED

Feb 02, 2021

Citation: Ayam Gupta, Shalin Rajagopal, Sonal Gupta, Ashwani Kumar Mishra, Prashanth Suravajhala (06/29/2021). A bioinformatics pipeline for processing and analysis of whole transcriptome sequence data. https://dx.doi.org/10.17504/protocols.io.brz8m79w

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LAST MODIFIED

Jun 29, 2021

PROTOCOL INTEGER ID

46880

Citation: Ayam Gupta, Shalin Rajagopal, Sonal Gupta, Ashwani Kumar Mishra, Prashanth Suravajhala (06/29/2021). A bioinformatics pipeline for processing and analysis of whole transcriptome sequence data. https://dx.doi.org/10.17504/protocols.io.brz8m79w

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