

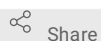


Jun 29, 2021

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

Ayam Gupta¹, Shalin Rajagopal¹, Sonal Gupta¹, Ashwani Kumar Mishra², Prashanth Suravajhala¹¹Birla Institute of Scientific Research, Jaipur; ²DNA Xperts, Noida

1 Works for me



Share

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

Systems Genomics

Prashanth Suravajhala

Birla Institute of Scientific Research, Jaipur

DISCLAIMER

DISCLAIMER – FOR INFORMATIONAL PURPOSES ONLY; USE AT YOUR OWN RISK

The protocol content here is for informational purposes only and does not constitute legal, medical, clinical, or safety advice, or otherwise; content added to protocols.io is not peer reviewed and may not have undergone a formal approval of any kind. Information presented in this protocol should not substitute for independent professional judgment, advice, diagnosis, or treatment. Any action you take or refrain from taking using or relying upon the information presented here is strictly at your own risk. You agree that neither the Company nor any of the authors, contributors, administrators, or anyone else associated with protocols.io, can be held responsible for your use of the information contained in or linked to this protocol or any of our Sites/Apps and Services.

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>

LICENSE

— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Feb 02, 2021

LAST MODIFIED

Jun 29, 2021

PROTOCOL INTEGER ID

46880