Impact of Biological Factos on Product Effectiveness Colgate-Palmolive

Clean Data

October 16, 2022

Intro Title

testing

Problem Statement

ntro Problem **Literature** Components Solutions Results Reference

Literature

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BIOINFORMATICS

Power analysis and sample size estimation for RNA-Seq differential expression

TRAVERS CHING, ^{1,2} SIJIA HUANG, ^{1,2} and LANA X, GARAIRE^{6,2}

Unbersily of Honest Concer Center, Honelda, Honest 96113, USA

Translated and Advanced Context Concerns 1987 (1988).

ARSTRACT

It is crucial for researchers to cotinize BNA-sex experimental designs for differential expression detection. Currently, the field

Keywords: RNA-Seq: sample size; power analysis; simulation; bioinformatics

Figure 1: Ching, Travers, et al. "Power Analysis and Sample Size Estimation for RNA-Seq Differential Expression." RNA, vol. 20, no. 11, 2014, pp. 1684–1696., https://doi.org/10.1261/rna.046011.114.

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Literature 2

Published online 16 July 2015

Nucleic Actds Reneurch, 2015, Vol. 43, No. 21 4146

Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package

Sonia Tarazona¹-², Pedro Furió-Tarí¹, David Turrà³, Antonio Di Pietro³, María José Nueda⁴, Alberto Ferrer³ and Ana Conesa¹-5.º

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ABSTRACT

As the use of PIRIA-seq-bas projunited, there is an inreseming consciousness of the importance of lexperimental design, bias removals, locurative quartification and control of last positives for project data enalyciative and project of the control of the control of the control and analysis of count data. We show have the available dispositio tools can be used to montion quality issues, make pre-processing decisions parametric NOIGIGOD effectivity control sales discoversis in experiments with Ecological repirations parametric NOIGIGO effectivity control sales discoversis in experiments with Ecological repirations of comparisons state-of-the-ort estimation. NOIGIG is for robust distal-exame analysis of RNA-seq differential expression.

Received April 21, 2015; Rayland June 12, 2015; Accepted July 51, 2015

Due of the most subsequent approximate of RNAsseq, so the transpop quantitions in the differential pair or in terminal pair or in the transpop quantities and the differential pair or in the second pair of the second pair o

Figure 2: Tarazona, Sonia, et al. "Data Quality Aware Analysis of Differential Expression in RNA-Seq with Noiseq R/Bioc Package." Nucleic Acids Research, 2015, https://doi.org/10.1093/nar/gky711.

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Literature 3



Figure 3: Tarazona, Sonia, et al. "Data Quality Aware Analysis of Differential Expression in RNA-Seq with Noiseq R/Bioc Package." Nucleic Acids Research, 2015, https://doi.org/10.1093/nar/gkv711.

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Components

Solutions

Deliverables

Future Plans

Preliminary Results

Conclusion

About References

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- ► There are 1400+ citation style files available: https://github.com/citation-style-language/styles
- ▶ {.allowframebreaks} can be useful if there are many citations

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