



genomics paper

-A Streamlined Approach to Pathway Analysis from RNA-Sequencing Data

-Task one / Abstract and Introduction Discussion

-Abstract

- The main concern with performing RNA-sequencing has drifted from being about budget and cost to the time obliged to process the data. This tremendous scale of raw data produced can be a great challenge to researches to gain vital knowledge about samples. While most companies submit basic reports about samples however, some sample comparisons might not be sufficiently identified. Utilizing different enrichment and mapping software platforms to highlight particular relations will lead us to evaluate these data within a wide range. The methodologies defined above intend to allow researches to handle RNA-sequencing via a more simple way to pathway analysis. The results will give valuable insights to generate samples.

-Introduction

- As current RNA-seq is increasingly available and low in cost, the limiting factors used in this evaluation tool have moved from budgetary to processing time. And it's due to the amount of data amplified by the comparison of a single experiment sample. Therefore the difficulty is how to choose the data containing significant details on the presented samples. Several RNA-seq organizations submit a primal evaluation of the data performance based on specific databases. For example, Novogene's services provide a detailed report that identifies pathways of interest (PoIs) based on pathway enrichment using KEGG database pathways and possible gene ontology (GO) ties. It might not cover all Pols. This is why these studies act as a basis for future assessments. This allows the correct tuning and generation of graphs and tables which best illustrated major comparative characteristics of the pathways and systems in question. Data processing flow detailed in this paper is based on Novogene data. The Protocol works for the differentially expressed genes on standardized datasets. This does not apply to gene discovery studies in non-model organisms. In the context of a particular collection of research questions, the main feature of this processing plan is to identify explicitly the scope of path searches and to confine information mining to these parameters. This is important because the creation of findings that illustrate the connection between samples due to selection distortion and the picking of obscure pathways, strengthening preconceived assumptions, is the common issue when assessing large data pools.

