

NGS TREX: next generation sequences transcriptome profile explorer

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Motivations

Next-generation sequencing (NGS) technology has exceptionally increased the ability to sequence DNA in a massively parallel and cost-effective manner. Nevertheless, the management and the analysis of NGS data requires significant expertise in bioinformatics and hardware infrastructure still beyond the possibilities of many laboratories focused on "wet biology". Moreover some projects only need few deep sequencing cycles and standard tools or workflows to carry out suitable analyses for the identification and annotation of genes, transcripts and splice variants found in the biological samples under investigation. The development of easy to use systems to automatically analyze and annotate NGS data is needed to allow researchers from different backgrounds to take full benefit of NGS technologies.

Results

We developed an automatic system targeted to the analysis of Next Generation Sequencing

data obtained from large-scale transcriptome studies. This system, we named NGS-Trex (NGS TRanscriptome profile Explorer) is available through a simple web interface and allows the user to upload raw sequences and easily obtain an accurate characterization of the transcriptome profile after the setting of few parameters required to tune the analysis procedure. The system is also able to assess differential expression at both gene and transcript level (i.e. splicing isoforms) by comparing the expression profile of different samples. By using simple query forms the user can obtain list of genes, transcripts, splice sites ranked and filtered according several criteria. Data can be viewed as tables and downloaded as text files to allow further analysis. Moreover a simple genome browser helps the visual inspection.

Availability

<http://www.ngs-trex.org/>