BITS :: Call for Abstracts 2022 - Oral communication

Type	Oral communication
Session	Algorithms for Bioinformatics
Title	3’-Tag RNA-sequencing
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Motivation

3’Tag-Seq is an approach to produce gene expression profiling data for small budgets. The main difference to traditional RNA-seq is that 3’Tag-seq produces one read per transcript and is not resequencing the whole mRNA. This procedure allows the user to request up to 10 times less reads for the same transcriptome analysis and therefore is confronted to a close to 10 times cheaper sequencing costs. 3’Tag-seq provides high quality expression data but lacks the additional information of alternative splicing events provided by the regular RNA-seq. Since most of the transcriptome analysis is focused on expression data and differential expression analysis, 3’Tag-seq is for these cases the approach of choice.

Methods

In our work we describe an algorithm to analyse such 3’Tag-seq data, evidence the problem of false positive counts due to expressed regions with poly T regions which could mimic in the mature RNA polyA tails. Further we highlighted that 3’Tag-seq can give information of the position of 3’UTR regions.

Results

In a test case of the expression analysis of cassava (Manihot esculenta) under our experimental conditions, we find read hits in only 10996 of the 26351 annotated 3’UTR (note that additional 15031 genes do not have a 3’UTR annotation), However, most of these genes contain read hits in the downstream regions up to 1500nt after the gene end. This technology not only give precise expression information but also data for alternative gene annotation in the region of the 3’UTR and differential polyA tail attachment.

Info

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filename	-

Figure

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Availability	non

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