samExploreR package: high-performance read summarisation with sequencing depth reduction simulation

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1 Introduction

In this vignette we introduce the samExploreR package.

The samExploreR package allows to perform a summarisation of NGS experiment reads for given annotation with simulation of reduced sequencing depth. During the summarisation process a fraction of reads is removed to simulate an NGS experiment with smaller library size.

2 Depth simulation

Function `samExplore` performs reads summarisation similar to `featureCounts` function from Rsubread package.

To simulate a sequencing depth, for given f that may be variated from 0 to 1 during the summarisation process a read is counted or not with probability f. This process is repeated N times.

`samExplore` takes an input list if SAM or BAM files containing mapped reads, annotation file with genomic features such as genes and exons to assign to and several perfomance parameters: some of them are the ones that are passed to `featureCounts` function and in addition fraction of reads to remove f and number of repeats N

3 Citation

4 Authors

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