

Simulating RNA-Seq in different Individuals

Hi Micha,

I am working on discovering isoforms and estimating isoform-specific expression from RNA-seq data. Therefore I would like to get reads for a single gene, and several individuals sharing a given number of isoforms. So I was wondering if flux-simulator could that and how to achieve it.

My first intuition was to provide a shortened input reference sequence to simulate from (basically the gene sequence in fasta format and the shortened corresponding GFF file). However, it doesn't solve the issue of simulating for several individuals with distinct isoform proportions.

My second thought was to simulate for each individual separately and to directly provide a LIB file, but I'm not sure how to simulate a good library and it would be redundant with what flux simulator is already doing.

Do you have any insight on this?

Thanks