

# Exact number of individual AS events

Dear all,

I am using FluxSimulator to create an artificial dataset in order to benchmark several RNA-Seq Isoform detection and quantification tools. Until now I have successfully ran FluxSimulator with a single fasta file (Human hg18 22nd chromosome) and GTF (hg18) using all -s, -x and -l parameters. I have no error code, everything seems running fine and output files seems correct. Unfortunately I am experiencing some issues finding the exact number of individual alternative splicing events. I might not be clear, by "individual alternative splicing events", I mean the exact number of Skip Exon, then the exact one of Intron Retention, the same information for alternative 5' splicing site, alternative 3' splicing site, Alternative first exon, alternative last exon, and eventually UTR information. Is it possible to find those particular informations ?

I just red the ".PAR Simulation Parameters" section of this web site and could not find any answer.

Many thanks in advance for your answers,

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