4.1.2 - Transcript Modifications

Parameters

Name	Default Value	Parameter Range	Description
TSS_MEAN	25	>0	rate of the exponential for deviation of simulated transcription starts from annotated transcription start point, set to NaN (i.e., "not a number") to deactivate simulated transcription start variability
POLYA_SCALE	300	>0	scale parameter of the Weibull distribution describing poly-A tail lengths, set to NaN (i.e., "not a number") to deactivate simulated poly-A tails
POLYA_SHAPE	2	>0	shape paramter of the Weibull distribution describing poly-A tail lengths, set to NaN (i.e., "not a number") to deactivate simulated poly-A tails

Algorithm

Input: Columnn 6 of the PRO_FILE, i.e., the absolute number of RNA molecules that is simulated for a certain transcript in the experiment and the parameters of transcription start (TSS_MEAN) and poly-A tail variation (POLYA_SCALE, POLYA_SHAPE).
Based on the number of RNA copies that is simulated for each transcript, genes are *in silico* expressed. In this process, assigned individual variations in transcription start and the length of the attached poly-A tail. The Flux Simulator models differences in the annotated transcription starts by an exponential distribution with an adjustable mean value (TSS_MEAN). During poly-adenylation in the nucleus usually 200-250 adenine residues get added to the primary transcript. Disregarding other poly-adenylation mechanisms (e.g., cytoplasmatic polyadenylation) the Flux Simulator describes poly-A lengths by a flexible Weibull distribution (POLYA_SCALE, POLYA_SHAPE).
Output: One line per simulated transcript molecule containing in the LIB_FILE.