

## 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 parameter 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:** Column 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.