

4.1.1 - Gene Expression Profile

Parameters

Parameter Name	Variable	Default Value	Parameter Range	Description
NB_MOLECULES		5,000,000	>0	number of expressed RNA molecules simulated
EXPRESSION_K		-0.6		exponent of the expression power law ("Pareto coefficient")
EXPRESSION_X0		9,500		parameter of the exponential decay
EXPRESSION_X1		9,500 ²		parameter of the exponential decay

Algorithm

Input: reference annotation (REF_FILE), transcript filtering parameter (LOAD_CODING, LOAD_NONCODING), expression parameters (NB_MOLECULES, EXPRESSION_K, EXPRESSION_X0, EXPRESSION_X1)

In the beginning, the Flux Simulator reads the transcripts of the reference annotation (REF_FILE) and clusters genomic overlapping ones into loci. Transcripts that are annotated as non-/coding can be selectively disregarded (LOAD_CODING, LOAD_NONCODING). Then to assign a random expression profile where not necessarily all transcripts of the reference are expressed. Expression levels are connected with the relative expression rank b by a mixed power- and exponential law of the general form

where b denotes the rank number of a gene, is the exponent of the intrinsic power law, and respectively control the exponential decay. The Flux Simulator assigns to the transcripts in the reference annotation randomly expression ranks which then are turned into relative expression levels by the modified Zipf's Law above, which determines the initial number of molecules by multiplication with the total numbers of molecules. Default values for parameters and have been estimated for mammalian cells by non-linear fitting to expression levels observed in experimental results.

Output: Columnn 1-6 of the PRO_FILE, i.e., (1) locus name, (2) transcript identifier, (3) coding flag, (4) length of the processed transcript, (5) relative fraction and (6) absolute number of the transcript species in the initial RNA extraction.

