# 4.1.1 - Gene Expression Profile

## Parameters

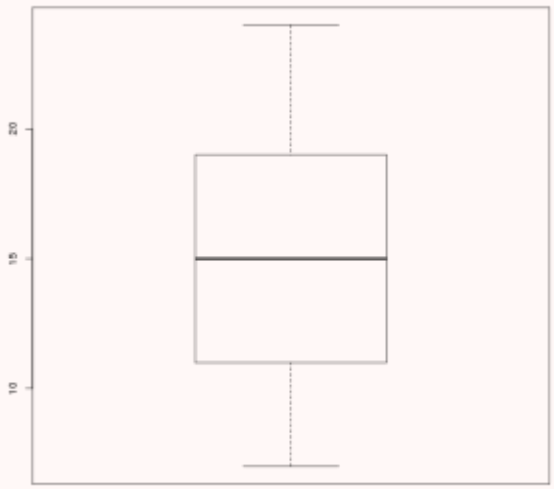
| Parameter Name | Variable | Default Value | Parameter Range | Description |
|---|---|---|---|---|
| NB_MOLECULES | | 5,000,000 | >0 | number of expressed RNA molecules simulated |
| EXPRESSION_K | Unknown macro: 'mathinline' | -0.6 | Unknown macro: 'mathinline' | exponent of the expression power law ("Pareto coefficient") |
| EXPRESSION_X0 | Unknown macro: 'mathinline' | 9,500 | Unknown macro: 'mathinline' | parameter of the exponential decay |
| EXPRESSION_X1 | Unknown macro: 'mathinline' | $9{,}500^2$ | Unknown macro: 'mathinline' | 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 Unknown macro: 'mathinline' are connected with the relative expression rank Unknown macro: 'mathinline' by a mixed power- and exponential law of the general form

Unknown macro: 'mathblock'

where Unknown macro: 'mathinline' denotes the rank number of a gene, Unknown macro: 'mathinline' is the exponent of the intrinsic power law, and Unknown macro: 'mathinline' Unknown macro: 'mathinline' respectively control the exponential decay. The Flux Simulator assigns to the transcripts in the reference annotation randomly expression ranks Unknown macro: 'mathinline' 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 Unknown macro: 'mathinline' and Unknown macro: 'mathinline' 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.




Although the Simulator program currently allows to set parameter EXPRESSION_K to a value of "0", please note that such settings remove the power-law distribution we ususally observe in cellular transcriptomes. Below a boxplot representation of the distribution of the simulated number of molecules for *all* transcripts in a reference annotation when EXPRESSION_K is set to "0", the distribution exhibits a mean of ~15 and a standard deviation of ~5.