

Table 1. The translational parameters calculated in the model.

par	mean	median	sd	min	max	description
L	513.3	430.5	365.2	37	4911	Length of the transcript CDS in codons.
x	7.8	2.7	28.9	0.140	591.3	Absolute number of transcripts in a yeast cell.
B	1.0e+4	677	7.7e+4	0.650	2.4e+6	Total amount of protein molecules produced from transcripts of a particular type.
g	1.1	0.8	0.9	0.003	6.6	Ribosome density in number of ribosomes attached to a transcript per 100 codons.
w	5.6	3.1	7.3	0.010	142	The absolute number of ribosomes on a transcript.
P	5.3e-5	3.6e-5	5.4e-5	1.5e-7	6.2e-4	The translation initiation frequency (the inverse of I).
Pz	2.2e-4	7.6e-5	8.0e-4	3.8e-6	1.6e-2	The relative rate of binding of free ribosomes to the 5' end of a transcript.
Ps	1.6e-2	6.4e-3	2.9e-2	5.2e-6	4.3e-1	The relative rate of a successful accomplishment of initiation once the ribosome-mRNA complex is formed, normalised by the maximal observed value of Ps, reported for gene YLL040C.
T	2:50	2:20	3:23	0:06	113:08	Total time of translation of one protein molecule from a given transcript (min:sec).
I	0:54	0:28	3:06	0:02	111:54	Total time required for translation initiation (min:sec).
E	1:56	1:36	1:24	0:04	17:54	Total time required for translation elongation of a transcript (min:sec).
mean_E	0.224	0.229	0.031	0.098	0.360	Mean time required for elongation of one codon of a transcript (sec).
h	2:45:51	1:31:44	3:59:18	0:00:19	42:27:31	Estimated half-life of a transcript (h:min:sec).
m	3:59:16	2:12:20	5:45:13	0:00:27	61:15:18	Estimated mean life-time of a transcript (h:min:sec).

Column descriptions: (1) name of the parameter; (2) mean value; (3) median value; (4) standard deviation; (5) minimal observed value; (6) maximal observed value; and (7) parameter description. For all parameters, except *B*, *h*, and *m*, the columns 2, 3, 4, 5, and 6 were calculated over the entire dataset of 4,470 yeast genes. For parameters *B*, *h*, and *m* the columns 2, 3, 4, 5, and 6 were calculated over the set of 4,192 genes.

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The following translational parameters were attributed to the yeast genes (for derivation, see the Materials and Methods): *L*, length of the transcript coding sequence (CDS) in codons; *x*, absolute number of transcripts in a yeast cell; *B*, total amount of protein molecules produced from transcripts of particular type; *g*, ribosome density in number of ribosomes attached to a transcript per 100 codons; *w*, the absolute number of ribosomes on a transcript; *T*, total time of translation of one protein molecule from a given transcript; *I*, total time required for translation initiation; *E*, total time required for translation elongation; *mean E*, mean time required for elongation of one codon of a transcript; *P*, translation initiation frequency; *Pz*, relative rate of binding of free ribosomes to the 5' end of a transcript, proportional to the concentration of the transcript; *Ps*, relative rate of successful accomplishments of initiation once the ribosome-mRNA complex is formed (the obtained values of the parameter *Ps* ranged from 3.4e-4 to 65.9. For clarity, we decided to normalise them by the maximal reported value of *Ps* obtained for the gene YLL040C. The normalised values of *Ps* range from 0 to 1 and allow more intuitive comparison); *h*, estimated half-life of a transcript; and *m*, estimated mean lifetime of a transcript. Parameters *T*, *I*, *E*, *mean E*, *h*, and *m* are given in SI units.