

A. Comparison of translation profile at maximum tRNA and standard parameters.

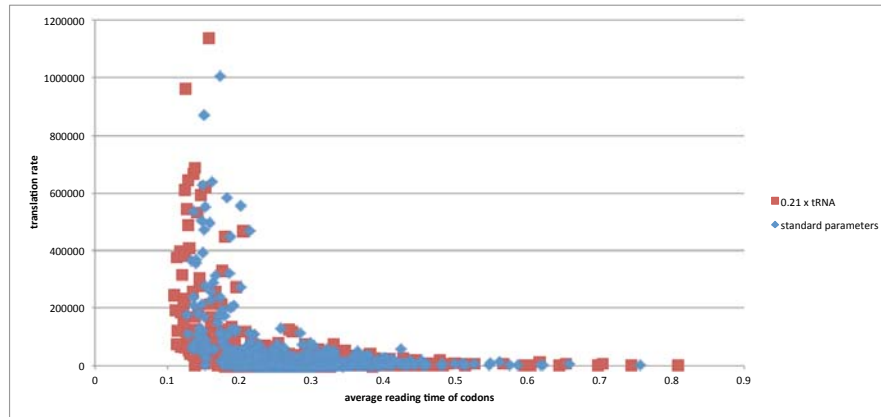


Figure 1: Every point represents a particular pair of (reading time,abundance) of a particular ORF. The horizontal axis represents the average reading time and the vertical axis the number of translation rounds in 1500s. At 0.21 tRNA ORFs are translated faster.

B. Key parameters used in the simulations:

Description	Parameter name	standard value
# a number which if set to a certain value ensures that each simulation will generate the same mRNA sequences. To change the sequences use a different number. To get a different value each time set this to 0	RANDOM_MRNA_SEED	0;
#the average length of IBS in nucleotides	IBS_LENGTH_AVG	54;
#the number of nucleotides per second at which the ribosome scans for the AUG site berthelot_2004	IBS_SCANNING_RATE	1000;
#number of ribosomes in the cell	NO_OF_RIBOSOMES	200000;
#this is true if the ribosome can unbind from the initial binding site if the AUG site is busy and false otherwise	UNBINDS_FROM_IBS_IF_BUSY	true;
#this is true if the ribosome can unbind from the termination site if the AUG site is busy and false otherwise	UNBINDS_FROM_TERMINATION_IF_BUSY	true;
# this is true if the ribosome can unbind from the current codon if the next one is busy and false otherwise	UNBINDS_FROM_CODON_IF_BUSY	false;
# the number of collisions before the ribosome unbinds. if <	COLLISIONS_BEFORE_UNBIND	0 then it never unbinds due to collisions. If 1 it unbinds from the first co
#waiting time for cognates	NON_COGNATE_WAIT_TIME	0.020655089315851884;
#waiting time for near cognates	NEAR_COGNATE_WAIT_TIME	0.03916395153681901;
#the tRNA binding rate(sec^-1)	TRNA_BINDING_RATE	140;
#the tRNA avg charge rate (sec^-1)	TRNA_CHARGE_RATE	47;
#the number of codons that the ribosome keeps occupied before the A site	NO_OF_RIBOSOME_SITES_BEFORE	6;
#the number of codons that the ribosome keeps occupied after the A site	NO_OF_RIBOSOME_SITES_AFTER	5;
#the total number of codons that the ribosome keeps occupied	NO_OF_RIBOSOME_SITES_TOTAL	12;
#the maximum number of translation per ribosome per mRNA	NO_OF_TRANSLATION_PER_RIBOSOME_MRNA_MAX	9;
#the minimum number of translation per ribosome per mRNA	NO_OF_TRANSLATION_PER_RIBOSOME_MRNA_MIN	1;
#the probability that a bound cognate tRNA will elongate fluitt_2007	ELONGATION_COGNATE_PROBABILITY	0.6515296869245238;
#the probability that a bound near-cognate will elongate fluitt_2007	ELONGATION_NEARCOGNATE_PROBABILITY	0.005494934334901434;
#the probability that a bound cognate will exit from codon recognition	ELONGATION_COGNATE_PROBABILITY_EXIT_RECOGNITION	0.31;
#the probability that a bound near-cognate will exit from codon recognition	ELONGATION_NEARCOGNATE_PROBABILITY_EXIT_RECOGNITION	0.989;
#the rate at which a cognate tRNA will elongate	ELONGATION_COGNATE_RATE	38.412041453105836;
#the rate at which a near-cognate tRNA will elongate	ELONGATION_NEARCOGNATE_RATE	25.547338887589383;
#the translocation rate If set to a negative number, it is infinite, except when stuck behind sbd.	ELONGATION_TRANSLOCATION_RATE	-58;
#probability that a non-cognate will elongate	ELONGATION_NONCOGNATE_PROBABILITY	0.0;

C. Ribosome capacity

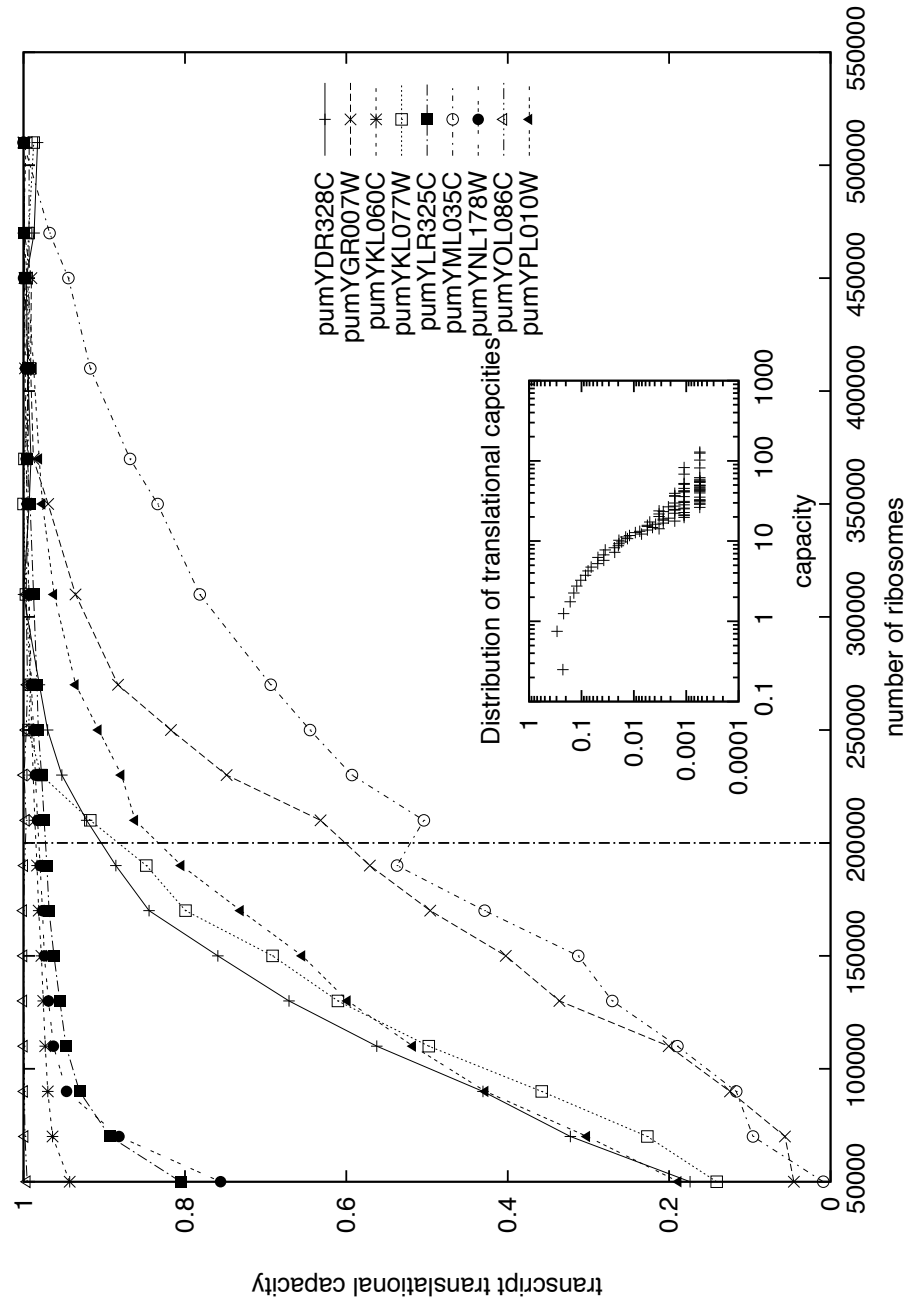


Figure 2: The relative translational capacity some highly expressed ORFs. For better readability we normalised each ORF by the maximum capacity in the plot. The dashed line indicates the standard parameters. The inset shows the distribution of capacities at standard parameters over all ORFs.

D. Changing Parameters

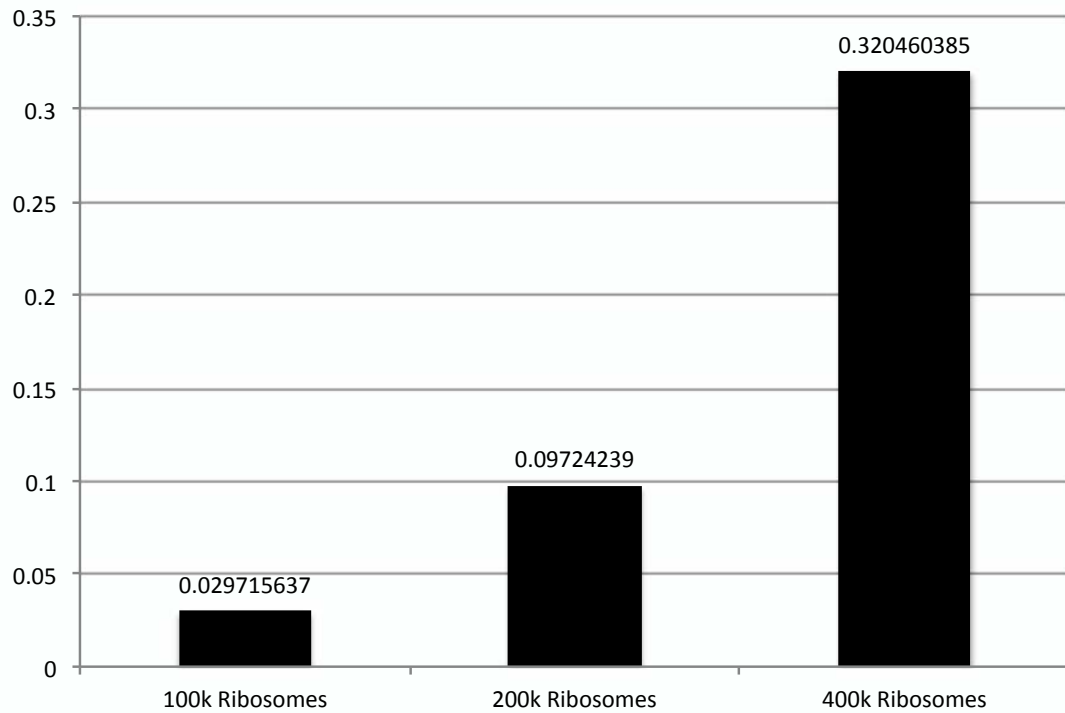


Figure 3: Comparing the average time to read an individual codon for different amounts of ribosomes. Note that the average is disproportionately impacted by very few highly expressed ORFs. The typical slowdown due to traffic jams is much smaller than the average one.

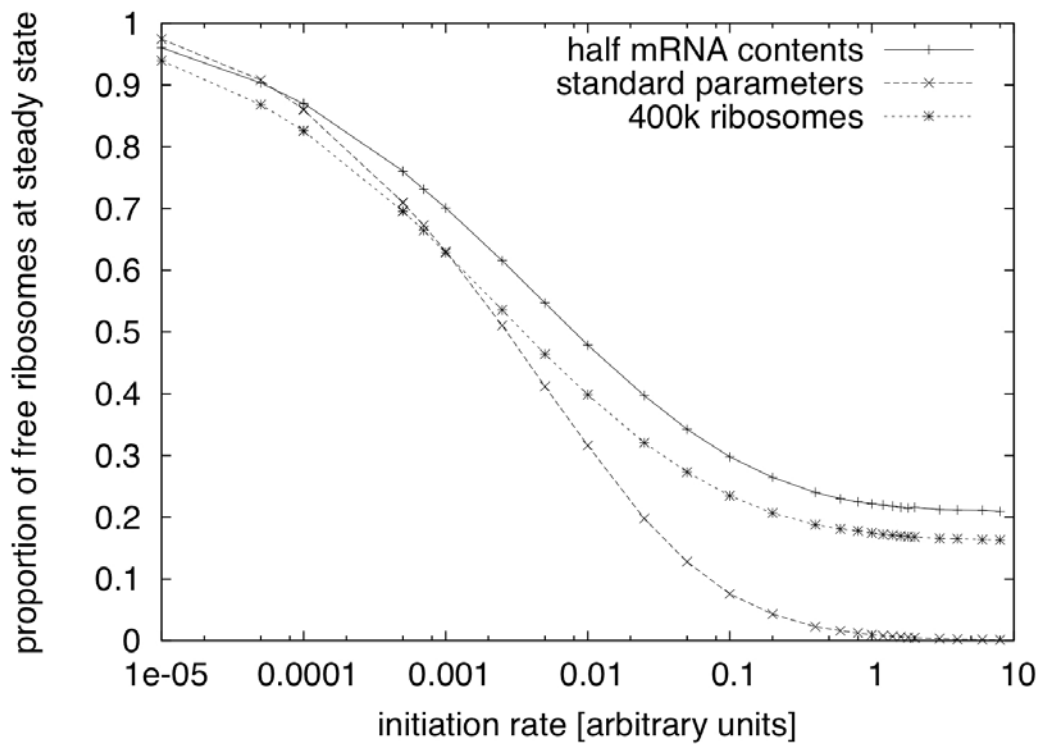


Figure 4: Fraction of free ribosomes. We compare the standard parameters with a halved number of mRNA. The line labelled "standard parameters" and "400k ribosomes" are the same as in figure \ref{initvar2}. Halving the mRNA leads to ribosomes saturating the RBS.

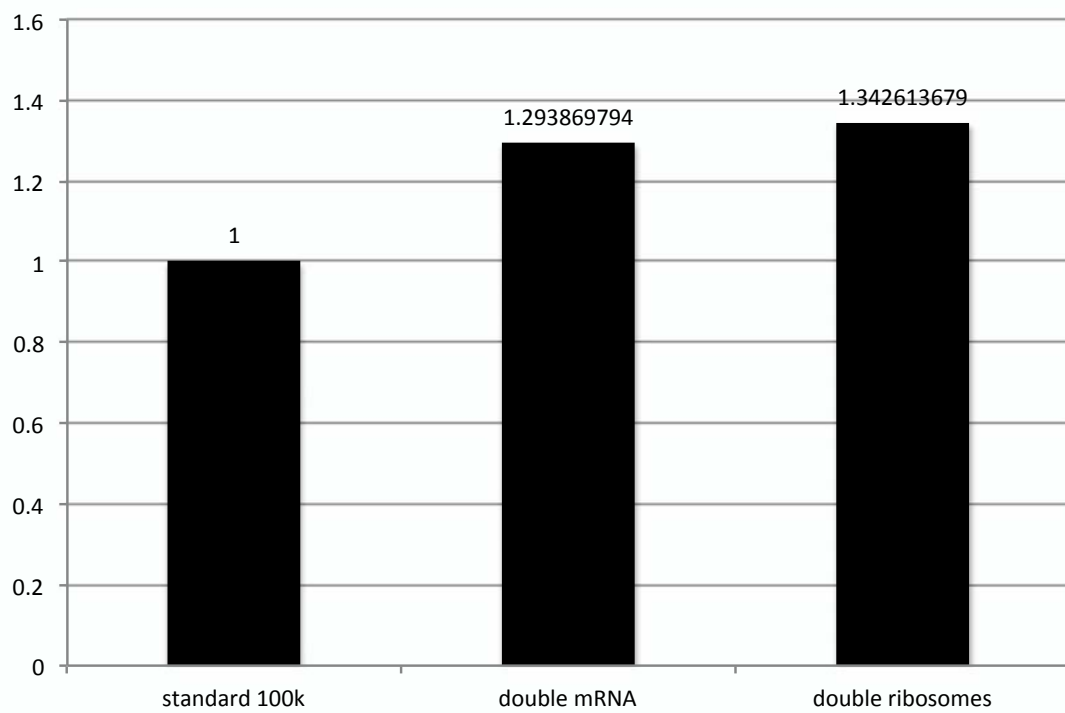


Figure 5: Bar chart showing the consequences of doubling the number of ribosomes/mRNA at standard parameters w/ 100000 ribosomes. The charts show the normalised translation rate.

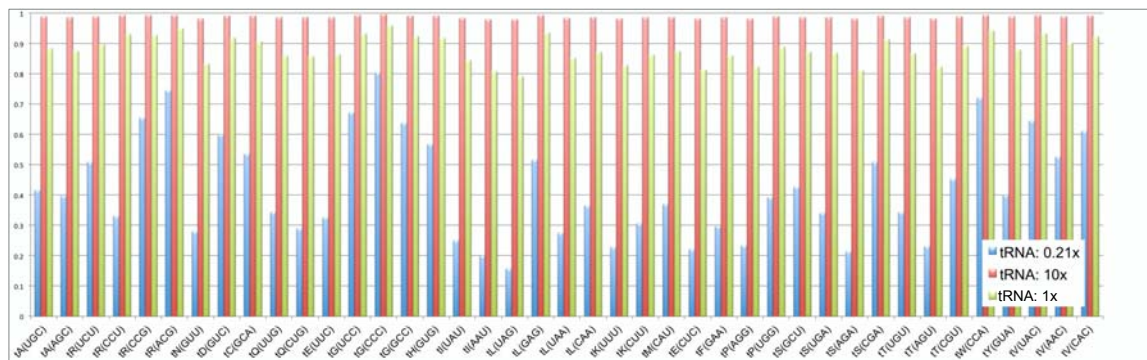


Figure 6: Availability of charged tRNA. The bar chart shows the fraction of aminoacylated and free tRNA for each species for standard parameters (1x tRNA), standard parameters with 10 times the amount of tRNA and at the translation rate maximum with 0.21 times the standard tRNA amounts.