## Introduction

The number of ribosomes depends on the growth velocity of the cells and it oscillates between 5,000 and 50,000 copies per cell (Raisman, 2013). Looking at the Chain Elongation, chains are likely to be single-RNA molecules in RNA transcription. The observed elongation rate is not uniform, with a peak rate of ≈40 nm/sec as well as a period of apparent transcriptional halting that lasts ≈10 sec. The average rate of ≈15 nm/sec.(Golding, I & Cox, E.; 2004). The rate of reproduction of E. coli in optimum conditions is seen in the tables below taken from Marr A.G (1991). In the graph we can see that E. coli`s growth is exponential and ideal at 37°C

Description	Symbol	Value, source, or unit
Parameters		
Concentration of *rrn* genes	$[rrn]$	0.025 μM
Maximum rate of *rrn* transcription	k_{rrn}	1.5 s^{-1}
Dissociation constant for ppGpp	K_g	40 μM
Cooperativity of ppGpp binding	h	2
Molar ratio of tRNA to rRNA	C_{tRNA}	0.25
Maximum rate of ppGpp formation	k_1	1 s^{-1}
First-order rate constant for ppGpp breakdown	k_2	0.035 s^{-1}
Dissociation constant for aminoacyl-tRNA	K_C	2.75 μM
Dissociation constant for uncharged tRNA	K_U	10 μM
Maximum rate of peptide synthesis	k_P	21 s^{-1}
Variables		
Protein expressed as amino acid	P	Eqn 10
Actual rate of peptide synthesis	r_P	Eqn 4
Specific growth rate	k	
Ribosomes	R	μM
Aminoacyl-tRNA	C	μM
Uncharged tRNA	U	μM
Guanosine tetraphosphate	G	μM
Amino acid	A	μM
Ratio of ribosomal to total protein	α_r	

TABLE 2. Computation of variables for steady states of growth[a]

k	R	C	U	G	A	r_P	α_r
0.1	29	0.6	6.5	283	1.4	2.5	0.08
0.2	27	1.4	5.4	203	3.3	5.3	0.08
0.3	28	2.3	4.7	162	5.2	7.6	0.08
0.5	31	4.2	3.7	115	8.8	11.0	0.09
0.7	36	6.0	3.0	88	11.9	13.2	0.11
0.9	41	7.7	2.4	69	14.7	14.5	0.13
1.1	45	9.3	2.0	56	17.4	15.5	0.15
1.3	49	10.7	1.6	45	20.3	16.2	0.16
1.5	53	12.1	1.3	36	24.0	16.7	0.18
1.7	57	13.3	1.0	28	29.5	17.1	0.20
1.9	61	14.5	0.7	20	41.3	17.5	0.22
2.0	63	15.1	0.6	16	57.9	17.6	0.23
2.13	65	15.9	0.3	0	1,000	17.8	0.24

[a] Specific growth rate, k, is expressed in reciprocal hours. Dimensions of other variables and values of parameters are given in Table 1. For the computation of A, the additional parameters were K_A = 20 μM, K_{U2} = 0.4 μM, and Q_{max} = 40 R.
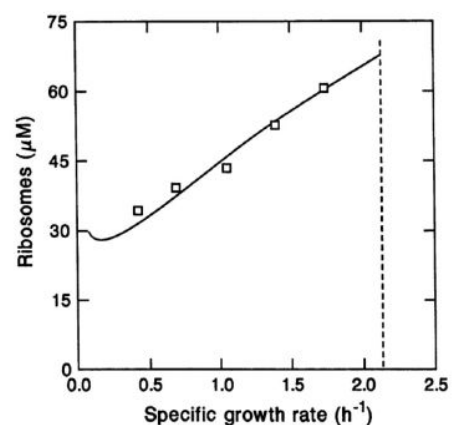
The TBG molecule has a single iodothyronine binding site. Optimal binding activity requires the presence of the L-alanine side chain, an unsubstituted 4′-hydroxyl group, a diphenyl ether bridge, and halogen (I or Br) constituents at the 3,5,3′ and 5′ positions. Compared to L-T4, rT3 binds to TBG with ~40% higher affinity, D-T4 with half that of the L-isomer and

tetraiodothyroacetic acid with ~25%. The protein loses its hormone binding properties by denaturation at temperatures above 55°C and pH below 4. The half-life of denaturation at 60°C is approximately 7 min. Denatured TBG does not bind iodothyronines. Further information about the protein can be found in the table below from (Krass et. al., 2007)

Table 1. Some properties and metabolic parameters of the prinicpal thyroid hormone-binding proteins in serum

	TBG	TTR	HSA
Molecular weight, kDa	54*	55	66.5
Structure	monomer	tetramer	monomer
Carbohydrate content, %	20	–	–
Number of binding sites for T4 and T3	1	2	several
Association constant, K_a (M-1)			
For T4	1×10^{10}	2×10^{8}**	1.5×10^{6}**
For T3	1×10^{9}	1×10^{6}	2×10^{5}
Concentration in serum			
(mean normal, mg/l)	16	250	40,000
Relative distribution of T4 and T3 in serum, %			
T4	75	20	5
T3	75	<5	20
In vivo survival			
Half-life, days	5***	2	15
Degradation rate, mg/day	15	650	17,000

HSA = human serum albumin; TBG = Thyroxine-binding globulin; TTR = transthyretin.
* Apparent molecular weight on acrylamide gel electrophoresis 60 kDa.
** Value given is for the high affinity binding site only.
*** Longer under the influence of estrogen.
Reproduced with permission from Hayashi and Refetoff: Molecular Endocrinology: Basic Concepts and Clinical Correlations. New York, Raven Press, 1995.

Our Mathematical Model

It is first important to note that for the numerical information that came as a range, ie. 1-5, we used the middle value, ie. 3. For the mathematical model we had to research the information regarding the translation for mRNA to protein and use it as the rate determining step to incorporate it to the formula. According to the Harvard Bionumbers (2008) database, the rate is between 12 and 21 for mRNA so we took it as 16.5 amino acids per second per ribosome. Then, we used the value for the ribosomes per bacteria, which according to Raisman J. (2013) is between 5,000 and 55,000 ribosomes, so we used 30,000 as the value. Then we multiplied the rate times the ribosomes per bacteria to get the amino acids per bacteria per second and divided that by the total amino acids in our protein to get the proteins per bacteria per second. We investigated that the bacteria took 30 minutes to double the population, so made that into a rate to calculate the bacterial population growth as $IB(2^{\frac{1}{1800}+3})$ where IB is the initial bacterial population and t is the time in seconds. By multiplying that times the rate of proteins per bacteria per second we got the rate of protein increase, so by integrating that we got the equation for the number of proteins per second.
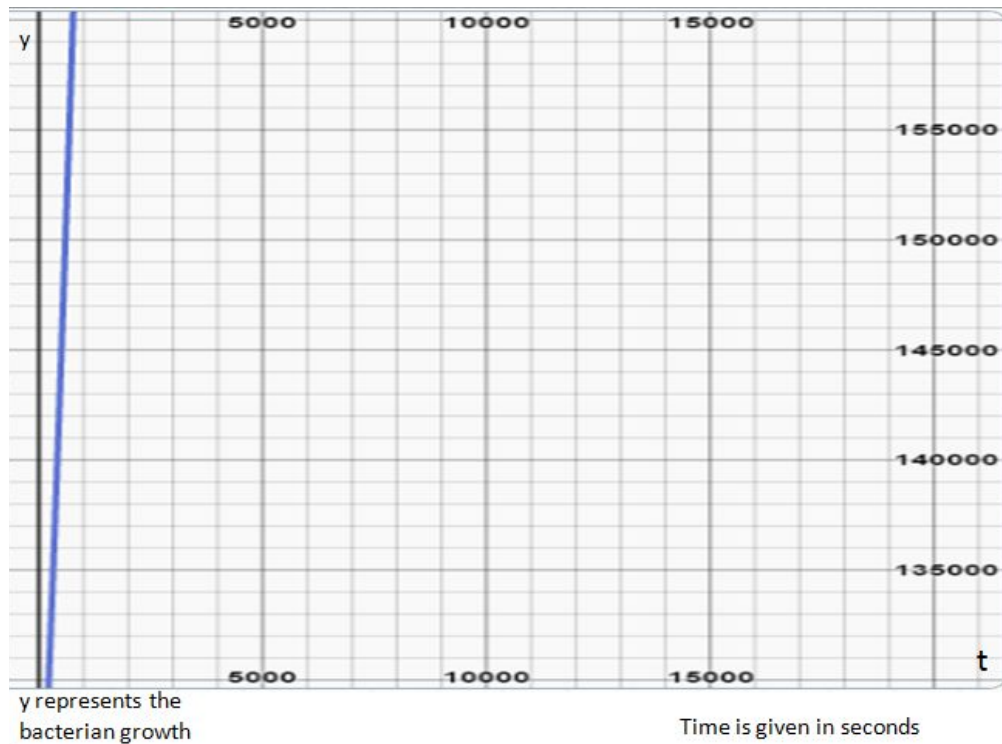
$$P.p.m = 1192.77 \int IB * 2^{\frac{t}{1800}}$$

that integrates to 1192.77 (({ IB 225 (2^[(t ÷ 1800) + 3])} / [Ln (2)]) +IB). That is the mathematical equation. We made a graph with that formula but made it by hour instead of seconds because the slope with seconds was very hard to read.

$$1192.77 \int_{T1}^{Te} \text{IB } 2^{\frac{t}{1800}+3}$$

$$(1192.77)\left(\frac{(IB\ 225\ (2^{\frac{t}{1800}+3})}{ln2} + IB\right)$$

$$1192.77([225 * IB * 2\hat{\ }(t/1800+3)]/ln(2)+IB)\ 28'800$$

y represents the bacterian growth

Time is given in seconds

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