

## Values for important parameters

Dominant timescale	r	m	r and m
$B_c = 1/(\tau cd)$	15873.016 cells/ml	256410.26 cells/ml	1111.11 cells/ml
$P_c = 1/(\tau d)$	2380952.38 virions/ml	38461538.46 virions/ml	166666.66 virions/ml
$B_0$	1000 cells/ml	66666666.67 cells/ml	55555.55 cells/ml
$P_0$	1e4 virions/ml	1 virions/ml	3333333.33 cells/ml
$\tau$	14 h	260 h	200 h
$w_{growth} = r\tau$	12.6	$2.6e - 08$	20.0
$w_{decay} = m\tau$	0.0042	26.0	20.0
Transition times	$t_1^c = 3.07$ h, $t_2^c = 7.79$ h, $t_3^c = 9.068$ h	$t_1^c = 19.50$ h, $t_2^c = 33.98$ h, $t_3^c = 81.46$ h	
Error Bacteria*	0.0952	0.0295	0.0
SD Bacteria	0.1448	0.0166	0.0
Error Phage	0.0321	0.0173	0.0
SD Phage	0.0241	0.0076	0.0
Error Total	0.0636	0.0234	0.0
SD Total	0.0683	0.0114	0.0

\*How the error was calculated:

1. For each point (time point)  $i$  take the concentration of bacteria and phage given by the full model ( $B_i^f$   $P_i^f$ ) and by the simplified model ( $B_i^m$   $P_i^m$ )
2. Calculate the absolute value of the relative error of bacteria  $|\epsilon_B|(i) = |\frac{B_i^f - B_i^m}{B_i^f}|$ , the absolute value of the relative error of phage  $|\epsilon_P|(i) = |\frac{P_i^f - P_i^m}{P_i^f}|$ , and their average:  $\epsilon_{Tot}(i) = 0.5(|\epsilon_B|(i) + |\epsilon_P|(i))$
3. Iterate over all points. This gives the vectors  $|\epsilon_B| = (|\epsilon_B|(1), |\epsilon_B|(2), \dots, |\epsilon_B|(n))$ ,  $|\epsilon_P|$ , and  $|\epsilon_{Tot}|$
4. The error of bacteria, phage, and the total error are the means of the vectors mentioned above:  $\overline{|\epsilon_B|}$ ,  $\overline{|\epsilon_P|}$ ,  $\overline{|\epsilon_{Tot}|}$