Supplementary Materials

Optimization of Bacteriophage Production in Batch Bioreactors

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TABLE S1: Lower and upper bounds for parameter estimation with references

Parameter	Lower bound	Upper bound	Reference
rn	0.1	2.0	[1]
K	10^{8}	10^{10}	[2]
a	10^{-10}	10^{-2}	[3]
ki	10^{-10}	10^{-5}	[4]
S	0.6	5.0	[4]
rr	0.1	1.0	[5]
b	20	200	[6]
p_decay	10^{-4}	10^{-1}	[7]

TABLE S2: Comparison of Model Calibration Iterations

Iteration	R^2	Adj. R^2	AICc	BIC
8p	0.9953	0.9934	827.58	827.65
-decay	0.9926	0.9903	834.37	835.96
-decay -rr	0.9953	0.9941	818.35	820.94
-decay -rr -a	0.9934	0.9921	823.40	826.53
-decay -rr -a -s	0.9962	0.9957	805.59	808.88

TABLE S3: Comparison of t-values across model simplification steps

Parameter	8p	-decay	-decay -rr	-decay -rr -a	-decay -rr -a -s
r_n	37.204	47.054	92.512	57.769	86.865
K	19.545	20.013	23.553	31.017	43.244
a	5.646	6.867	0.031	_	_
k_i	10.096	2.959	30.867	3.334	3.212
s	2.885	1.741	6.201	1.889	_
r_r	1.546	1.718	6.529	_	_
b	3.141	1.803	_	1.948	3.253
$p_{ m decay}$	0.367	_	_	_	_

TABLE S4: Non-significant parameters in each model iteration $\left(|t|<2\right)$

Iteration	Non-significant parameters
8p	r_r, p_{decay}
-decay	s, r_r, b
-decay -rr	a
-decay -rr -a	s,b
-decay -rr -a -s	_

TABLE S5: Parameter Values Across Model Calibration Iterations (Split View)

Parameter	8p	-decay	-decay -rr
r_n	1.81872	1.77619	1.82063
K	1.06399×10^{8}	1.16129×10^{8}	1.06356×10^8
a	4.99278×10^{-6}	0.00954×10^{-3}	4.99642×10^{-6}
k_i	5.96398×10^{-9}	1.61681×10^{-9}	5.99062×10^{-9}
s	0.600012	2.77948	0.600012
r_r	0.582558	0.582064	_
b	20.4265	23.1149	20.3955
$p_{ m decay}$	0.0996885	_	_

TABLE S6: Parameter Values Across Model Calibration Iterations (Split View)

Parameter	-decay -rr -a	-decay-rr-
r_n	1.77024	1.77408
K	1.1562×10^{8}	1.14137×10^8
a	_	_
k_i	1.5734×10^{-9}	1.86483×10^{-10}
s	2.47758	_
r_r	_	_
b	24.6669	194.213
$p_{ m decay}$	_	_

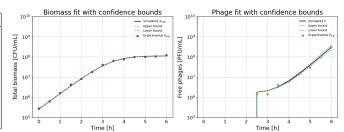


Fig. S1: Model fit and confidence bounds for biomass and phage concentration.

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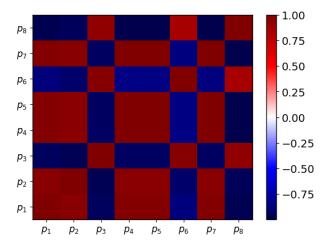


Fig. S2: Correlation matrix between parameters of the full model (8 parameters).

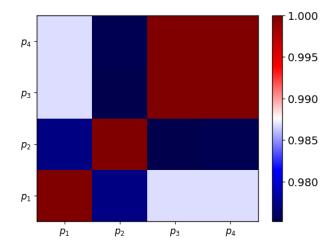


Fig. S3: Correlation matrix between parameters of the reduced model (4 parameters)

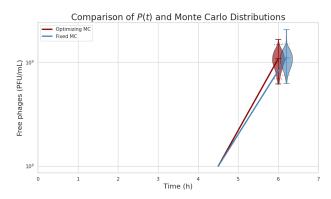


Fig. S4: Comparison of final phage titer distributions in Monte Carlo simulations

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