

UNIVERSITY OF AMSTERDAM

MASTERS THESIS

Mathematically Modeling the Interactions Between Phages, Bacteria, and the Environment

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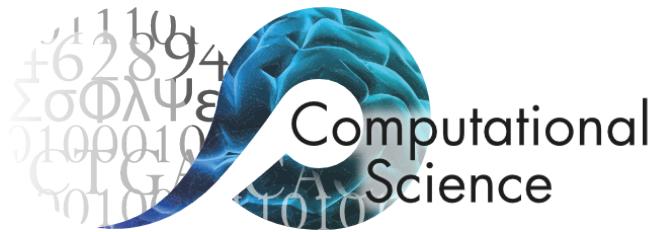
*A thesis submitted in partial fulfillment of the requirements
for the degree of Master of Science in Computational Science*

in the

Computational Science Lab

Informatics Institute

June 2025



Declaration of Authorship

I, Victor PIASKOWSKI, declare that this thesis, entitled ‘Mathematically Modeling the Interactions Between Phages, Bacteria, and the Environment’ and the work presented in it are my own. I confirm that:

- This work was done wholly or mainly while in candidature for a research degree at the University of Amsterdam.
- Where any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated.
- Where I have consulted the published work of others, this is always clearly attributed.
- Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.
- I have acknowledged all main sources of help.
- Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself.

Signed:

Victor Piaskowski

Date: June 3, 2025

“All models are wrong, but some are useful“

George E. P. Box

UNIVERSITY OF AMSTERDAM

Abstract

Faculty of Science
Informatics Institute

Master of Science in Computational Science

**Mathematically Modeling the Interactions Between Phages, Bacteria, and
the Environment**

by Victor PIASKOWSKI

Include your abstract here Abstracts must include sufficient information for reviewers to judge the nature and significance of the topic, the adequacy of the investigative strategy, the nature of the results, and the conclusions. The abstract should summarize the substantive results of the work and not merely list topics to be discussed. Length 200-400 words.

Acknowledgements

I would like to thank my parents for loving me despite some of my faults, and for supporting me through my Bachelor and Master studies even if they don't exactly know what I am studying. Without them, I wouldn't know where my life would be right now, and I certainly would be a different person if it were not for them.

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Thank you to Sofia Blaszczyk for finding the Master thesis opening and suggesting that I email Dr. Gralka for an introductory meeting. She acted as my [rubber duck programming buddy](#), and watched my cringe screen recordings that I sent her at 2am showcasing various demos of my project. If she wouldn't have found this opening, I wouldn't know what I would be doing as my thesis.

If I hadn't followed Dr. Rik Kaasschieter's and Dr. Martijn Anthonissen's courses "Introduction Computational Sciences" and "Numerical Linear Algebra" in my Bachelors, I would not have been interested in Computational Sciences. I would not have found the MSc Computational Sciences program, as Computational Sciences fits my interests and skill sets better than any other program I could have taken. For Rik and Martijn have forever altered my career trajectory.

Thank you to Sarah Flickinger for showing me the research that she has been doing in the lab. She allowed me to really connect my research and models to real life, reminding me that what I am doing has real life use cases than just a purely theoretical or programming challenge.

And finally, thank you to all of my friends for keeping me sane and helping me through both of my programs.

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List of Algorithms

Abbreviations

ABM	Agent Based Modelling
ARD	Arms Race Dynamic
BVP	Boundary Value Problem
CBASS	Cyclic oligonucleotide-Based Antiphage Signalling Systems
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
DDE	Delay Differential Equation
DNA	DeoxyriboNucleic Acid
FSD	Fluctuating Selection Dynamics
GUI	Graphical User Interface
IC	Initial Condition
IVA	Initial Value Analysis
OD	Optical Density
ODE	Ordinary Differential Equation
PA	Parameter Analysis
PDE	Partial Differential Equation
RNA	RiboNucleic Acid
SIE	SuperInfection Exclusion
SNP	Single Nucleotide Polymorphism
ST	Serial Transfer
TAB	Tail Assembly Blocker
UA	Ultimate Analysis
UvA	Universitiet van Amsterdam

Chapter 1

Experiments and Results

1.1 Graph Behavior

[Table 1.1](#) elaborates how a change in parameter value changes the shape and population level of the agents. ”[A Good Curve](#)”, whose agent and parameter default values can be found in the first column of [Table 1.1](#) and in [Table 2.1](#) are used as a reference. Each parameter was individually changed to a higher and lower value from the reference value, and the changes were noted in [Table 1.1](#). It should be noted that [Table 1.1](#) provides illustrative examples rather than an exhaustive analysis. The observed behaviors reflect typical trends when varying each parameter in the indicated direction, but may not generalize to all possible values and cases, or the magnitude of the change. The results can also not be generalized to cases where two parameters values are changed at a time. [Table 1.1](#) can be used in conjunction with [SOBOL Sensitivity Analysis Results](#) to gain a better idea of how sensitive the output is to that specific parameter.

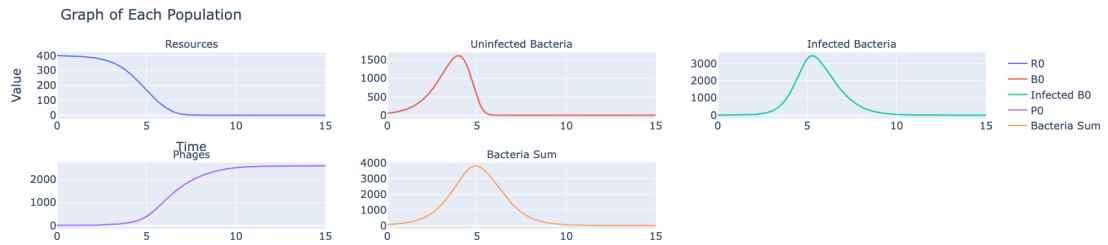
1.2 A Good Curve

Assuming a very simple model, with no washin or washout rate, a good bacteria growth curve looks like a mountain, with a clear rise, peak, and fall in population levels. For a given IC, the bacteria start to consume resources and replicate leading to exponential growth. The phages start to infect the bacteria and eventually the bacteria start to die, releasing new phages. The new phages infect more bacteria, putting pressure on the bacteria growth. Eventually, more bacteria are being infected than being created, causing the decline in bacteria population. [Figure 1.1a](#) shows an example of a good curve. [Figure 1.1b](#) is the same plot but with a logarithmic y-axis.

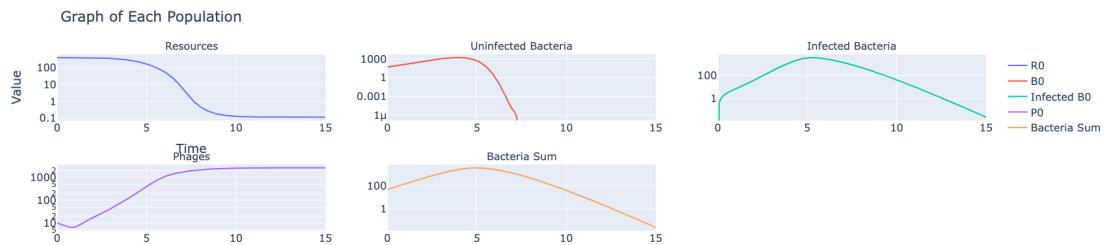
Parameter	Tested Value	Description of Behavior
R (400)	500	More uninfected and infected, slightly more phages
	300	Slightly less uninfected and infected, earlier resource depletion
U (50)	70	Slightly more phages and uninfected and infected bacteria
	30	Less uninfected and infected bacteria, slower resource depletion, not all resources used, slightly less phages
P (10)	20	Less resources consumed, less uninfected, bacteria peaks earlier, slightly less phages
	5	Resources consumed faster, more uninfected, infected, and phages
τ (2.14)	10	Faster resource depletion, faster bacteria peak, plateau, then fall in population. more uninfected and infected, less phages
	0.5	Barely any resource consumption, little bacteria growth and uninfected, more phages
$\omega^i(0)$	15	Slightly more bacteria, resource replenish after bacteria die out
e (0.03)	0.1	Faster resource depletion, sharper decline in uninfected, less infected and phages
	0.01	Less resource consumption, slightly more bacteria
v (1.2)	1.8	More phages, significantly more bacteria, earlier and sharp peak in uninfected, ,
	1	Less phages and bacteria, less resource consumption, earlier bacteria peak
K (10)	100	Less resource consumption, less bacteria and phages, earlier bacteria peak
	1	Faster resource depletion and sudden stop instead of gradual slowdown, earlier bacteria peak
r (0.01)	0.1	Less consumption, less infected and phages, earlier peak in bacteria
	0.001	Faster resource consumption rate, more infected and phages, delay in bacteria peak, sharp bacteria peak, small plateau in bacteria count before drop
β (20)	50	More phages, earlier bacteria peak, less resources consumed, less bacteria
	10	Faster resource consumption, more uninfected, less phages, sharper bacteria peak
$\omega^o(0)$	0.02	Faster resource depletion, more bacteria and sharper peak, later peak, and less phages.

Table 1.1: A table that compares how moving one individual parameter value up or down relative to the “A Good Curve” changes the general shape of the curve. This table is not meant to be exhaustive, cover edge cases, or extreme cases, or cover every exact detail and change in the population graph, but just to give an idea of how a change in parameter influences the graph shape, such as the rate of resource depletion, maximum number of bacteria and phages, and change in peak time. Reference parameter values are provided in the parentheses, from [Table 2.1](#).

As the bacteria population grow, the resource consumption speeds up until there are trace amount of resources left at $t = 8$. The uninfected and infected bacteria exhibit exponential growth, peaking at 1617 at $t = 3.99$ and 3463 at $t = 5.27$ respectively. The delay in the uninfected to infected bacteria's peak is due to the infection stages and latent period of the phage infection. The bacteria sum do not have as stark of a peak in comparison to the uninfected and infected bacteria, due to the graph measuring all bacteria populations, but the peak of 3805 at $t = 4.89$ is still clear. The phages saw a significant increase in population count at around $t = 4$, coinciding with the peak in uninfected bacteria. At this point in time, the infection rate is larger than the bacteria replication rate, so the bacteria are starting to die out even though there are still sufficient resources remaining. At around $t = 4$ is when the the resource consumption rate inflects. The rate at which the resources are being consumed starts to slow down, showing a decreasing sigmoid shape. The total bacteria population reached a peak of 3805 at $t = 4.89$, a 76.1x increase in population count from the initial 50 starting uninfected bacteria. The phage population reached a peak of 2584 phages at $t = 15$, a 258.4x increase in population count.



(a) Linear y-axis for a "good" plot.



(b) Logarithmic y-axis for a "good" plot.

Figure 1.1: The log plot allows to see behavior happening at values near 0 and to plot data on a logarithmic scale. The parameters used for this plot can be found in [Table 2.1](#).

1.3 SOBOL Sensitivity Analysis Results

It is important to understand how a change in parameter value affects the change in output of a model. Models will have parameters that are more important and have a larger effect on the model output than other parameters.

[Figure 1.2a](#) shows the impact that the parameter had on the final value of the population at $t = 15$. The average value and variance of population value were intentionally left out of the analysis, despite being a part of the dashboard because the SOBOL sensitivity values are almost identical to the final sensitivity values. There were some very minor differences from bar to bar across plots, but the difference was imperceptible. Since the plots all look similar, only an analysis on the final value, [Figure 1.2a](#) will be done.

The parameters that were tested include all the parameters listed in the extended golden model, except for Uninfected Bacteria and M . Uninfected Bacteria was left out as it doesn't make sense to already add infected bacteria to the system M , the number of stages that the infection goes through, can not be tested as M hardcodes the number of infection stages that the bacteria has to go through. The hardcoding is done before the simulation framework starts. As such, it is not possible to change M without rerunning the program from the very start.

1.3.1 Final Value Analysis

1.3.1.1 Resources

The ω^i /washin rate had the largest influence on the final, average and variance value. Without a washin rate, the resources will most likely have been consumed by the time the simulation ended at $t = 15$. The final values for Resources, Uninfected, Infected, and Phages would often be something similar to $(0, 0, 0, 10000)$ at $t = 15$, where all the resources were consumed and the bacteria died out due to the phages, leaving only the phages remaining. The final value of the resources would often be 0, no matter what parameter values were used, with $\omega^i, \omega^o = 0$. With the addition of the washin, new resources were constantly being re-added. Once the bacteria died out, the resources could accumulate, with the accumulation dependent on the rate of the washin rate, hence why the washin rate has such a large impact on the final, average, and variance of population value for the resources. The final value would be dependent on when the bacteria died out, in turn allowing the resources to accumulate at a rate proportional to $\omega^i - \omega^0 \cdot R$. Resources were less dependent on higher order interactions, unlike the uninfected, infected, phages, and total bacteria sum.

1.3.1.2 Uninfected

The uninfected bacteria population sensitivities depend on many higher order interactions between the parameters as $ST_i \gg S1_i$. The uninfected are highly dependent on β/B_matrix and initial phage population, as the initial phage population will determine how many bacteria become infected, and how quickly the phages can proliferate through the bacteria population. Surprisingly, r/r_matrix did not have as big of an influence on the uninfected as β did, even though the infection rate is dependent on r . The larger or smaller r is, the faster or slower the infection rate is. If r is really small, the infection rate would take forever, potentially allowing the bacteria to keep a stable population. r is equally as important at explaining the final value as τ/\tauau_vector , $washin$, e/e_matrix , and $washout$ of sensitivity around 0.25.

1.3.1.3 Infected

Since $ST_i \gg S1_i$ for the infected bacteria, where $S1_i \approx 0$ for nearly all of the parameters, the infected bacteria heavily depend on many interactions happening at the same time. This makes intuitive sense after looking at ???. The infected (and uninfected) bacteria directly interact with R , U , P , v , K , r , τ , and ω^o (M is not included as it was left out of the analysis). So due to the high coupling of parameters, the infected (and also the uninfected) have large global sensitivities compared to the local sensitivity.

However SOBOL had some difficulties assigning a good sensitivity score to each parameter for the ST and $S1$ tests as noticed by the slightly larger error bars in the infected than the uninfected or resources. This is most likely due to the infected bacteria going through multiple stages of infection, causing a delay and uncertain behavior in the final value, despite the ODE model being deterministic.

1.3.1.4 Phages

The most important factor for the final phage value is r , followed by β , ω^o and P . The r value allows the phages to infect the uninfected. When r is decreased, the final phage population is counterintuitively higher than when r is larger. The behavior is counterintuitive because one would expect that a higher infection rate would lead to more infections and thus more phages. With a higher r value, more phages are being removed from the phage population and infecting the bacteria. It can be seen as a way of "more phages are needed to infect a bacterium", therefore getting less phages out as a result as more phages are needed to infect a single bacteria.

Washout has a noticeable influence on the phage population, as not the phage population is being reduced at a rate proportional to the washout rate. The larger the washout rate, the larger the drawdown of phages. When the infected all die out, the phage population wont grow anymore. Given the phage population at that point in time, the phage removal rate is proportional to the washout rate.

1.3.1.5 Total Bacteria

Total bacteria is the sum of both uninfected and infected bacteria, so it makes sense for total bacteria to have similar values to uninfected and infected bacteria. Apparently the uninfected bacteria have a stronger influence on the output variance than the infected bacteria. The total bacteria sensitivities resemble the sensitivities of the uninfected bacteria more than the infected bacteria. It would have been expected for the total bacteria to resemble more of an average between the uninfected and infected.

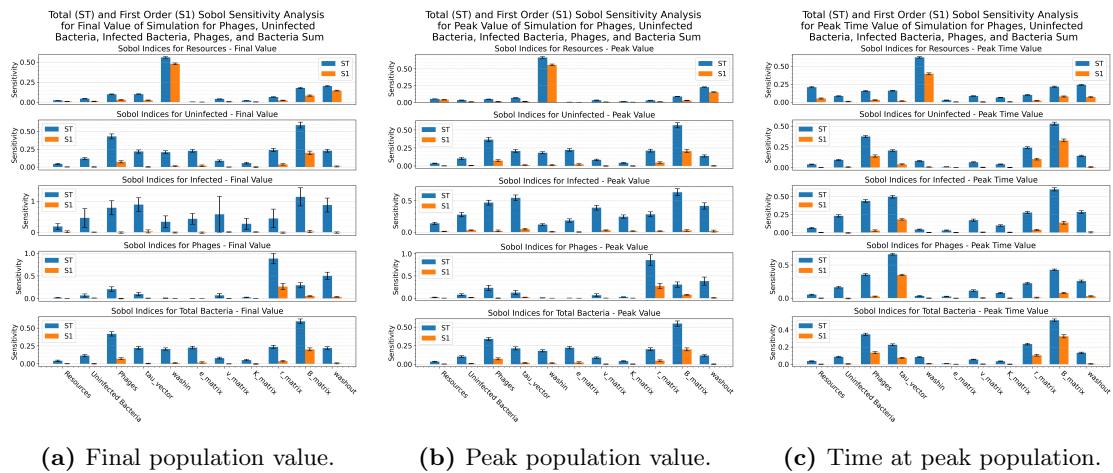


Figure 1.2: SOBOL analyses for the average, peak, and peak time. The data was saved from the dashboard and plotted using Matplotlib. The average and variance analysis results were left out for nearly identical results to the final value. The values used for this SOBOL test can be found in [Table 2.3](#). The data used in [Figure 1.2a](#) was used for [Figure 1.2b](#) and [Figure 1.2c](#). The plot of the average and variance analysis can be found at [Figure 3.1a](#) and [Figure 3.1b](#)

1.3.2 Custom SOBOL Analysis - Peak Value and Peak Time

Due to the similarity of the final, average, and variance value as seen in [Figure 1.2a](#), [Figure 3.1a](#), and [Figure 3.1b](#) a custom SOBOL analysis that isn't included in the dashboard might result in a different SOBOL analysis result. To create the custom SOBOL analyses, the peak value and the time at the peak of the population is measured and analyzed. The peak is defined as the point where the population reaches 95% of its absolute maximum value. The time at peak is measured at the point in time that the

population reaches 95% of the maximum value. This removes unintended side effects of the simulation. For populations that are only increasing in value, this prevents the measured peak from bunching up at the end of the simulation, skewing the data. As the peak is defined at 95% of the absolute maximum value, populations that have a faster increase on population count at the end will have a time value closer towards the end of the simulation. For populations that reach a plateau, the 95% rule will push the peak time towards the beginning of the simulation, while still "respecting" the absolute final value since $95\% \approx 100\%$. The 95% rule can fail under certain situations, such as when there is cyclic behavior. See [Why 95%?](#) for a more detailed explanation on why the 95% rule is used.

The results of the SOBOL peak and time at peak analyses can be seen in [Figure 1.2b](#) and [Figure 1.2c](#). Although some of the bars between the final, peak, and time at peak values are the same, some are different. But overall, similar values can be seen across the the final, peak, and time at peak analyses. The peak infected values are more certain compared to the final infected values, which could be due to the 95% rule removing some of the noise of the simulation. The time at peak values have less error compared to the final and peak value. This is due to the restricted range of values. The time at peak value can only fall somewhere between 0 and 15, the start and end values of the simulation respectively. The final and peak values can fall anywhere between 0 and any value, depending on the IC and how high the population can rise, and how fast the population can fall, *if* the population count falls.

1.3.3 SOBOL Analysis - Without Washin and Washout

In many of the plots, the washin and washout rate had a large influence on the final, peak, and time at peak value. [Figure 3.2](#) ran the same input as [Figure 1.2](#), but left the washin and washout rate out. The sensitivity plots for the final, average, variance, peak, and time at peak plots look different form one another. The final resource value depended heavily on the washin and washout rate, but without the washin and washout, the final resource depended heavily on the initial resource population. Since $S1 \approx ST$, the resource parameter does not depend on other higher order interactions.

The peak value for the resources without washin and washout only depended on the initial resource consumption. Since there was no washin, no resources could be added, so the peak for the resources was always at $t = 0$, and was dependent on the initial resource value. The time at peak value is always 0 as the resources are only being depleted, so no matter the change in parameter values, the parameter had no effect on the peak time, so SOBOL gives a value of 0 to every parameter for the resources. β

consistently had a large effect on the final, average, variance, peak, and time of peak value as

1.4 Initial Value Analysis Results

The IVA section of the dashboard allows the user to visualize how a change in parameter value affects the population growth of the agents.

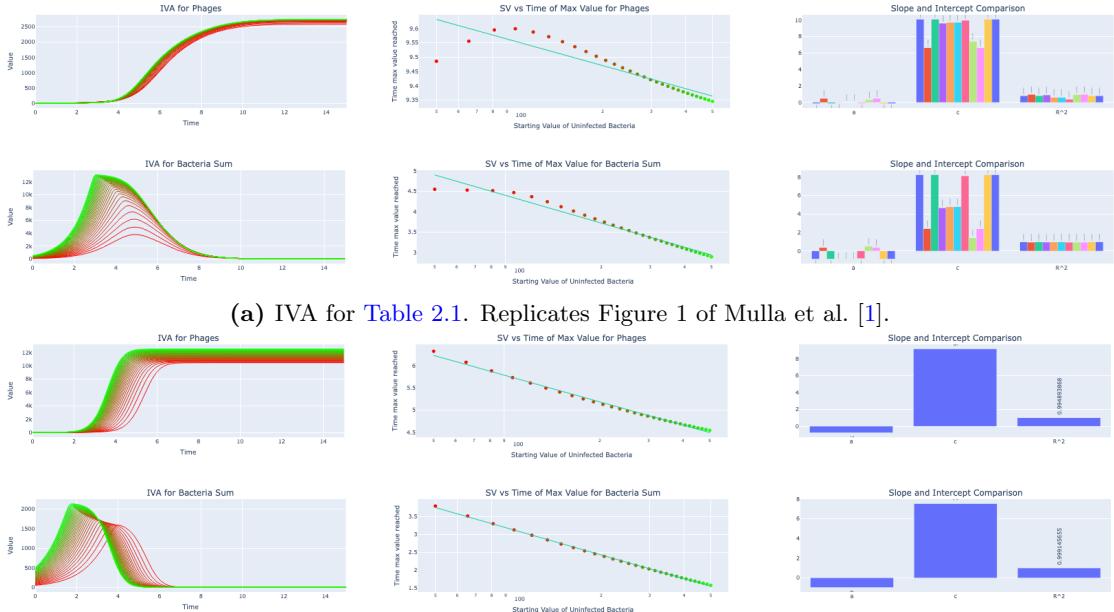
In Figure 1 of Mulla et al. [1], they vary the initial concentration of bacteria and measure the time until bacterial collapse. The initial concentration value and time of collapse is plotted on the x and y-axis with a tight linear regression fit on the data. The observed logarithmic decrease suggests that the phage kinetics is adsorption-limited meaning that [Figure 1.3b](#) replicates this graph.

[Figure 1.3a](#), even considered a "good" curve, shows interesting behavior that diverges from that of [Figure 1.3b](#). Then though the behavior should be similar, changing other parameter values can alter how a parameter works. It would be expected that for 100 initial uninfected bacteria and less the bacteria sum peak time would follow the linear regression line, but at around 100 uninfected bacteria and less, the peak curve goes horizontal. This suggests that something is restricting the bacterial growth. The lack of resources is actually restricting the bacteria growth.

1.5 Phase Portrait

[Figure 1.4a](#) shows a phase portrait varying the initial resource and phage concentration. For phages that start above 25.98, the phage population can proliferate (until the washout would eventually removes the phages). For phage populations that start below 25.98, the washout removes the phages before the phages had time to infect and kill the bacteria. Both regions of phages exhibit consistent behavior, of either going to 0 or proliferating. If the phage population started at exactly 25.98, if the initial resources was 260 or above, the phages died out. If the initial resources was 255 or below, the phages would proliferate.

[Figure 1.4b](#) simulates a wider range of values. The initial resource values span from 100 to 500, and the initial phage values range from 25.5 to 26.5, each with 100 unique values sampled. It shows if a set of initial conditions allowed the phages to proliferate (red boxes) or if the phages died (white boxes). A boundary between the dead and proliferating phages can be curve-fit. The curve follows a logarithmic $y = 21.484 \cdot \ln(x +$



(a) IVA for Table 2.1. Replicates Figure 1 of Mulla et al. [1].
(b) IVA for Table 2.2. For uninfected bacteria less than 100, the phage-bacteria interaction is resource limited. For 100 and higher, it is adsorption limited.

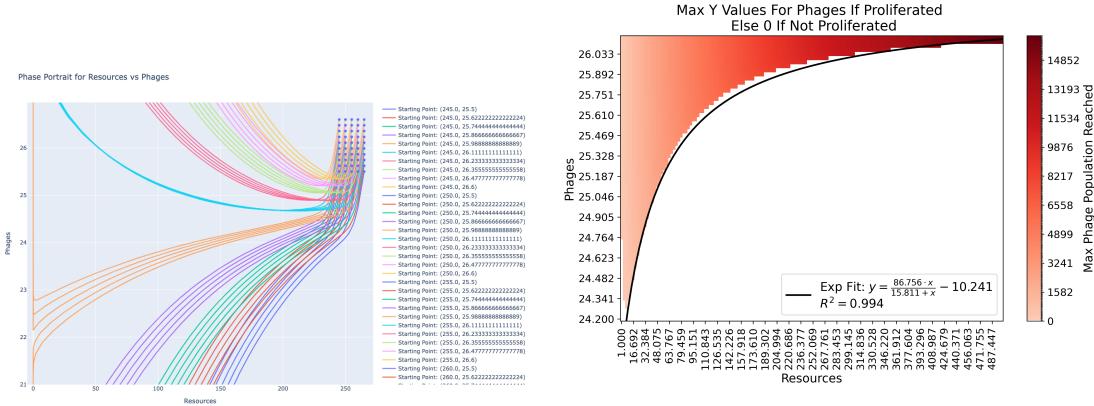
Figure 1.3: Varying initial Uninfected Bacteria concentration, from 50 to 500, with 30 unique values tested over two different instances of "good" curves. Even with two "good" curves, even varying the default parameter values a tiny bit can have a large influence on how changing the initial bacteria concentration can have an influence on the dynamics of the system, changing the behavior of the peak time. The default values for Figure a) and b) can be found at Table 2.1 and Table 2.2.

3.353) – 21.810 with an R^2 value of 0.994. There appears to be a non-linear tradeoff between initial resources and phages when there is washout. The washout non-linearly affects if the phages proliferate or not.

Phage populations are coupled to bacteria populations who are in turn coupled to resource populations. By varying the initial resource concentration, the bacteria growth rate is affected, in turn affecting the phage population, with a non-linear effect.

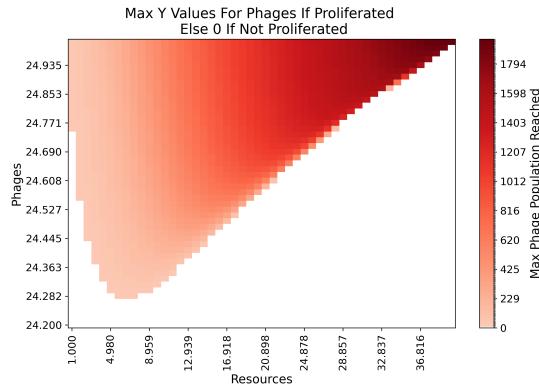
1.6 Plotting Parameter Change - $3 \times 2 \times 3$ Model

Figure 3.4, Figure 3.4, and Figure 3.4, show a 7×7 matrix of different r and β initial conditions for a $3 \times 2 \times 3$ model. For each simulation, if r or β is equal to a value not equal to inf , as identified by the title above each subfigure, then each value of r or β has that value. If r or β is equal to inf , then the simulation uses the original data as defined in the IC, vector, and matrix section of the dashboard. As a small example for the $3 \times 2 \times 3$ model, when $r = 0.200$, the simulation framework uses $r = \begin{pmatrix} 0.200 & 0.200 \\ 0.200 & 0.200 \\ 0.200 & 0.200 \end{pmatrix}$ as the input matrix to the ODE model. It is important that in the user-implemented



(a) Zoomed in plot of a phase portrait with varying resource and phage population from 40-60 and 60-70 respectively. Each row has its own line color. Diverging behavior can be seen for the orange line (phage=25.98).

(b) Phage population proliferation as a function of initial resource and phage concentrations. While the color appears uniform along the vertical axis, each cell is actually a slightly different value. The phage-resource proliferation boundary follows a fitted Monod equation.



(c) Zoomed in to analyze the regime of behavior change near resources= 10.

Figure 1.4: Varying initial resources and initial phages and the resulting curve and proliferation. The clear phage proliferation boundary follows a shifted Monod curve. Proliferation is defined as when the phage population reached at least 2 times the initial starting population. This simulation values used can be found in [Table 2.2](#), but with washout set to 0.02 instead of 0.

ODE model, the user needs to check if an edge exists between two nodes first before calculating the new values. The values

When $r = \inf$, the simulation framework uses $r = \begin{pmatrix} 0 & 0.11695 \\ 0.144459 & 0 \\ 0.11895 & 0.13065 \end{pmatrix}$ as the data to simulate the interactions with.

Chapter 2

Appendix E: Parameter Values Used

2.1 A Good Curve

IC	Resources	Uninfected Bacteria	Infected Bacteria	Phages
	400	50	[0 0 0 0]	10
Vector Data				
τ		ω^i		
2.14		0		
Matrix Data				
e	v	K	r	β
0.03	1.2	10	0.01	20
Environment Data				
M		ω^o		
4		0		

Table 2.1: The parameter values used for Figure 1.1.

2.2 A Good Curve 2

2.3 SOBOL Analysis

2.4 Complex Model

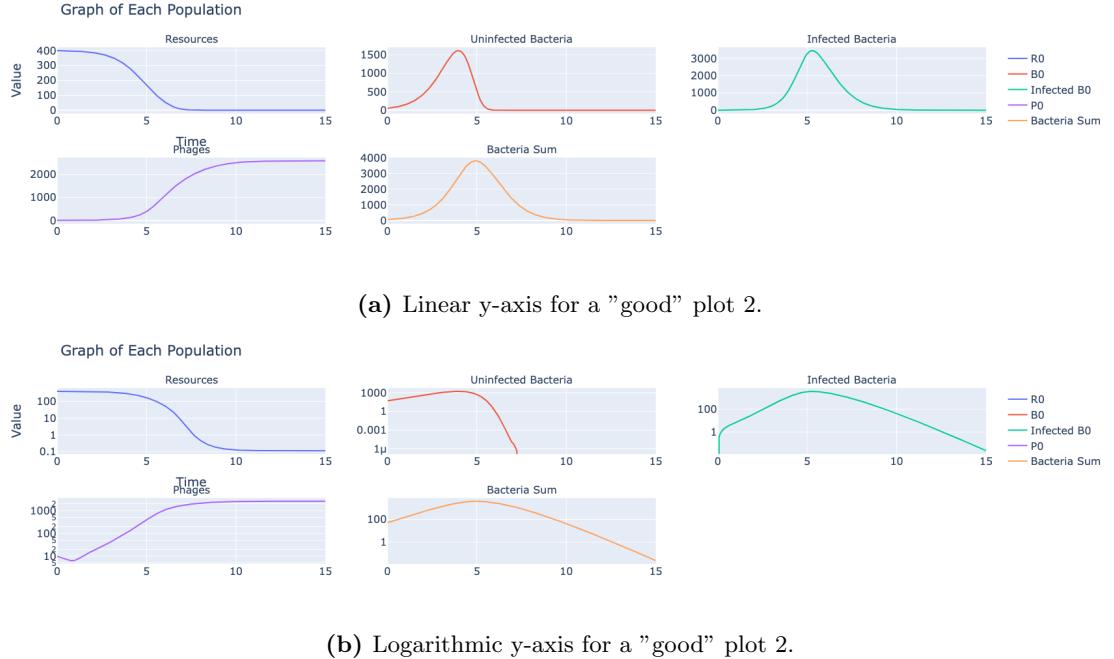


Figure 2.1: The log plot allows to see behavior happening at values near 0 and to plot data on a logarithmic scale. The parameters used for this plot can be found in [Table 2.1](#).

IC	Resources	Uninfected Bacteria	Infected Bacteria	Phages
200	50		$[0 \ 0 \ 0 \ 0]$	10
<hr/>				
Vector Data	τ	ω^i		
0.7	0			
<hr/>				
Matrix Data				
e	v	K	r	β
0.12	1	10	0.001	10
<hr/>				
Environment Data				
M		ω^o		
4		0		

Table 2.2: Another set of "good" curves. The linear and logarithmic plot of this data can be seen in [Figure 2.1](#)

IC				
Resources	Uninfected Bacteria	Phages		
100-500	1-100	1-50		
Vector Data				
τ	ω^i			
0.5-3.5	0-100			
Matrix Data				
e	v	K	r	β
0.05-0.25	0.8-1.9	10-250	0.001-0.2	0-100
Environment Data				
ω^o				
0-0.1				
Other Data				
Seed Value	2nd Order	Number Samples	Simulations Run	Simulation Length
0	False	15	$2^{15}(11 + 2) = 425984$	15

Table 2.3: The parameter values used for the SOBOL sensitivity analysis in [Figure 1.2](#), [Figure 3.1](#) and [Figure 3.2](#).

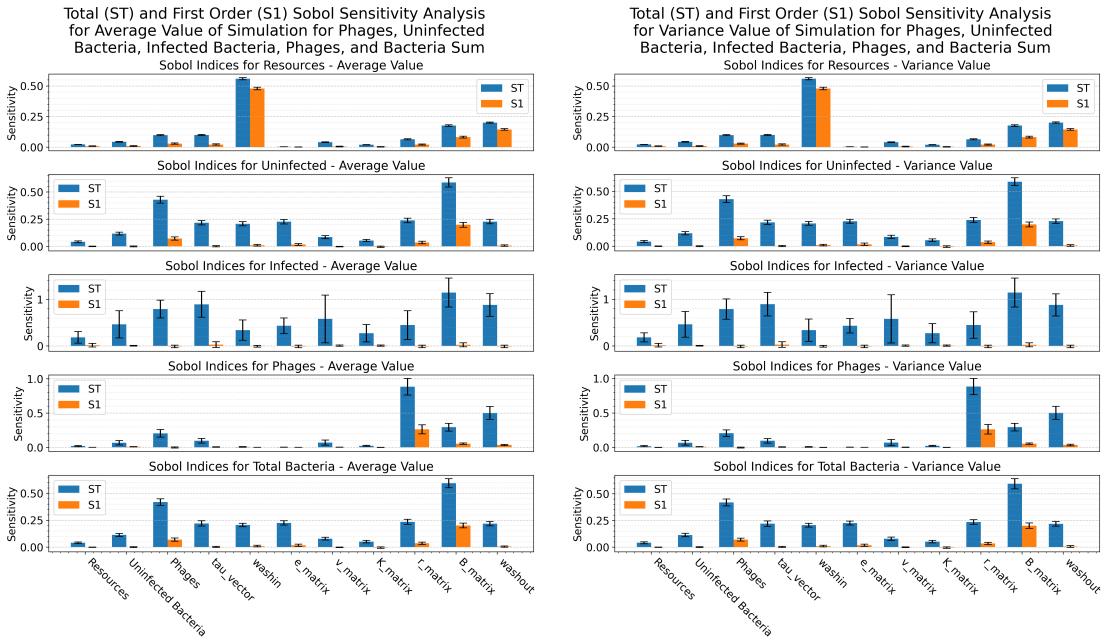
IC				
Resources	Uninfected Bacteria	Infected Bacteria	Phages	
[236 287 270]	[53 69]	$\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$	$\begin{bmatrix} 10 & 5 & 8 \end{bmatrix}$	
Vector Data				
τ_b	ω_r^i			
[2.73340 2.25015]	[0 0 0]			
Matrix Data				
e_{br}	v_{br}			
$\begin{bmatrix} 0.15680 & 0.10871 & 0 \\ 0 & 0 & 0.18009 \end{bmatrix}$	$\begin{bmatrix} 1.27601 & 0.86393 & 0 \\ 0 & 0 & 1.22625 \end{bmatrix}$			
K_{br}	r_{pb}	β_{pb}		
$\begin{bmatrix} 139.58353 & 12.83058 & 0 \\ 0 & 0 & 82.86684 \end{bmatrix}$	$\begin{bmatrix} 0 & 0.11695 \\ 0.144459 & 0 \\ 0.11895 & 0.13065 \end{bmatrix}$	$\begin{bmatrix} 0 & 15 \\ 34 & 0 \\ 11 & 57 \end{bmatrix}$		
Environment Data				
M	ω^o			
4	0			

Table 2.4: The parameter values used for the $3 \times 2 \times 3$ network model rounded to 5 decimal points. In the matrix data, if a value is 0, then the edge does not exist between p and b or between b and r , depending on the subscript.

Chapter 3

Appendix F: Extra Plots and Figures

3.1 Extra SOBOL Analyses



(a) The ST and $S1$ sensitivity for the average Resource, Uninfected, Infected, Phage, and Total Bacteria population.

(b) The ST and $S1$ sensitivity for the variance of the Resource, Uninfected, Infected, Phage, and Total Bacteria population.

Figure 3.1: SOBOL analyses for the average, peak, and peak time. The data was saved from the dashboard and plotted using Matplotlib. The values used for this SOBOL test can be found in Table 2.3. The same data used in Figure 1.2 was used for Figure 3.1a and Figure 3.1b.

3.1.1 SOBOL Analysis Without Washin and Washout

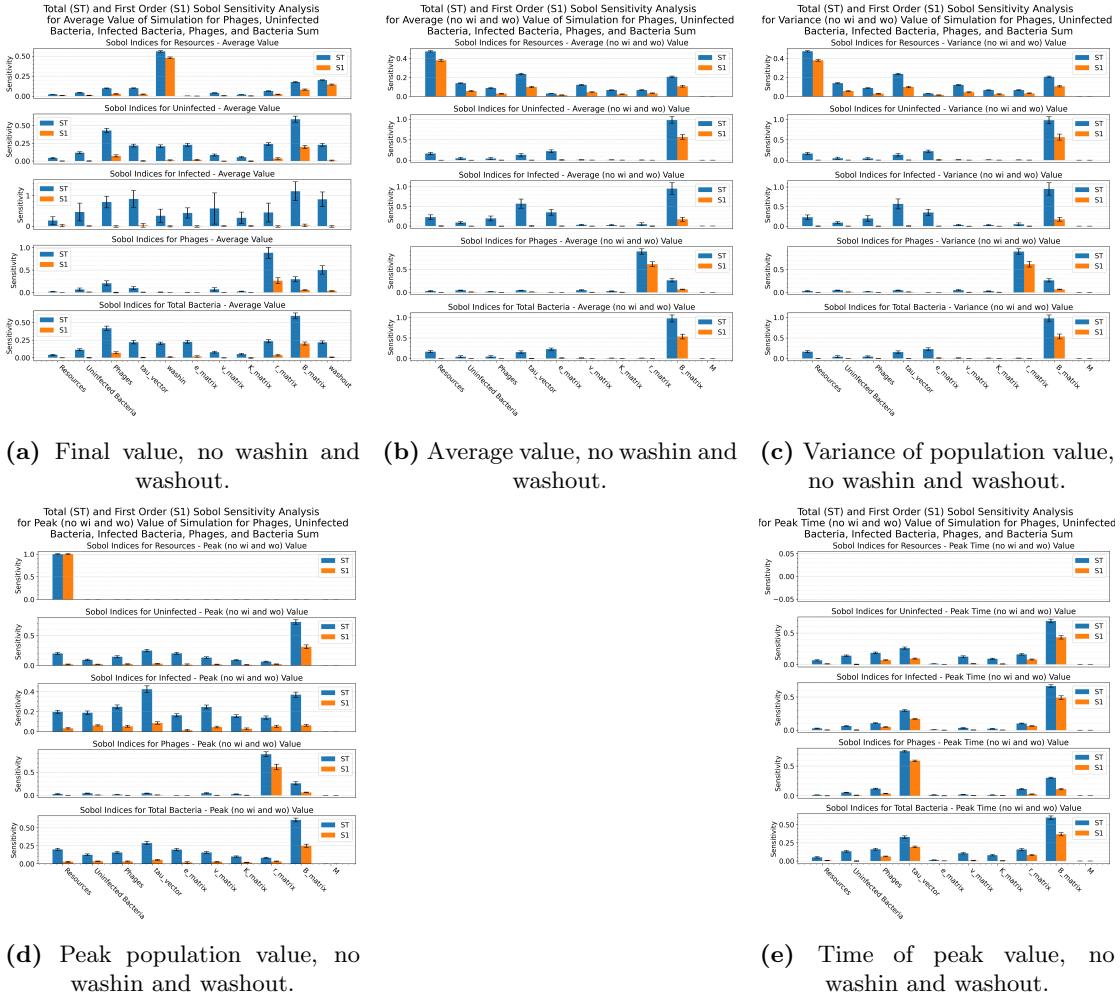


Figure 3.2: SOBOL analyses for the final, average, variance, peak, and peak time, without a washin and washout rate. The data was saved from the dashboard and plotted using Matplotlib. The values used for this SOBOL test can be found in [Table 2.3](#), except washin and washout have been set to 0.

3.2 Why 95%?

The 95% rule helps in the IVA analysis. Due to the solver, when taking the absolute peak value, the same time value can occur. Or in an ever increasing value like phages, the peak values occur at the last time step of the simulation, or plateaus and doesn't grow anymore. However, as the parameter value is changing, each graph for every input change will change the growth rate of the agent, changing how fast the agent population grows.

[Figure 3.3](#) shows how using the 95% rule vs the 100% rule for finding the max value reached helps smooth out computational errors from the ODE solver and smooths out

the shape. For the phages, using the 100% rule ([Figure 3.3b](#)) shows that the population peaked at the end of the simulation, $t = 15$, for all e values. However at $t = 15$, the population plateaued, as evident by the line graph. Plotting the same plot, but calculating the peak at 95% of the actual peak ([Figure 3.3a](#)) shows that the green line ($e = 0.25$) "reached" its peak at $t = 8.4$ before the red line ($e = 0.05$) at $t = 9.4$, a full unit of time after $e = 0.25$. The user can thus conclude that for this instance, larger e values will cause the phage population to reach its "peak" faster than smaller e values.

[Figure 3.3c](#) and [Figure 3.3d](#) likewise show how the 95% rule can improve analysis of the change in peak time. [Figure 3.3d](#) shows how apparently the peak is reached at set time values. Due to how `solve_ivp()` from SciPy works, it automatically chooses time values that it thinks would best capture the dynamics of the system without calculating too many steps. The user can control the step size by decreasing the absolute and relative error bounds, as well as by minimizing the time steps. The user can also provide their own time range with the number of steps to run, increasing the control of the time values chosen. It takes about 0.02321 seconds to run a simulation for 15 time units, where 200 time steps are selected and solved by the solver. Comparatively, a simulation with 1000 time units and 1000000 (a 5000x increase in samples) equidistant time samples takes about 1.71651 seconds to run, a 73.95562258x increase in time spent computing the simulation. The total time taken to run the whole method call, a call to the simple graph maker at the top of the dashboard took 1.76130 seconds vs 17.70634 seconds.

Alternatively instead of controlling the solver, the user can use the 95% rule. Although some accuracy is lost. Going from the 100% rule to the 95% rule, the solver still captures the peak values and the dynamics, but the accuracy is lost. The 100% rule shows that for $e = 0.25$, the time the uninfected population reached its peak occurred at $t = 3.2$. But for the 95% rule, the time at which the peak occurred at is at $t = 3.05$. The slope (the a value) and the intercept (the c value) are somewhat similar, with very high and similar R^2 values (0.97), suggesting a good linear fit of the data.

[Figure 3.3e](#) shows how the by increasing the time sampling to more fine grained results in a more accurate graph. Instead of having the solver choose the time values to test, 1000 equidistant time values were selected between 0 and 15. The solver can more accurately calculate the population values and calculate the proper peak time. Comparing the 100% rule without the custom time values with the 100% rule with the custom time values shows the same time values were calculated. in both, the $e = 0.25$ resulted in a time of peak at 3.2 and for $e = 0.05$, the time of peak occurred at $t = 3.95$. This is in stark comparison to the 95% rule vs 100% rule without the custom time, showing a difference of 0.15 time units. The custom time values also preserved the shape of the

curve e -value vs time curve, being almost identical to that of the 95% rule as seen in [Figure 3.3c](#) and [Figure 3.3e](#).

Another issue that arises with the custom time is that it doesn't solve the issue seen with the phages, where the time of peak is at $t = 15$.

The user can control the % rule with a value input on the dashboard. They can select to use the 95% rule, or 100% rule, or even 83% rule if they want by changing the value they use. The user can use their own custom time values, to ensure that they get high quality curves.

3.3 Varying r and β In A $3 \times 2 \times 3$ System

[Figure 3.4](#), [Figure 3.5](#), and [Figure 3.6](#) show a 7x7 matrix of figures, each with a unique parameter set. In each sub-figure, the values of r and β are varied as follows: $r = 0.5, 1.1, 1.7, 2.3, 2.9, 3.5, \text{inf}$; $\beta = 0, 20, 40, 60, 80, 100, \text{inf}$. "inf" in the figures, represented as `np.inf` in the code, the representation of ∞ , represents the original parameter values used in the IC, vector data, or matrix data. Each figure shows the effect of varying the washout rate, with values set to 0, 0.02, and 0.05, respectively. The default values for the parameters can be found in [Table 2.4](#).

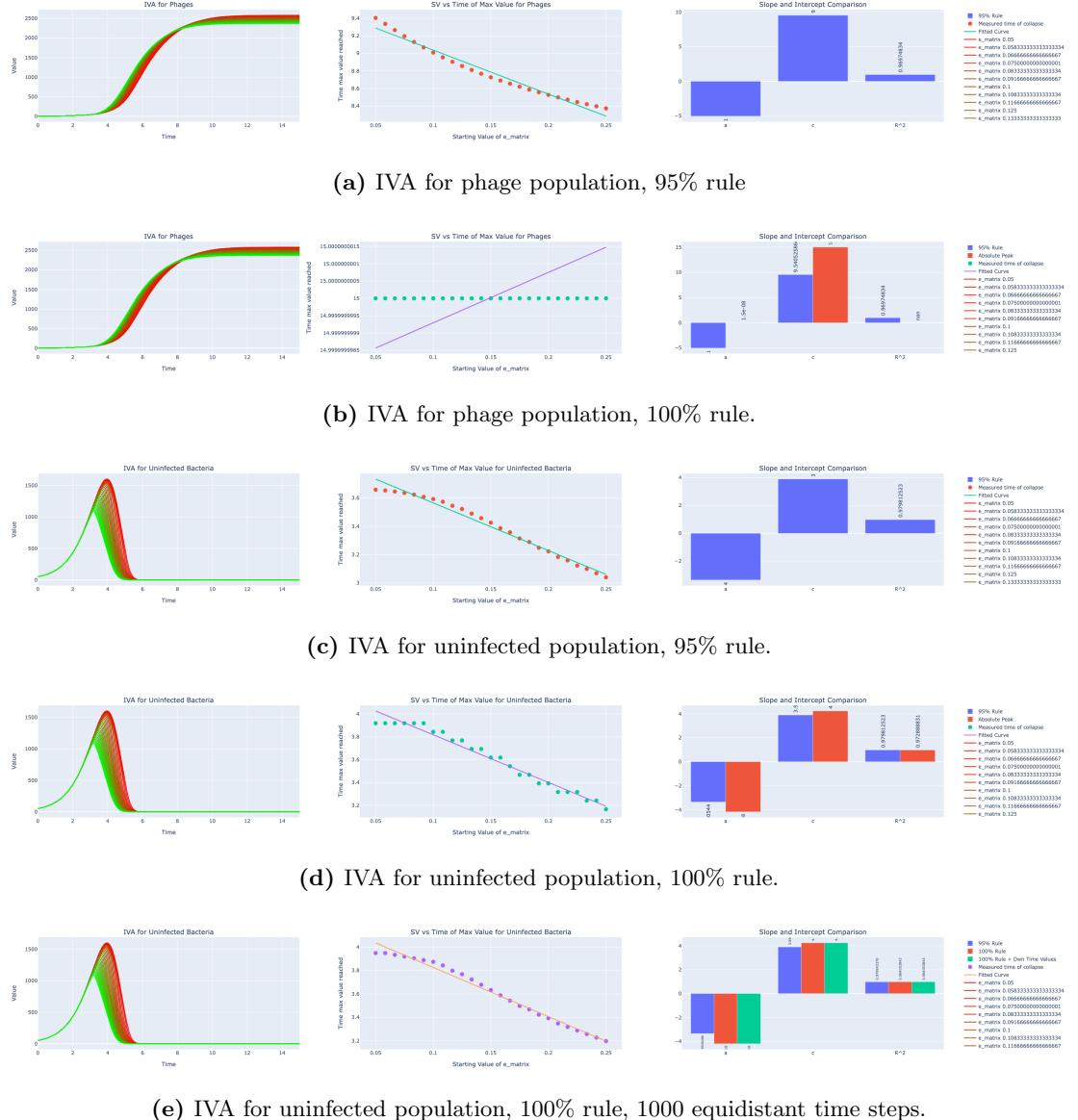


Figure 3.3: Testing the 95% rule vs the 100% rule, where the time at the absolute peak is taken and plotted in the second plot. A comparison of phages and uninfected bacteria is shown. Verification of the graph shape between the 95% rule graph and a frequent time step with 100% rule can be seen between c) and e). The e value is changed, ranging from 0.05 to 0.25.

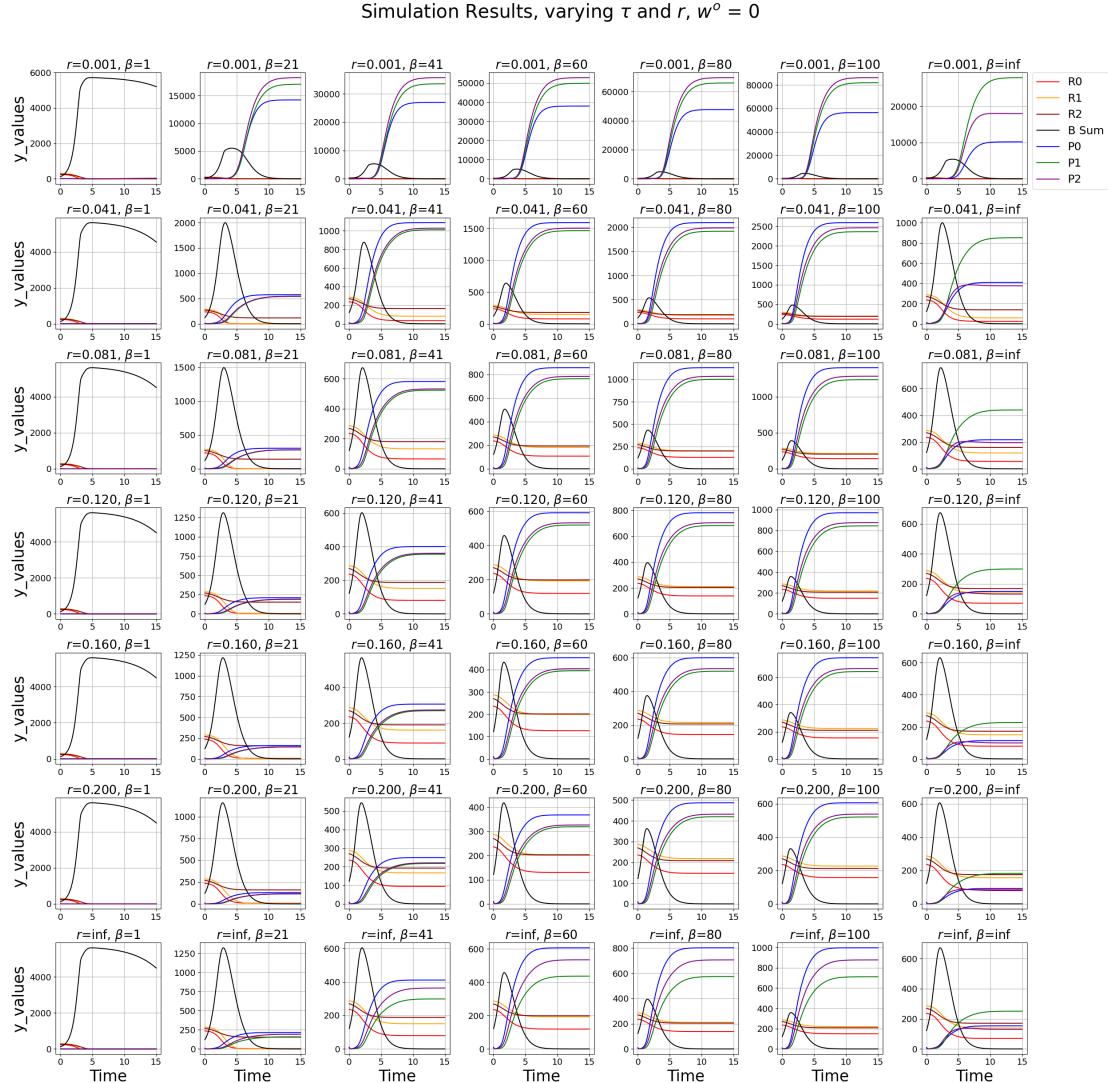


Figure 3.4: Washout $\omega^o = 0$.

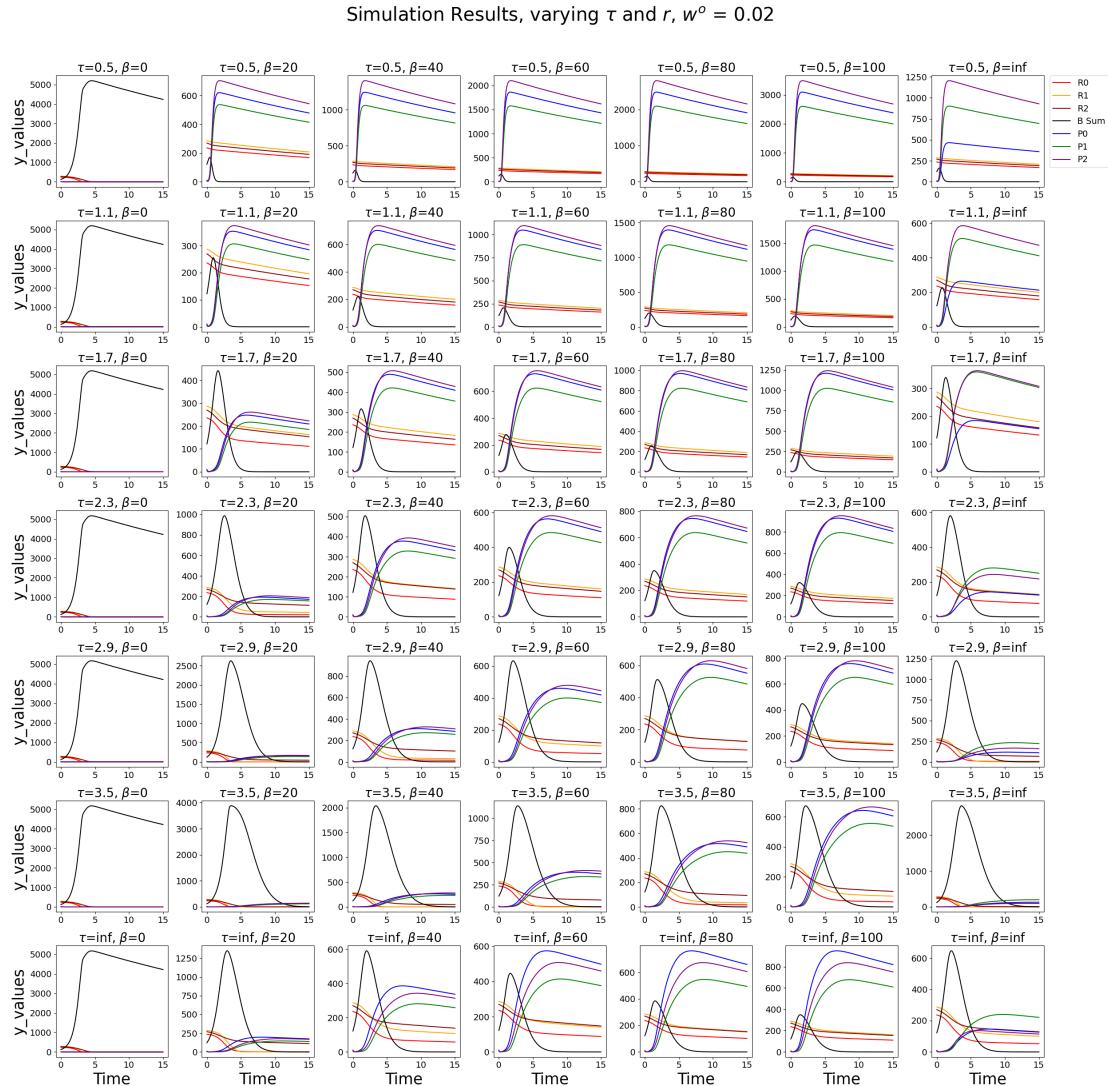


Figure 3.5: Washout $\omega^o = 0.02$.

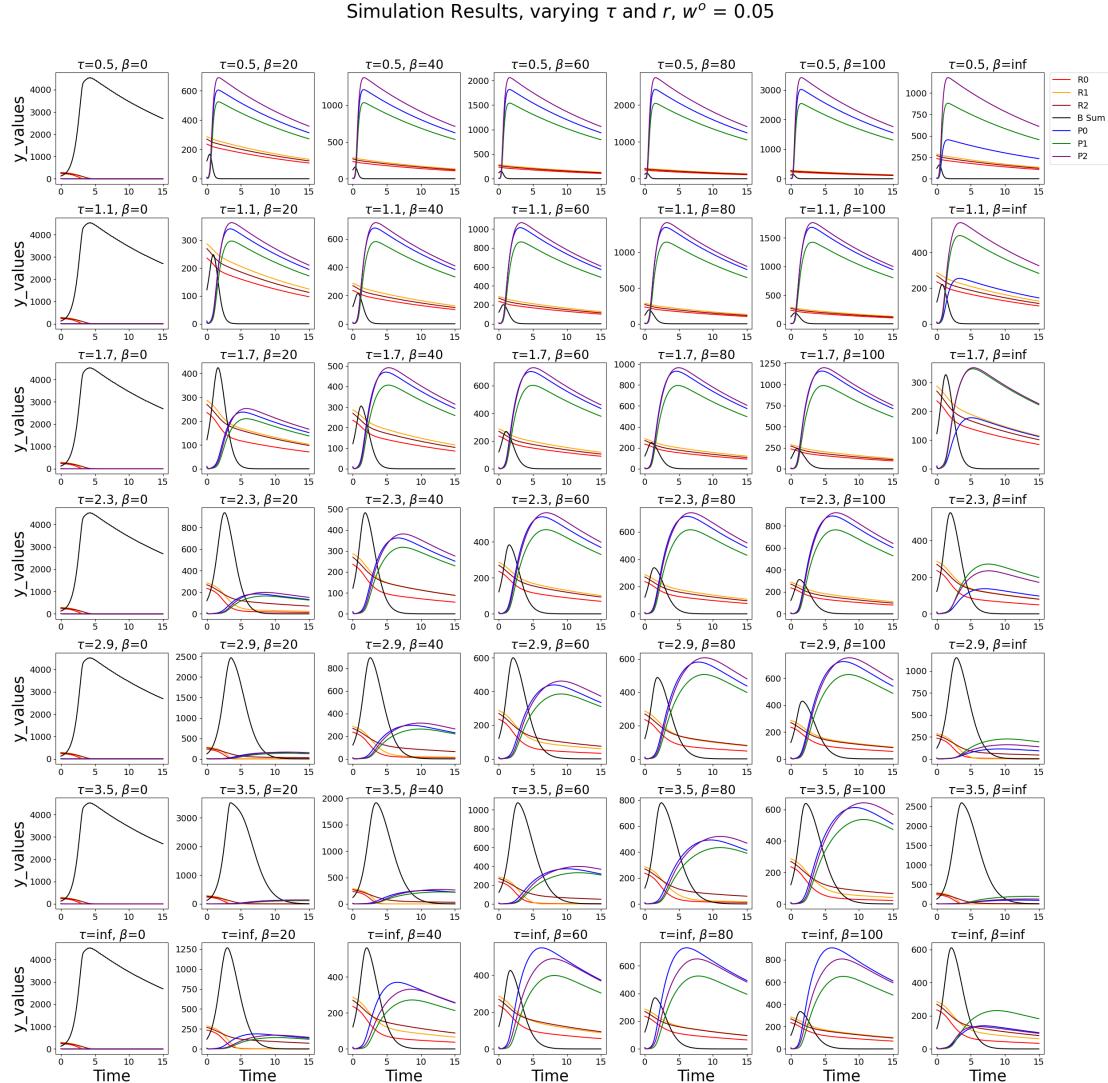


Figure 3.6: Washout $\omega^o = 0.05$.

Bibliography

- [1] Yuval Mulla, Janina Müller, Denny Trimcev, and Tobias Bollenbach. Extreme diversity of phage amplification rates and phage-antibiotic interactions revealed by PHORCE, December 2024.