



Analyzing the Dynamics of an Inflammatory Response to a Bacterial Infection in Rats

Allison Torsey¹ Amy Carpenter² Dr. Julia Arciero³

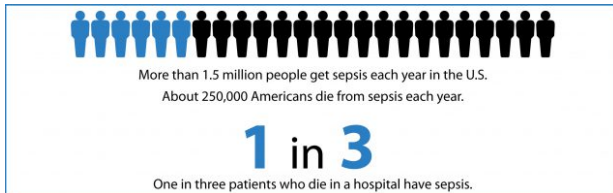
¹Department of Mathematics, SUNY Buffalo State

²Department of Natural Sciences and Mathematics, Lee University

³Department of Mathematical Sciences, IUPUI

January 26th, 2019

Sepsis



- | Sepsis is a life threatening condition that results from an overwhelming inflammatory response to a bacterial infection



Inflammation

- | Inflammation is the body's response to an infection
- | Too much inflammation can cause damage to healthy tissue
- | Bacterial infections that often cause sepsis:
 - | *Staphylococcus aureus* (*staph*)
 - | *Escherichia coli* (*E. coli*)
 - | some types of *Streptococcus*



Virulence

- | The strength of the pathogen
 - | Low virulent strains - large quantity in blood does not cause significant damage
 - | High virulent strains - small quantity will cause significant damage
- | We interpret virulence as a pathogen's ability to cause more inflammation
- | Bacteria are constantly mutating, so the virulence may vary over time

Experimental Observations

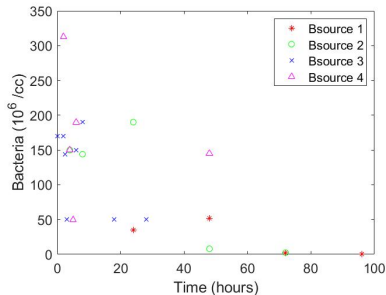
- | Rats were injected with a fibrin clot containing four different levels of bacteria (*E. coli*)
 - | For very high levels of bacteria, the clot was saturated and the bacteria was released immediately
- | The bacteria levels in the blood were measured over time
- | Once the bacteria levels in the blood reached a certain level, the rats were unable to recover
- | Used the data to parameterize sepsis model and predict health or disease outcome



Data Set: Time Dynamics

Dose administered to rats:

Bsource	Amount ($\times 10^6$ /cc)
1	128
2	248
3	505
4	1940





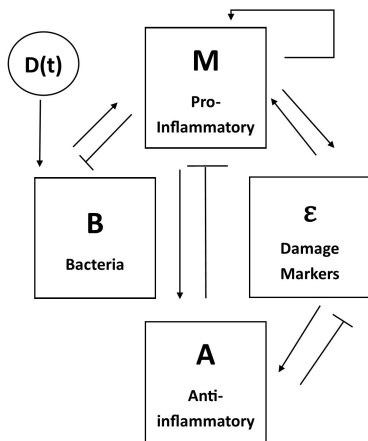
Expected Outcomes

- | **Septic death:** bacteria remains in the blood
- | **Aseptic death:** bacteria is eliminated but damage remains elevated
- | **Health:** both bacteria and damage are eliminated

Objective

Our goal is to use a mathematical model to predict the survivability range in rats for an infection while varying the initial dose, growth rate, or virulence of the bacteria

Model Schematic





Model

Bacteria:

$$\frac{dB}{dt} = D(t) + k_1 B \left(1 - \frac{B}{B_1}\right) - \frac{k_2 S_I B}{1 + k_3 B} - \frac{k_5 B M}{1 + k_A A} \quad (1)$$

Pro-inflammatory Response:

$$\frac{dM}{dt} = \frac{a_1 (k_M M + k_B c_1 B + k_4)}{(a_2 + k_M M + k_B c_1 B + k_4)(1 + k_A A)} - M M \quad (2)$$

Anti-inflammatory Response:

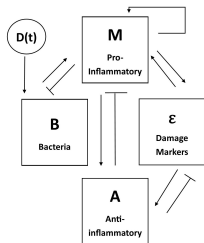
$$\frac{dA}{dt} = s_A + \frac{a_1 (M + k_4)}{(1 + M + k_4)(1 + k_A A)} - A A \quad (3)$$

Damage Markers:

$$\frac{d}{dt} = \dots + \frac{[f M T]_+}{1 + k_A A} \quad (4)$$



Model: Bacteria

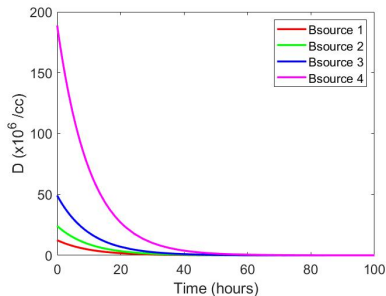


$$\frac{dB}{dt} = \underbrace{D(t)}_{\text{Dosing function}} + \underbrace{k_1 B \left(1 - \frac{B}{B_1}\right)}_{\text{growth}} - \underbrace{\frac{k_2 S_I B}{1 + k_3 B}}_{\text{local immunity}} - \underbrace{\frac{k_5 B M}{1 + k_A A}}_{\text{immune response}}$$

Dosing Function

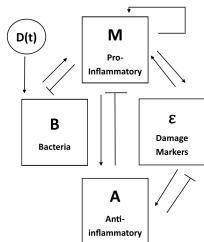
$$D(t) = k_D B_{source} e^{-k_D t}$$

- | The dosing function simulates how bacteria is released from the fibrin clot
- | No initial bacteria in the blood, $B(0) = 0$
- | Constant rate of decay, k_D





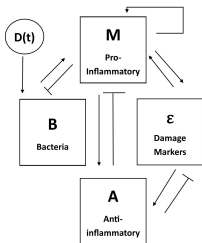
Model: Bacteria



$$\frac{dB}{dt} = \underbrace{D(t)}_{\text{Dosing function}} + \underbrace{k_1 B \left(1 - \frac{B}{B_1}\right)}_{\text{growth}} - \underbrace{\frac{k_2 S_I B}{1 + k_3 B}}_{\text{local immunity}} - \underbrace{\frac{k_5 B M}{1 + k_A A}}_{\text{immune response}}$$



Model: Pro-inflammatory Response

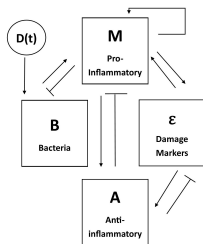


$$\frac{dM}{dt} = \frac{1(k_M M + k_B c_1 B + k)}{\underbrace{(2 + k_M M + k_B c_1 B + k)}_{\text{inflammation activation}} (1 + k_A A)}$$

$\frac{M}{Z}$
natural decay



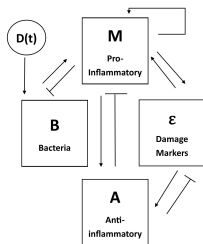
Model: Anti-inflammatory Response



$$\frac{dA}{dt} = \underbrace{\{S_A\}}_{\text{source term}} + \underbrace{\frac{a_1(M + k_4)}{(1 + M + k_4)(1 + k_A A)}}_{\text{anti-inflammation activation}} - \underbrace{\{Z\}}_{\text{natural decay}} A$$



Model: Damage



$$\frac{d}{dt} = \frac{[fM T]_+}{1 + k_A A} \Big|_{\{Z\}}$$

repair damage from pro-inflammatory response

Model Parameters

	Description	Value/ unit	Reference
k_1	pathogen growth rate		varied
B_∞	maximum carrying capacity	$145 \times 10^6 = CC$	optimized
k_2	rate at which the non-specific local response eliminates pathogen	.6/ I-units/h	Reynolds (2006)
s_I	source of non-specific local response	.005/ I-units/h	Reynolds (2006)
l	decay of non-specific local response	.002/h	Reynolds (2006)
k_3	rate at which the non-specific local response is exhausted by pathogen	.01 B-units	Reynolds (2006)
k_5	rate at which activated inflammatory response consumes pathogen	1.6/ M-units /h	optimized
k_A	inhibition rate of the anti-inflammatory response	2.6/ A-units	optimized
1	source of pro-inflammatory response	.08 M-units/h	Reynolds (2006)
2	decay of pro-inflammatory response	.12/h	Reynolds(2006)
k_M	activation of resting inflammatory response by activated inflammatory response	.01/M-units/h	Reynolds (2006)



Model Parameters Cont.

	Description	Value/unit	Reference
k_B	activation of resting inflammatory response by pathogen	.1 /B-units/h	Reynolds (2006)
C_1	virulence of pathogen		varied
k_ϵ	activation of resting inflammatory response by damage	.02/ -units h	Reynolds (2006)
M	decay of pro-inflammatory response	.12/h	Reynolds (2006)
S_A	source of anti-inflammatory response	.0125 A-units/h	Reynolds (2006)
a_1	maximum production rate of anti-inflammatory response	.04 A-units/h	Reynolds (2006)
k_4	relative effectiveness of pro-inflammatory response and damage inducing the production of the anti-inflammatory response	48 M-units/ -units	Reynolds (2006)
A	decay of the anti-inflammatory response	.1/h	Reynolds (2006)
	rate of recovery from damage		estimated
f	maximum rate of damage produced by the pro-inflammatory response	15 /M-units h	optimized
T	threshold for damage		estimated

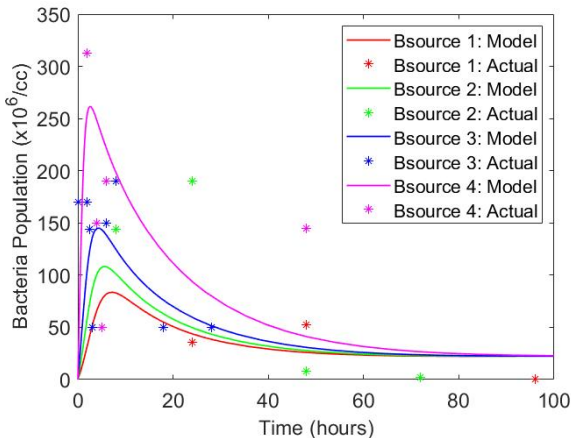
Parameter Estimation

- Using least squares optimization, the following parameters are fit to the data set

- k_A
- k_5
- f
- B_∞
- k_D

$$\min \left[\frac{\sum_{i=1}^P (B_{\text{actual},i} - B_{\text{model},i})^2}{\sum_{i=1}^P B_{\text{actual},i}^2} \right]$$

Fitting the Model to the Data





Steady States

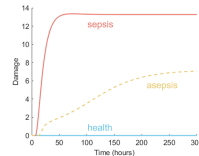
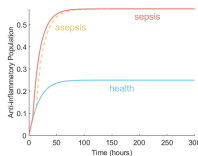
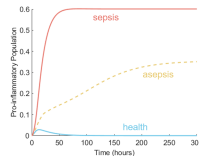
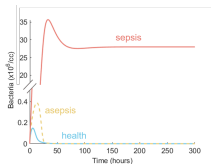
$$(B, M, A,)$$

- | Health: $(0, 0, A_1, 0)$
- | Aseptic Death: $(0, M_2, A_2, 2)$
- | Septic Death: $(B_3, M_3, A_3, 3)$



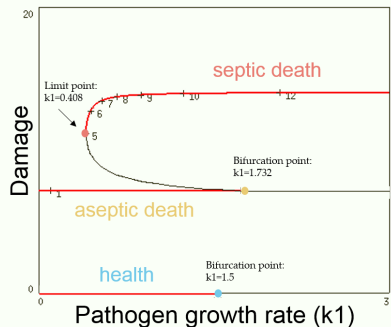
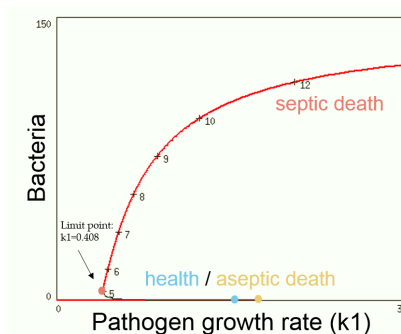
Time Dynamics

- | Sepsis:
 $B_{source} = 2$
- | Asepsis:
 $B_{source} = 1.3$
- | Health:
 $B_{source} = 1$
- | $k_1 = .5$



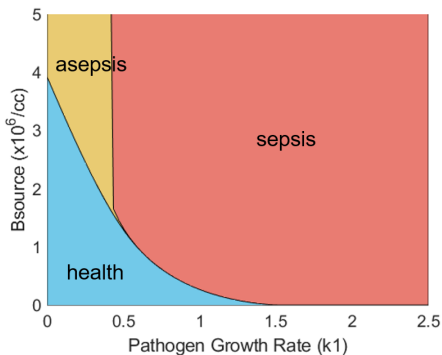


Bifurcations





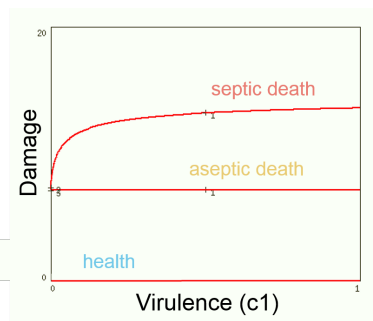
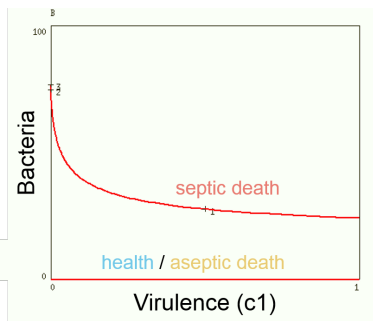
B_{source} vs. Pathogen Growth Rate





Bifurcations - Virulence

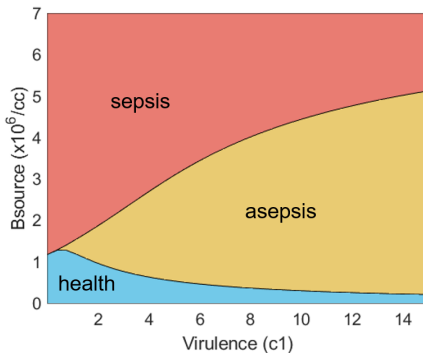
($k_1 = 0.5$)





Bsource vs. Virulence

$$(k_1 = 0.5)$$





Conclusions

- | This model highlights the balance between the pro-inflammatory response and the damage caused to the healthy tissue
- | Parameters ranges are predicted that yield outcomes: health, aseptic death, and septic death
- | May be useful for determining optimal treatment strategies (e.g. timing and amount of antibiotics or anti-inflammatory medication)



Future Work

- | Collect more data to be able to improve parameter estimation
- | Compare model to patients with peritoneal sepsis

Acknowledgements



This work is supported by the National Science Foundation
Mathematical Sciences Research Experiences for Undergraduate
Program and by the Mathematical Biosciences Institute
Thank you to our mentor, Dr. Arciero, for her assistance and
guidance on this project
SUNY Buffalo State for supporting my travel



References

- | Arciero, J. C., Ermentrout, G. B., Upperman, J. S., Vodovotz, Y., & Rubin, J. E. (2010). Using a mathematical model to analyze the role of probiotics and inflammation in necrotizing enterocolitis. *PLoS One*, 5(4), e10066.
- | Center for Disease Control and Prevention. (2018). Sepsis: Basic Information. Retrieved from <https://www.cdc.gov/sepsis/basic/index.html>.
- | Reynolds, A., Rubin, J., Clermont, G., Day, J., Vodovotz, Y., & Ermentrout, G. B. (2006). A reduced mathematical model of the acute inflammatory response: I. Derivation of model and analysis of anti-inflammation. *Journal of theoretical biology*, 242(1), 220-236.



Questions?