

1 **Supplemental Material**

2 **Video captions**

3 **Video S1.** Growth of attached *S. aureus* (green) in a control experiment without added
4 neutrophils (4 h).

5 **Video S2.** *S. aureus* biofilm growth visualized by brightfield microscopy from time $t = 0.5$ to 8
6 hours in 10% serum. This is the same field of view as Video S3.

7 **Video S3.** *S. aureus* biofilm growth visualized by overlaid brightfield and fluorescence
8 microscopy from time $t = 0.5$ to 8 hours in 10% serum. Green fluorescence consistently overlaps
9 all bacterial biomass (Video S2) indicating retention of the GFP-encoding plasmid.

10 **Video S4.** Interaction of neutrophils (red) with attached *S. aureus* (green) at an intermediate
11 neutrophil density of ~ 3000 per cm^{-2} and N:B ratio of 0.24 (4 h).

12 **Video S5.** Interaction of neutrophils (red) with attached *S. aureus* (green) at a high neutrophil
13 density of ~ 13000 per cm^{-2} and N:B ratio of 0.66 (4 h).

14 **Video S6.** Interaction of neutrophils (red) with attached *S. aureus* (green) when neutrophils were
15 added after giving bacteria a 3 h head start (4 h).

16 **Video S7.** Computational simulation of neutrophil-bacteria interaction on a two-dimensional
17 surface during a 4 h interval. Six bacterial colonies survive the interaction. Figure 5A illustrates
18 the paths taken by neutrophils during this simulation.

19 **Video S8.** Computational simulation of neutrophil-bacteria interaction on a two-dimensional
20 surface during a 4 h interval with alternative initial cell locations. This case uses parameter
21 values identical to the simulation presented in Video S7 (initial bacteria = 12, neutrophils = 8)

22 except that the initial locations of both cell types are different as they have been randomly
23 placed. In this simulation, 3 bacterial colonies survive to the end of the 4 h simulation period.

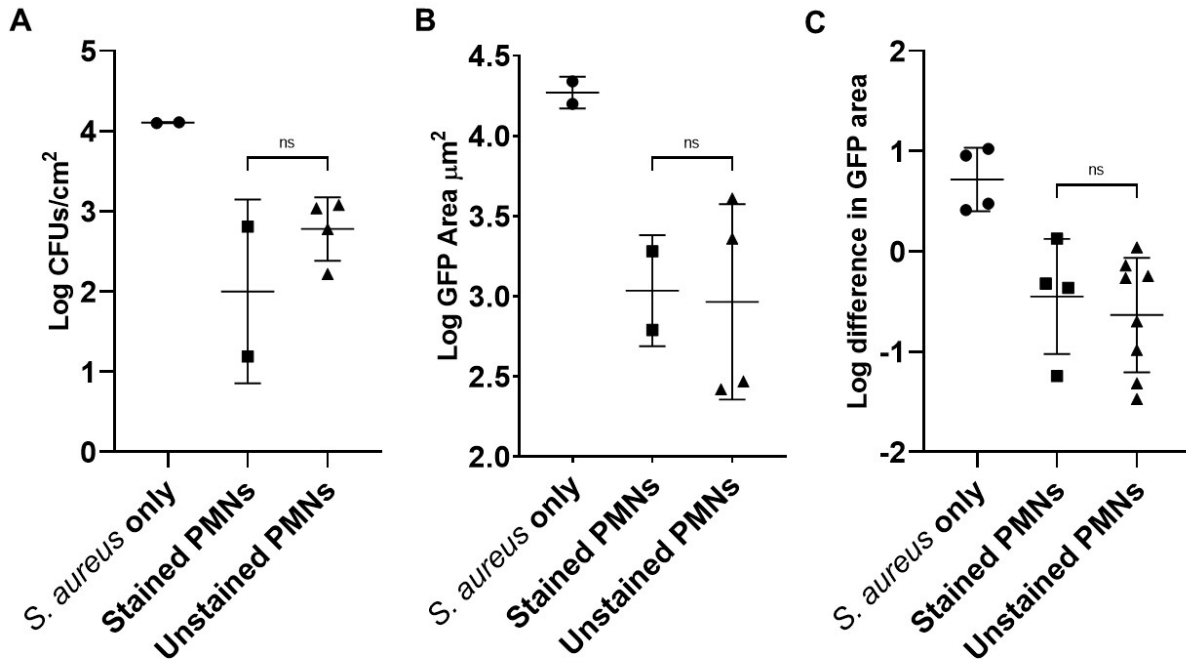
24 **Video S9.** Computational simulation of neutrophil-bacteria interaction on a two-dimensional
25 surface during a 4 h interval with identical cell locations. This case uses parameter values and
26 initial cell locations that are identical to the simulation presented in Video S7 to show that the
27 paths taken by neutrophils are quite different as these are stochastic in nature.

28 **Table S1.** Random motility coefficient from mean square displacement versus time analysis. The
 29 coefficient did not vary significantly between fields of view where there were bacteria and
 30 neutrophils or where neutrophils were alone.

Condition	<i>n</i>	(cm ² s ⁻¹)	(cm ² s ⁻¹)	Mean <i>R</i> ²
		<i>D</i> _m	SD	
Neutrophils alone	4	2.15 x 10 ⁻⁸	0.72 x 10 ⁻⁸	0.950
Neutrophils + bacteria	4	3.17 x 10 ⁻⁸	0.35 x 10 ⁻⁸	0.988
All	8	2.67 x 10 ⁻⁸	0.75 x 10 ⁻⁸	0.969

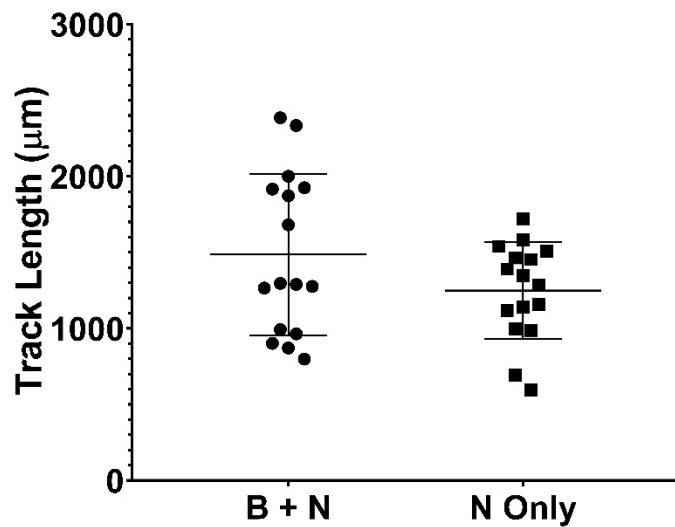
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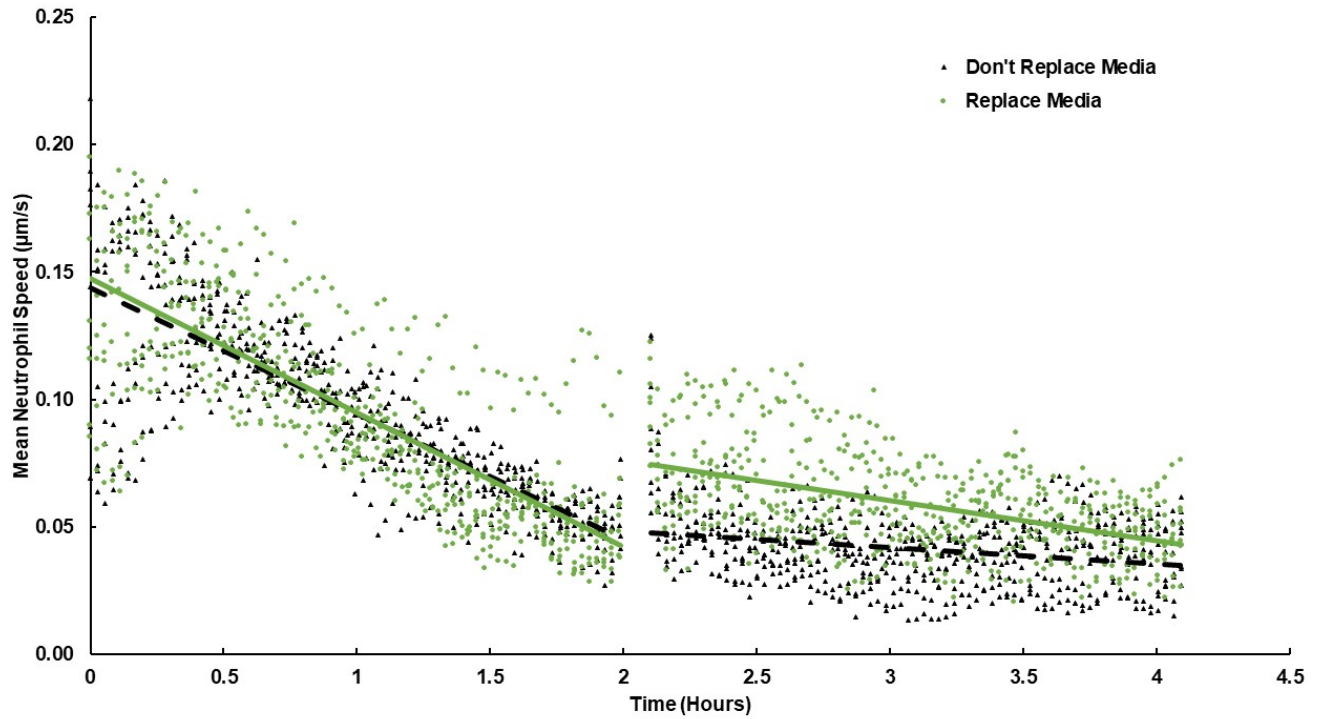
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35 **Figure S1.** LysoBrite staining does not affect killing of *S. aureus* by neutrophils. Approximately
 36 10^3 CFUs/cm² were attached to the surface and challenged with neutrophils that had been stained
 37 with LysoBrite or received a sham treatment. (A) Bacteria were scraped from the surface,
 38 vortexed, and plated on tryptic soy agar to determine remaining viable bacteria on the surface. n
 39 = 2 (control and stained PMNs) or 4 (unstained PMNs) from 2 independent experiments. (B) A
 40 stitched image of the entire well was generated using the 10x objective to determine the total
 41 amount of GFP area remaining in each well after a 4 hour challenge with neutrophils. $n = 2$
 42 (control and stained PMNs) or 4 (unstained PMNs) from 2 independent experiments. (C) The log
 43 difference in GFP area over 4 hours for each field of view. $n = 4$ (control and stained PMNs) or 8
 44 (unstained PMNs) fields of view from 2 independent experiments. Error bars represent standard
 45 deviation of the sample. Differences between stained and unstained neutrophils were not
 46 significant by an unpaired t test.



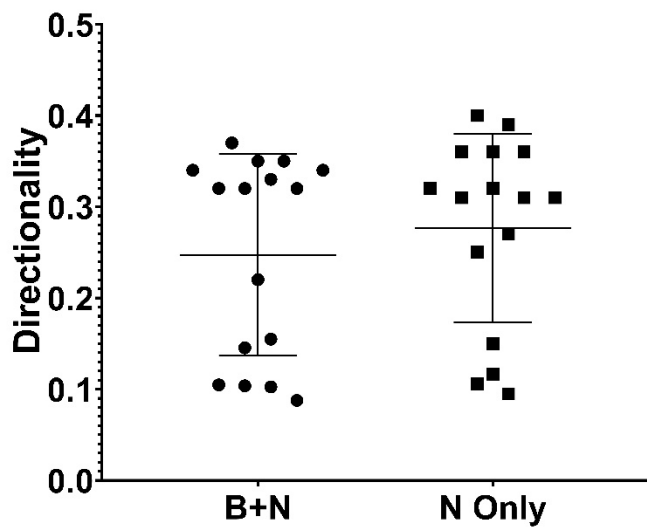
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49 **Figure S2.** Neutrophil track length is similar on a sterile surface or on a surface seeded with *S.*
50 *aureus*. The average speed of all neutrophils in a field of view was calculated for each frame and
51 then integrated with respect to time to obtain an average track length value. The average distance
52 traveled by a neutrophil did not vary between wells with bacteria and wells without bacteria ($p =$
53 0.1368 by an unpaired t test). $n = 16$ fields of view each from 5 independent experiments. B+N
54 denotes bacteria with neutrophils; N only denotes neutrophils in the absence of bacteria. Error
55 bars represent standard deviation of the sample.



56

57 **Figure S3.** Mean neutrophil speed with and without medium supplementation. Experiments were
 58 performed with bacteria present. Old medium was gently removed via pipette and replaced with
 59 10% human serum in HBSS from the same donor (serum was kept on ice and warmed to 37°C
 60 prior to addition) at 2 h. Neutrophil speed was not restored to starting levels when fresh medium
 61 was added, however a slight increase in speed was observed compared to control wells ($p <$
 62 .0001). $n = 8$ fields of view, 2 independent experiments.

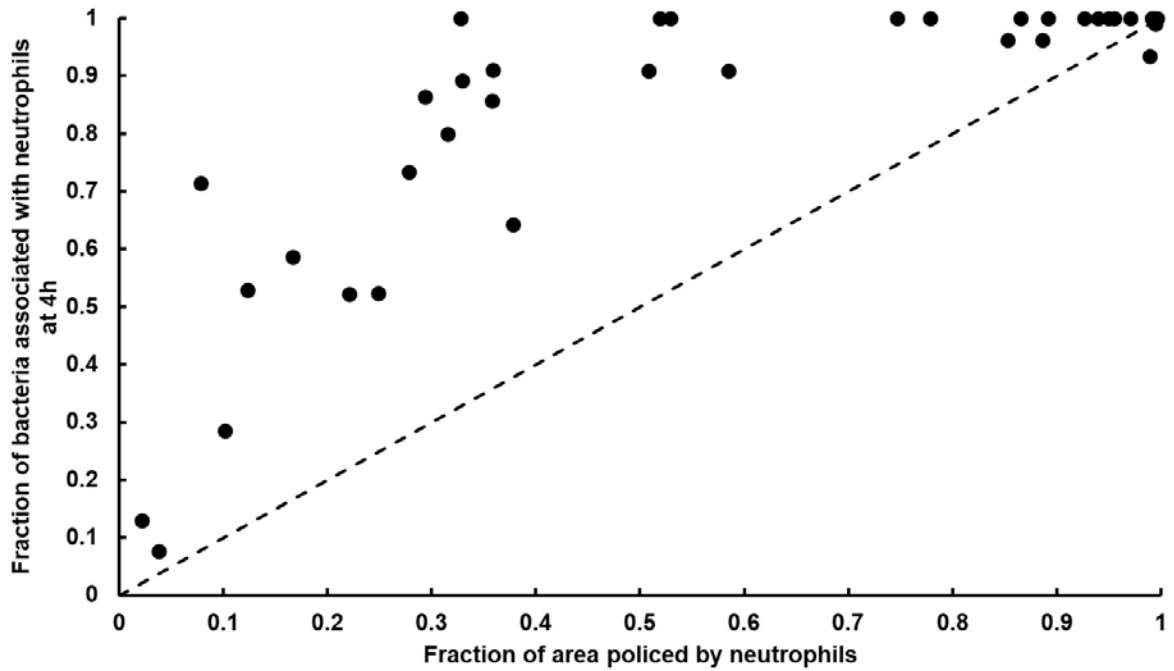


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64 **Figure S4.** Neutrophil directionality measured by dividing displacement by total distance
 65 traveled. No statistically significant difference was observed between experiments with bacteria
 66 and neutrophil only controls ($p = 0.4453$ by an unpaired t test). $n = 16$ fields of view each from 5
 67 independent experiments. B+N denotes bacteria with neutrophils; N only denotes neutrophils in
 68 the absence of bacteria. Error bars represent standard deviation of the sample.

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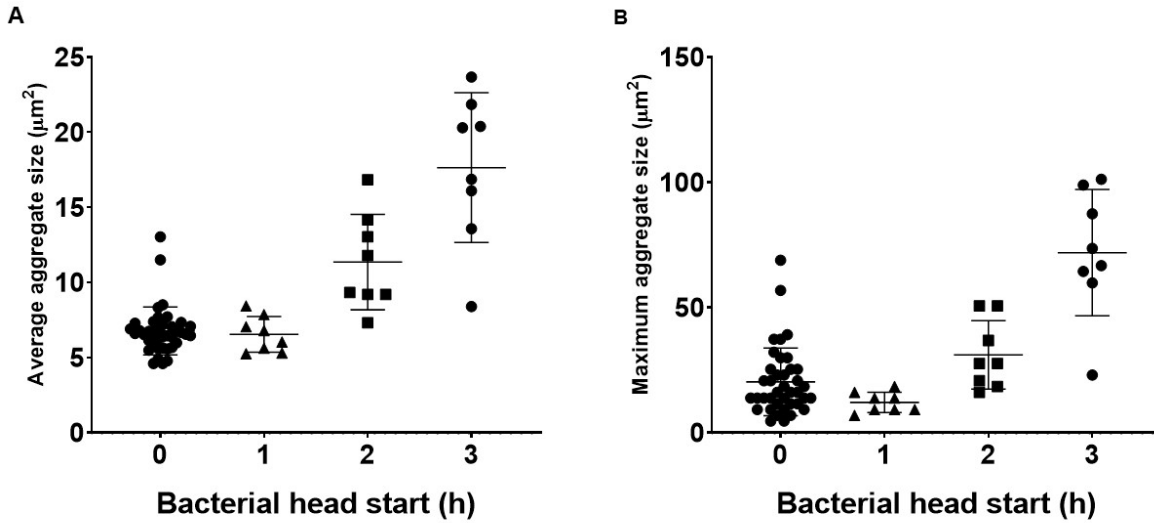
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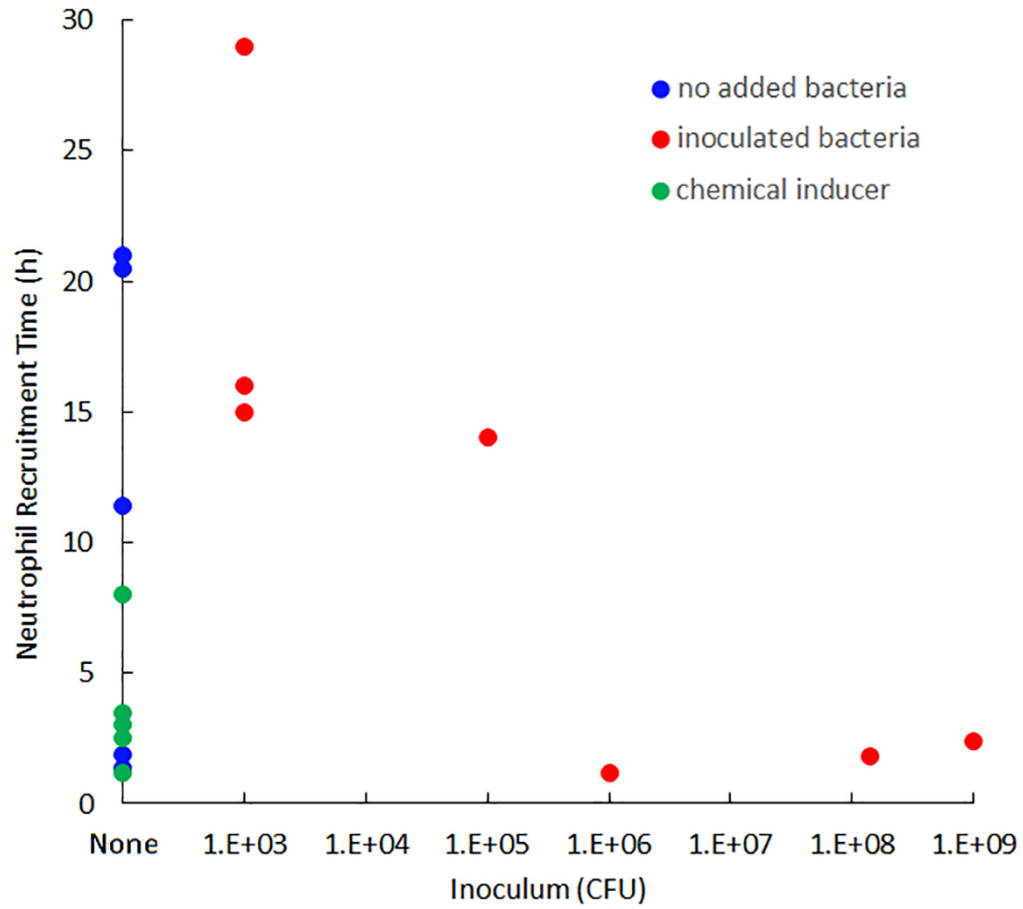
72 **Figure S5.** Fraction of bacterial objects discovered as a function of the fraction of the surface
73 area patrolled by neutrophils. The fraction of bacterial aggregates that were discovered by a
74 neutrophil within the 4 hour observation window were determined manually. The dashed line
75 represents the expected curve if aggregate discovery was purely random. $n = 39$ fields of view
76 from 9 independent experiments.

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79 **Figure S6:** *S. aureus* aggregate sizes at $t = 0$. (A) The average size of a *S. aureus* aggregate at the
80 start of imaging given different head start times. Each point represents the average size of all
81 aggregates in a field of view. (B) The maximum observed aggregate size in a field of view at the
82 start of imaging. $n = 24$ fields of view from 4 independent experiments for head start data. $n = 39$
83 fields of view from 9 independent experiments for without head starts. Error bars represent
84 standard deviation of the sample.



85

86 **Figure S7.** Neutrophil recruitment times measured in murine models. See the supplemental
 87 methods that follow for details.

88

89 **Methods for literature survey of neutrophil recruitment times in murine models.** We
90 identified 18 published data sets from 14 papers (Table S2) that contained sufficient quantitative
91 information to extract a numerical value of a characteristic neutrophil recruitment time. This
92 time was estimated by fitting a logistic function, which is an S-shaped curve, to neutrophil signal
93 versus time data of the form

94
$$N(t) = \frac{N^*}{1 + \exp(-k(t - t_o))}$$

95 where $N(t)$ is neutrophil signal as a function of time, N^* is the plateau neutrophil signal at long
96 time, t is time, k is a parameter reflecting the steepness of the response, and t_o is the characteristic
97 time for the response to occur. The parameter t_o is the time value plotted in Figure S5. This time
98 corresponds to the inflection point of the S-shaped curve.

99 The data sets analyzed are summarized in Table S2 below. The data include experiments with
100 chemical inducers (no added bacteria), inoculated *Staphylococcus aureus* or *Staphylococcus*
101 *epidermidis* (other microorganisms were excluded from the search), and some controls in which
102 implants without added bacteria were investigated.

103

104 **Table S2.** Summary of neutrophils recruitment times, anatomical sites, stimuli, and sources.

Site	Stimulus	no bacteria (h) t_0	bacteria (h) t_0	chemical (h) t_0	Inoculum (cfu)	Source
skin on back	punch biopsy (no inoculation)	11.4			none	1
subQ	Ti disk, uninfected	20.5			none	2
subQ	Ti disk coated with <i>S. aureus</i>		21		NR	2
spine, L4 process	Stainless steel (SS) implant - control	21			none	3
spine, L4 process	SS implant inoculated with <i>S. epidermidis</i>		29		10^3	3
subQ	agar bead containing <i>S. aureus</i>		1.2		10^6	4
knee joint	SS implant, <i>S. aureus</i> strain Xen 40		16		10^3	5
knee joint	SS implant, <i>S. aureus</i> strain ALC2906		15		10^3	5
peritoneum	injection 30 μ g LPS			8	none	6
knee joint	injection of <i>S. aureus</i>		14		10^5	7
pleural cavity	injection of 100 μ g zymosan			3	none	8
air pouch on back	injection of 0.5 μ g MIP-2			1.2	none	9
peritoneum	injection of 1 mg zymosan			3.5	none	10
liver	sterile thermal injury	1.9			none	11
skin on back	6 mm full thickness punch biopsy	1.4			none	12
peritoneum	injection of 5 mg/kg peptidoglycan			2.5	none	13
peritoneum	injection of <i>S. aureus</i>		2.4		10^9	13
peritoneum	injection of <i>S. aureus</i>		1.8		1.4×10^8	14
	Mean	11.2	12.6	3.6		
	SD	9.6	10.1	2.6		

105 NR – not reported; SD – standard deviation.

106 **References**

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Supplemental Material: Solution of the Chemoattractant Concentration Equation. The chemoattractant concentration $u(\mathbf{x}, t)$ satisfies the equation

$$u_t = D_1 \nabla^2 u + 2\beta \sum_{j=1}^{12} \sum_{k, \ell \in \mathbb{Z}} c_j(t) \delta(\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))),$$

with initial and boundary conditions

$$u(\mathbf{x}, 0) = 2\beta \sum_{j=1}^{12} \sum_{k, \ell \in \mathbb{Z}} \delta(\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))), \quad \frac{\partial u}{\partial z}(x, y, 0, t) = 0.$$

Here,

$$c_j(t) = \begin{cases} e^{rt} & 0 \leq t < T_j \\ 0 & t \geq T_j \end{cases}$$

is the population of colony j , and T_j is the time of first encounter of a neutrophil with that colony (T_j may be larger than the total run time of 240 min.).

Note by linearity that we can decompose

$$u(\mathbf{x}, t) = \sum_{j=1}^{12} u_j(\mathbf{x}, t)$$

where u_j is the contribution to total chemoattractant concentration from bacteria colony j , where u_j satisfies

$$(u_j)_t = D_1 \nabla^2 u_j + 2\beta \sum_{k, \ell \in \mathbb{Z}} c_j(t) \delta(\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))),$$

with initial and boundary conditions

$$u_j(\mathbf{x}, 0) = 2\beta \sum_{k, \ell \in \mathbb{Z}} \delta(\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))), \quad \frac{\partial u_j}{\partial z}(x, y, 0, t) = 0.$$

For $t < T_j$ these systems have solutions

$$\begin{aligned} u_j(\mathbf{x}, t) &= \sum_{k, \ell \in \mathbb{Z}} \int_0^t \frac{2\beta c_j(\hat{t})}{(4\pi D_1(t - \hat{t}))^{3/2}} \exp\left(-\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|^2}{4D_1(t - \hat{t})}\right) d\hat{t} \\ &= \sum_{k, \ell \in \mathbb{Z}} \frac{\beta c_j(t)}{4\pi D_1 |\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|} \\ &\quad \left[\exp\left(-|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))| \sqrt{\frac{r}{D_1}}\right) \operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1 t}} - \sqrt{rt}\right) \right. \\ &\quad \left. + \exp\left(|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))| \sqrt{\frac{r}{D_1}}\right) \operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1 t}} + \sqrt{rt}\right) \right], \end{aligned}$$

where $\operatorname{erfc}(z) = 1 - \operatorname{erf}(z) = \frac{2}{\sqrt{\pi}} \int_z^\infty e^{-t^2} dt$ is the complementary error function.

For $t \geq T_j$, the solution is

$$\begin{aligned}
u_j(\mathbf{x}, t) &= \sum_{k, \ell \in \mathbb{Z}} \int_0^{T_j} \frac{2\beta c_j(\hat{t})}{(4\pi D_1(t - \hat{t}))^{3/2}} \exp\left(\frac{-|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|^2}{4D_1(t - \hat{t})}\right) d\hat{t} \\
&= \sum_{k, \ell \in \mathbb{Z}} \frac{\beta c_j(t)}{4\pi D_1 |\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|} \\
&\quad \left\{ \exp\left(-|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))| \sqrt{\frac{r}{D_1}}\right) \right. \\
&\quad \left[\operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1 t}} - \sqrt{rt}\right) - \operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1(t - T_j)}} - \sqrt{r(t - T_j)}\right) \right] \\
&\quad + \exp\left(|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))| \sqrt{\frac{r}{D_1}}\right) \\
&\quad \left. \left[\operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1 t}} + \sqrt{rt}\right) - \operatorname{erfc}\left(\frac{|\mathbf{x} - (\mathbf{x}_j + (800k, 800\ell, 0))|}{\sqrt{4D_1(t - T_j)}} + \sqrt{r(t - T_j)}\right) \right] \right\}
\end{aligned}$$