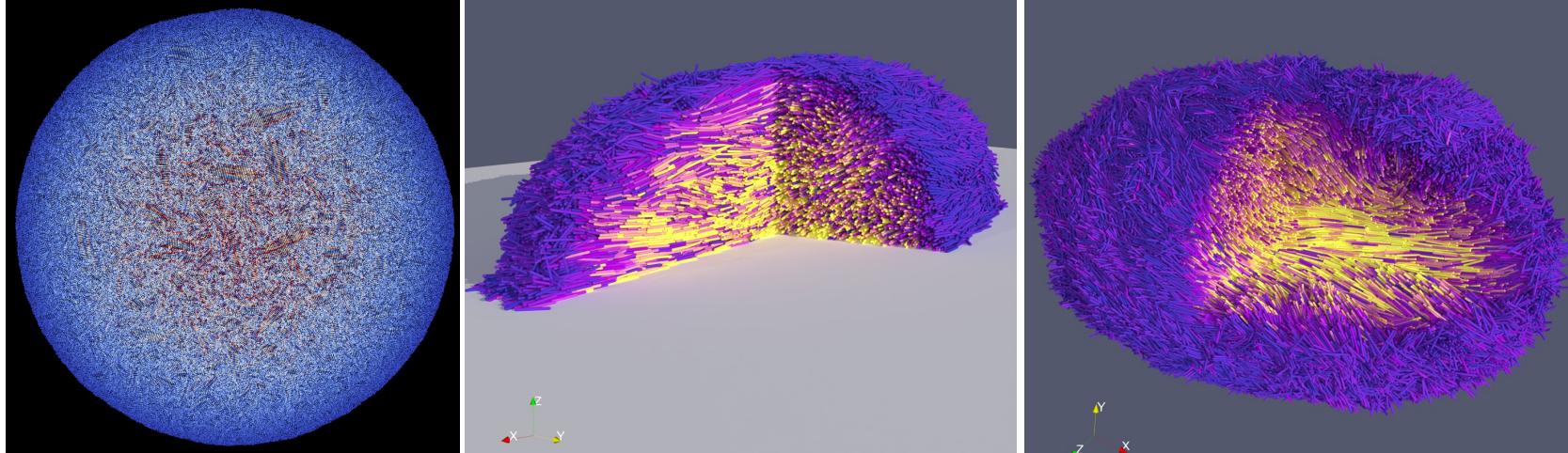


# Modeling of bacteria growth via aLENS



**Taeyoon Kim**

Associate Professor, Purdue University  
Visiting Scholar, Flatiron Institute

# Bacteria population exponentially grows over time



E-coli

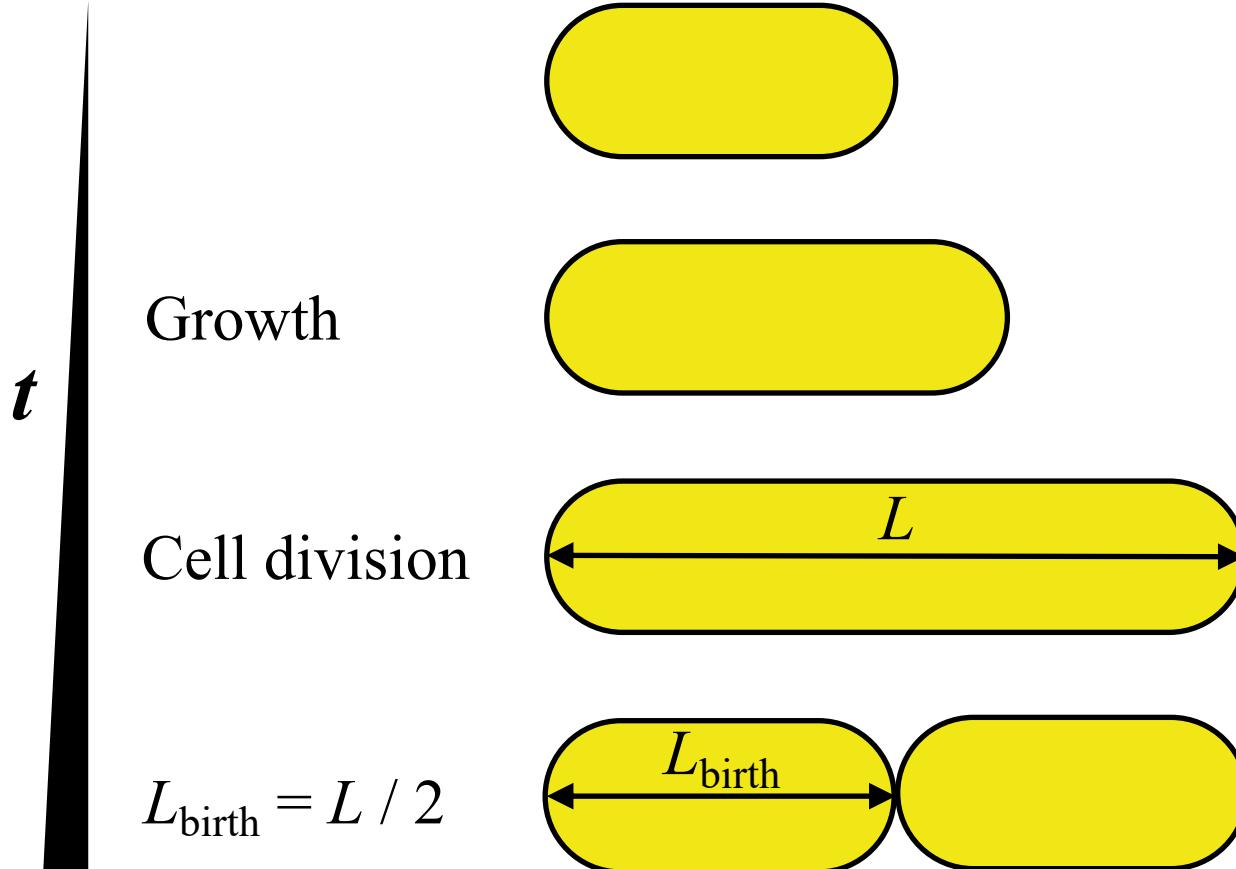
[<https://youtu.be/gEwzDydcIWc>]



Lactobacillus

[<http://www.davidbarlowarchive.com>]

# Growth of bacteria population can be simply described an exponentially increasing function



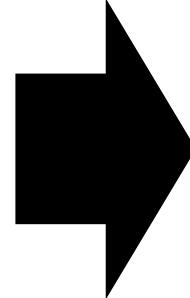
$$P(t) = P_0 e^{kt}$$

$P(t)$ : # of bacteria at time  $t$

$P(0)$ : # of bacteria at time = 0

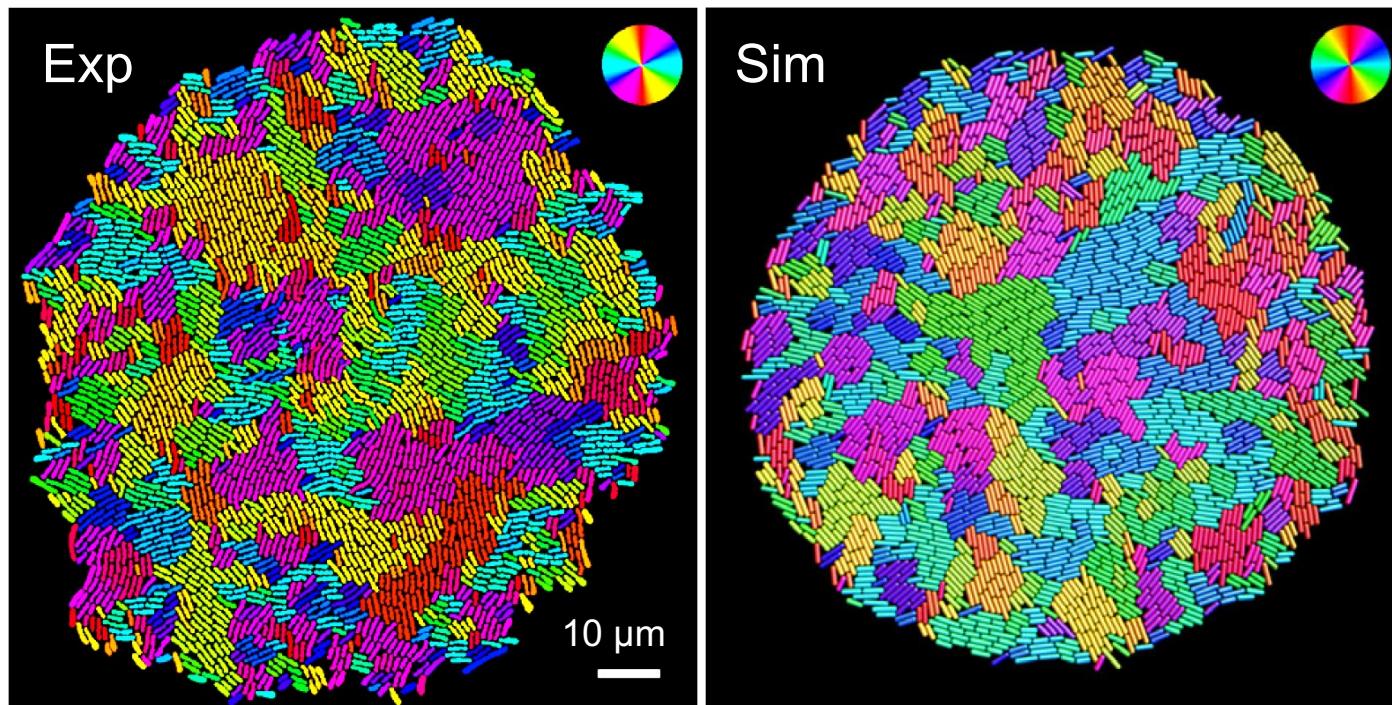
$k$ : positive constant of growth

**For discrete computational modeling, bacteria are often simplified into spherocylinders that elongate and divide**

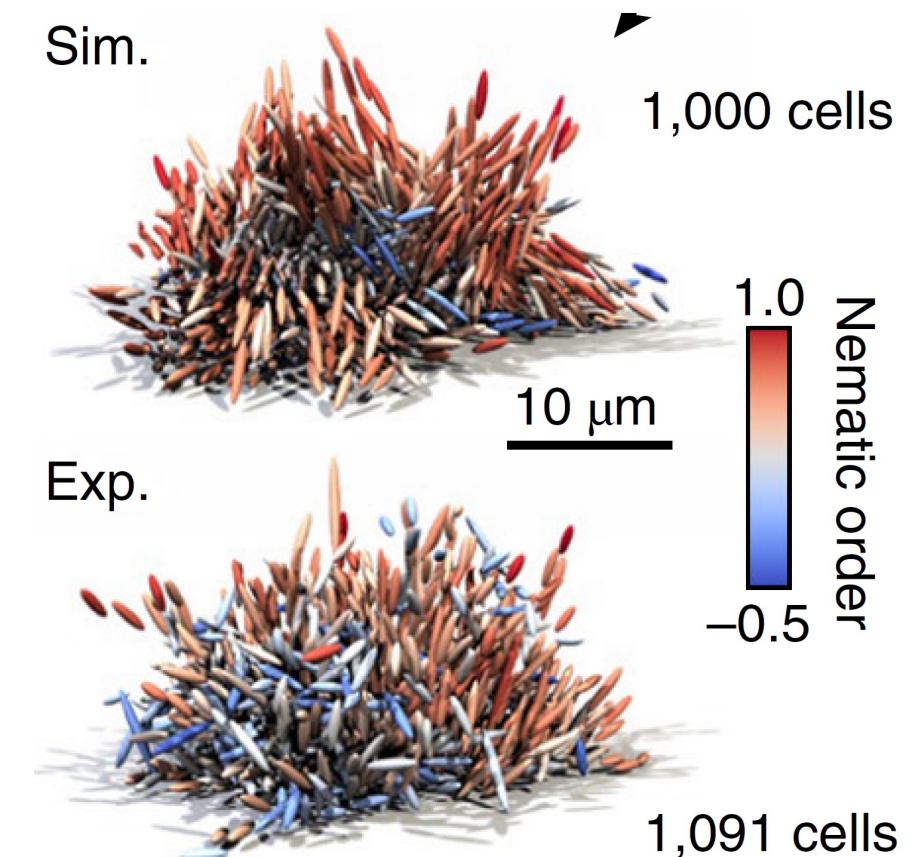


[<http://my.clevelandclinic.org/>]

# Bacteria growth in 2D and 3D have been investigated in numerous computational studies



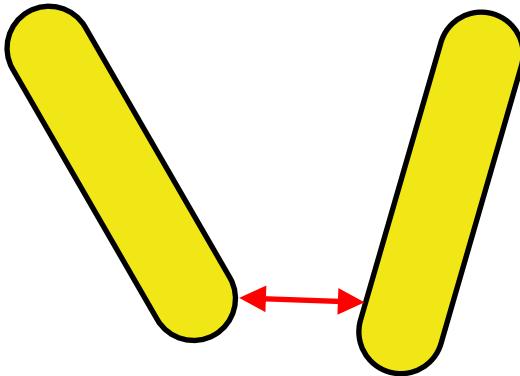
Formation of nematic domains by *E. coli*  
[R. Hartmann et al., Nat Phys, 2019]



Biofilm development by *V. Cholerae*  
[R. Hartmann et al., Nat Phys, 2019]

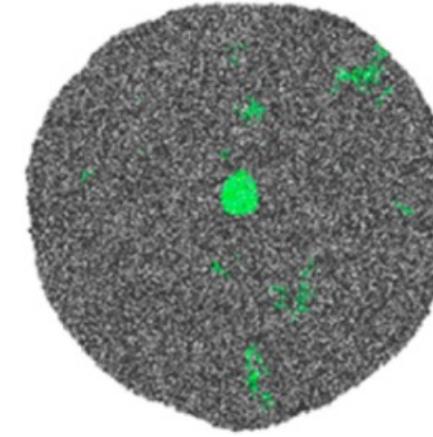
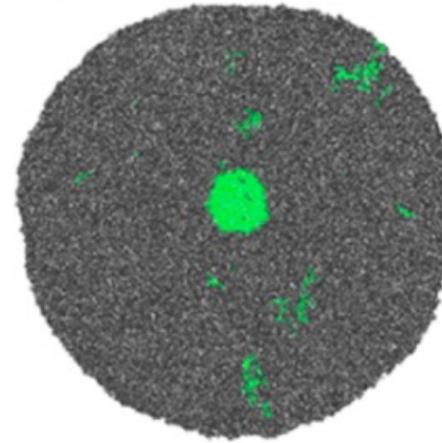
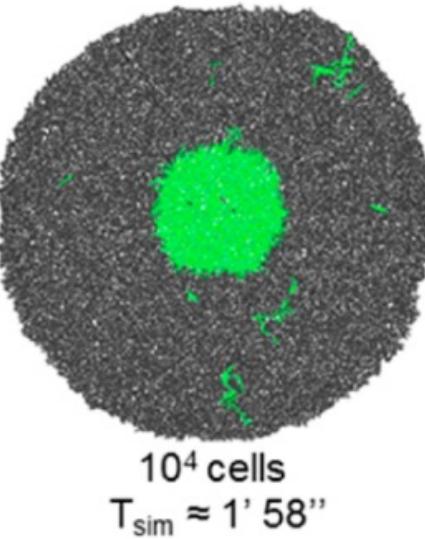
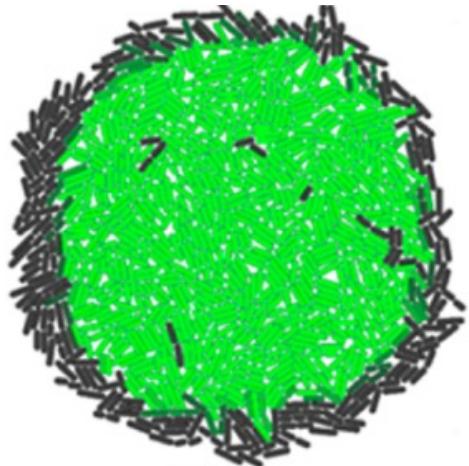
# Current computational models for bacteria growth have critical limitations

- Significant overlaps between bacteria can occur during the exponential growth because most of the models use “soft repulsion.”

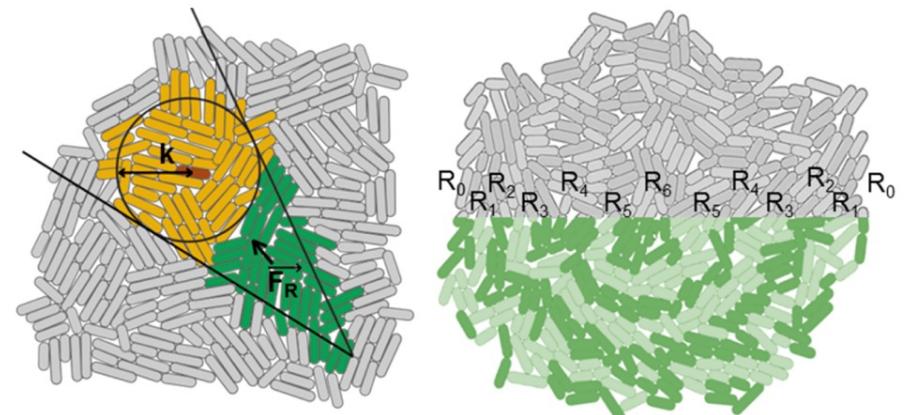


- The maximum number of bacteria that can be simulated is relatively low due to several reasons. (e.g., no parallel computing, inefficient algorithm)

A model called “gro” can simulate a very large number of bacteria, but it is only for 2D circular shapes, and the calculation of internal pressure/stress buildup is not possible



A screenshot of a web browser showing the `gro` software interface. The URL is `depts.washington.edu/soslab/gro/`. The interface displays a 2D simulation of a bacterial colony with various colored cells (green, red, yellow) and a grid of gray rod-shaped bacteria. The word "gro" is prominently displayed in large, bold letters. Below the interface, the text "The cell programming language" and "Guarded Command Programming + Cell Signaling + Micro-Colony Simulation" is visible.



# aLENS can be used to simulate very large bacteria population without such limitations

2D



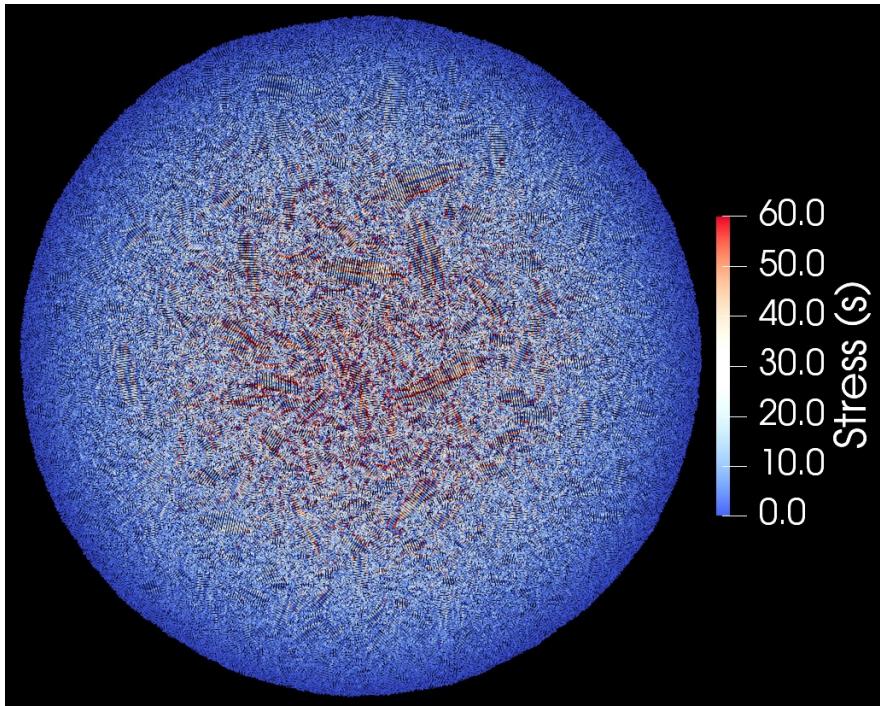
3D



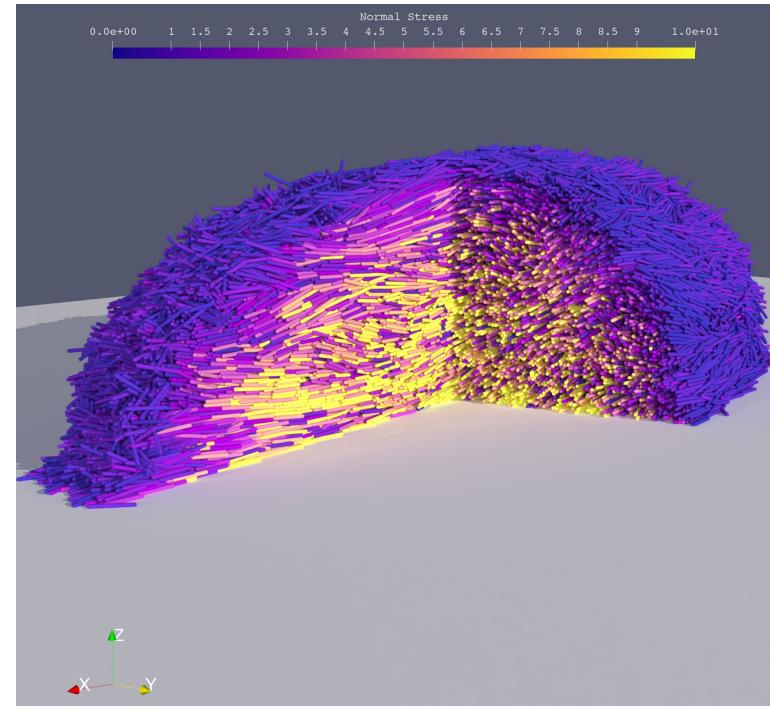
- Minimal overlaps between bacteria
- Accurate estimation of internal stress/pressure
- Good scalability (up to ~1M bacteria)

# aLENS can be used to simulate very large bacteria population without such limitations

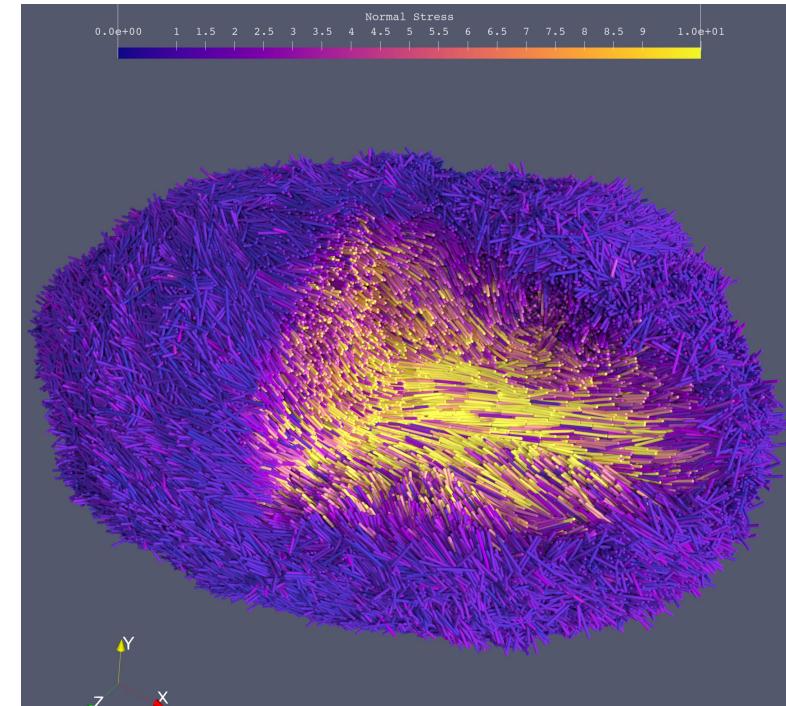
2D



2.5D

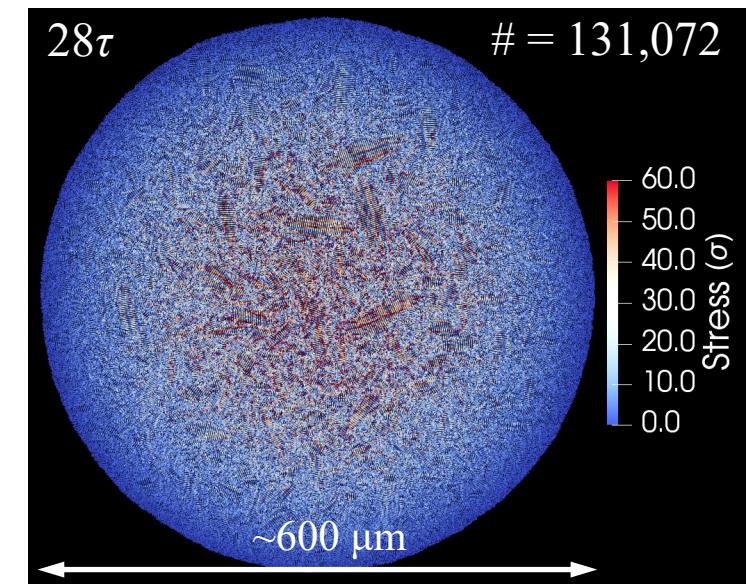
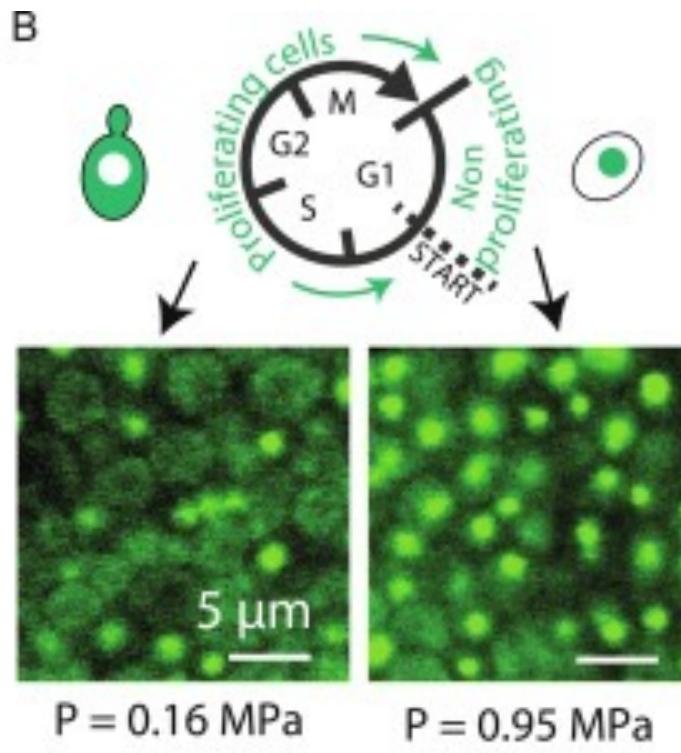
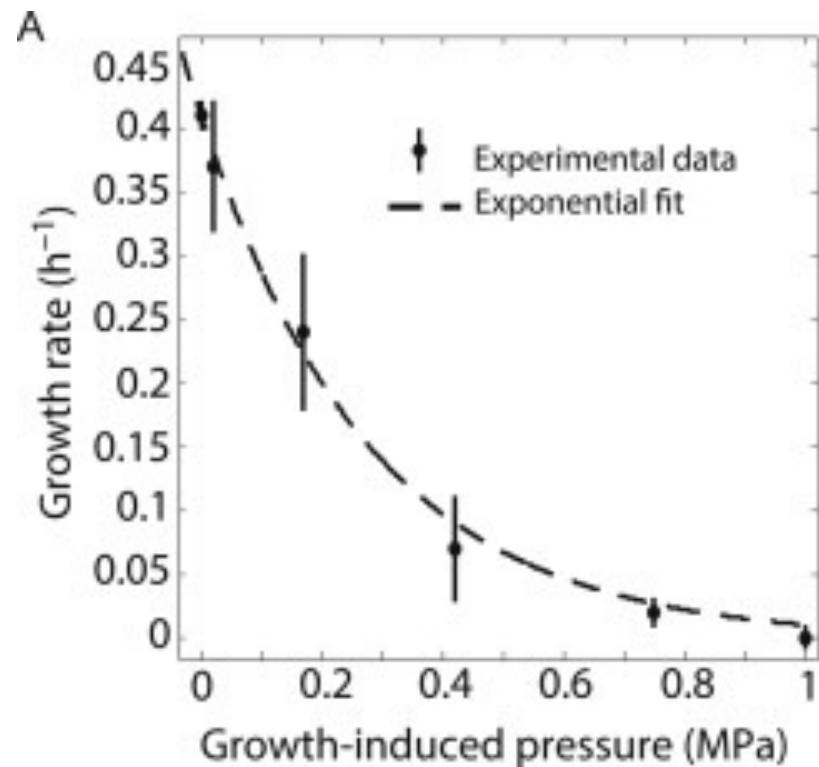


3D



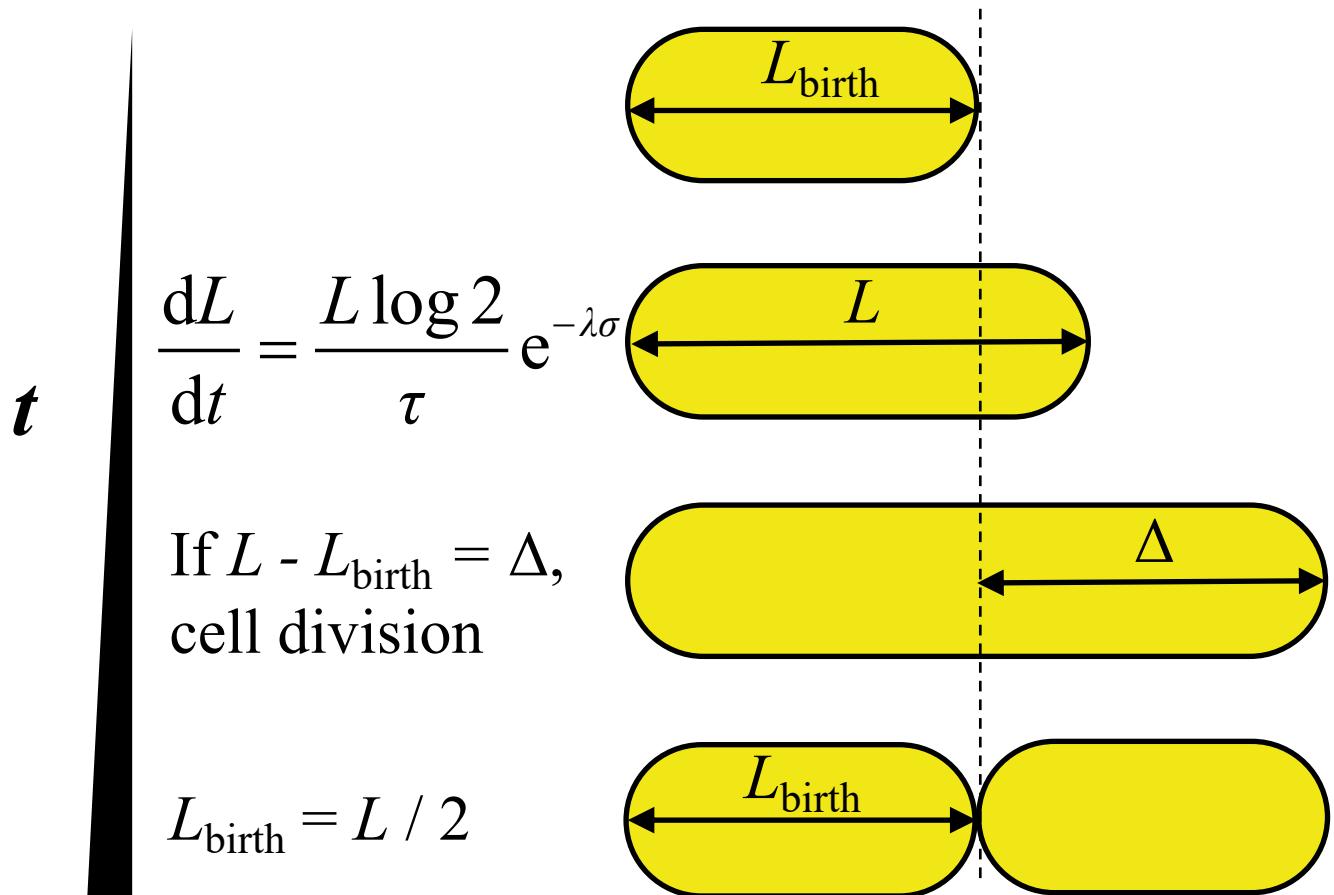
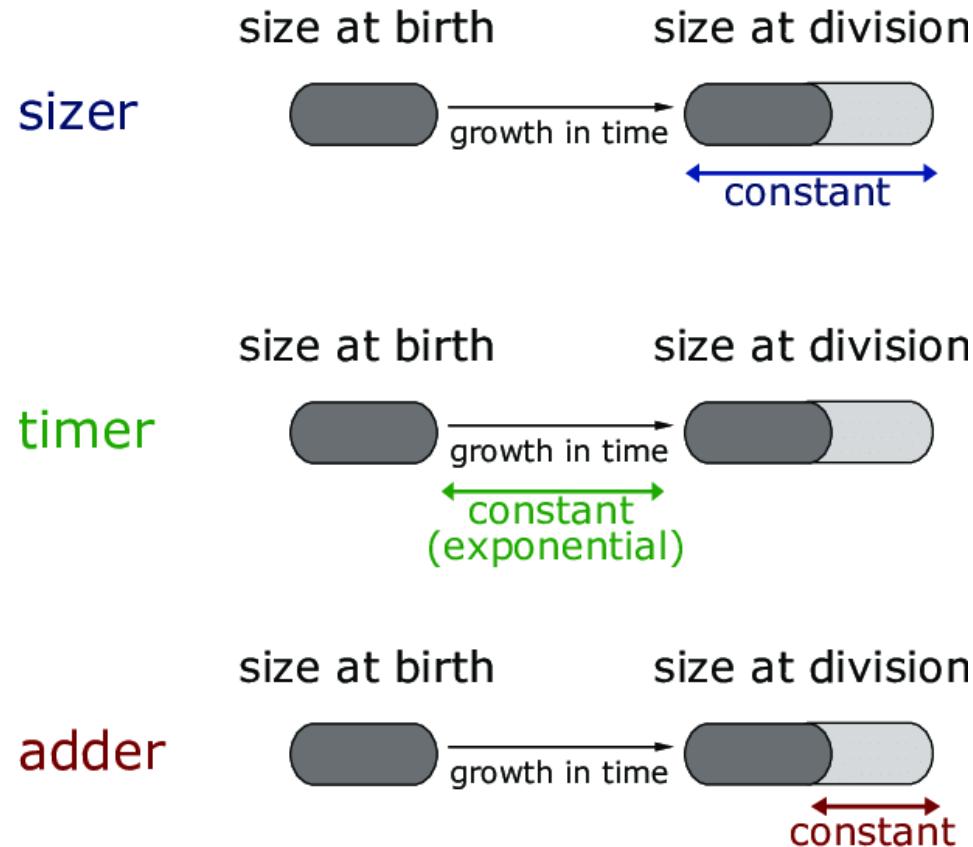
- Minimal overlaps between bacteria
- Accurate estimation of internal stress/pressure
- Good scalability (up to ~1M bacteria)

# In case of yeast, a growth rate decreases roughly exponentially as a function of growth-induced pressure



[DOI: 10.1016/bs.mcb.2018.06.010]

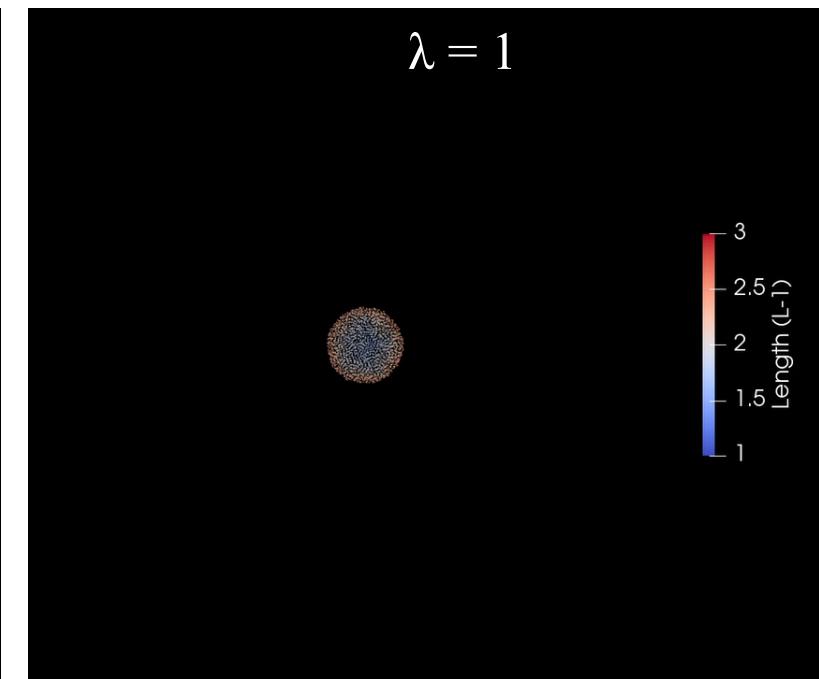
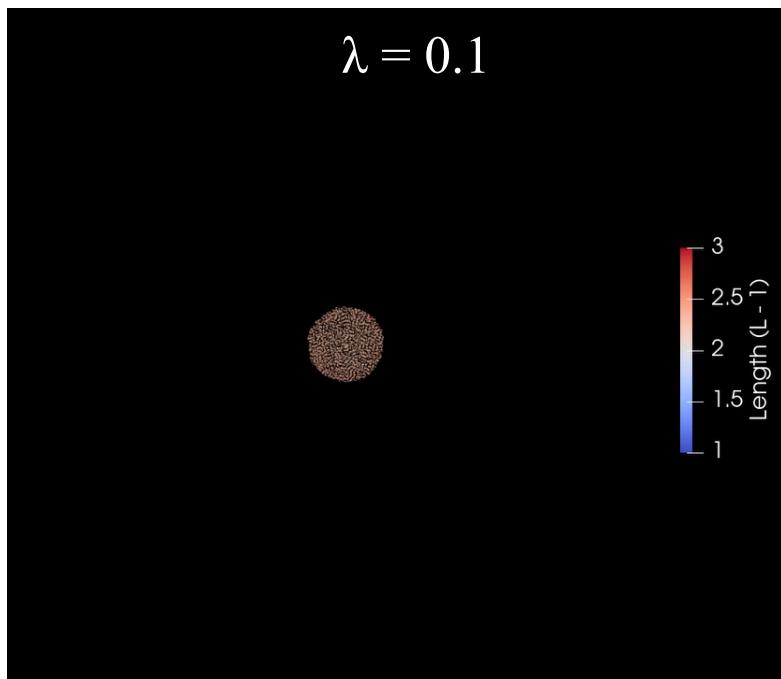
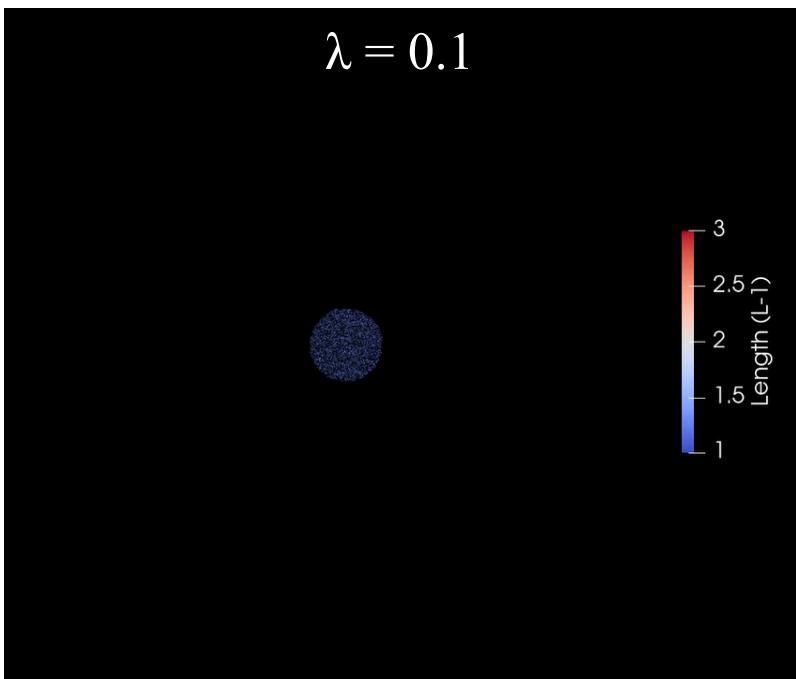
# We currently investigate the role of stress-sensitivity in the growth of bacteria population, based on the adder model

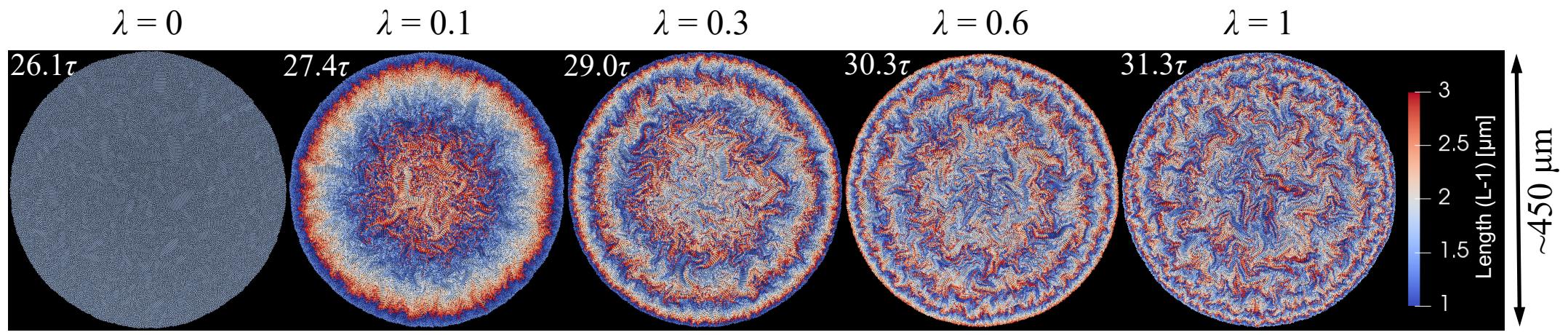


[DOI: 10.18388/abp.2018\_2798]

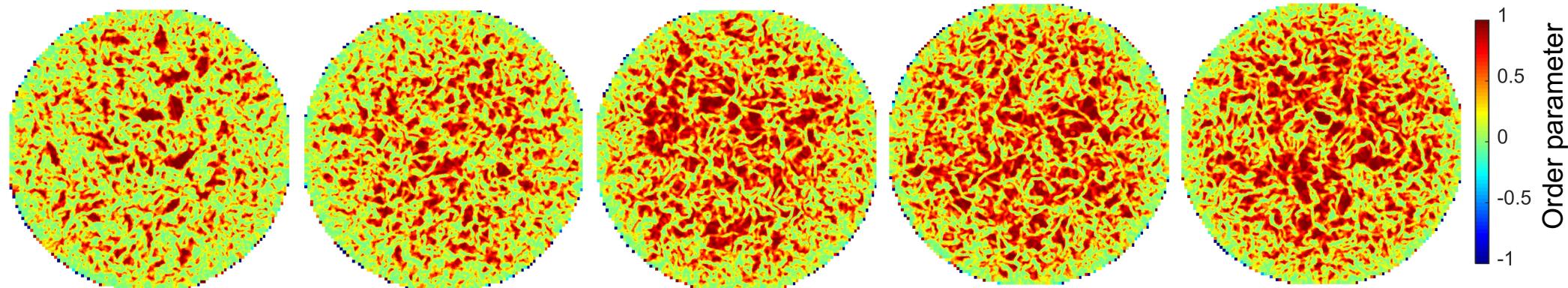
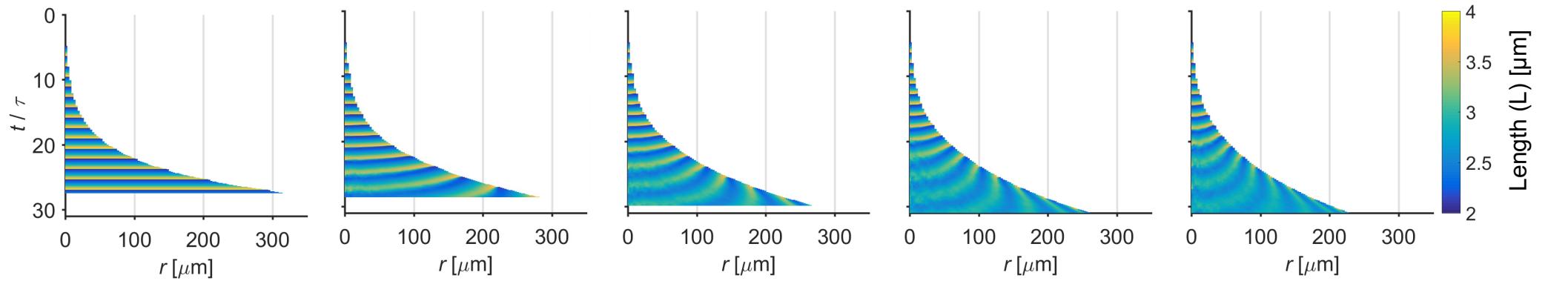
# Stress dependence of the growth of short bacteria results in a wave-like distribution for bacteria length

Stress sensitivity





# =  $\sim 65,000$



# Stress dependence of the growth of long bacteria leads to smaller nematic domains and different topological defects

