Multiscale Model of Human Pathogen Growth on Fresh Produce

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Abstract

Introduction:
Predictive food microbiology currently first requires experimental data for growth on fresh produce and then fitting an empirical or semi-empirical model to the data, making extrapolation to other conditions (temperature, type of produce) difficult (Marks, 2008). Herein, we develop a mechanistic model for the growth of human pathogenic bacteria (Escherichia coli O157:H7 a spherocylinder shaped bacteria) on spinach using geometry acquired from μCT (Figure 1). By knowing the initial substrate profile on the leaf and number of bacteria, we show how you can predict the number of bacteria at any time, predict the colony morphologies and migration, and conduct what-if scenarios that will improve food safety mitigation strategies.

Use of COMSOL Multiphysics® software:
The Livelink™ with MATLAB® was used to couple the individual based model, (MATLAB®), with the nutrient field, (COMSOL) (Figure 2). Transport of diluted species was used to solve the nutrient field. The leaf geometry was acquired from μCT and converted to a parametric surface, used in MATLAB® and COMSOL.

Results:
The results for colony morphology (Figure 3b) are similar to that of literature (Figure 3a, (Tecon and Leveau, 2012)). The results show good agreement with literature in terms of growth at one temperature (Figure 3c (Huang, 2012)) and will be validated versus other temperatures. The nutrient field (example in Figure 4 of glucose) calculated in COMSOL shows good qualitative agreement with lower concentrations at colony locations and higher concentrations elsewhere.

Conclusion:
The impact of the results is that predictive food safety models will be improved by having a mechanistic way of determining the risk associated with a contamination event. Moreover, microbiologists will conduct fewer, more impactful experiments because they will be able to do what-if scenarios first with the simulation. The simulation can also be used to study biofilm formation in other research areas, outside of food.

The impact of the results are also demonstrating how a sophisticated solver (COMSOL) can be coupled with an individual based model to study more complicated problems in microbiology where traditionally the environmental physics was solved with simplified in-house codes.

Reference

Huang, L., 2012. Mathematical modeling and numerical analysis of the growth of non-O157 Shiga toxin-producing Escherichia coli in spinach leaves. International Journal of Food Microbiology 160: 32-41.

Marks, B., "Status of microbial modeling in food process models."Comprehensive reviews in food science and food safety 7.1 (2008): 137-143.

Tecon, R., and Leveau, J., 2012. The mechanics of bacterial cluster formation on plant leaf surfaces as revealed by bioreporter technology. Environmental Microbiology 14:1325-1332.

Figures used in the abstract

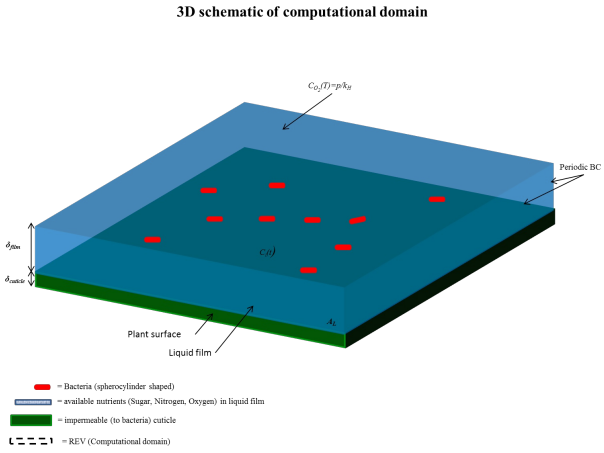

Figure 1: Simplified schematic of problem formulation. A liquid film on a plant surface of area (AL) with periodic boundaries on lateral sides and no flux at the film/leaf interface. At the top of the film, there is no flux for all species except for oxygen, which has a constant concentration in equilibrium with the air. Initially, there are ten bacteria in the liquid film (in red). The nutrients in the film are carbon (glucose), nitrogen (ammonium), and oxygen (dissolved oxygen gas).

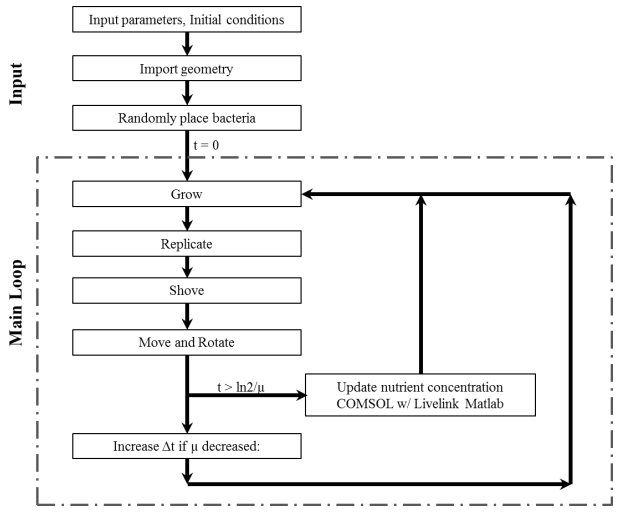

Figure 2: Flow diagram for computational algorithm. The input parameters, initial conditions, geometry, and bacteria locations (random) are entered. Then, the individual based model runs in a loop: growing, replicating, shoving, and moving. At certain time intervals, based on the growth rate, the simulation calls COMSOL to update the nutrient field which affects the growth rate and migration direction via the concentration gradients.

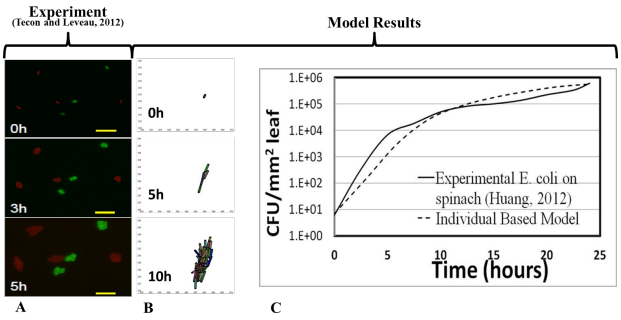

Figure 3: A) Experimental results of fluorescent tagged P. applomerans on agarose gel, bars are 20 μm; B) Individual based model of one colony; C) Validated model results versus literature.

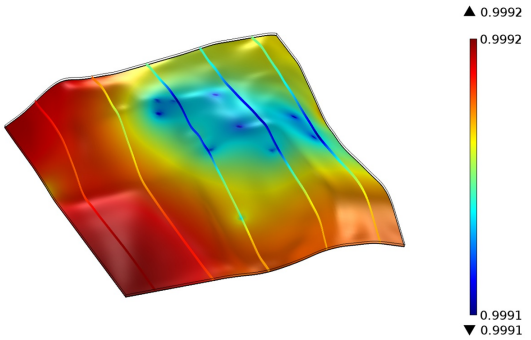

Figure 4: Glucose concentration field (normalized to the initial) in the liquid film. The points of lowest concentration are where the highest biomass is.