Project 3B
Generic Bacteria Simulation on Human Body
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We conduct literature search to have a basic idea of the status quo of similar research topic. However, we cannot find research works that are very close to our proposal. Most simulations related with bacteria do not focus on its behavior within the circulation of the blood system. Instead, they focus more on the generation, reproduction and mutation of the bacteria itself. Some researchers attempt to simulate actual cell in details but their complicate model is not suitable for our project [1]. Therefore, we search for research works that are related to the circulation of the blood system. In fact, there are quite a lot simulations conducted for the simulations of the flow of the blood cells [2][3][4]. Observed on a high level, blood cell itself does not have a very sophisticated structure and therefore their tasks in the metabolic system is a more interesting topic. Since the space of our conceptual model of our project is a complete network of human blood circulation system, these research works can help us developing the simulation system. The problem left is the model of generic bacteria. There are not many research works that we can learn from for the model of generic bacteria. We would mostly build the bacteria model from scratch based on the biomedical knowledge we have.

Our project aims to simulate the spread of any bacteria in a human body. We intend to design the simulator as loosely constrained as possible so that the user may tune the parameters of the simulator to reflect both real and imaginary bacteria. The project is beneficial for people who want to learn the blood system and the behavior of bacteria which can be either preexistent or not. Since there already exist many implementations of the simulations of the blood system. We will focus more on the flexibility of the model of generic bacteria. The most difficult problem in this project is to formulize the interaction mechanism between different kinds of bacteria and the blood system.

Our milestone for part C will be the setup of the space of our conceptual model. This part will mainly focus on blood cells, blood system network and other kinds of cells that need to be taken into account. In part D, we will build the model of the generic bacteria and incorporate the bacteria model into the blood system. In this part, since we focus more on setup the interaction mechanism, we may not give much flexibility for the bacteria model. In the last part, we will give full flexibility to our bacteria model and visualize the simulation process.

[1] Tomita, Masaru. "Whole-cell simulation: a grand challenge of the 21st century." Trends in biotechnology 19.6 (2001): 205-210.
[2] Pries, A. R., et al. "Blood flow in microvascular networks. Experiments and simulation." Circulation research 67.4 (1990): 826-834.
[3] Tsubota, Ken-ichi, Shigeo Wada, and Takami Yamaguchi. "Particle method for computer simulation of red blood cell motion in blood flow." Computer methods and programs in biomedicine 83.2 (2006): 139-146.
[4] Jamshidi, Neema, et al. "Dynamic simulation of the human red blood cell metabolic network." Bioinformatics 17.3 (2001): 286-287.