DTU Compute
Department of Applied Mathematics and Computer Science

Automated Blood Flow Analysis in Connection with Malaria

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Introduction

Malaria is a disease caused by parasites which are spread to humans through the bites of infected mosquitoes. The pathogenesis of malaria is not completely understood, which is why a lot of research is done in the field. It is widely accepted theory that the endothelial glycocalyx layer (EGL), which is covering the inside of the veins and contributes to a laminar blood flow by repulsing the red blood cells (RBCs), is decomposed as a consequence of malaria. As a step towards investigating this hypothesis further, the aim of this project is to develop an algorithm which, given a temporal series of images of a blood vessel, can track the paths of the RBCs using image analysis techniques. The data set, which is used to develop and test the algorithm contains videos captured with a CytoCam microscope. A CytoCam is a microscope that creates images on which the RBCs stand out, which makes it a very useful tool in this project.

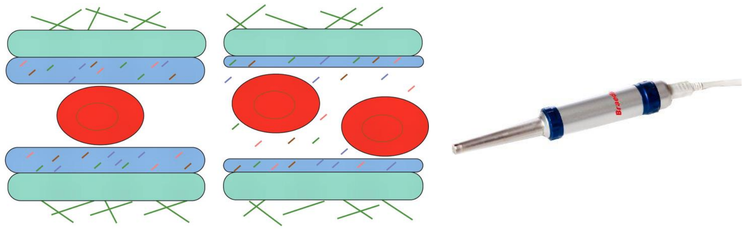

Figure 1: Left: Healthy EGL with laminar RBC flow and decomposed EGL with a more turbulent RBC flow. Right: The CytoCam microcirculation microscope.

Data

The data set consists of videos showing the flow of the RBCs, and is acquired in the village of Magu in Tanzania, using the CytoCam microcirculation microscope. Since we are only interested in individual or small groups of RBCs, the original data is cropped to show only capillaries.

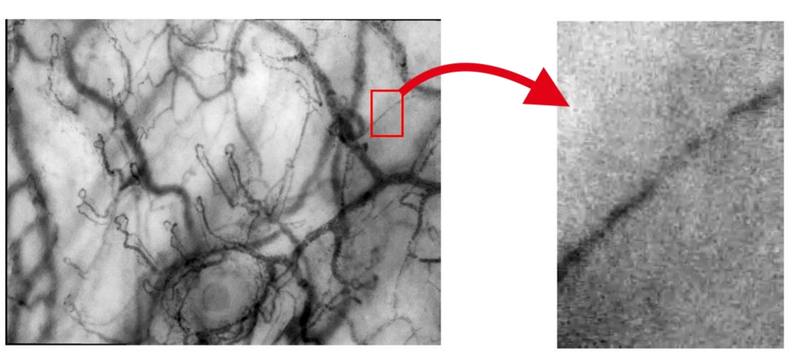

Figure 2: An example of how the data set is extracted from the raw data.

Cell Detection

The RBCs are detected using template matching within a specified region of interest. A Gaussian and a Laplacian of Gaussian distribution (figure 3, left) are used as templates, while the matching score is computed as the average absolute difference (AAD). The number of RBCs in a frame is estimated automatically by detecting a predefined number of cells and evaluating all the matching scores. The approach is based on a theory, that the matching score will reach a more or less constant level once the algorithm begins detecting tissue as cells, resulting in a break in the AAD graph. Using linear regression and orthogonal projection the break point is detected and used as the estimated number of cells in the frame. The method is illustrated in figure 3, right.

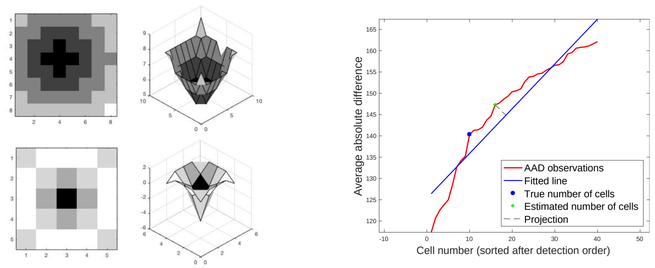

Figure 3: Left: The templates used for the template matching in 2D and 3D. Right: Illustration of the method used to estimate the number of RBCs in a frame.

Cell Matching

The Hungarian algorithm for the assignment problem is used to match each of the detected RBCs in one frame to the corresponding RBC in the next frame. The cost matrix contains the similarity between each pair of cells, which is computed using normalized cross correlation (NCC), along with constraints assuring that an RBC does not flow backwards or move to somewhere far from expected. Cells entering or exiting the field of view between the two frames are not considered in the matching.

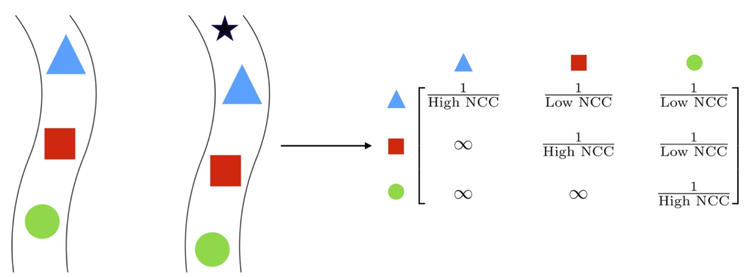

Figure 4: An illustration of the structure of the cost matrix used in the Hungarian algorithm for the assignment problem. Notice that the black star is incoming, hence not taken into account in the assignment.

Results

The algorithm makes it possible to track RBCs in a temporal series of frames, which makes it possible to estimate the trajectories of the RBCs for further analysis. An example of a matching is shown in figure 5, while an example of RBC trajectories is shown in figure 6. The RBCs are detected with an accuracy of 88.48 % and matched with an accuracy of 82.81 % compared to a manual detection and matching.

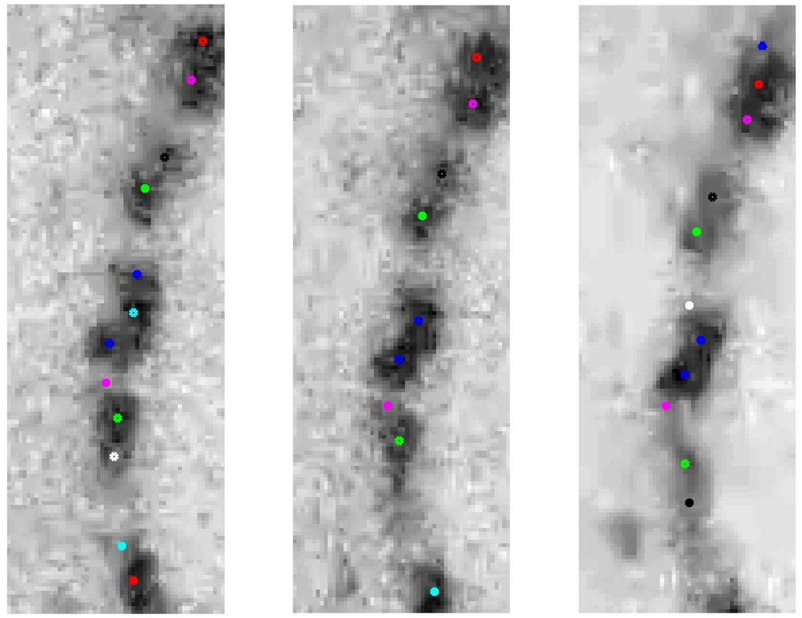

Figure 5: An example of RBCs tracked in a series of 3 frames. Notice how the bottom red RBC in the first frame exits, and how there is one incoming RBC in the last frame.

Remaining Work

The remaining work includes investigating whether the RBC flow is significantly more turbulent for malaria patients, based on an analysis of the trajectories. The idea is to compare the trajectories to the optimal path through the vessel, and determine by how much the travelled distance deviates from the optimal distance. Hypothetically, the deviation would be smaller for healthy people than for malaria patients.

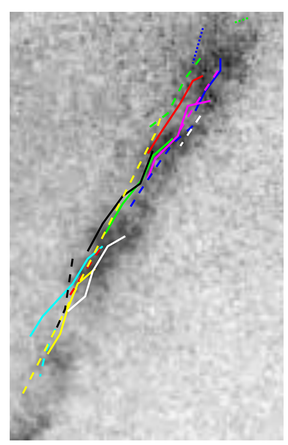

Figure 6 (right): An example of the resulting trajectories of an automatic RBC detection and matching.