Postdoctoral Position in Computational Systems Biology and Bioengineering is available in the laboratory of Prof. Igoshin in the Dept of Bioengineering at Rice University. In our research we use computational and theoretical tools of engineering to study microbiological systems. We are recruiting one postdoctoral researcher to work on statistical image analysis and quantification of the dynamic biofilms formed by Myxobacteria.

PROJECT BACKGROUND:
In recent years the ubiquity of microbial communities in nature has become apparent: for instance, most bacteria related to human diseases are associated with biofilms. However, it is still not clear how individual cells self-organize in these communities and how community as a whole responds to environmental cues. This project aims to discover the mechanisms of self-organization in dynamic single-species biofilms (swarms). In these swarms, bacteria display collective surface motility, cooperatively sense the environment, execute collective developmental programs and often differentiate into distinct cell types performing specialized functions. This research focuses on self-organization in spreading or aggregating biofilms formed by Myxococcus xanthus – an important model organism for studying microbial cooperation, development, and collective motility.

The main project for this position would be to determine quantitative pattern descriptions (features) that describe biofilm phenotypes and distinguish mutant strains from wild-type strains. We will analyze the spreading and aggregation phenotype of biofilms formed by various mutant strains. Subsequently, we will use the information to find a set of quantitative features (pattern descriptions, order parameters) that comprehensively characterize given biofilm phenotypes.

RESPONSIBILITIES:
The postdoctoral fellow will be responsible for the image quantification and data analysis based on available biological data of our collaborators. Statistical quantification and processing of experimental data (time-lapse microscopy images) will be primary computational techniques. Furthermore, statistical analysis techniques like clustering, factor analysis and PCA would be used to quantify the distinction between the mutant strains. The research will be conducted in tight collaboration with experimental colleagues and the main results are at least partially expected to be published in biological journals.

QUALIFICATIONS:
PhD in science or engineering is required for this position. Candidates are required to have experience in mathematical and computational modeling or statistical analysis of biological images as well as some knowledge of basic biology. Candidates with publications in the field of mathematical/computational biology are strongly preferred. Previous experience in statistics, image processing computational biophysics, mathematical biology, or bioinformatics is a plus. Strong interest in interdisciplinary collaboration and English proficiency are also expected.

ABOUT RICE AND HOUSTON:
Rice is consistently ranked as one of the nation’s best teaching and research universities. It is a member institution of the world largest Medical Center (TMC). The Department of Bioengineering is consistently ranked among the nation’s top 10 bioengineering graduate programs. Rice is situated in the Museum district of Houston, TX – forth largest city in the US.

CONDITIONS:
Rice University is committed to affirmative action and equal opportunity employer and offers competitive postdoctoral salary and benefits. The position is open from August 1, 2010 until filled. The initial appointment is for 1 year with possible continuation for the second year upon satisfactory performance. Please visit http://igoshin.rice.edu/ or contact Prof. Igoshin for more information. Applicants should submit their resume and letter stating their research interests to igoshin@rice.edu