

Title: Classification of chromosomes using multi-color image analysis

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Overview of the research

This project will develop image processing and analysis approaches based on multi-color fluorescence in-situ hybridization (M-FISH) imaging. The M-FISH imaging technique has been used for the characterization of chromosomal translocations, to search for cryptic rearrangements, and to study mutagenesis, tumors, and radiobiology. In this technology chromosomes are labeled with five dyes and a DNA stain known as DAPI that attaches to DNA and labels all chromosomes. A fluorescent microscope equipped with a filter wheel is used to capture the chromosome images. Each dye is visible in a particular wavelength and can be captured using a specific filter. Therefore, M-FISH signals can be obtained as multi-spectral or multi-channel images, in which a chromosome was stained to be visible (signed as '1') or not visible (signed as '0'). By simultaneously viewing six different channel images, pixel-wise classification of human chromosome is possible. This technique is also called color karyotyping in cytogenetics. Even though many attempts have been made to automate image analysis procedure, the reliability of the diagnosis technique has not reached the level for clinical use due to a number of factors including non-homogeneity of staining, variations of intensity levels within and between image sets, and emission spectral overlaps between fluorophores. The sizes of the misclassified regions are often larger than the actual chromosomal rearrangements or lost, which often lead to incorrect interpretation by cytogeneticists. The key problem with the technique is the detection of chromosomal abnormalities with accurate pixel-wise classification techniques. To improve the detection of chromosomal abnormalities for clinical diagnosis, accurate segmentation and classification algorithms have to be developed.

Project objectives

The goal of this project is to develop novel image processing and machine learning algorithms to accurately classify chromosome images and visualize the classification using computer programming.

Prerequisites and experience required

Some knowledge of digital image processing and programming skills in Matlab