

Auburn Montgomery

Department of Mathematics

Colloquium/*MAMS*

Time: Friday, August 17, 2007, 2:00pm

Place: Auburn Montgomery, Goodwyn Hall, Room 202

Speaker: Vladimir V. Ufimtsev, Northeastern University, Pursuing a graduate degree in Mathematics under supervision of Dr. Mikhail Malioutov.

Title: Coding Theory: DNA Library Design and Group Testing

Abstract:

A DNA library, or DNA code, is a large collection of carefully designed single stranded DNA sequences that can be algorithmically filtered to store monumental quantities of information which can be retrieved in a massively parallel chemical reaction. DNA strands can also be implemented in biomolecular computing. Cross-hybridization between two single strands of DNA within a library is an erroneous process which can occur, thus leading to memory misreads akin to signal-to-noise ratio. Effective design techniques of strands must be implemented in order to effectively store information in a DNA library. The insertion-deletion metric is commonly used to measure discrete distances between DNA strands. New and more advanced versions of the insertion-deletion metric take into account t-stems, as well as the Gibbs free energies associated with DNA bases. The new metrics, along with effective code generation techniques, have provided a more accurate and robust hybridization prediction model. Bounds on parameters for codes in the t-stem metrics will be presented. New code generation techniques and critical distance fractions will also be discussed.

Group testing is a mathematical technique which can be employed in the design of screening experiments, with the objective of finding a specified number of defective (hazardous) units among a large population with no defects. It should be noted that group testing methods could gain a great deal of implementation in the defense of humanity against global epidemics or pandemics such as HPAI, AIDS, cancer, as well as in environmental screening. Group testing is also a vital element of DNA library screening. By employing a Superimposed Code based on the Reed-Solomon Code we derive a much improved upper bound on the minimal number of tests required in a specific group testing model. New group testing techniques will also be presented.

Refreshments will be served at 1:30pm; colloquium begins at 2:00pm.