

Fall
2015

Mathematical Sciences/RTG Seminar
Colloquium

Computational techniques for identifying driver mutations in cancer genomes

ABSTRACT: Cancer is a class of diseases that are characterized by abnormal cell growth and the ability to spread to other parts of the body. Different combinations of genetic mutations cause different types of cancer, and identifying the combinations of mutations responsible for cancer is essential for finding more effective treatments. Identifying these mutations, which necessitates separating driver mutations from a much larger number of passenger mutations, is a difficult task. However, the advent of inexpensive next-generation sequencing techniques, coupled with the development of novel algorithms that incorporate areas of biology, computer science, and mathematics, provides the potential for more personalized and more targeted cancer treatments. In this talk, we first briefly review the biology of cancer. We then overview various computational methods for identifying driver mutations in cancer along with their mathematical motivations. We finally explore our work on a particular computational technique for identifying groups of driver mutations using biological networks and mutation data.

Speaker: Matthew Reyna

(Computer Science Department, Brown Univ.)

Monday, November 30, 2015

Time: 4:00 – 5:00 PM

Location: AE214



