

## MAY 1 (BERT 012)

9:30 am: Matthew Segar

### Short-read simulator for Next-Generation Sequencing

With the advent of cheaper and faster DNA sequencing technologies, assembly methods have greatly changed. Instead of outputting reads that are thousands of base pairs long, new sequencers parallelize the task by producing read lengths between 35 and 400 base pairs. However, testing new assemblers is a difficult task. Simulated genomes aid researchers by providing real-life, but smaller, data sets for testing an assembly. Therefore, we present srSim as an all-in-one program for generating short-read data. Composed of three separate steps, srSim combines a genome creation, fragmentation, and quality value simulation all in one solution. First, a genome is generated using a Hidden Markov Model that models AT-rich and CG-rich regions. The genome is then fragmented following a normal Gaussian distribution length at a random location. Finally, quality values are simulated using actual, real-world quality value distributions from Roche/454 technologies. To test, a 1,000,000 length genome with 8x coverage and an average read length of 100 was generated. The data set was run through the sequence quality assessment tool FASTQC and passed every test.

9:50 am: Kin Fung Kei

### Chaos in a three-level tropic food chain

We present preliminary results for the dynamics of a type II three-level tropic food chain using molecular dynamics simulations.

## APRIL 24 (BERT 012)

10:10 am: Kota Suenaga

### Simulation of Yahtzee Strategies

Yahtzee, one of the most popular board games, has been studied for its moderate complexity. The strategies are not as simple as ones of Tic Tac Toe, yet the study of Yahtzee is feasible unlike of chess. Previous study has solved for a computer operated optimal strategy. However, it does not suggest a strategy that a player can follow. In this talk, we present computer simulation results which suggest simplified strategies for a human player.

10:30 am: Miles Dawson

### Age Distribution in Global Flu Pandemics

Globalization has enabled diseases to rapidly spread throughout the world as infected individuals move via air travel. Children, who are more prone to catching and spreading diseases, play an important role in the growth of a pandemic and countries with high proportions of children are at greater risk of being overrun by a deadly virus. We use a modified S-I-R model to simulate the spread of a flu pandemic across the five most populated cities from eight strategic regions in the world. Infected citizens spread the disease to susceptibles in their own city as well as cities they travel to. Each city has its own proportion of children to adults, and this variable significantly affects both the duration of the pandemic and the height of infection in that city. We find that in the cities with higher proportions of children, the infection spreads faster and affects more people than in cities with fewer children. Our model and results can help governments plan for a potential pandemic by optimizing their vaccination strategy and restricting air travel from higher risk cities.