Elevated intracranial pressure (ICP) is a condition that arises from a number of causes, from traumatic brain injury to idiopathic intracranial hypertension and hydrocephalus. Currently, the only ways to accurately measure ICP is through either a probe inserted through the skull or by conducting a lumbar puncture, both of which are invasive procedures. Distortion product otoacoustic emissions (DPOAEs) have been shown to change systematically with ICP. Due to their inter-subject variability, DPOAEs are currently being investigated as a means to measure ICP in a clinical population for which a baseline measurement can be taken.

The change in DPOAEs with ICP is hypothesized to be due to physical changes in the structure of the ear as the pressure in the surrounding cranium increases. There are several existing lumped element models of the ear, but none that include the capability to predict DPOAEs. The aim of this project is to design a model of the ear with the capability to predict DPOAEs.

Repeated measurements of power reflectance were made on eight subjects on a weekly basis for four to eight weeks. At each session, measurements were made at three locations: the standard insertion depth (foam plug being flush at the entrance to the ear canal) and plus and minus 3mm from the standard depth. This measurements were made in order to determine whether there is significant variability between the left and right ear measurements, whether the position of the probe makes significant differences to the measurement, and how the intra-subject variability compares to the inter-subject variability.

The mean power reflectance at each position over all sessions was calculated for each subject and was found to depend on the location of the probe in the ear for low to mid-range frequencies. T-tests were conducted to test whether there was a difference in left and right means at each position for every subject for the range of frequencies of the measurement, and the results varied by frequency depending on the subject. The individual standard deviations of a subjects’ mean absorbance at each position were calculated and compared to the difference in mean positions and also varied depending on subject but the overall trend was that the difference in the position means were smaller than the standard deviation of measurements taken at each position."

Phyllotaxis is the arrangement of plant organs (leaves, bracts, flowers, etc.) on the plant axis. This arrangement initiates at the microscopic level at the shoot apical meristem (SAM). The most common pattern of organ arrangement is helical, spiraling around the plant axis. As the plant grows, the meristem produces new undifferentiated cells and periodically, cells that differentiate as primordia, embryonic leaves or other organs. Mathematicians have been proposing and modifying models to explain the spiral
Understanding the motions of biological molecules is important for examining their functions; however, experimental methods for analyzing these motions are time-consuming and not applicable to large datasets. Rigidity analysis is a fast computational method for decomposing a molecule into rigid and flexible regions, which provides information about which atoms in a structure are likely to move together. KINARI-Web is a freely available server for protein rigidity analysis developed by Professor Ileana Streinu’s Linkage Lab. My research is focused on extending KINARI-Web to analyze the rigidity of DNA molecules in the absence of structural information.

As a first step toward this goal, I have extended KINARI-Web to analyze nucleic acids and nucleic acid protein complexes with known structures. However, there is a huge excess of DNA sequence information (> 135 million sequences in GenBank) as compared to structural information (about 4,000 Protein Data Bank files), so it is of interest to develop a method to analyze these DNA sequences. I have developed a preliminary proof-of-concept for this computational tool. In addition, I am also working with Professor Suarez to analyze the flexibility of specific DNA molecules using 2-D NMR. Once our tool for DNA sequence-based rigidity analysis is further developed, the results will be compared to the rigidity analysis of DNA molecules with known structures, and to experimental NMR data on DNA flexibility.
Morphology of some organisms is developmentally plastic which allows individual organisms to respond to environmental variation within a single generation. One example of this is the “arms race” between snails and crabs. When snails sense the presence of crabs, they increase their defenses by altering their shell morphology. Crabs respond to these changes by altering their morphology to overcome the snail defenses. This project uses *Littorina littorea*, the common periwinkle native to the Atlantic coast, and *Carcinus maenas*, the invasive green crab, as a model system through which to investigate the dynamics of an ecological arms race.

In this experiment we compared shell shape parameters of snails in two treatments, with and without crab cues present. Previously, students had developed a program based on David Raup’s work on the geometry of snail shell coiling. My work involved writing a program to find the parameters that best fit the shapes we observed. Ultimately these results will influence future work to understand the arms race dynamics.

**April 1 Presentation**

**Zeke Nierenberg (Hampshire ’14)**
Lee Spector (Hampshire, Computer Science)
with Martina Steurer-Muller, MD

**Opinion: Researchers, Hire Hackers; Clinical researchers need programming support**

Heroic investigations of life and disease have put us on the verge of a healthcare revolution. Meanwhile, the software industry is booming; tech startups crop up faster than you can say “medical informatics.” But at the intersection of these two complex fields lies dysfunction. Researchers and clinicians are shackled to software that no one in their right mind would use voluntarily, spending immeasurable hours manually copying data from one system to another. And this separation of software development and clinical research is costing lives.