1135-92-2982 **Devin Mattoon*** (dmattoon@missouriwestern.edu), **Altan Tutar**, **Hannah S Sinks**, **Autumn Estrada**, **David Sullivan**, **Daniel Zweerink**, **A. Malcolm Campbell**, **Todd T Eckdahl**, **Jeffrey L Poet** and **Laurie J Heyer**. *Modeling directed evolution with coupon-collecting and mixing problems.* Preliminary report.

Our interdisciplinary, interinstitutional team of undergraduate researchers sought to evolve a DNA sequence in a bacterial virus, using natural selection to alter the specificity of an RNA regulatory element called a riboswitch. We modeled random mutations in the virus, accounting for lethality due to damaged genes. We applied a generalized solution of the coupon collector's problem to calculate the expected value and a confidence interval for the number of viral genomes required to observe all possible single, double and triple base substitutions in the DNA sequence, after removing from the population all viruses with lethal mutations. We used our probability model to ensure that the spatial and temporal scale of the wet lab experiment was sufficient to explore the extremely large space of all possible DNA sequences of a given length. Further, we used differential equations to predict the time required for a small molecule to reach each of its target concentrations in a dynamic solution, and for particular virus genomes to dominate the population in each of three parallel compartments of a chemostat. Finally, we built web tools to make generalized versions of our probability and differential equation models available to biologists for the design of future experiments. (Received September 26, 2017)