Poster Presentation:

COMPUTATIONAL INVESTIGATION OF RNA EDITING IN MAMMALIAN TRANSCRIPTOMES. Justin Talbot, Shuba Gopal, Department of Biological Sciences

The flow of genetic information was originally thought to be simple, that DNA was the precursor to RNA, and that RNA was the precursor to proteins. As we have learned, however, this central dogma is in fact rather more complex. A significant factor adding to this complexity is RNA editing. RNA editing is defined as a modification of RNA that changes the coding capacity and is distinct from RNA splicing, capping, or 3' processing. The type of RNA editing. This is the process of chemically modifying the base pair cytosine, and converting it into the base pair uracil. We have been trying to identify where this editing occurs in mice and humans. In order to identify these edit locations we have taken a computational approach. We have been building a data set of ESTs from both mice and humans, which we shall use to map against the mouse and human genomes. A dataset of C - T base pair mismatches was acquired(1). Using megaBLAST(2) we mapped the dataset to the mouse genome to see if the C - T mismatches were consistent across species and to gain evidence that they were not errors or unknown polymorphisms.

References:

1) Furey, Terrence S. et al. (2004). "Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing," Genome Res. 2004 Oct;14(10B):2034-40.

2) Zhang Z., Schwartz S., Wagner L., & Miller W. (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.