

## **An Investigation of Codon Usage Bias Including Visualization and Quantification in Organisms Exhibiting Multiple Biases**

Douglas W. Raiford  
Wright State University  
Computer Science Department (Bioinformatics Research Lab)  
3640 Colonel Glenn Highway  
Dayton, Ohio University

Detection of codon usage bias is an important tool in the analysis of genomic data, particularly as a predictor of gene expressivity. There are several algorithmic methods for identifying this bias, all of which are susceptible to being obscured by the presence of other biases (such as a dominant GC bias) that coexist in the genome's codon usage space. Presented here are novel techniques for measuring genome-wide adherence to a pair of biases, and visualizing the genomic adherence to the biases through the use of a bipolar bias view.