

Poster presentation

## Buffered codons in human transcriptional units

Rami Mahdi and Eric C Rouchka\*

Address: Department of Computer Engineering and Computer Science, University of Louisville, Louisville, KY 40292, USA

Email: Eric C Rouchka\* - [eric.rouchka@louisville.edu](mailto:eric.rouchka@louisville.edu)

\* Corresponding author

from UT-ORNL-KBRIN Bioinformatics Summit 2008  
Cadiz, KY, USA. 28–30 March 2008

Published: 8 July 2008

*BMC Bioinformatics* 2008, **9**(Suppl 7):P8 doi:10.1186/1471-2105-9-S7-P8

This abstract is available from: <http://www.biomedcentral.com/1471-2105/9/S7/P8>

© 2008 Mahdi and Rouchka; licensee BioMed Central Ltd.

### Background

Codon usage is well established for a number of different species. Multiple models have been proposed to show codon bias as a balance between mutation and selection. Most of these models emphasize controlling the speed of protein translation from the mRNA and increasing the accuracy where this bias is dependent on the abundance of the available tRNA. We show codon usage bias from a different angle based on a new hypothesis where selection is expected to act in a direction to favor codons that are more buffered, or protected, from mutation than those sensitive to mutation. It is anticipated that the more buffered the original coding sequence, the higher the survival chance for the whole organism since the resulting protein sequence remains unchanged. Two different complementary measures are developed to compute the average buffering capacity in a given sequence. We show that the buffering capacity of coding sequences is in general higher than that of randomly generated sequences and that of shifted reading frames. Highly expressed genes are shown to have an even higher buffering capacity than non-house-keeping genes.

### Acknowledgements

This work was supported in part by NIH-NCRR Grant P20RR16481 and NIH-NIEHS Grant P30ES014443. Its contents are solely the responsibility of the authors and do not represent the official views of NCRR, NIEHS, or NIH.