

Automating the Classification of

Authorship & Acknowledgement

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Motivation

- > Explore the automation of classifying acknowledgment & authorship
- > Bootstrap the use of existing ontologies to increase the reliability of our own classifications

Data

- > Corpus of articles from the field of Bioinformatics (n= 9741)
- > Extracted authorship statements and acknowledgments (see below) for each article
- > Manually classified a subset (n = 300) of each paratext using the Scholarly Contributions and Roles Ontology (Shotton and Peroni, 2013)

UCSC Genome Browser

Identification and Classification of Conserved RNA Secondary Structures in the Human Genome

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The discovery of microRNAs and ribozymes, among others, have shown functional RNA to be biologically more important and genetically more prevalent than previously appreciated. We have developed a general computational pipeline to identify RNA secondary structures in the human genome and used it to survey an eight megabase window adjacent of the human, chimpanzee, mouse, rat, dog, chicken, zebra fish, and pufferfish genomes for deeply conserved functional RNA. We have identified four conserved RNA motifs, including 108 motifs in human 3'UTR exon loops, and various types of human protein-coding elements. Among the highest scoring new predictions are 160 new miRNA candidates, as well as new candidate telomerase transcripts. RNA editing targets RNA motifs in conserved sites, and more folds that have signatures or small functional RNA families of completely unknown function. While the role of this position in the result is difficult to estimate and it likely to be redundant, the results nevertheless provide evidence for many new human functional RNAs and present specific predictions to facilitate their further characterization.

Genome Research, Volume 18, Number 10, October 2008, Pages 1811-1821. doi:10.1093/gnr/kfn181

Introduction

Many new classes of functional RNA structures (RNAs) such as miRNAs, siRNAs, piRNAs, and ribozymes [1, 2] have been discovered over the last few years. These structures function both as regulatory molecules and as part of RNA viruses. These new discoveries have led to the discovery of new RNA structures and their potential roles in the cell, suggest that perhaps only small fractions of the RNA in the genome are currently understood. The development of computational methods that can effectively identify RNAs are currently needed to address this gap.

We have developed a computational pipeline to identify conserved RNA structures across the human genome. This pipeline uses a recently derived model structure, a phylogenetic likelihood, and a dynamic programming algorithm to identify conserved RNA structures. This pipeline is available as a web-based tool and can be used to identify conserved RNA structures in the human genome. The pipeline is available as a web-based tool and can be used to identify conserved RNA structures in the human genome. The pipeline is available as a web-based tool and can be used to identify conserved RNA structures in the human genome.

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