

RNA Gene Finding

Project Assignment – *Topics in Computational Biology*

2nd – 6th of June, 2009

Objective To give a presentation of about 1 hour at the end of the week covering key aspects of non-coding RNA genes, such as functionality, evolution, and computational detection.

Most focus in molecular biology is on proteins and the regions of a genome encoding proteins, i.e. protein coding genes. However, parts of the genome have other important roles. One significant class is the class of non-coding, or RNA, genes. These describe regions that are transcribed to RNA, but not a messenger RNA that is translated to a protein. Instead the RNA molecule itself carries out a functional, structural, or regulatory task. Probably the two most well known types of RNA genes are transfer RNAs and ribosomal RNAs that play a crucial part in the translation of messenger RNAs into proteins. Some of the questions you may want to address in your presentation are:

- What are the main classes of RNA genes? What are their roles, how do they function, and what are their structures?
- What theories exist about the introduction of RNA genes into biological systems?
- Where are RNAs found in the genome and how are their transcription regulated?
- What are the main features of RNA molecules' structure?
- How do RNA genes evolve, compared to other parts of the genomes? What types of selection have been identified?
- Are there difficulties in experimental identification of RNA genes?
- What are the approaches to finding RNA genes, known and *de novo*, by computational means?

Suggested literature

- Sean Eddy. Non-coding RNA genes and the modern RNA world. *Nature Reviews Genetics*, 2:919–929, 2001.
- Walter Gilbert. Origin of life: The RNA world. *Nature*, 319:618, 1986.

- Sam Griffiths-Jones, Simon Moxon, Mhairi Marshall, Ajay Khanna, Sean R. Eddy, and Alex Bateman. Rfam: annotating non-coding RNAs in complete genomes. *Nucleic Acids Research*, 33:D121–D124, 2005.
- C. Hudelot, V. Gowri-Shankar, H. Jow, M. Rattray, and P. Higgs. RNA-based phylogenetic methods: Application to mammalian mitochondrial RNA sequences. *Molecular Phylogenetics and Evolution*, 28(2):241–252, 2003.
- Robert J. Johnston and Oliver Hobert. A microRNA controlling left/right neuronal asymmetry in *Caenorhabditis elegans*. *Nature*, 426:845–849, 2003.
- Neokles B. Leontis and Eric Westhof. The non-Watson–Crick base pairs and their associated isostericity matrices. *Nucleic Acids Research*, 30(16):3497–3531, 2002.
- John S. Mattick. A new paradigm for developmental biology. *Journal of Experimental Biology*, 210:1526–1547, 2007.
- Irmtraud M. Meyer and István Miklós. Co-transcriptional folding is encoded within RNA genes. *BMC Molecular Biology*, 5:10, 2004.
- Naila K. Mimouni, Rune B. Lyngsø, Sam Griffiths-Jones, and Jotun Hein. An analysis of structural influences on selection in RNA genes. *Molecular Biology and Evolution*, 26:209–216, 2009.
- Jakob Skou Pedersen, Gill Bejerano, Adam Siepel, Kate Rosenbloom, Kerstin Lindblad-Toh, Eric S. Lander, Jim Kent, Webb Miller, and David Haussler. Identification and classification of conserved RNA secondary structures in the human genome. *PLoS Computational Biology*, 2(4):e33, 2006.
- Laura Schramm and Nouria Hernandez. Recruitment of RNA polymerase III to its target promoters. *Genes & Development*, 16:2593–2620, 2002.
- S. Smit, J. Widmann, and R. Knight. Evolutionary rates vary among rRNA structural elements. *Nucleic Acids Research*, 35(10):3339–3354, 2007.
- Stefan Washietl, Ivo L. Hofacker, and Peter F. Stadler. Fast and reliable prediction of noncoding RNA. *Proceedings of the National Academy of Sciences of the United States of America*, 102(7):2454–59, 2005.