

FRISYS Group-Seminar

September 30th, 2010
15 ct, room 0.043, Schänzlestraße 1



Computational RNomics: The long and the short of non-coding RNA prediction.

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The past few years have revealed that the transcriptional output of eukaryotic cells is much more pervasive and multi-layered than previously anticipated. Recent efforts in transcriptome deep sequencing suggest that eukaryotic genomes are almost entirely transcribed. Thousands of regulatory non-protein coding RNAs (ncRNAs) have been detected and their functional importance is broadly recognised. In general we distinguish between short (~20-200nt) and long ncRNAs (>200nt, up to several kilobases). This heterogeneity is only one reason why the number of bioinformatic approaches reliably predicting ncRNA genes in genomic sequence data is still limited. Here, we highlight recent advances of computational ncRNA gene-finding.



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