

The Brave New World of RNA

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Large international transcriptomics projects such as ENCODE and FANTOM showed that nearly the mammalian genomes are almost completely described, putting an end to idea of “Junk DNA”. Since then, we have learned that transcription is more extensive and more complex also in other eukaryotes, and even in prokaryotes. In contrast to the common organizational principles governing the protein-coding minority, the collection of transcripts forms a surprisingly heterogeneous zoo of RNAs differing in processing, transport, and function. Complex hierarchical processing pathways, furthermore, generate multiple RNA species from the same genomic information that can act in ways that are unrelated in both biochemical mechanism and biological function. The unexpected observation has not only changed the paradigms of gene expression but also enforced a fundamental re-thinking of the concept of the “gene” itself.

For bioinformaticians, new challenges keep popping up, ranging from the technicalities of analysing huge amounts of high throughput sequencing data to ncRNA annotation and the quest for a sensible taxonomy of ncRNA classes.