Computational genomics: searching for new proteome components

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Modern methods of experimental analyses generate large volumes of raw data on mRNA and protein profiles in different cells, tissues and stages of development. These data provide a valuable source for reconstruction of biological pathways and regulatory circuits.
However, such a reconstruction demands not only well-developed techniques of computational analyses but also a reliable background (i.e., genome structure, transcriptome and proteome contents, etc.).
Currently, genome annotation procedures are based on certain premises limiting accuracy of gene structure predictions. In particular, it is commonly considered that a typical eukaryotic mRNA can encode only one protein. However, it was recently demonstrated that a considerable part of mRNAs could contain several alternative start codons from which translation of functionally different protein isoforms (or unrelated peptides) can be initiated. A contribution of alternative translation to eukaryotic proteome complexity is discussed.

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