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Heterogeneous data analysis for annotation of microRNAs and novel genome assembly

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STELLINGEN

Behorende bij het proefschrift

Heterogeneous Data Analysis for Annotation of microRNAs and Novel Genome Assembly

1. Heterogeneous data integration is no doubt the trend for the analysis of biological data. - *This thesis*
2. Genomic location plays a role in the mechanism of microRNA-mediated gene regulation. Many genes are physically located close to their regulatory microRNAs. Also many functionally similar microRNAs are located in clusters. - *This thesis*
3. microRNAs have potential binding preference at the end of the 3' UTR sequences. - *This thesis*
4. RNA-Seq data can not only measure gene expression level but also reveal the exonic regions within a gene. For the genes that do not undergo alternative splicing, RNA-Seq libraries can be used to guide genomic sequence scaffolding. - *This thesis*
5. For each algorithm, it is desirable to achieve both high sensitivity and high specificity. However, there is a trade-off between the measures. The crux of computation is to find the balance.
6. A good definition of annotation is that genome annotation is the process of taking the raw DNA sequence and adding the layers of analysis and interpretation necessary to extract its biological significance and place it into the context of our understanding¹.
7. microRNAs are short. This makes them very suitable as master regulators of gene expression.
8. In the application of next-generation sequencing technologies, the costs associated with downstream data handling and analysis could match or surpass the data-production². This is often forgotten in the setup of an experiment.
9. A delicate usage of make-up enhances your beauty. The same holds for scientific writing.
10. In life sciences, research is driven by impact factor.
11. The Thesis Repulsor Field (TRF) is a model of the forces experienced by an individual in the final stages of graduation³. In TRF, the motivation of completing the thesis is inversely proportional to the amount of work remained.
12. The spirit of "Nee heb je, ja kun je krijgen" often works in Holland but seldom works in China.

¹L. Stein. Genome annotation: from sequence to biology. *Nature reviews. Genetics*, 2(7):493503, July 2001

²Michael L. Metzker. Sequencing technologies - the next generation. *Nature reviews. Genetics*, 11(1):3146, January 2010.

³PhD comics. <http://www.phdcomics.com/comics/archive.php?comicid=1354>