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Integration and visualization of non-coding RNA and protein interaction networks

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17 Fully automated RNA-seq Analysis Pipeline.

Jesper Culmsee Tholstrup, Francesco Favero, Asli Ozen, Yuan Mang, Jacob Bock Axelsen, Michael Thorsen, Maria Wrang Teilum, Peter Mouritzen, Niels Tolstrup.

Exiqon, Vedbæk, Denmark.

Modern sequencing technologies generate large amounts of raw data and even comparably small experiments generate data in quantities, which pushes or exceeds the computational capabilities of personal computer sized machines. Consequently, to deliver overnight analysis results larger computers are required. However, with larger computers comes more complexity and the analysis scheduling mechanism can quickly turn into a bottleneck.

Exiqon has developed a RNA-Seq analysis pipeline, which features completely automated analysis all the way from raw fastq input to analysis results, such as differential expression analysis and unsupervised analysis. The pipeline features an internal scheduling system, which support asynchronous analysis of samples in parallel as well as analysis merge and branch points. The pipeline is able to handle projects containing hundreds of individual samples and is able to utilize large computers efficiently. The modular design of the pipeline allows Exiqon to offer many different types of analyses and we currently support analysis of miRNA, smallRNA, mRNA, and totalRNA samples. In addition, the modular design gives us the flexibility to offer new types of analysis while staying in a robust and tested core framework. In the poster, we will present an overview of the pipeline, resource usage graphs, and actual analysis results

18 Integration and visualization of non-coding RNA and protein interaction networks.

Alexander Junge, Jan C. Refsgaard, Christian Garde, Xiaoyong Pan, Alberto Santos, Christian Anthon, Ferhat Alkan, Christian von Mering, Christopher T. Workman, Lars Juhl Jensen, Jan Gorodkin.

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Non-coding RNAs (ncRNAs) fulfill a diverse set of biological functions relying on interactions with other molecular entities. The advent of new experimental and computational approaches makes it possible to study ncRNAs and their associations on an unprecedented scale. We present RAIN (RNA Association and Interaction Networks) - a database that combines ncRNA-ncRNA, ncRNA-mRNA and ncRNA-protein interactions with large-scale protein association networks available in the STRING database. By integrating ncRNA and protein networks, RAIN provides a more complete picture of the cell's complex interaction network. RAIN aggregates associations and (predicted) interactions of a vast collection of ncRNA classes, including microRNAs and long ncRNAs, collected from a wide range of resources: a) curated knowledge, b) experimentally supported interactions, c) predicted microRNA-target interactions, and d) co-occurrences found by text mining Medline abstracts. Each resource was assigned a reliability score by assessing its agreement with a gold standard set of microRNA-target interactions. RAIN is available at: <http://rth.dk/resources/rain>