

Project: miRNA annotation pipeline

Micro RNAs (miRNAs) are short segments of RNA that regulate many important biological functions of an organism. In collaboration with the Department of Pathology and Molecular Medicine at Queen's, this project is concerned with analyzing miRNAs data for cancer diagnosis and prognosis and in the study of depression.

The abundance of miRNA in a sample is measured through a sequencing technique. The expression of miRNAs in a sample is then calculated by processing the sequences and determining the sequence read counts for each miRNA present in the sample. This is done through the alignment of the sequenced data to a reference genome, which is made tricky by the very short (19-24 bases) length of the miRNAs, and our evolving understanding of which sequence characteristics actually denote a miRNA within the genome. Many methods of data filtering, trimming and alignment are available, but the optimized pipeline for using these has not been determined. This project involves identifying the best setup for accurate evaluation of miRNA sequence read counts in a data sample.

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