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isomiR-SEA: miRNA and isomiR expression level detection in seven RNA-Seq datasets

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Why identifying and quantifying miRNAs and isomiRs?
The role of miRNAs in multi-factorial diseases such as cancer is well assessed. Indeed, miRNAs can act by inhibiting or promoting both oncogenic or metastatic processes. Conversely, the role of isomiRs has to be clarified. However, deregulated isomiR patterns were pointed out in some cancers as the gastric one. Furthermore, miRNAs are considered good bio-markers, making their adoption for disease characterization highly desirable.

What’s new in isomiR-SEA approach?
IsomiR-SEA\(^1\) implements a miRNA-specific alignment procedure that results in very accurate miRNA/isomiR expression levels and precise evaluations of miRNA-mRNA conserved Interaction Sites. As first activity, isomiR-SEA identifies miRNA seeds within the tags. If the seed is found, the alignment is extended and the positions of the encountered mismatches recorded and analysed to distinguish among miRNAs and isomiRs, and to assess the conservation of the interaction sites.

Experiment 1: Large scale analysis
We analysed 23 human miRNA-Seq Samples (GSE13370, GSE19812, GSE21279, GSE22918, GSE23090, and GSE26516) for reporting on the overall isomiRs expression level and the conserved miRNA-mRNA Interaction Sites spectrum.

Experiment 2: Two samples analysis
We analysed a human embryonic stem cells (hESCs) and a neural steam cells (NSCs) samples from Tan\(^2\) for pointing out trends in both isomiRs expression levels and conserved miRNA-mRNA Interaction Sites profiles. These trends cannot be appreciated from the overall miRNAs expression profile.

Conclusions
Analyses performed with isomiR-SEA proven the wide spectrum of information hidden into miRNAs-Seq data. Being designed around miRNAs-specific alignment algorithm IsomiR-SEA is capable to:

i) Provide accurate miRNAs expression profiles;
ii) Distinguish and classify each read mapped on a miRNA as exact mature form or as isomiR;
iii) Report the spectrum of mapped reads conserving miRNA-mRNA Interaction Sites.

The evaluation of isomiR-SEA results could help to gain novel insights into miRNAs mediated cell behaviours and to better characterize the miRNAs associated diseases and conditions.

The impact of NGS on miRNA/isomiR analysis
The analysis of data coming from transcriptome sequencing potentially accounts for an accurate identification and quantification of both known and novel miRNA and isomiR molecules. To this aim, several methodologies working on miRNA-sequencing (miRNA-Seq) data were devised in the last decade. However, many of these tools do not provide any information concerning isomiRs and miRNA-mRNA Interaction Sites spectrum.

References: