A dry lab for exploring miRNA functions and applications in cancer subtype discovery

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microRNAs (miRNAs) are important gene regulators controlling a wide range of biological processes and they are involved in different types of cancers. Computational methods are proved to be effective in studying miRNA functions.

For exploring miRNA functions and discovering cancer subtypes based on miRNA and mRNA expression data, in the last 2 years, we have developed 4 Bioconductor packages:

- ***miRLAB***[1], a package providing 12 computational methods for predicting miRNA targets from expression data. The package also provides tools for validating the predictions, comparing different methods, and incorporating target binding information to the expression data based methods.
- ***miRsponge***[*], which includes 7 computational methods for identifying miRNA sponge interactions and modules. The package also provides tools for validating competing endogenous interactions and functional enrichment analyses.
- ***miRBaseConverter***[*], a package providing the tools for converting and retrieving miRNA names, ID, and other information in different versions of miRBase. The package is useful for working with multiple miRNA datasets where different miRBase versions are used for the miRNA naming convention.
- ***CancerSubtypes***[2], which provides 6 machine learning methods for identifying cancer subtypes, including our own method for stratifying cancer subtypes based on miRNA-Transcription Factor-mRNA network information. The package also contains 4 pre-selecting gene methods and 4 stastistical methods for evaluating the subtyping methods.

In this talk, I will present the motivations and utilities of the 4 Bioconductor packages. I will demonstrate their ease of use and present some typical scenarios of using the packages.

References:
(1)   Thuc D. Le et al. (2015). miRLAB: an R based dry lab for exploring miRNA-mRNA regulatory relationships. ***PloS One***, *10*(12), e0145386.
(2)   Taosheng Xu, Thuc D. Le, et al. (2017). CancerSubtypes: an R/Bioconductor package for molecular cancer subtype identification, validation, andvisualization. ***Bioinformatics***, 33(19): 3131-3133.
(*)   Papers describing the packages are under review.