Bibliographic Information:

Pham VH, Zhang J, Liu L, Truong B, Xu T, Nguyen TT, Li J and Le TD, "Identifying miRNA-mRNA regulatory relationships in breast cancer with invariant causal prediction", Pham et al BMC Bioinformatics (2019) 20:143, https://doi.org/10.1186/s12859-019-2668-x.

Key Points:

In this paper, the authors proposed an approach to identify miRNA-mRNA regulatory relationships in "Breast Cancer" by exploiting the invariant causal prediction technique. The key points of this paper are described below:

- Existing computational methods for inferring miRNA-mRNA regulatory relationships have high computational complexity in case of large dataset. In this paper, parallel processing-technique has been employed for the casual method jointIDA by using its parallel implementation in the ParallelIPC. The breast adenocarcinoma (BRCA) dataset of The Cancer Genome Atlas (TCGA) is classified into 5 different breast cancer subtypes. These subtypes are called "different environment".
- The proposed approached has three main steps:
  - ➤ Selecting miRNAs and mRNAs with most expression variability: The matched miRNA and mRNA expression samples are extracted from the BRCA dataset of TCGA. In total 503 samples with matched miRNA and mRNA expression are selected and stored in additional file. Then FSbyMAD function of the Cancersubtypes package has been used to select miRNA and mRNA with the most different Median Absolute Deviation.
  - ➤ Categorizing samples into different experiment settings: The Pam50 method has been used to categorize BRCA samples into different environment settings to identify miRNA targets across different cancer subtypes. After categorization, they have 107samples in Basal subtype, 75 samples in Her2 subtype, 147 samples in LumA subtype, 116 samples in LumB subtype, and 58 samples in Normal-likesubtype.
  - ➤ Predicting casual effects of miRNAs on mRNAs: finally, invariant casual prediction has been employed to find the miRNA-mRNA regulatory relationship across subtypes by estimating the causal relationships of miRNAs on each mRNA through the hiddenICP funciton of the InvariantCausalPrediction package.
- If breast cancer spreads, it might affect other parts of the body such as: liver, lungs, muscles, bones and brain. So early detection of breast cancer will reduce the death rate. Bioinformatics play an important role to early detect of breast cancer. That's why I think it's an important application of Bioinformatics.

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