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## iMiR: Identifying miRNA Regulation in Diseases: Bioinformatics Tool

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# iMiR: Identifying miRNA Regulation in Diseases

## Bioinformatics Tool

### Introduction

Human cells are extremely complicated machineries. Cancer mutations are a resulting occurrence of a wide-variety of biological factors and cellular mechanisms involving genes, miRNAs, transcription factors (TFs), chemicals etc. within a cell. Hence, determining drug and therapeutic approaches require for biologists and drug researches to understand the activity and role of all these factors precisely and comprehensively. Inability to understand the larger scenario of these factors inter-working may lead to misleading or slanted prognosis.

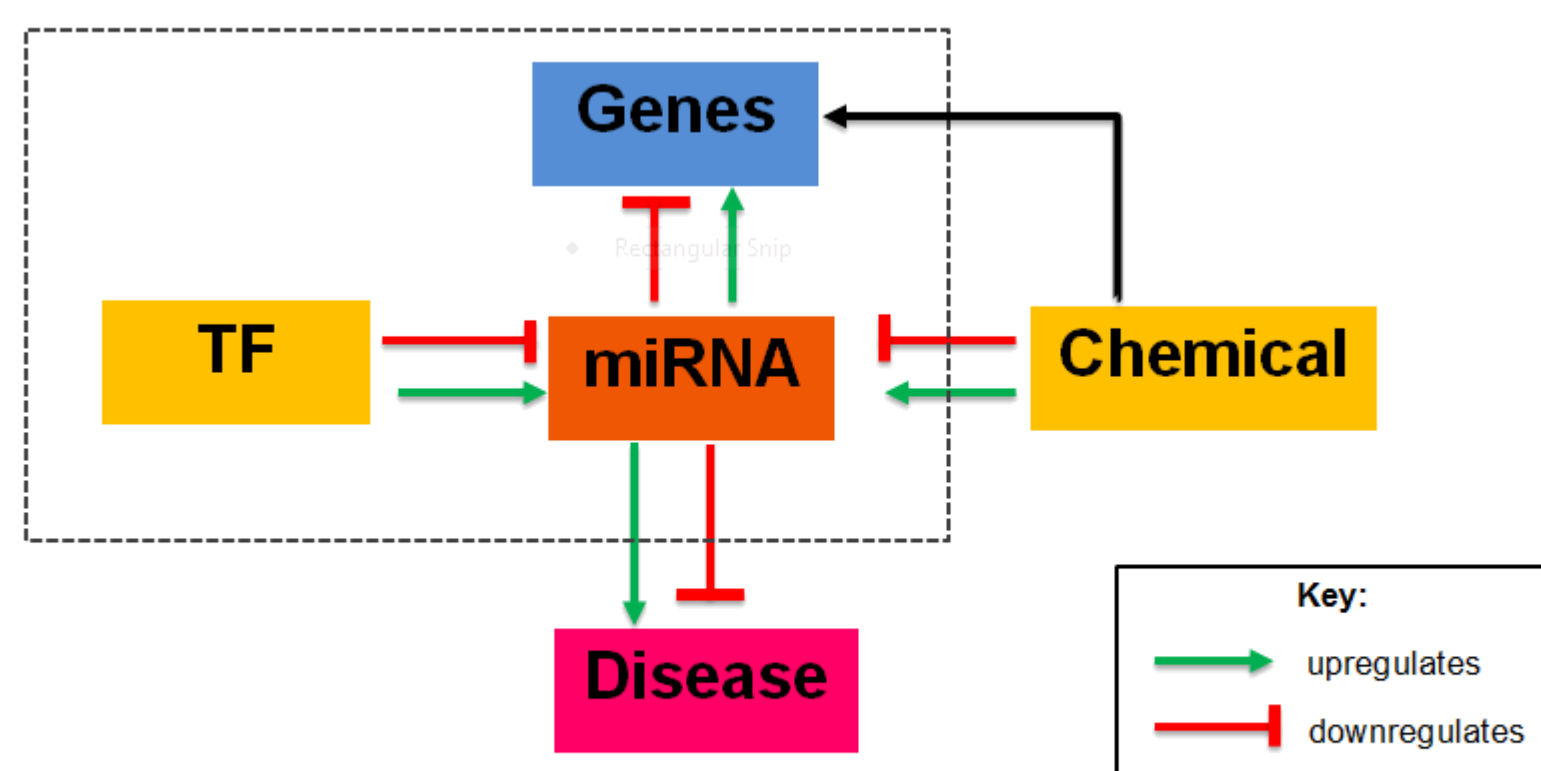


Figure 1: A schematic representation

### Objective

Chemicals and TFs regulate miRNAs. miRNAs up/down regulate mRNAs and modulate gene expressions which further lead to changes in biological processes and eventually diseases. The goal is to provide a comprehensive tool to discover and identify targets, and essential miRNAs critical in the mutation of cancer diseases.

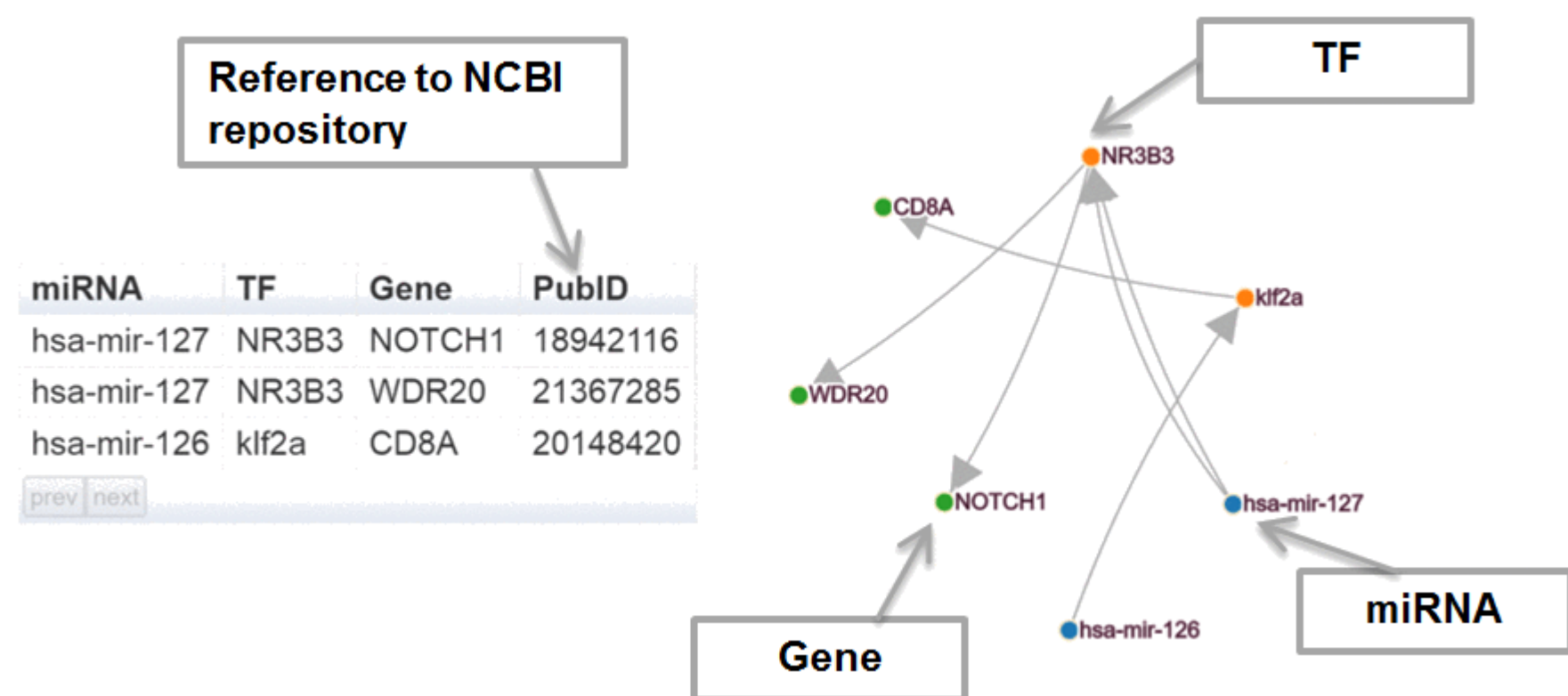


Figure 2: Regulation of miRNAs, TFs, and genes

### iMiR

Our software, 'iMiR' allows researchers to **search** and **extract** the multi-level interactions between miRNAs, diseases, genes, drugs, and transcription factors from the NCBI data repository. The tool provides **global** and **local** view of the disease-regulation scenario by giving the user multi-dimensional views of responsible miRNAs [Figure 3], their subsequent regulations [Figure 4], the literature references [Figure 5], the impact of miRNA-disease association, the over-all regulating miRNA-gene pairs.

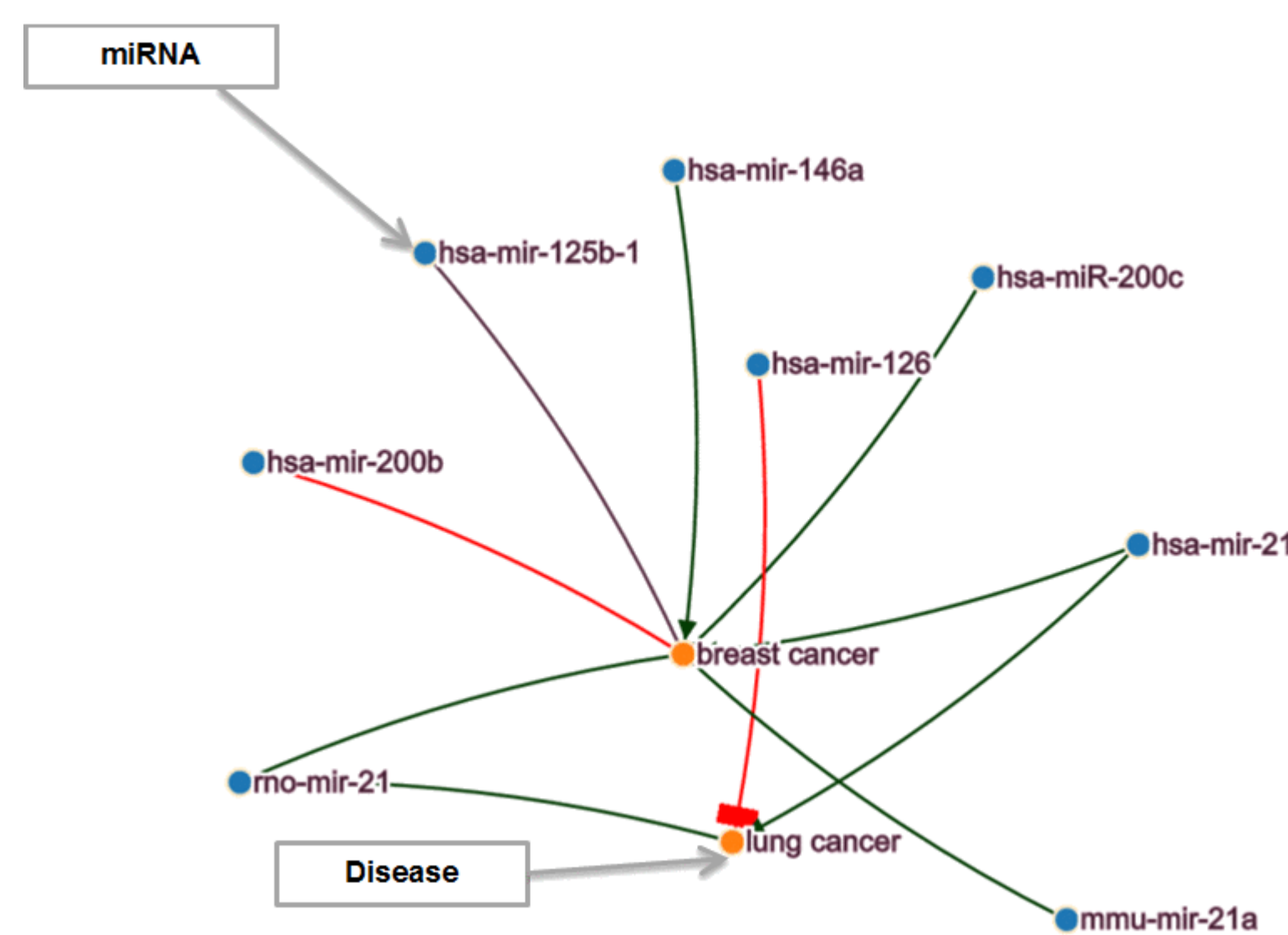


Figure 3: miRNA regulation in diseases

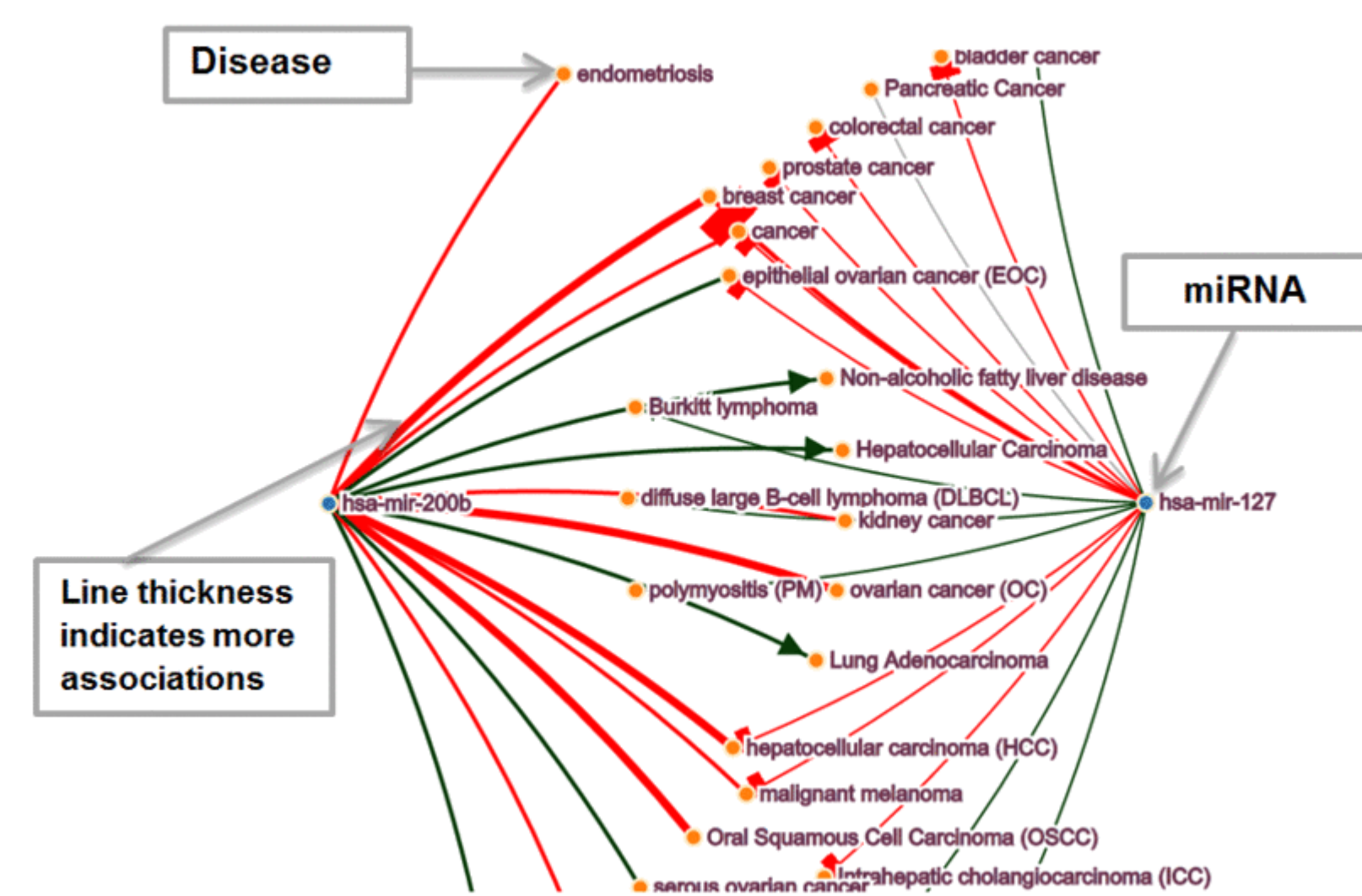


Figure 4: miRNA's regulating multiple diseases

### iMiR features

- Network visualization allows intuitive comprehension of the information.
- Diagrams follow standard practices of color and symbols for easy understanding of biological associations.
- Users can interact with the information and observe their topology.
- Tabular presentation allows more details in addition to the network display.
- Multi-tab design allows for easy progression on the tool to study various factors.

### iMiR framework

- Database: MySQL
- Middleware: PHP
- Frontend: HTML, Ajax, Javascript, D3.js for visualization

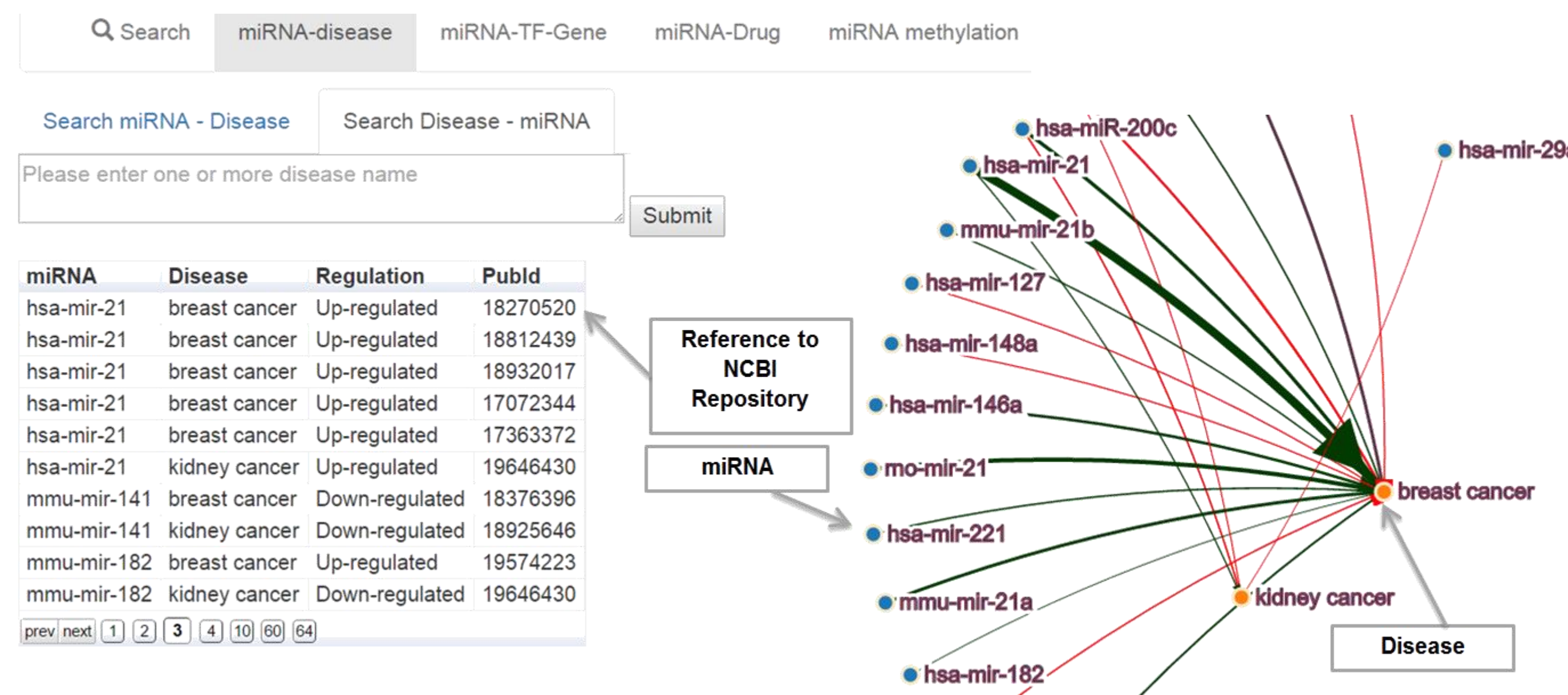


Figure 5: iMir tool features

### Conclusion

iMiR is a one-stop web portal for biologists and drug researchers to study the biological factors responsible for disease regulation in cells via miRNA, genes, and drugs through an easy-to-visualize bioinformatics tool.