

Immuno-Navigator, a batch-corrected coexpression database, reveals cell type-specific gene networks in the immune system

The huge amounts of data in public databases contain an enormous potential for elucidating complex dynamics in cellular biology. However, traditional biology lacks the mean to analyze such “big data”. Moreover, it is hard to compare between data of different laboratories. Thus, the extraction of meaningful information from public data is very difficult in practice.

In this interdisciplinary study, we developed Immuno-Navigator (<http://sysimm.ifrec.osaka-u.ac.jp/immuno-navigator/>), a platform which allows researchers to use thousands of samples for addressing key questions in immunology. Using our platform, researchers can explore information hidden in the data without worries about technical obstacles, and generate hypotheses regarding gene functions.

In one application of our platform we successfully predicted known and new candidate regulators in naturally occurring regulatory T cells. For one promising gene, integrin $\beta 8$ (Itgb8), we experimentally validated an association between Treg-specific epigenetic characteristics and Itgb8 expression in Foxp3⁺ T cells. Furthermore, our analysis also suggests that the expression of Treg-specific genes within Treg cells is relatively independent of Foxp3 expression, supporting recent studies which reported a Foxp3-independent component in the development of Treg cells.

We believe that our Immuno-Navigator will be of great use in increasing our understanding of human disease and accelerate drug discovery.

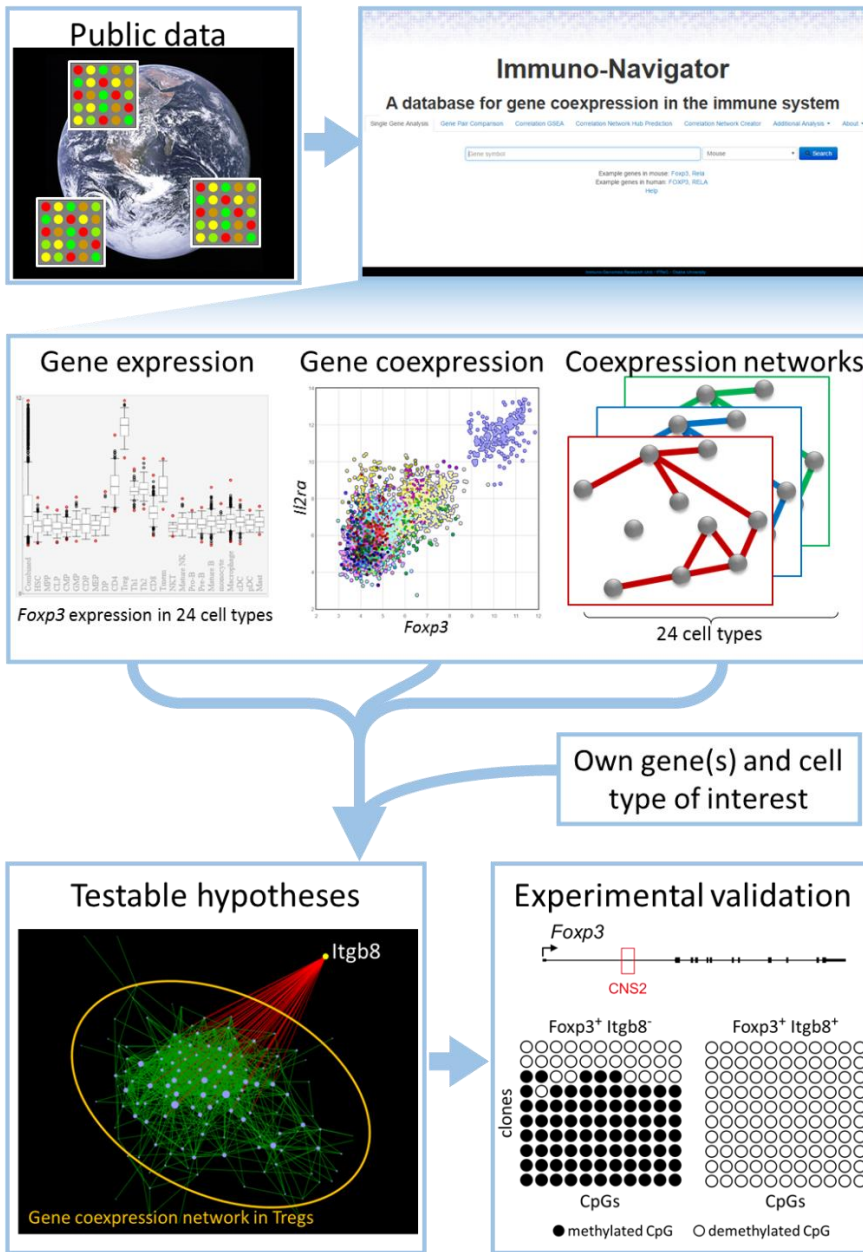
Keywords

Gene expression, network inference, database, bioinformatics, regulatory T cells

Article & journal

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Conceptual overview of the usage of the Immuno-Navigator database.