



tigeR: Tumor immunotherapy gene expression data analysis R package

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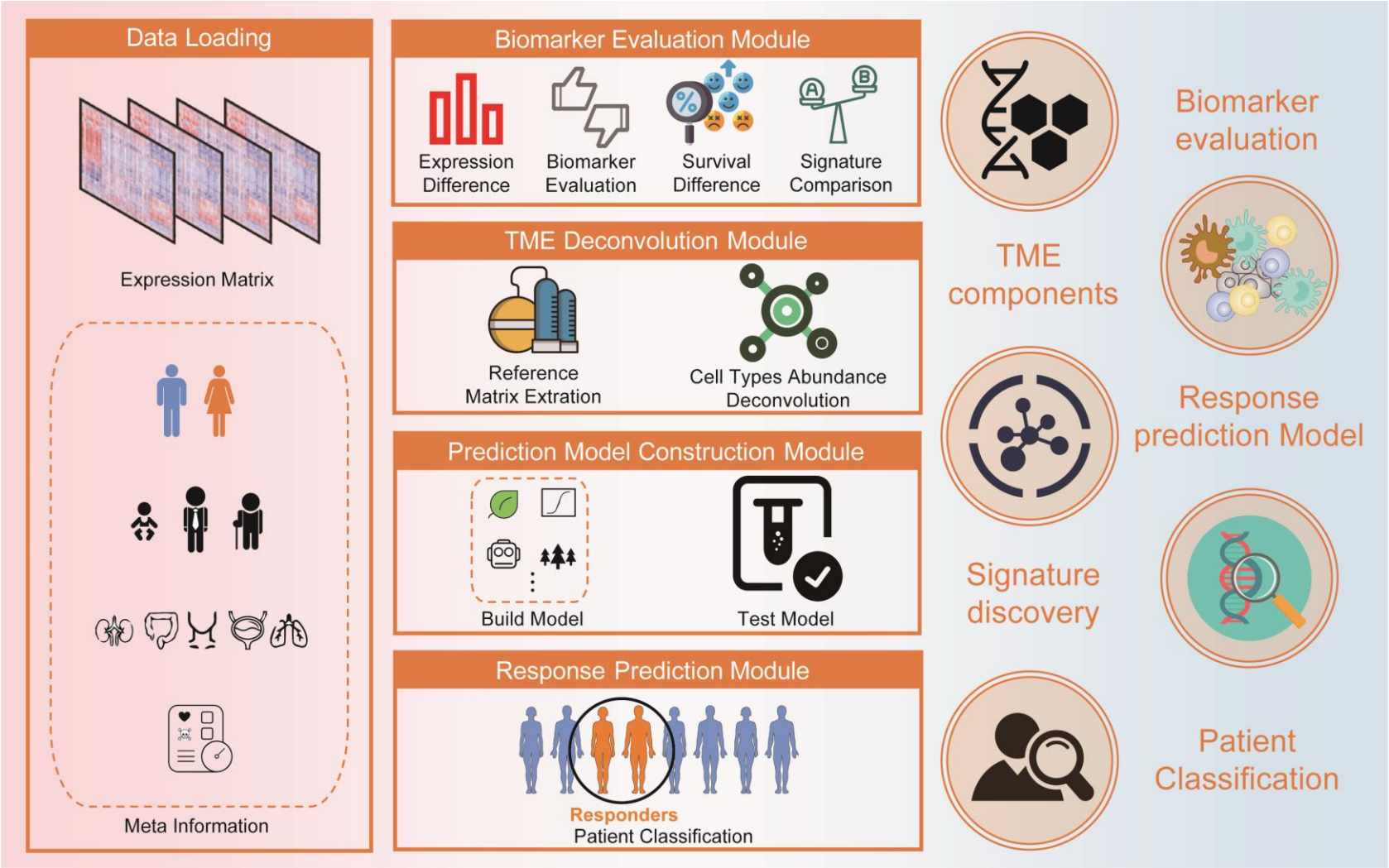
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Introduction

A powerful tool for identifying immune therapy efficacy biomarkers and constructing predictive models



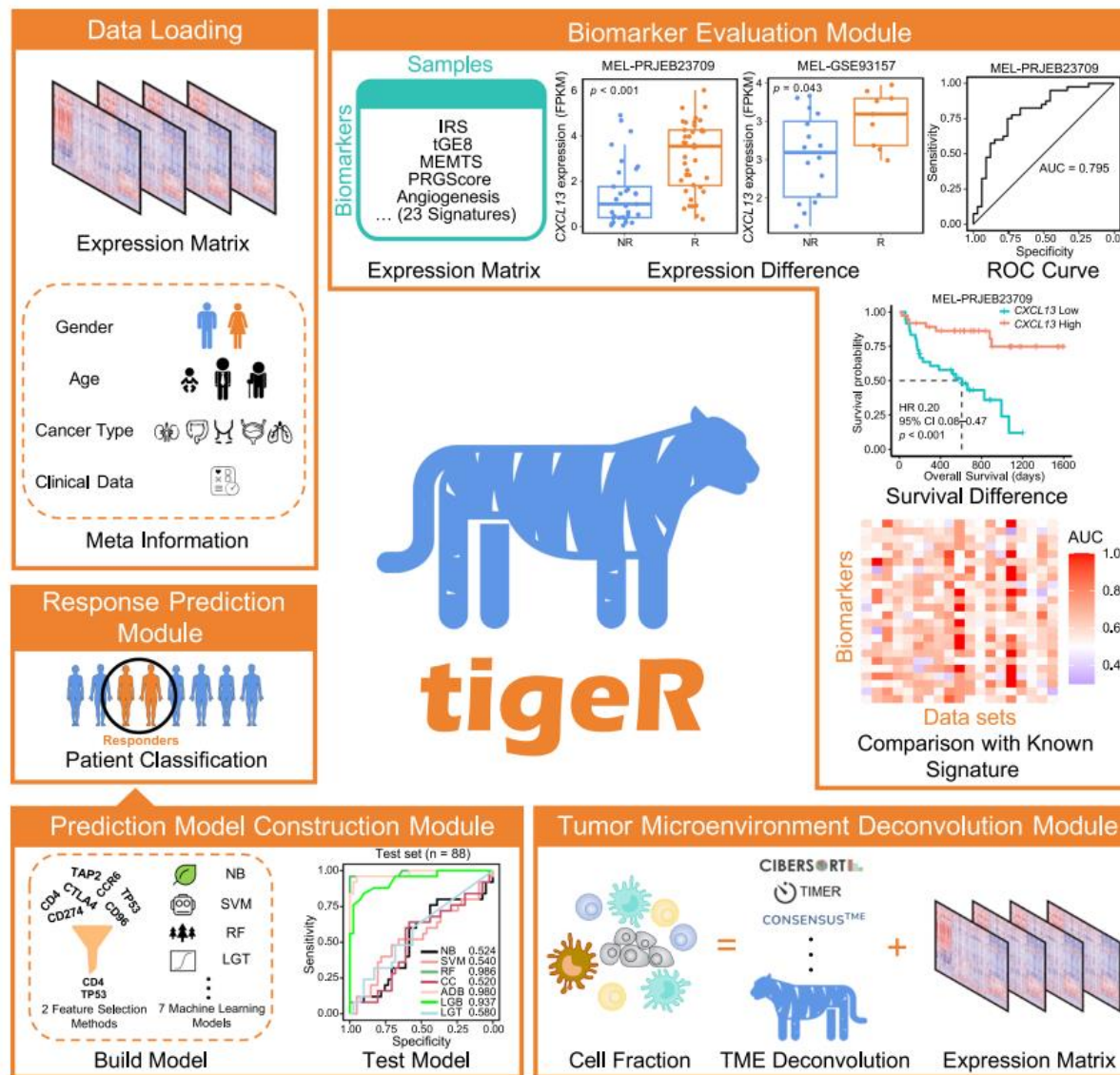


Highlights

- tigeR is an effective R package to explore biomarkers and construct predictive models to predict immunotherapeutic outcomes.
- tigeR enables the flexibility to load built-in or custom gene expression data with immunotherapy outcome information.
- tigeR encompasses four distinct yet closely interconnected modules, including the Biomarker Evaluation module, Tumor Microenvironment Deconvolution module, Prediction Model Construction module, and Response Prediction module.



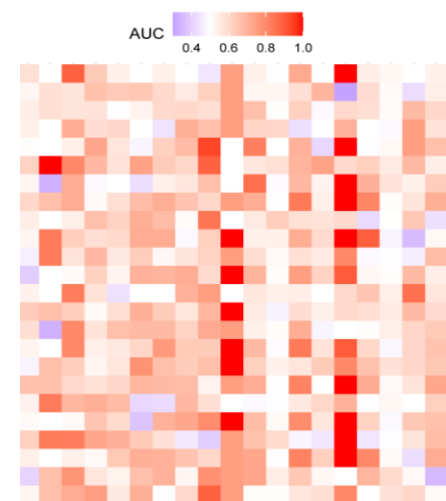
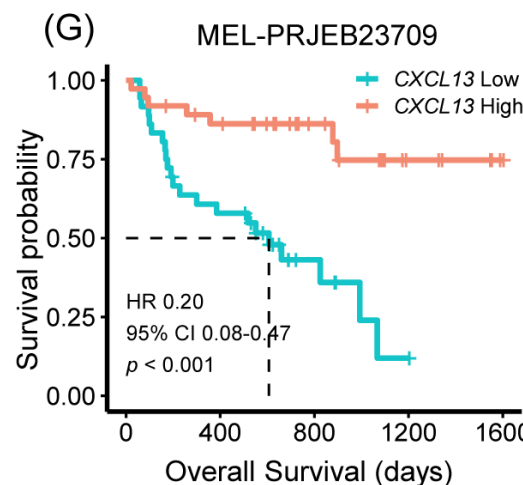
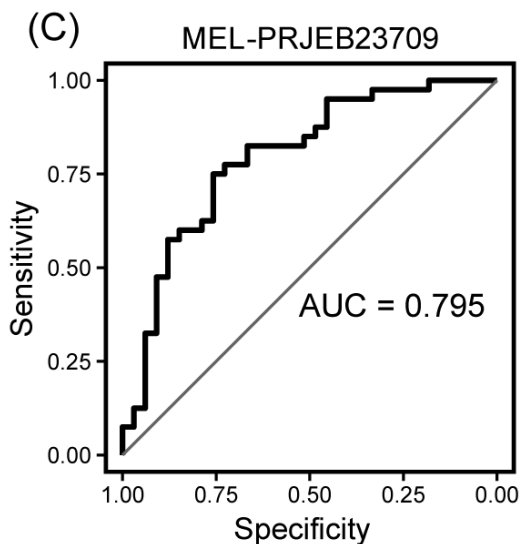
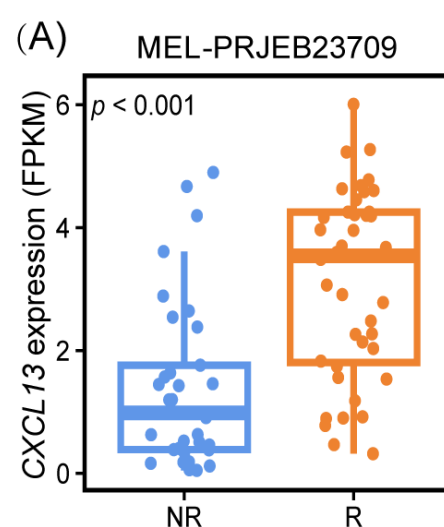
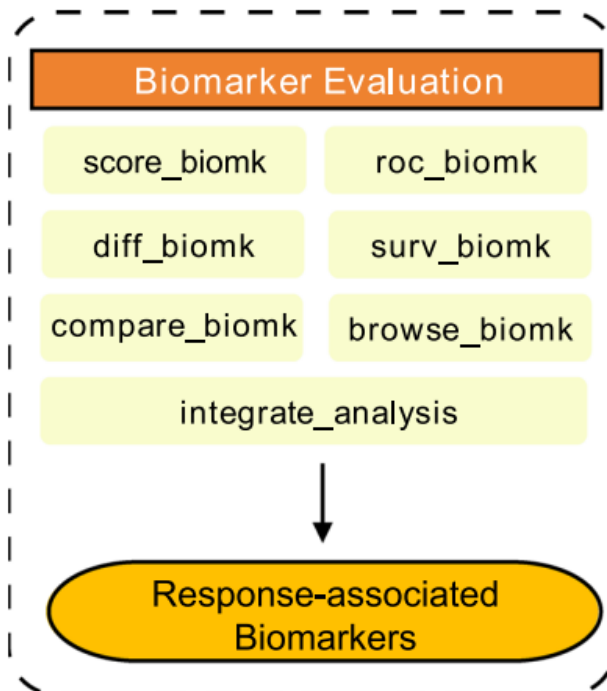
Overview of tigeR



tigeR supports exploration of both built-in datasets and user-defined datasets, including four different but highly interconnected analysis modules: the Biomarker Evaluation module, the Tumor Microenvironment Deconvolution module, the Prediction Model Construction module, and the Response Prediction module.



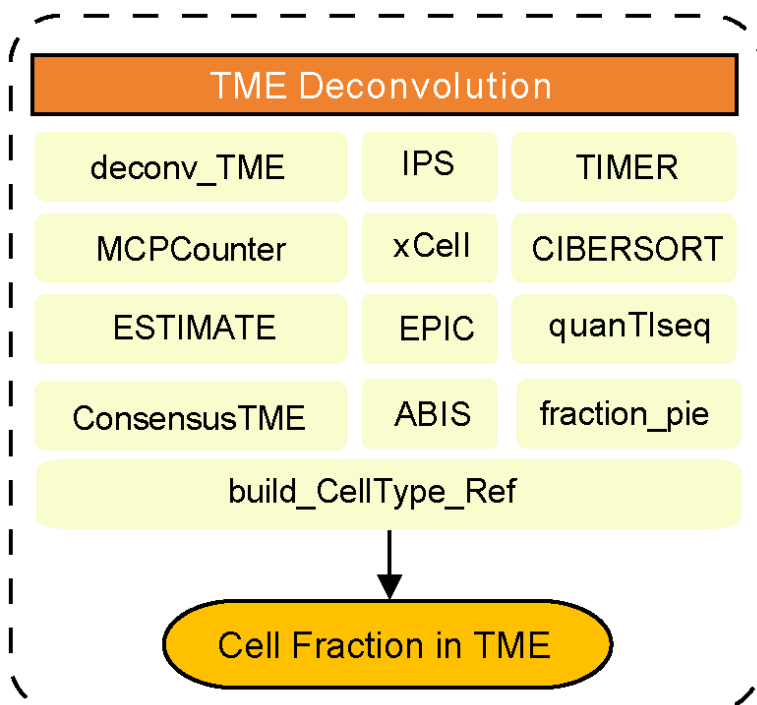
Biomarker Evaluation module



- **diff_biomk()**: visualizes differential analysis result (Responder vs Non-Responder or Pre-Treatment vs Post-Treatment).
- **roc_biomk()**: visualizes the Receiver operating characteristic (ROC) curve.
- **surv_biomk()**: establishes an association between biomarker and improved overall survival in patients undergoing ICB therapy, which is visualized using Kaplan-Meier curve.
- **compare_biomk()**: compare the biomarkers of interest with these existing biomarkers.

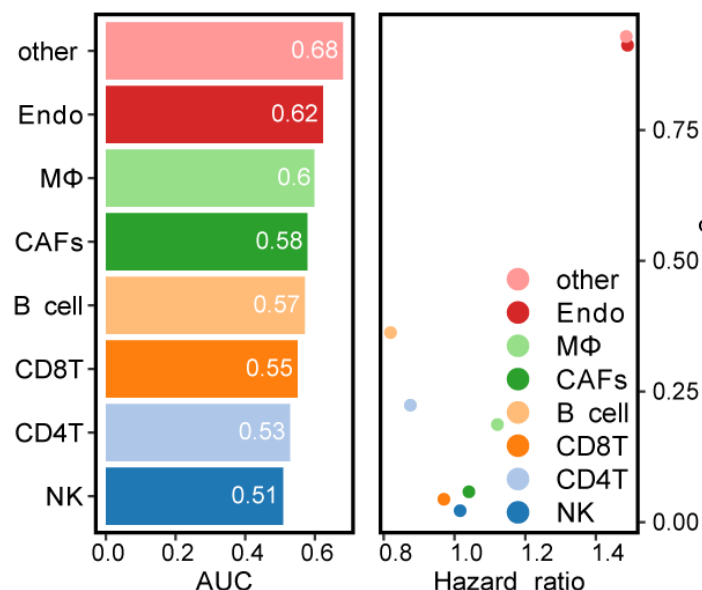
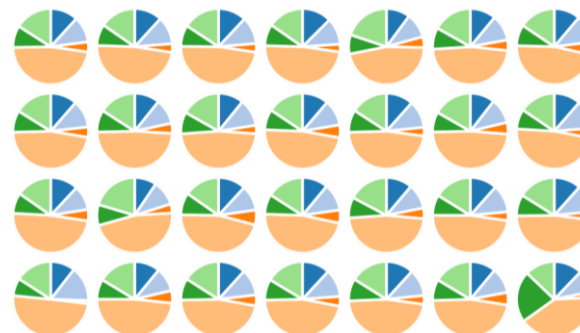


Tumor Microenvironment Deconvolution module



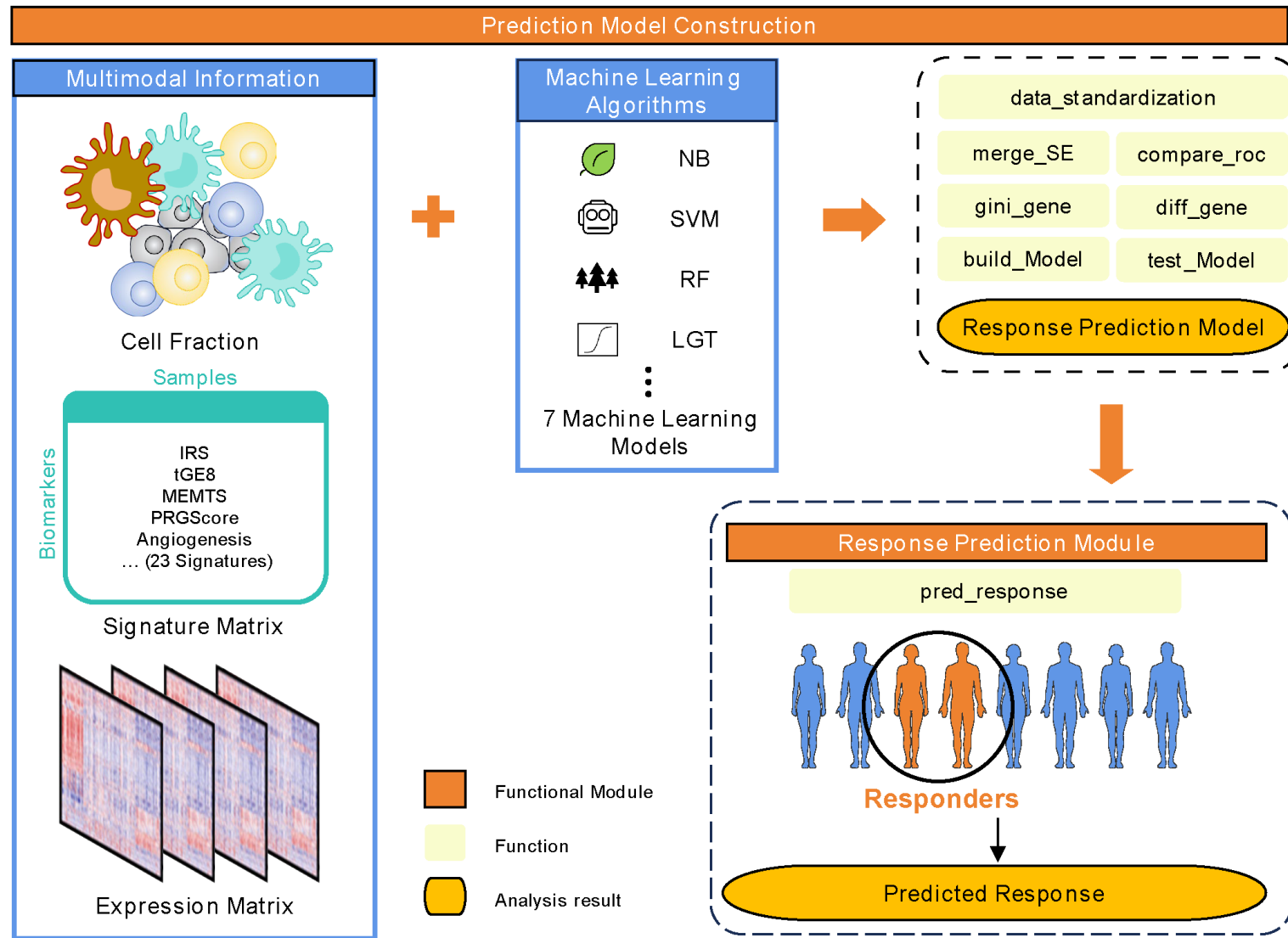
Legend for cell types:

- T cells CD4 (Blue)
- Neutrophil (Light Blue)
- Macrophage (Orange)
- mDCs (Light Orange)
- B cells (Green)
- T cells CD8 (Light Green)



- **deconv_TME()**: derive the proportions of different tumor microenvironment cell types from gene expression data with 10 open-source algorithms.
- **fraction_pie()**: generate pie charts illustrating the cell abundance for each sample.
- **build_CellType_Ref()**: generate a cell type signature matrix from scRNA-seq analysis results.
- **browse_biomk()**: generate a single layout comprised of a bar plot representing AUC and a dot plot denoting Hazard Ratio and P-value.

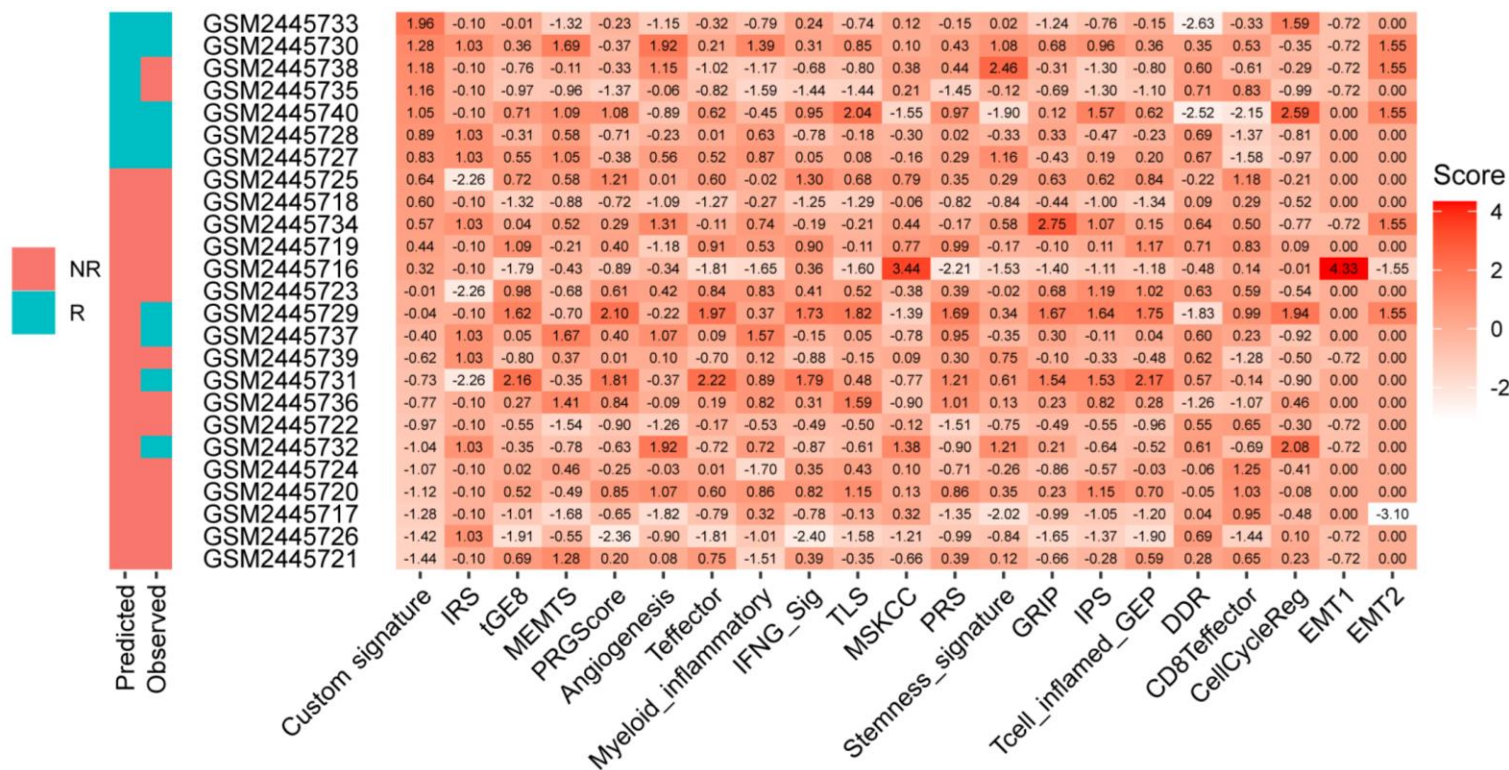
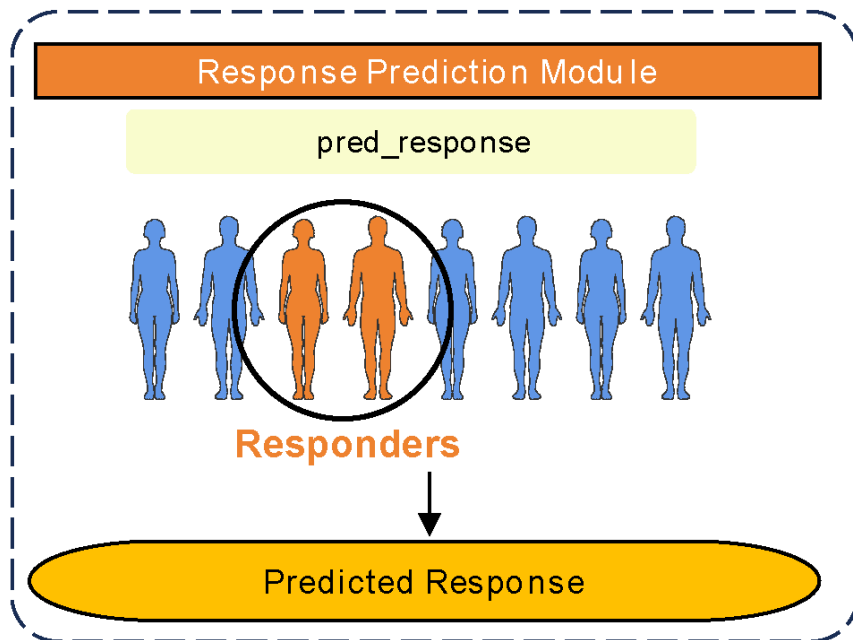
Model Construction module



build_Model(): build machine learning prediction model for immunotherapy response.
test_Model(): test prediction model for immunotherapy response.



Response Prediction module



- **pred_response()**: predict immunotherapy response for individual patient.

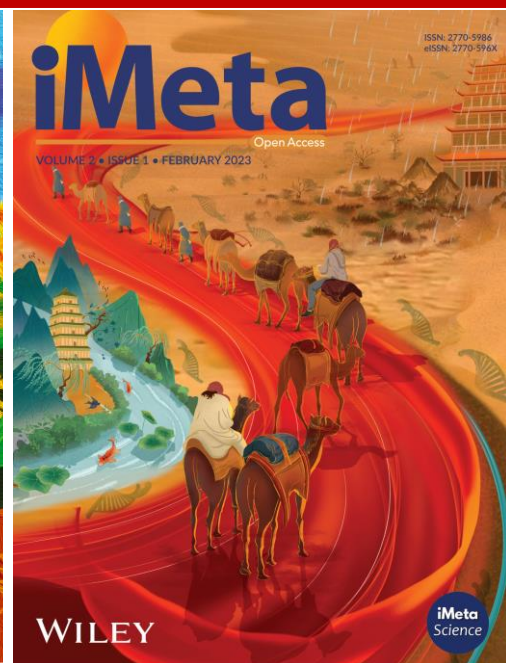
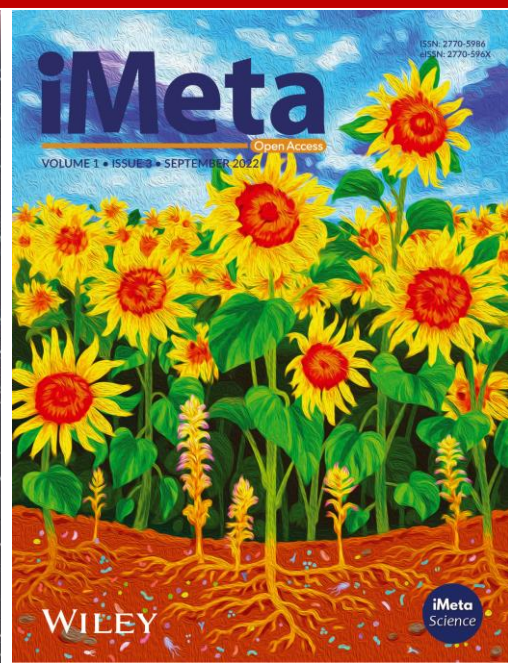


Summary

- ❑ In this study, we introduced tigeR, an R package specifically designed to help users explore the complexities of immunotherapy response.
- ❑ Currently, tigeR is equipped with 4 distinct yet interconnected functional modules, 1060 samples with immunotherapy clinical information, 23 immunotherapy response-related biomarkers from the literature, and 10 open-source TME methods which facilitates a deeper understanding of the molecular mechanisms underlying treatment response.
- ❑ As the field continues to evolve, tigeR stands poised to remain at the forefront, driving innovation and insights in the pursuit of enhanced cancer treatments.
- ❑ Website: <https://github.com/YuLab-SMU/tigeR>


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