CAMOIP: A Web Server for Comprehensive Analysis on Multi-Omics of Immunotherapy in Pan-cancer

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Introduction

- The exploration of biomarkers that can effectively distinguish immune responders from non-responders is important for predicting the effect of immunotherapy. RNA-Seq data and mutation data of patients receiving ICIs provide opportunities to find candidate drug targets and screening biomarkers relevant to immunotherapy. Through genome-wide sequencing and multi-omics analysis, we may comprehensively evaluate the tumor immune status of patients and identify suitable ICI-relevant biomarkers.
- We developed Comprehensive Analysis on Multi-Omics of Immunology in Pan-cancer (CAMOIP), a web-based tool that provides fast and customizable analysis.

Home

- CAMOIP provides a graphical interface that briefly introduces all clinical cohort information used in this project.
- Users are able to find the sample number of the immunotherapy cohort corresponding to each tumor in the body diagram provided by the interface.

Expression

- The user can select tumor type and gene expression data for differential analysis and visualization (Figure 5A).
- In addition to the differential analysis of single gene expression, users can also perform a differential analysis on all expression data of each tumor type based on gene mutation grouping and visualize the results as a volcano map (Figure 5B).

Immune Infiltration

CAMOIP provides an opportunity for users to analyze changes over time in immune cells, immune checkpoint molecules, immune related scores, and immune related genes.

Kaplan-Meier plotter

CAMOIP can be used for survival analysis according to either gene mutation level or gene expression level. This function allows users to select a tumor type and perform survival analysis for specific genes.

Drug Sensitivity

Users can select the tumor type and gene of interest and analyze the differences in drug sensitivity.

Mutation Landscape

- This function allows users to display an overview of gene mutation under different mutations or alterations groups.
- According to the specific tumor type and input of a specific gene, the user is able to group the non-synonymous mutation status or change the status of the gene and further compare the difference in mutation frequency of other genes in the same cohort under the grouping variable.

Immunogenicity

CAMOIP provides users with a simple way to analyze immunogenicity.

Conclusions

- With continuous user feedback and further enhancement, CAMOIP has the potential to become an integral part of routine data analysis for experimental biologists.

References


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