



RTypes

Cristian Ayala, Elias Brezine, Bruce Choe, Erik Marsh
Instructors: David Feil-Seifer, Devrin Lee, Sergiu Dascalu, Vinh Le
Advisor: Tin Nguyen

Department of Computer Science and Engineering, University of Nevada, Reno

CSE

Description

Main Goal

RTypes provides an accessible, intuitive interface for performing disease subtyping analysis.

Features

RTypes takes .RData files as input, and uses data from The Cancer Genome Atlas as a template. RTypes uses Similarity Network Fusion (SNF) and Neighborhood based multi-omics clustering (NEMO) as the main subtyping tools. RTypes visualizes results using heatmaps and alluvial plots. Figure 2 displays the heatmap result of a NEMO analysis.

Architecture

RTypes is a web application. RTypes receives visualization requests from the front-end user interface and sent to the back-end for processing. The results are displayed on the front end. Figure 1 displays a collection of saved visualizations.

Abstract

RTypes is a web application that performs disease subtyping analysis. Disease subtyping analysis uses genomic data to cluster similar patients in order to identify disease phenotypes. The application takes .RData files with patient information as input, and creates heatmaps and alluvial plots to visualize the disease subtyping analysis. The aim of the project is to expand the accessibility of subtyping tools. RTypes allows non-computational medical professionals and researchers to access subtyping tools without the need for any coding. Improving accessibility to subtyping tools will improve health outcomes and standards of care for patients.

Future Work

- Support .csv files as input
- Add more R modules for subtyping analysis
- Support for subtyping tools written in Python
- Refine account system with email verification, password security requirements, and two-factor authentication
- Support zooming and panning on the generated visualizations

Figures

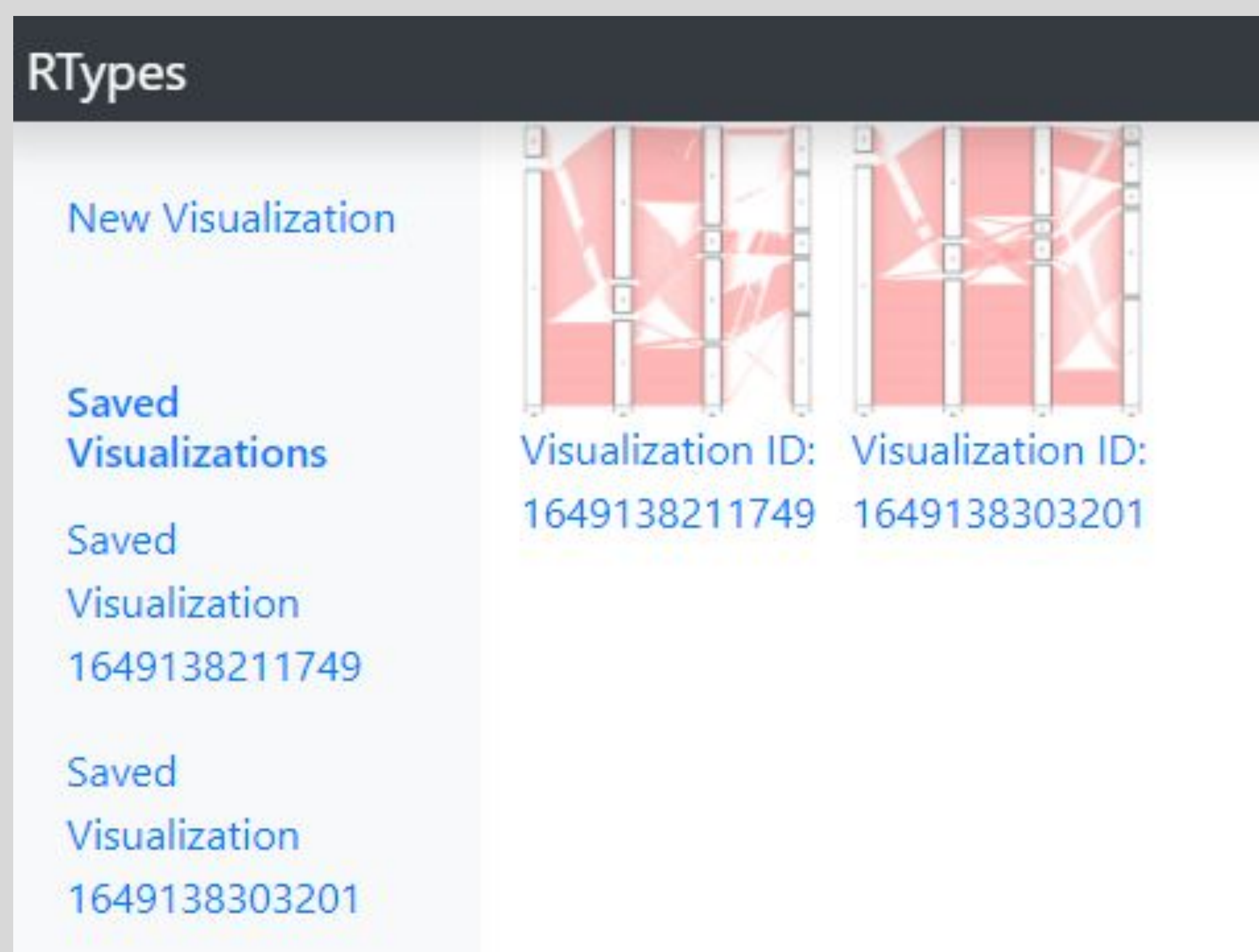


Figure 1: The saved visualization page of RTypes, showing two saved visualizations with thumbnails of their alluvial plots.

Conclusions

RTypes functions as a framework for aggregating disease subtyping tools. RTypes has the architecture to allow the inclusion of additional subtyping tools and visualization options in the future.

Expanding the use of disease subtyping tools to nontechnical users is an important step in elevating subtyping analysis to become a standard of care. As a standard of care, subtyping analysis is beneficial as it allows patients to identify their risk level.

Figures

