

Spectre R package - Home Page

Overview: Spectre is an R package and computational toolkit that enables comprehensive end-to-end integration, exploration, and analysis of high-dimensional cytometry data from different batches or experiments. Spectre streamlines the analytical stages of raw data pre-processing, batch alignment, data integration, clustering, dimensionality reduction, visualisation and population labelling, as well as quantitative and statistical analysis; with a simple, clear, and modular design of analysis workflows, that can be utilised by data and laboratory scientists.



The Spectre Home Page has moved!

You can now find the Spectre home page at <https://immunedynamics.github.io/spectre>