Package: cytofWorkflow (via r-universe)

October 1, 2026

Title CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets

Version 1.37.0

Date 2023-10-28

Description High-dimensional mass and flow cytometry (HDCyto) experiments have become a method of choice for high-throughput interrogation and characterization of cell populations. Here, we present an updated R-based pipeline for differential analyses of HDCyto data, largely based on Bioconductor packages. We computationally define cell populations using FlowSOM clustering, and facilitate an optional but reproducible strategy for manual merging of algorithm-generated clusters. Our workflow offers different analysis paths, including association of cell type abundance with a phenotype or changes in signaling markers within specific subpopulations, or differential analyses of aggregated signals. Importantly, the differential analyses we show are based on regression frameworks where the HDCyto data is the response; thus, we are able to model arbitrary experimental designs, such as those with batch effects, paired designs and so on. In particular, we apply generalized linear mixed models or linear mixed models to analyses of cell population abundance or cell-population-specific analyses of signaling markers, allowing overdispersion in cell count or aggregated signals across samples to be appropriately modeled. To support the formal statistical analyses, we encourage exploratory data analysis at every step, including quality control (e.g., multi-dimensional scaling plots), reporting of clustering results (dimensionality reduction, heatmaps with dendrograms) and differential analyses (e.g., plots of aggregated signals).

Depends R (>= 3.6.0), BiocStyle, knitr, readxl, CATALYST, diffcyt, HDCytoData, uwot, cowplot

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Encoding UTF-8

LazyData true

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

VignetteBuilder knitr

Suggests knitcitations, markdown, rmarkdown

NeedsCompilation no

Workflow true

URL https://github.com/markrobinsonuzh/cytofWorkflow

BugReports https://github.com/markrobinsonuzh/cytofWorkflow/issues

Config/pak/sysreqs cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl zlib1g-dev

Repository https://bioc.r-universe.dev

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RemoteUrl https://github.com/bioc/cytofWorkflow

RemoteRef HEAD

RemoteSha bd00dfcf2284b72b718d1761dfa241650155f6d4