Motivation

- Most gating from flow cytometry is manual and not reproducible
- Need for transparency within flow data analysis
- Visualize impact of each step of analysis:
  - pre-processing/normalization
  - Gating
    - Autogating or manual
  - Population expression
- Enable exploration of data by researchers
  - Understand what is reproducible

Assessing Quality Control across Samples

- Heatmap gives an overview of variability of marker expression across samples
- Individual markers can be compared and colored by condition
- Violin plots for each marker/sample can be visualized for technical variability. Samples can be flagged for poor quality and removed from downstream analysis.

Assessing Gating

- Full gating hierarchy for each population/sample can be assessed for reliability. Bad gating results can be flagged and removed
- Waterfall plots: allow user to assess correlations between populations and conditions
- Dotplots: allow user to assess association of population percentages within categories

Population Expression

- Violin plots allow to assess reproducibility of expression within a population and aggregate data within conditions and populations

Implementation

- Implemented in R/Shiny/plotly as modules
  - Modules can be mixed and matched for a customized dashboard
  - data.table used for fast subsetting of data structures
- Data and display options encapsulated in R6 objects
  - Automates building of dashboard from objects
  - Objects are derived from either flowSet or gatingSet objects from flowWorkspace (Bioconductor)

Check it out!

http://github.com/laderast/flowDashboard

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