

Analyzing flow cytometry data in Bioconductor

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A decorative graphic consisting of several horizontal lines of varying lengths and colors (teal, white, and light blue) extending from the right side of the slide.

Flow cytometry

- R – Bioconductor packages
 - Open source

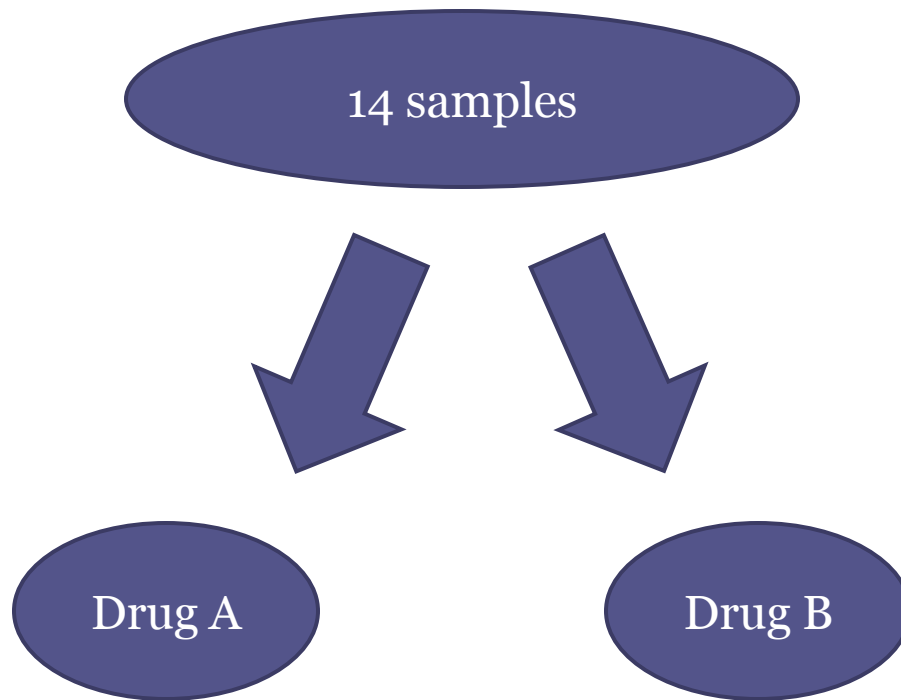
- flowCore
- flowViz
- flowQ
- flowStats

- flowUtils
- flowClust
- flowMerge
- flowFP
- flowFlowJo

Overview

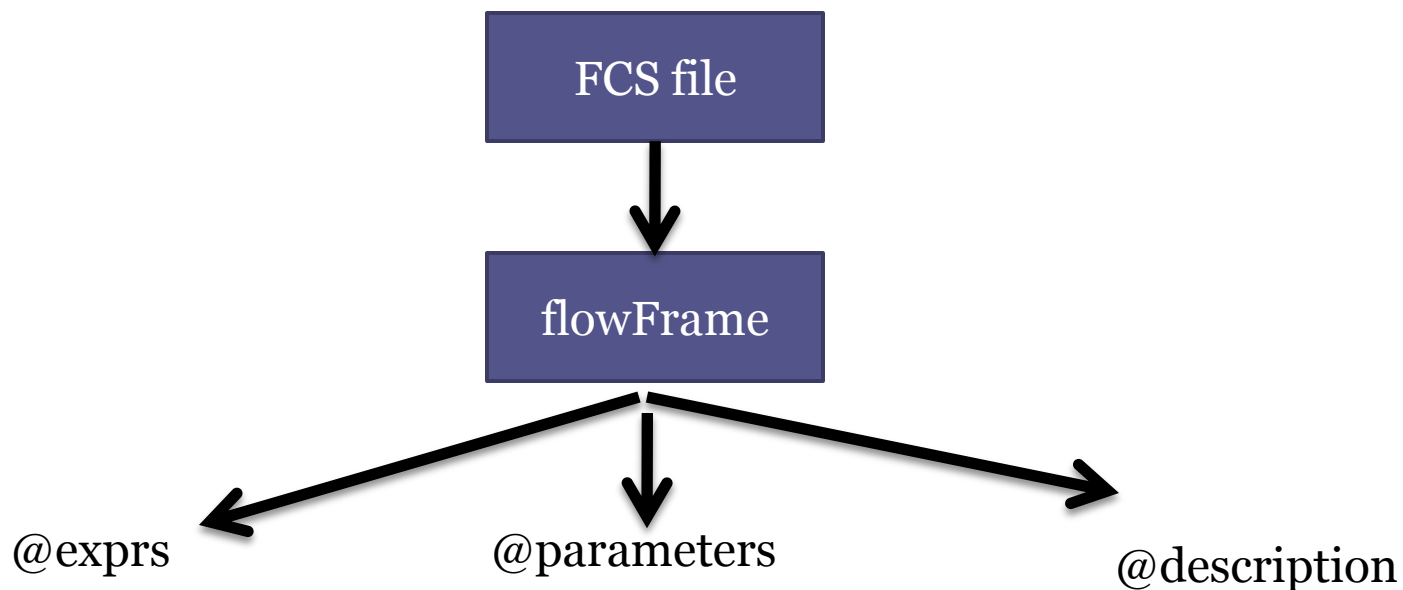
- Walk through a simple flow data analysis
 - FCS files
 - Data structures in flowCore
 - Quality control reports
 - Transformation, sequential gating , visualization
 - Workflows

FCS files



CD8
CD69
CD4
CD3
HLADr

Data structures - flowFrame



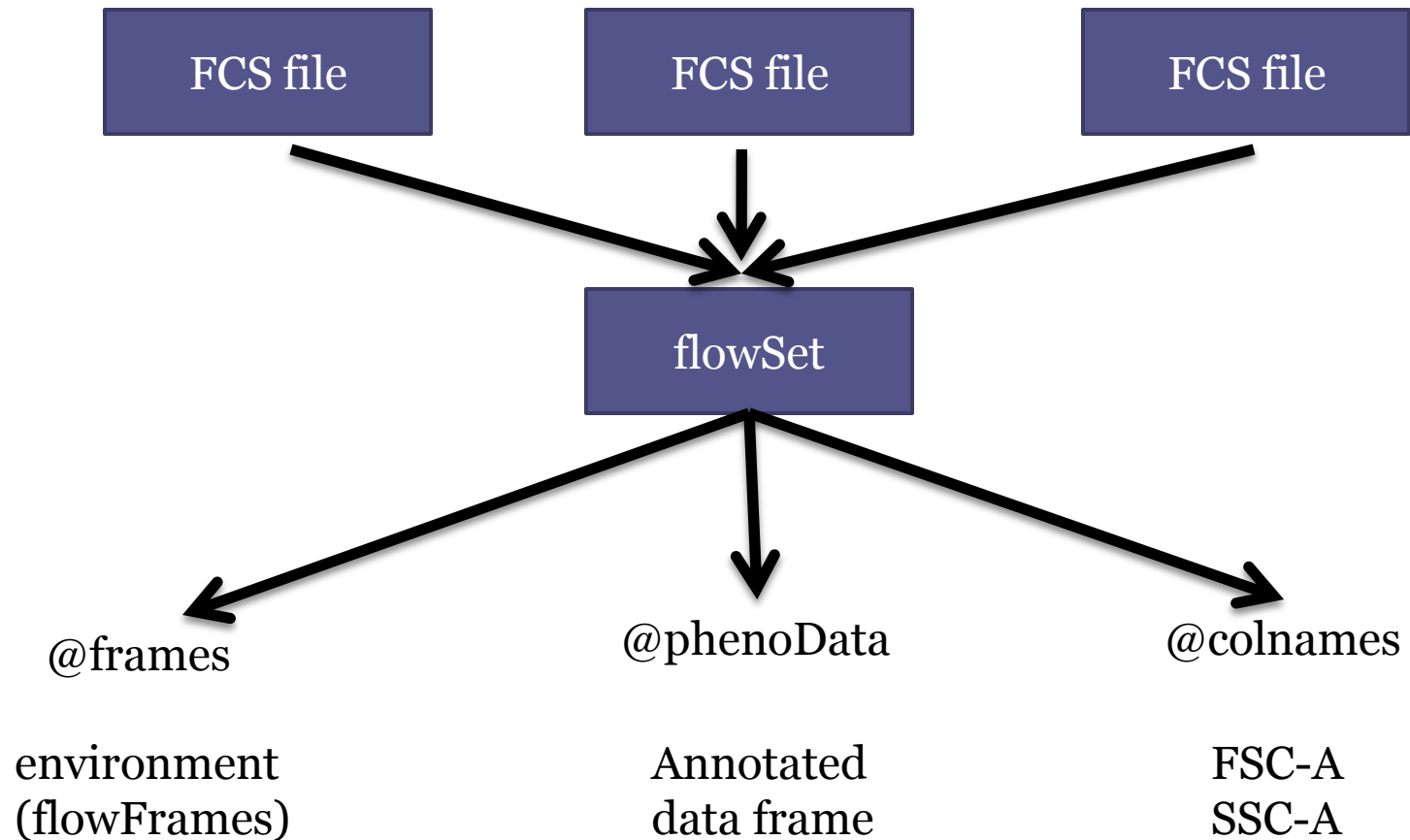
FSC	SSC	FITC-A	PE-A
600	444	4.5	5.4
500	333	3.4	4.5
700	450	4.3	3.3

Annotated data frame

- Stain
- Channel
- Range

List containing meta data information

Data structures -flowSet



R session 1

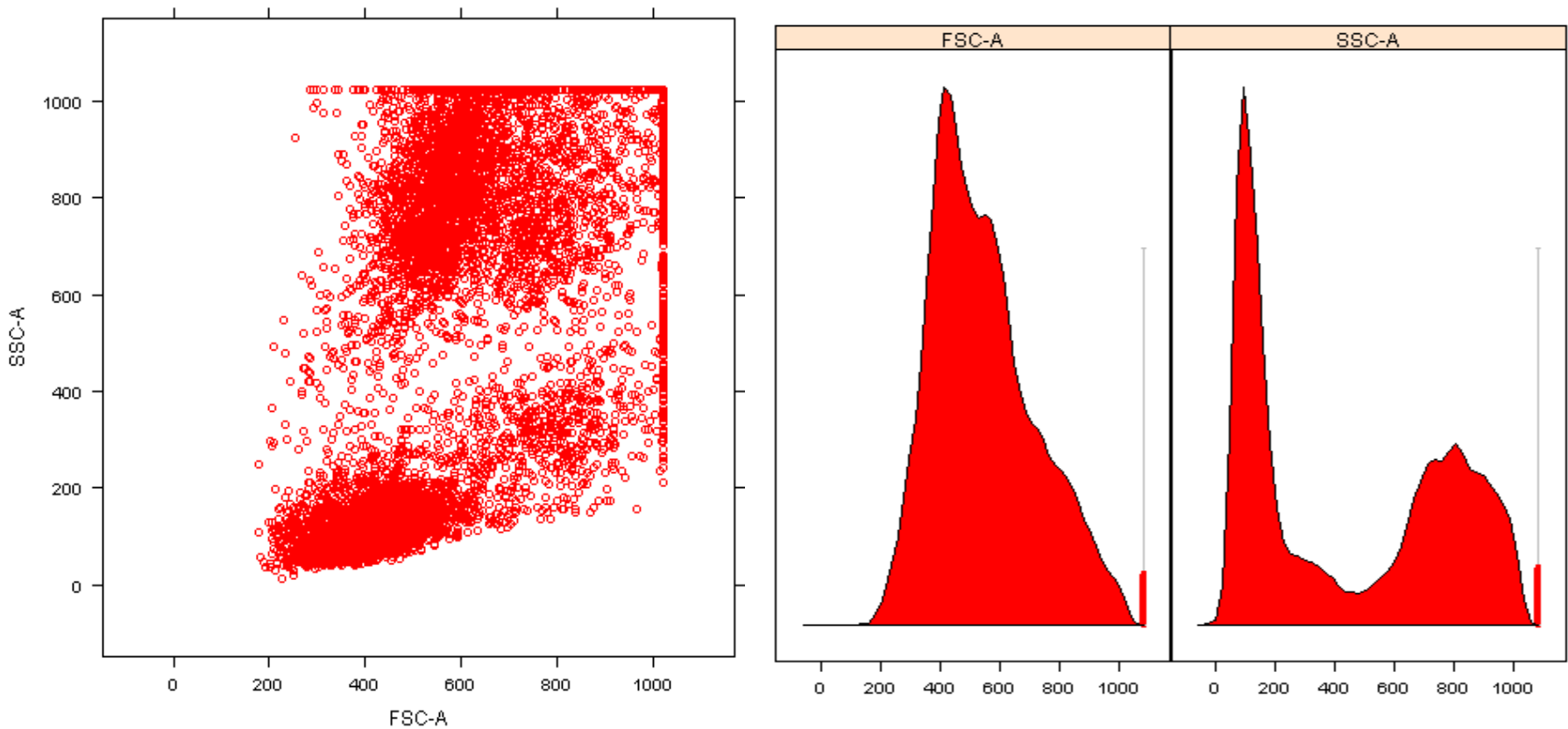
- Create a flowSet
- Transform Data using asinh transformation
 - `transform()`
 - FITC-A, PE-A, FL3-A, PE-CY7-A , APC-A
 - `transformList`
- Visualize data

Quality Assessment - flowQ

- Boundary events
- Cell number
- Time Line
- ECDF plots
- Density plots
- KL distance plots

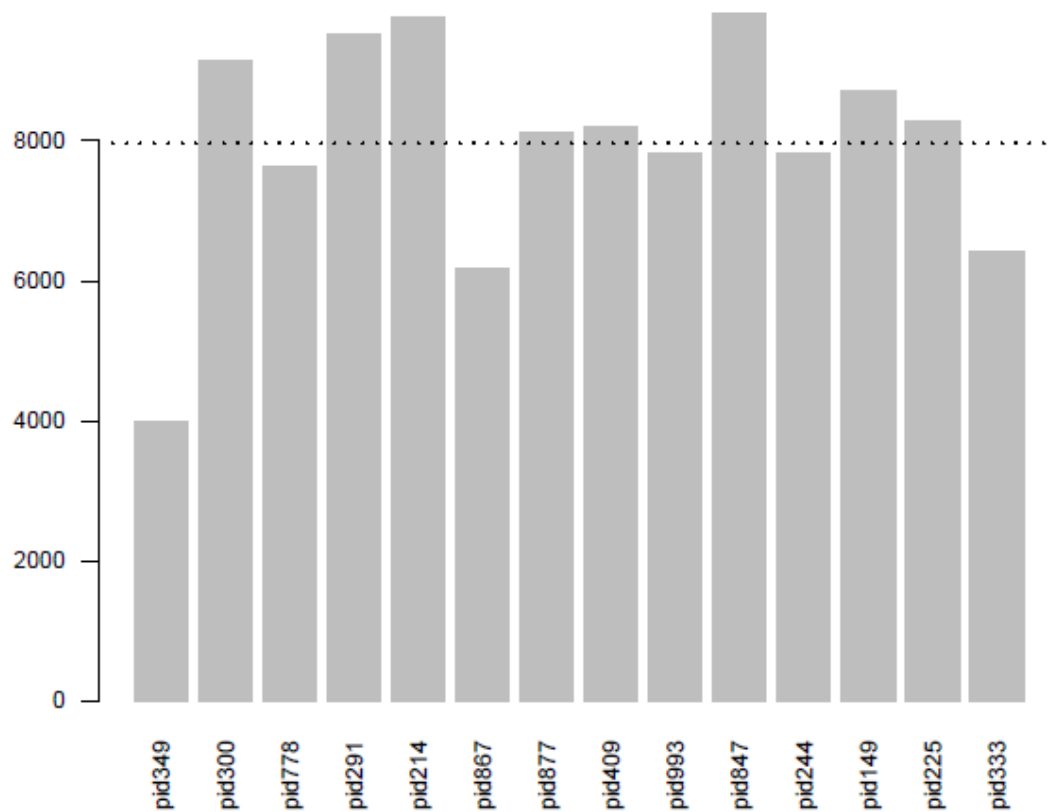
Boundary events

- `qaProcess.marginevents()`



Cell number

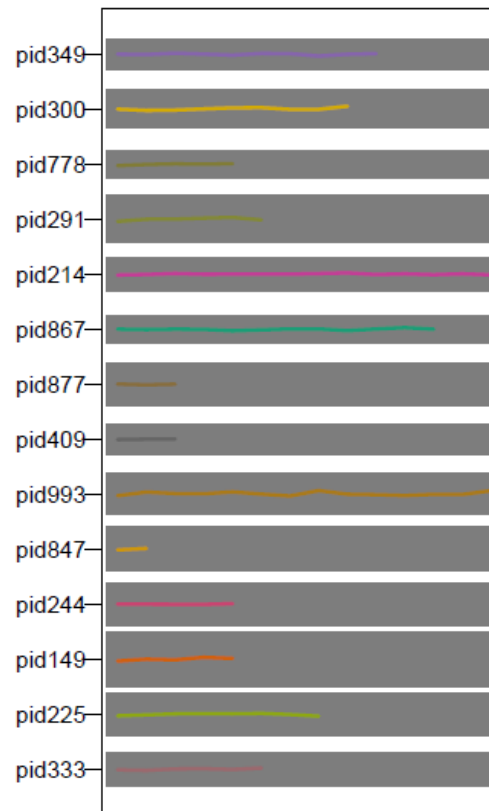
- `qaProcess.cellnumber()`



Time line

- `qaProcess.timeline()`

time line for FSC-A



R session 2

- Generate quality reports

Goals

Compare amongst two treatment protocols -
Drug A & B

- T helper cells that exhibit HLADr activation marker
- T cytotoxic cells that exhibit HLADr activation marker

Sequential gating strategy

