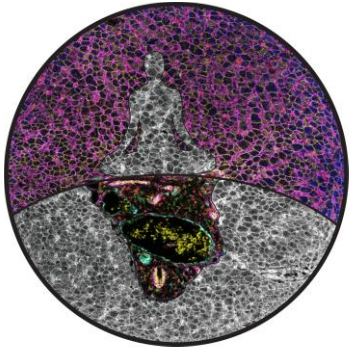

Centenary Institute
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Making sense of flow cytometry data in R

Felix Marsh-Wakefield

Latest updates

- Batch alignment in Spectre
  - https://immunedynamics.io/spectre/cytonorm/
  - Development branch has a few options
- SuperCellCyto for subsampling data
  - https://phipsonlab.github.io/SuperCellCyto/
  - Retains rare cell populations
  - Includes workflows with batch alignment
  - Putri et al., 2024 (*Genome Biology*)
- Spectre Rshiny app (thanks to Thomas O'Neil)
  - https://drthomasoneil.github.io/CVR-site/apps.html

Today’s workshop!

- https://shorturl.at/Ppqcn

Flow data preparation

https://shorturl.at/Ppqcn

- Compensation
- QC gating (live single cells)
- *Data transformation (arcsinh, biexponential, etc.)
- Export as CSV
  - "Channel values" in FlowJo
- Can use 'CytoExploreR'
  - https://dillonhammill.github.io/CytoExploreR/

Special thanks to...

- Thomas Ashhurst
- Givanna Putri
- ACS

https://shorturl.at/Ppqcn

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