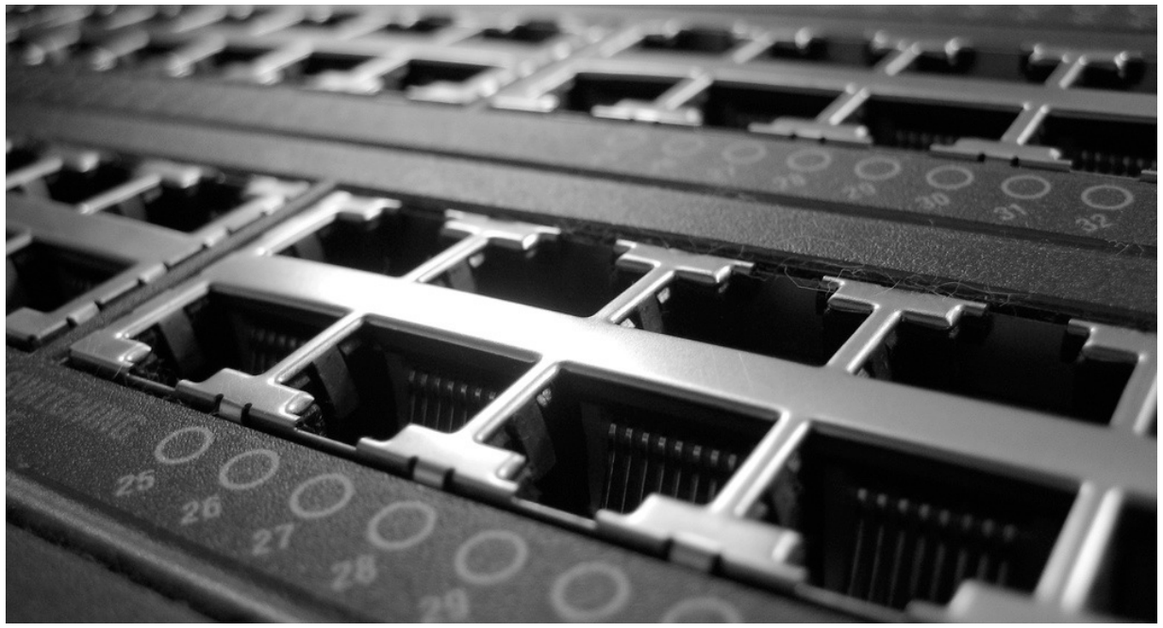

Supporting Single Cell RNA-seq Analysis: A Core's Perspective

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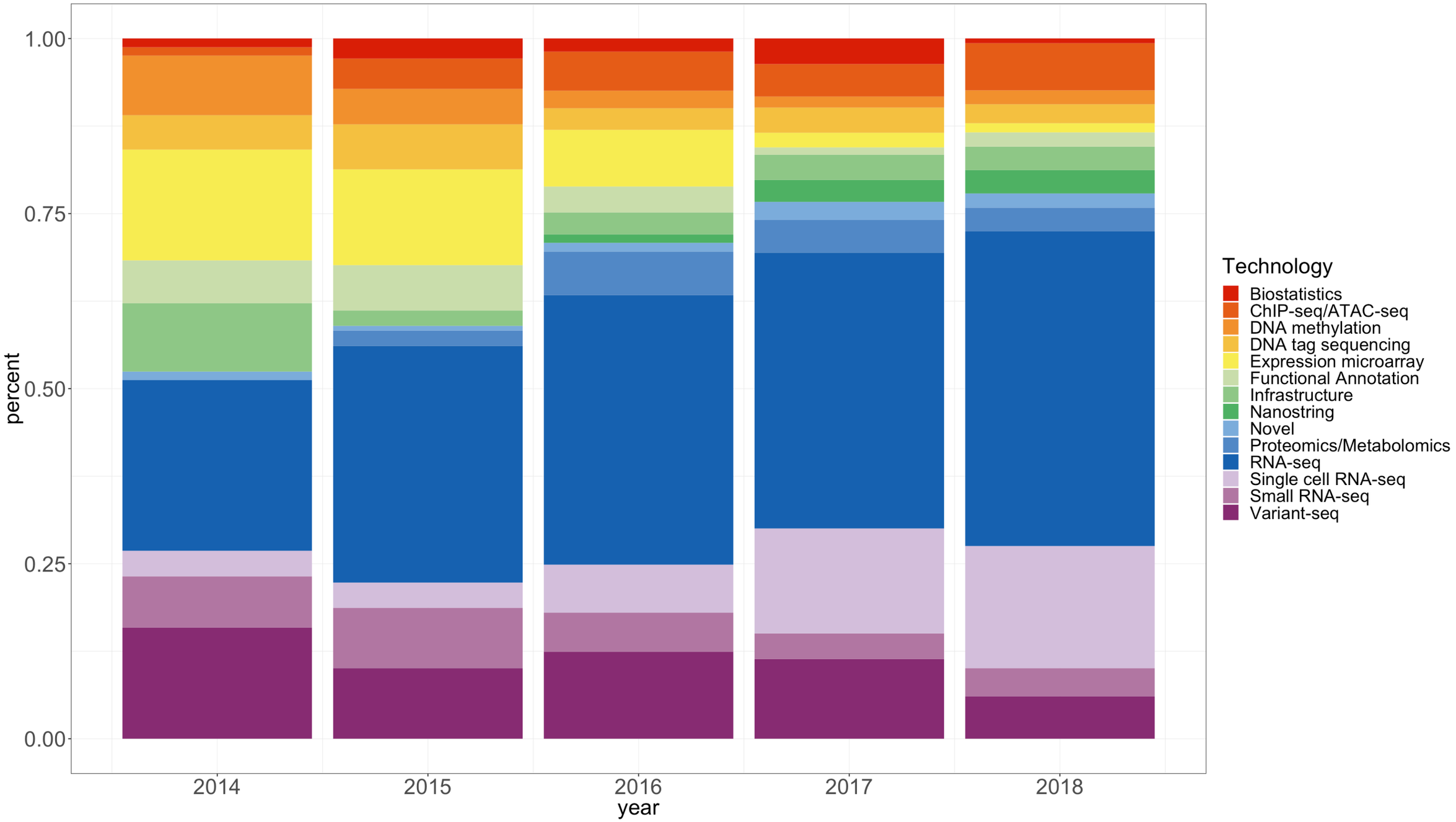
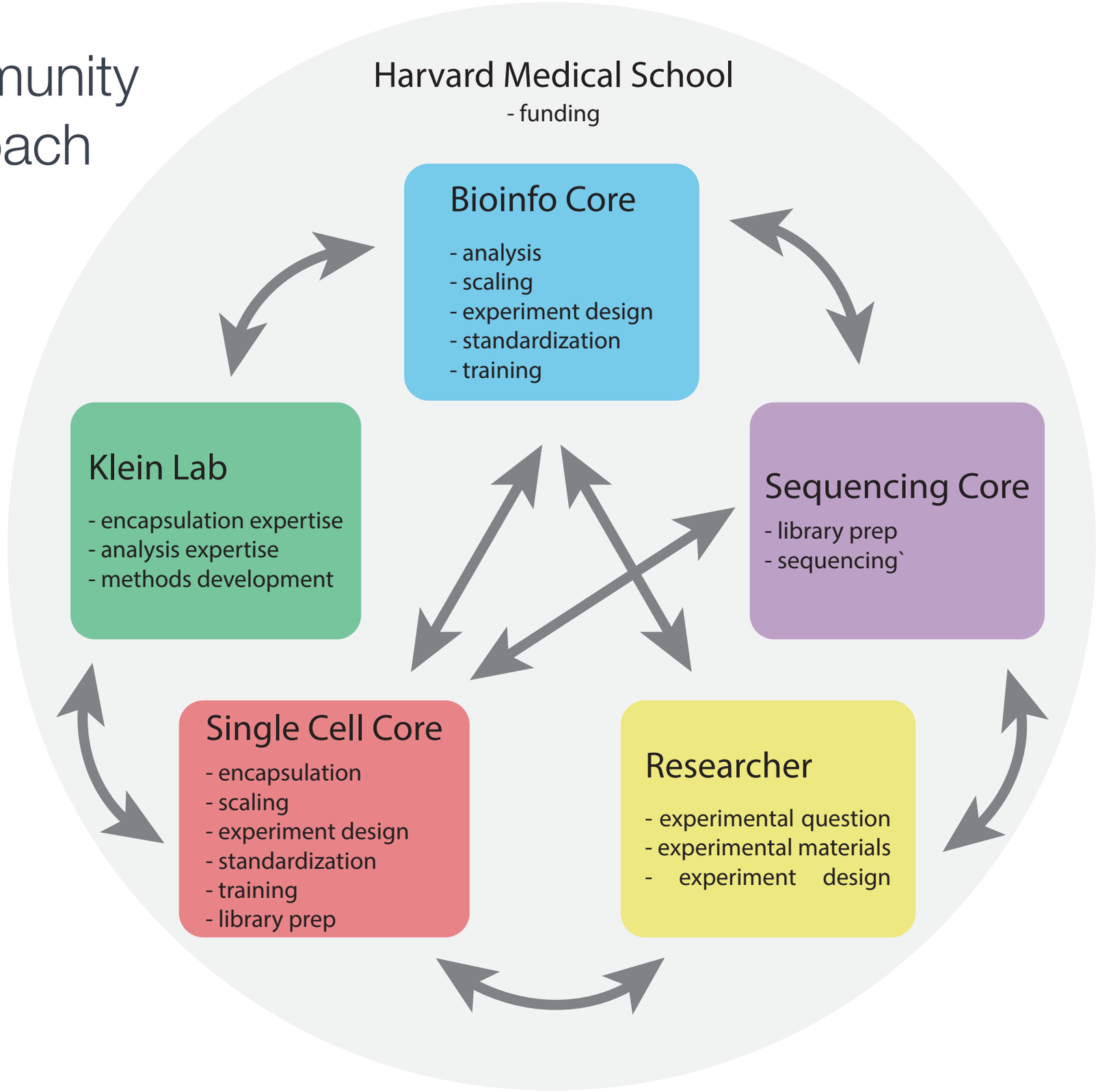
Common applications of scRNA-seq

- Explore which cell types are present in a tissue
- Identify unknown/rare cell types or states
- Elucidate the changes in gene expression during differentiation processes or across time or states
- Identify genes that are differentially expressed in particular cell types between conditions (e.g. treatment or disease)
- Explore changes in expression among a cell type while incorporating spatial, regulatory, and/or protein information

Growing demand for scRNA-seq support



A Community Approach



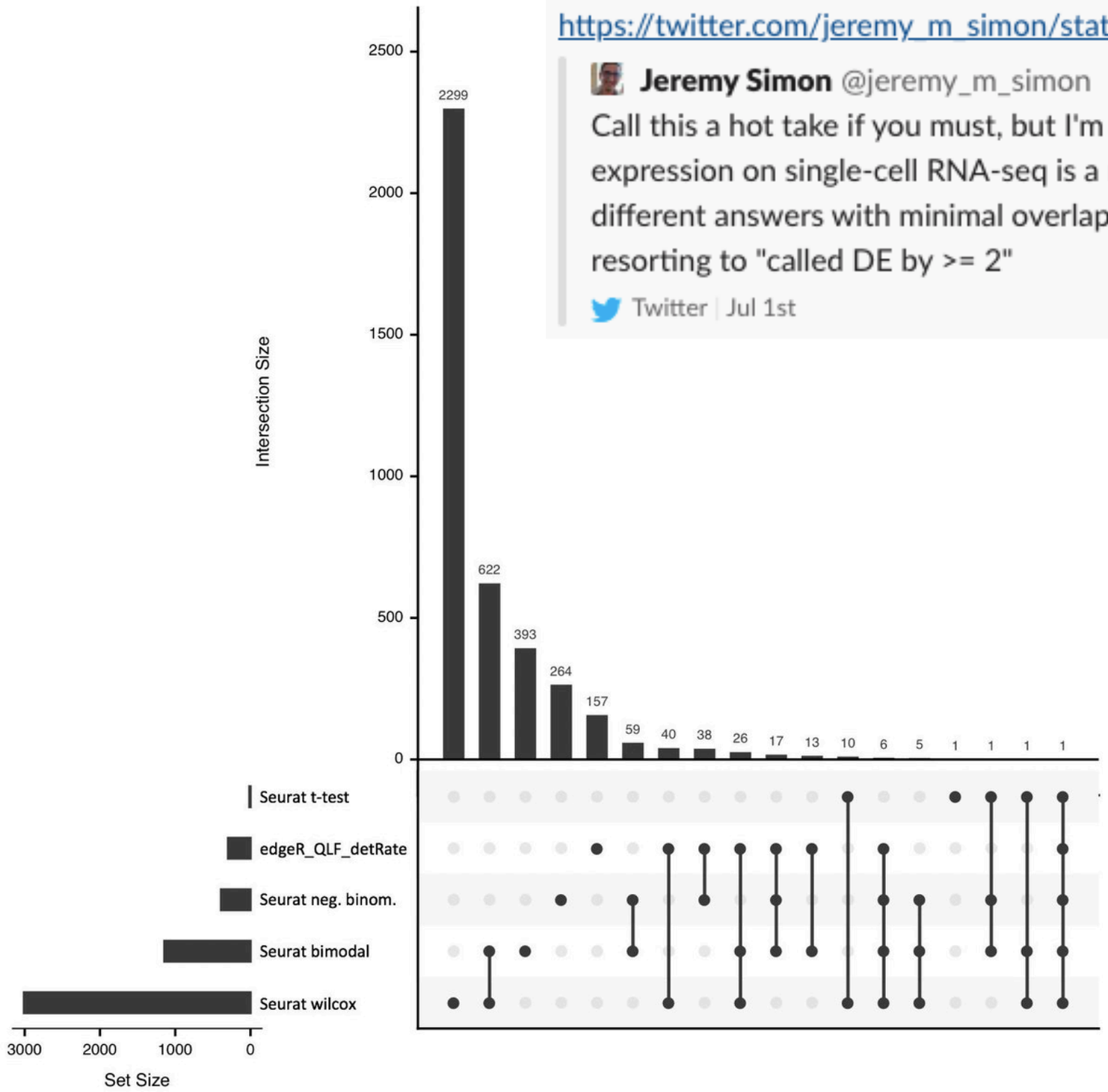
Standardizing using reproducible, scalable, validated best practice workflows

bcbio-nextgen

Python toolkit to automate best practice NGS pipelines

Challenges and Opportunities

- Complex designs - replicates, batches, technologies
- Close collaborations to allow for rapid, iterative analyses
- Rapidly emerging methods and evolving tools
  - Which ones to use?
  - Keeping versions consistent/synchronized (esp. among computing environments)
  - Different results from different methods
  - Lots of open questions

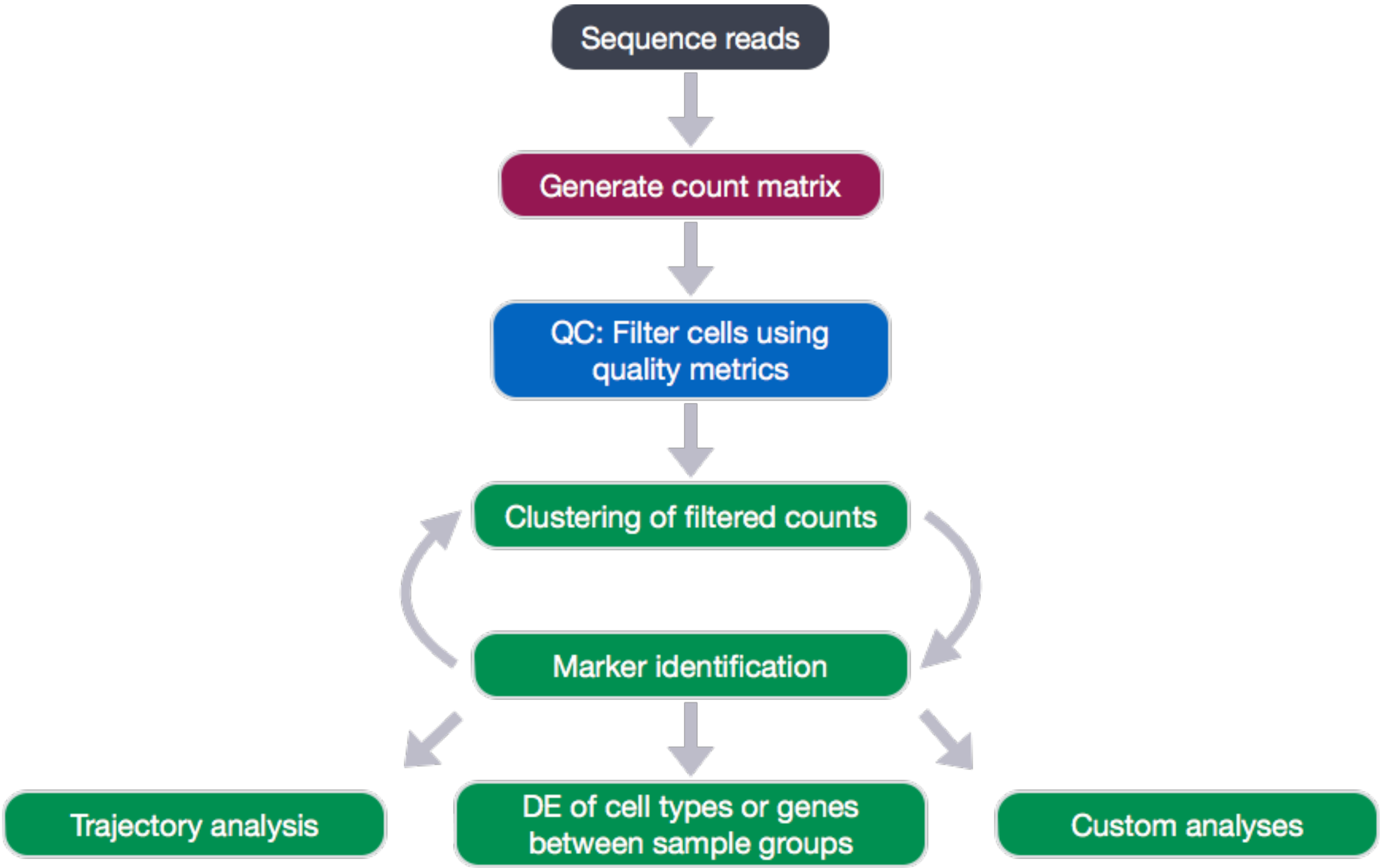


https://twitter.com/jeremy_m_simon/status/1145754750110990336?s=19

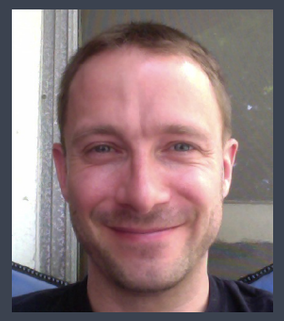
> **Jeremy Simon** @jeremy_m_simon
> Call this a hot take if you must, but I'm going on record and saying it: differential expression on single-cell RNA-seq is a mess. 10 different methods = 10 wildly different answers with minimal overlap. Hard to believe it's 2019 and we're likely resorting to "called DE by >= 2"
> Twitter | Jul 1st

Challenges and Opportunities

- Projects take longer to complete
- Practical approach to training
    - Internal training through retreats, development of materials, group discussions
    - Community training through our Bioinformatics Training Program


Sequence reads
Generate count matrix
QC: Filter cells using quality metrics
Clustering of filtered counts
Marker identification
Trajectory analysis
DE of cell types or genes between sample groups
Custom analyses

John Hutchinson
Associate Director



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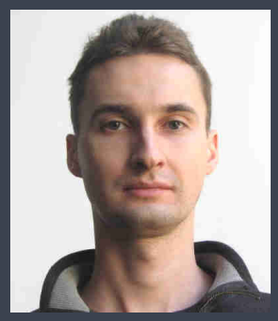

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