Search for and transformation of human cells and cell types with latent space representations

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Abstract

Project Team

- Elana Fertig
- Loyal Goff
- Casey Greene (Submitter)
- Tom Hampton
- Stephanie Hicks
- Mike Love
- Rob Patro

- Base enabling technologies:
    - Low dimensional representations, ProjectR (Elana, Loyal)
    - New methods published by other groups (scVI, etc - others)
    - Fast & improved quantification (Rob)

Aim 1

- Fast search: (in low dimensions, quantifying differences between case and reference maps, twist: shared latent spaces / k-mers)
    - Stephanie: differences b/w maps
    - Rob: new models for UMI deduplication accounting for transcript-level information
        - Parsimony & likelihood based, integrated with gene-level uncertainty
    - Rob: everything FAST! API for search against HCA reference?
    - Casey & Rob: k-mer / quantified latent spaces

Aim 2

- Transformation of latent spaces
    - Loyal & Elana: search tool for perturbations / signatures in latent-space(s)
    - Elana: latent space transformations for progression? Consider jawns for semi-supervised learning?
    - Loyal transfer of signatures *between* tissues

Aim 3

- Reference Cell types
  - Cell-type summarized expression profiles
  - Versioning & provenance of cell types as the reference dataset changes
- Delivery
  - Training / teaching (scRNAseq, low-dimensional representations, RFA-developed tools)
  - Software hardening/testing
  - Bioconductor integration

References