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

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Abstract

Five Key References

Project Team (750 words each)

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

Proposal Body (2000 words)

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

Aim 1

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

Aim 2

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

Aim 3

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

References