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

This manuscript (permalink) was automatically generated from greenelab/czi-seed-rfa@c97109d on October 11, 2018.

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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)
 - Incorporation of uncertainty estimates in low dimensional representations (Rob / Mike / Elana) - note this can be done w/o modification in scCoGAPS

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

- Eschewing marker genes: Practical exploration of the HCA in latent spaces
 - Search tool for perturbations / signatures in latent-space(s) (Loyal)
 - Differential analysis of latent space usage across contexts

- Latent space transformations for progression? Consider jawns for semi-supervised learning? (Elana)
- Transfer learning of signatures between/across tissues (Loyal)
- · Reference Cell types
 - Cell-type summarized expression profiles (Mike, Loyal)
 - A 'reference catalog' of reduced dimensional representations
 - Versioning & provenance of cell types / features as the reference dataset changes (Mike)
 - 'Power-user' application of latent-space discovery in novel dataset and projection of HCA into new learned spaces.

Aim 3

- Delivery
 - Training / teaching (scRNAseq, low-dimensional representations, RFA-developed tools)
 (Tom)
 - Software hardening/testing (Casey software eng)
 - Bioconductor integration (Stephanie, Mike)

References