**1,600 words max**

**Proposed title:** Bayesian matrix factorization for multimodal integration of time-course single cell and bulk omics data

**Summary** Single-cell analysis of gene expression (scRNA-seq) analyses have demonstrated that population-level gene expression and the “transcriptional identity” of individual cells arises from combinations of dependent and independent discrete biological processes1. The dynamics and relationships of these processes change as organisms develop. Inter-individual genetic variation and pharmacological perturbations from treatment of complex diseases induce further changes. Thus, learning developmental trajectories and timing of state transitions requires analytical techniques to delineate cellular composition from dynamic biological processes in single cell transcriptional data.

When representing genomics data as a data matrix, the discrete biological processes that distinguish developmental dynamics from transcriptional identity are each represented as basis vectors in that matrix. Decomposition methods can learn these bases directly from the input data matrix. Specifically, this class of algorithms decomposes data into a continuously-valued vector associating the relative amount of a gene’s expression in a given biological process with a corresponding continuously-valued vector indicating the activity of that process in each sample (**Fig 1**). Our sparse, Bayesian non-negative matrix factorization algorithm CoGAPS (Coordinated Gene Activity in Pattern Sets)2 accounts for both gene reuse and biological parsimony by encoding sparsity and non-negativity in its atomic prior3. CoGAPS learns quantitative trajectories associated with pathway perturbations4, therapeutic resistance5,6, and ageing7 from bulk transcriptional data. It can also distinguish individual and tissue-specific differences8 from static, bulk transcriptional data. Because CoGAPS is Bayesian, it can also encode disparate error models to learn these trajectories across data from distinct measurement technologies6,9. These models have enabled previous multi-model genomics data integration6,9.

CoGAPS unique takes as input both expectation and variance measures of expression consistent with the quantification methods for single-cell RNA-seq such as those developed by collaborative network member Patro10. Preliminary data in single-cell RNA-sequencing has suggested that CoGAPS can likewise differentiate developmental trajectories in different cell types in the retina from single-cell data (**Fig 2**). Together, these results suggest that CoGAPS integration of bulk and single-cell developmental datasets in the Human Cell Atlas will learn patterns in the data that distinguish gene interactions associated with individual variation from gene interactions along developmental trajectories.

The central aim of this research proposal is to address challenges pervasive to the large sample size of transcript level single cell data (**Aim 1**)and model distinct distributions when decomposing multimodal data (**Aim 2**). These approaches build upon gene-level parallelization of CoGAPS in GWCoGAPS8 and modeling distributions of the sparsity hyperparameter in the CoGAPS atomic prior3, respectively. Together, these aims are essential to realize the project goal of “analytical methods … to solve multimodal integration [and] inference of state transitions” in the comprehensive, dynamic datasets of the Human Cell Atlas. Although optimized for CoGAPS, the parallel processing methods and Bayesian models of sparsity will be generally applicable to other unsupervised approaches for genomics data being developed as part of the HCA consortium. They will also be inter-dependent on preprocessing, signature interpretation, data generation, and visualization efforts of the both proposed collaborative network and broader consortium.

**Project Aims, and how they address program goals**:

**Aim 1 Parallel Gene Activity in Pattern Sets (P-GAPS) to learn state transitions and developmental trajectories from large, time-course omics data.** Similar to most NMF algorithms, CoGAPS is limited to O(1000) genes for guaranteed convergence. Some techniques address this convergence by applying feature compaction prior to analysis11,12. However, associating genes or transcripts with inferred patterns from inferred from groups of compacted features may be challenging. Recently, we showed that CoGAPS can be performed directly on genome-wide data using parallel analysis across random gene sets in an algorithm called GWCoGAPS8. Both compaction and parallelization algorithms are possible to perform across genes because of the considerable redundancy between co-regulated genes. Growing scale of time-course, single cell omics data will introduce large sample sizes with similar convergence issues. Independence of expression in specific cell types or stages may limit similar application of these approaches across samples. To ensure both solution optimization and computational efficiency, we will develop a message passing system to parallelize CoGAPS pattern detection in genome wide data for large sample sets. We will apply this algorithm to randomly selected subsets of time-course genomics data benchmark data to assess the sensitivity of the resulting trajectory inference to distributions of cell types, states, and dynamic stages selected for parallel analyses. The resulting gene associations will be linked to function with unsupervised groups, such as those learned by collaborative network member Casey Greene. **Program goal:** The P-GAPS algorithm will enable efficient inference of state transitions and developmental trajectories from HCA time-course omics data.

**Aim 2** **Modeling the impact of sparsity on technical variation between bulk and multi-platform single cell RNA-sequencing.** The atomic prior in CoGAPS provides a dynamic sparsity constraint. In this model, lowly expressed genes being constrained towards zero and highly expressed genes constrained away from zero, with corresponding constraints to limit the number of patterns to which each gene is associated3. We will modify the hyperparameters in the prior distribution for CoGAPS to model different levels of sparsity between bulk and single cell-RNA sequencing data. We will apply the modified algorithm to time-course bulk and RNA-seq data from samples from similar developmental phases. We will model the resulting common biological patterns across sequencing platforms as a function of the sparsity hyperparameter. **Program goal:** Learning an adaptive, sparsity parameter across bulk and single-cell RNA-seq data will enable inference of state transitions and developmental trajectories from multimodal, time-course omics data.

**Prior contributions in the area and preliminary results:**

We have performed numerous genomics analyses of data from complex experimental designs in cancer4,5,9,13-30. Our work on analyses of multi-modal genomics data from distinct procurement techniques lead to methods for integrating both technical and biological data types6,9,20,27. We have demonstrated that CoGAPS infers trajectories associated with the dynamics of therapeutic response and acquired therapeutic resistance4-6.

Recently, we have adapted CoGAPS to simultaneously delineate between cell cycle dynamics, technical artifacts, and cell fate trajectories from single cell RNA-seq data during retinal development from collaborative network member Loyal Goff. Like other CNS systems, all the different cell types in the retina arise from a common precursor pool in a stereotyped birth order. Since each progenitor has the potential to differentiate into any of the seven cell types of the mature retina, determining the key factors that regulate the selection of an individual retinal progenitor cell (RPC) to exit the cell cycle and differentiate is a critical question in neural development. CoGAPS’s unique ability to parse these concurrent signals represents a major step toward determining how this stereotyped temporal birth-order of retinal cell types is determined. Further, the algorithms ability to concomitantly account for technical artifacts makes it uniquely suited to scRNA-seq data which are highly susceptible to both batch effects and the risk of creating false structure in the data when attempting to correct for technical variation.

**Proposed work and deliverables:**

**Aim 1 Parallel Gene Activity in Pattern Sets (P-GAPS) to learn state transitions and developmental trajectories from large, time-course omics data.**

**P-GAPS algorithm development.**

**Sensitivity to sample sets** Using the 1,000 genes most variable genes, we will apply the parallel approach of GWCoGAPS to samples instead of genes. This approach will be applied to large, time-course genomics datasets, such as the retinal development data in **Fig 1** from collaborative network member Loyal Goff. We will compute the similarity of gene weights among parallel runs as a function of the extent of confounding between cell type and cell states in each sample set. Assessing the robustness of such pattern detection by sample composition will also implicate the impact of batch effects on time course data. It will also provide robust quantification of pattern robustness, to assess optimal grouping for sample-level compaction.

**Parallelization** We will divide the HCA benchmark datasets into groups of random, but overlapping sets of genes and samples. CoGAPS will be run in parallel for each set. During the MCMC iterations in CoGAPS, message passing between the parallel chains will be employed to determine the current state of the factorization. Approximate Bayesian computation across all of the chains will determine the consensus patterns and gene weights across all random sets of genes and samples, and chains will be continued from the consensus solutions in a new algorithm called P-GAPS.

**Pitfalls and proposed solutions.** (1) The P-GAPS algorithm may converge at different rates based upon the distribution of cell types, states, and times in each set, resulting in an imbalanced algorithm. In this case, timing will also be assessed in the sensitivity analysis and used as a basis for set selecting in P-GAPS analysis. (3) Efficient factorization methods are emerging rapidly in the computer science literature, including those developed in collaborative network member Patro’s proposal. These will be incorporated in CoGAPS if found to be more efficient than the proposed P-GAPS algorithm.

**Aim 2 Modeling the impact of sparsity on technical variation between bulk and multi-platform single cell RNA-sequencing.**

**Sparsity parameter algorithm development.** Currently, CoGAPS is a unique factorization algorithm in modeling both the variance of the data and sparsity. Previously, this algorithm has been tuned for microarray data2 and RNA-sequencing8 data. To tune the algorithm for single-cell RNA-sequencing, we will modify the existing algorithm to utilize different sparsity hyperparameters for different samples within a dataset that contains mixed bulk and single-cell RNA-sequencing. We note that this same hyperparameter will facilitate application of matrix factorization to future work beyond this proposal comparing analysis for different transcriptional quantification methods for both expected abundance and uncertainty, including methods from collaborative network member Patro.

**Statistical analysis for systematic comparison of the impact of sparsity on data from distinct sequencing technologies**. We will apply CoGAPS with mixed sparsity hyperparameters to the combined bulk and single cell RNA-sequencing data sets from matched samples in **Table 2**. Run CoGAPS for a range of sparsity hyperparameters for each of the Smart-Seq2 and 10X sequencing separately. Robustness will be estimated by comparing the number of shared patterns across data platforms as a function of these hyperparameters.

**Pitfalls and proposed solutions.** (1) If missing data from single cell RNA-sequencing results in poor convergence, we will apply denoising techniques such as those from collaborative network member Krishnaswamy31. (2) If variance stabilization is an ill-fitting error model, we will adapt the MCMC framework of CoGAPS to include a negative binomial error model.

**Deliverables**: (1) R/C++ code for P-GAPS encoded in the R/Bioconductor package CoGAPS. (2) R/C++ code to modify the sparsity hyper-parameter by sample encoded in the R/Bioconductor package CoGAPS. (3) R scripts to reproduce all analyses in the project aims. (4) Manuscript(s) on algorithm and results.

**Proposal for evaluation and dissemination of methods, resources, or results**

**Testing of methods** CoGAPS has been tested by comparing the inferred patterns to known phenotypes in multiple publications5-9,16,32. Similar assessment will be performed in this proposal, notably by comparing pattern robustness across random sets as described above. Results will be compared with trajectories, patterns, and gene signatures inferred with methods such as those developed collaborative network members Krishnaswamy33 and Greene34 using model comparison methods such as those developed by network member Goff.

**Engineering support** Engineering support from CZI in message passing code and access to sufficient cloud-based computing resources would ensure efficiency of the P-GAPS algorithm.

**Statement of commitment to share proposals, methods, data, and code with other researchers funded by this RFA and with CZI**

**Primary data:** All scripts will be openly shared consistent with the PI’s standard practice (e.g., <https://sourceforge.net/projects/psva/>, <https://github.com/FertigLab/EGFRFeedback>).

**Proposal:** The proposal has already been developed in collaboration with the collaborative network and shared publicly on https://github.com/FertigLab/HCA.

**Methods:** Methods will be published, and posted on Bioarxiv during journal submission.

**Software:** Any algorithms will be released as part of the open-source CoGAPS Bioconductor package2. Bioconductor is a centralized, peer-reviewed database and release there will support future application and development by the broader community.

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