Community-wide hackathons establish foundations for emerging single cell data integration

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Draft outline

Full outline described in 01.outline.md but as comment if you need to go back to the big picture.

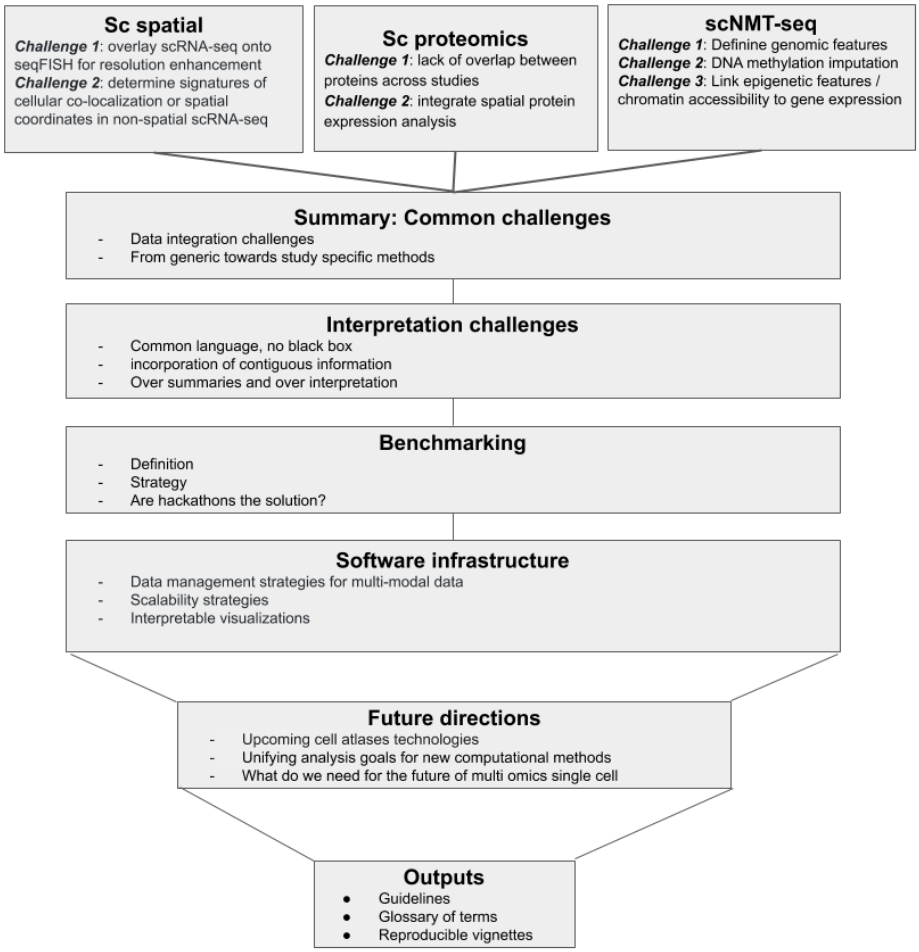

Figure caption: Main challenges discussed during our brainstorming sessions from the hackathons

Figures, Tables and online resources

Figures

- Figure 1: Outline of manuscript (Provided below)
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Tables

- Table 1: Summary of tasks and methods across all hackathons highlighting methods and common challenges (Provided below)
- Table 2: Glossary of terms, consensus terms will be used throughout the manuscript
- Table 3: Benchmarking single cell data sets

- Table 4: List of single cell analysis software

Online resources

- Online resource 1: Three hackathon datasets (github)
- Online resource 2: R packages with open source reproducible vignettes (12 vignettes)

Abstract

Introduction

Comprehensive characterization of biological systems with multi-omics

- Single cell community has advanced technologies to enable concurrent processing of biological systems at multiple molecular resolutions
- The lack of prior knowledge and gold standard benchmark naturally leads to a data-driven approach

New single cell multi omics initiatives:

- Human Cell Atlas (HCA): assess variation in normal tissues
- Brain initiative and Allen Brain
- Human Tumor Atlas Network (HTAN): Single-cell, longitudinal, and clinical outcomes atlases of cancer transitions for diverse tumor types.

What bulk multi-omics (e.g. TCGA, ENCODE) have taught us:

- Type of omics that can answer a specific biological question
- The value of open resources for methodological developments
- New hypotheses

Using hackathons to illustrate analysis standards and challenges for capturing biological information from multi-omics technologies

- Brief overview of our three hackathon studies highlighting state of the art challenges (e.g., spatial transcriptomics, cross-study analysis, epigenetic regulation)

- Challenges include issues with noise and experimental design, Time lag between regulatory levels not addressed and many open questions remain (e.g methylation / gene expression), Direction of regulation not captured

- We present our findings from hackathon case studies that helped us obtain benchmarks and define a common language for multi-omics

- **Objectives of this paper**

    - Provide guidelines on tools / data / technologies / methods and needs to model the multi-scale regulatory processes in biological systems for a computational biologist audience

- **Outline and messages**

    - Cellular and molecular regulation is fundamentally multi-scale and captured by distinct data modalities
    - Traditional hypothesis-driven multi-omics/view studies only consider one facet of these technologies, but more can be learned through a holistic approach extending into atlases

- We present our findings from hackathon case studies that helped us obtain a broader picture and language

Outline of the paper:

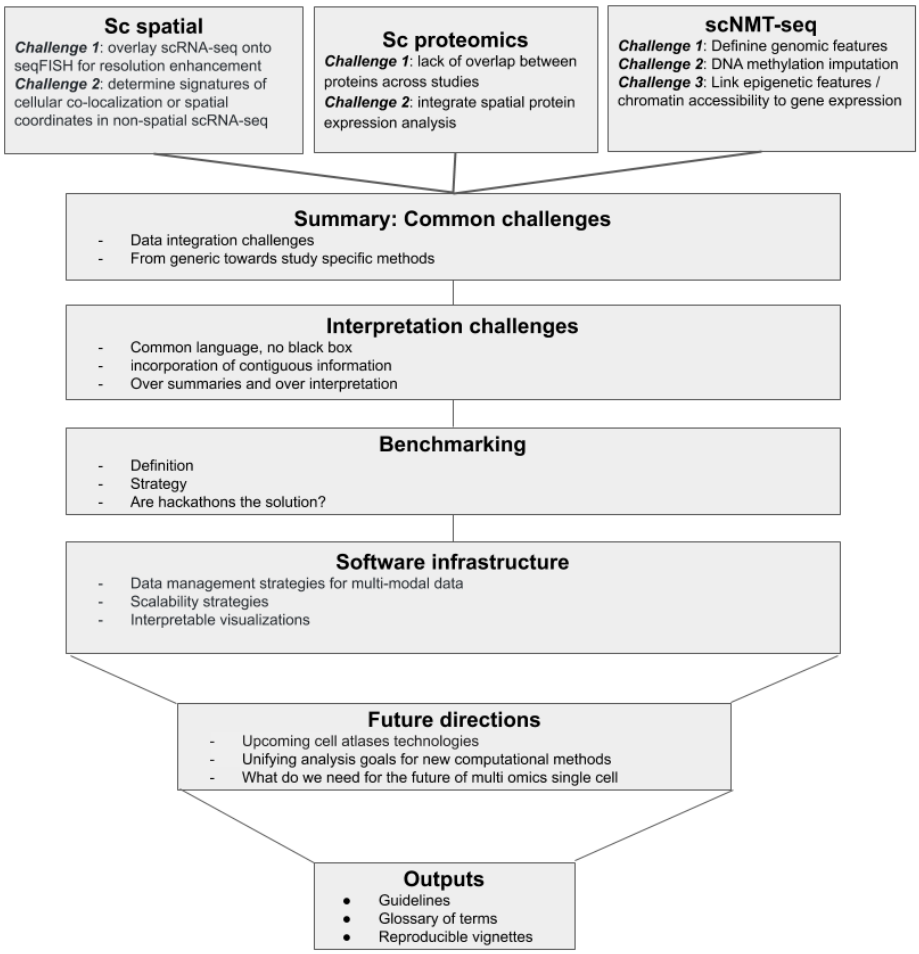


Figure caption: Main challenges discussed during our brainstorming sessions from the hackathons

scRNA-seq + FISH as a case study for spatial transcriptomics

Overview and biological question

Single cells are considered the smallest units and building blocks of each tissue, but they still require proper spatial and structural three-dimensional organization in order to assemble into a functional tissue that can exert its physiological function. In addition, most tissues are composed of multiple cell types whose identity and function can be inferred through their unique transcriptomic profile. In the last decade single-cell RNA-seq (scRNA-seq) played a key role to capture single cell gene expression profiles, which allowed us to map virtually all the different cell types and states in whole organisms. Despite this remarkable achievement this technology is based on cellular dissociation and hence does not maintain spatial relationships between single cells.

More recently technologies have begun to emerge that can profile the transcriptome of single cells within their original environment. These technological advancements offer the possibility to examine how gene expression is influenced by cell-to-cell interactions or organized in a spatially coherent manner. One such approach is sequential single-molecule fluorescence in situ hybridization (seqFISH), which can identify single molecules at (sub)cellular resolution with high sensitivity. Nevertheless, and in contrast with scRNAseq, seqFISH and many other spatial transcriptomic technologies often pose significant technological challenges and hence the number of profiled genes per cell is usually restricted to a smaller number (10-100s).
To overcome the lack of spatial information with scRNAseq and the common limited coverage in spatial datasets, we sought to combine and integrate a matching scRNAseq and seqFISH dataset, since both were generated from the mouse visual cortex region. More specifically, in this hackathon we explored a number of strategies to identify the most likely cell types in the seqfish dataset based on information obtained from the scRNAseq dataset. And in the opposite direction, we sought out how to transfer spatial information obtained from the seqfish dataset to that of the scRNAseq dataset.

Computational challenges

Challenge 1: overlay of scRNA-seq onto seqFISH for resolution enhancement

[suggestion 1]
Sequencing and imaging based single-cell transcriptomic profiling have complementary strengths. Whereas single-cell RNAseq generates transcriptome-wide information, it does not have spatial information. On the other hand, seqFISH (Lubeck 2014; Shah 2016) provides single-cell resolution spatial information, but typically profiles the expression level of only 100-300 genes. Although the newer generation of seqFISH technology (called seqFISH+) has greatly enhanced its capacity which can now be used to profile 10,000 genes (Eng 2019), the technology is significantly more complex and costly. As such, it is desirable to develop computational approaches to effectively integrate scRNAseq and seqFISH data analyses.

In this hackathon, the participants were provided with seqFISH (Zhu 2018) and scRNAseq (Tasic 2016) data corresponding to the mouse visual cortex and challenged to accurately identify cell-types by integrating both datasets. Cell type labels, derived from scRNAseq analysis (Tasic 2016) and previous seqFISH/scRNAseq integration (Zhu 2018) were also provided as reference. A variety of computational approaches were applied to achieve this goal, including: supervised classification with support vector machines (Coulumb, Xu), semi-supervised self-training (Singh), and unsupervised matrix factorization methods (Sodicoff). While the methodologies are different, a number of themes recur, such as the importance of gene selection and batch effect correction. As expected, the ability to identify refined cell-type structure relies on the selection of cell-type specific marker genes in seqFISH data, suggesting a potential benefit of using single-cell RNAseq data to guide seqFISH experimental design. Batch effect is another important factor affecting the accuracy of data integration. While a number of batch effect correction methods have been developed (COMBAT, Seurat, Scanorama, etc), it remains challenging to distinguish technical from biological variations if the biological samples do not match exactly.

[suggestion 2]
The mouse visual cortex consists of multiple complex cell types, however the number of profiled genes in the seqFISH dataset is limited to 125 genes. Moreover, these genes were not prioritized based on their ability to discriminate between cell types and thus assigning the correct cell identity is challenging. In contrast the scRNAseq dataset is transcriptome wide, thus including the 125 aforementioned genes. As such we first used all genes to identify the cell type labels for each cell in the scRNAseq data with high certainty. Next, we leveraged that information to build a classifier based on (a subset of) the 125 common genes only. This classifier could subsequently be applied to the seqFISH dataset in order to assign cell types to each cell with high probability.

During the hackathon we tested various machine learning or data integration models, but also noted that initial dataset normalization strategies might have a significant impact on the final results (see common challenges [**???**]). Although unique molecular identifier (UMI) based scRNAseq and seqFISH can both be considered as count data, we observed dataset specific biases that could be attributed to either platform (imaging vs sequencing) or sample specific sources of variation. Here we opted to apply a quantile normalization approach which forces a similar expression distribution for each shared gene. The hackathon participants selected two machine learning classifiers, a supervised support vector machine (SVM) and a semi-supervised lasso and elastic-net regularized generalized linear model (glmnet). To further improve the SVM model the participants tried multiple kernels and searched for optimal hyperparameters using a combined randomized and zoomed search. In addition, different flavors of recursive feature elimination was used to find the optimal or minimum number of genes needed to correctly classify the majority of the cells. Importantly, participants tested different classification accuracy metrics to alleviate the major class imbalance in the dataset, since more than 90% of cells were excitatory or inhibitory neurons. The glmnet approach used a iterative model building approach, which combines both datasets and initially only retains the highest confidence labels and then gradually adds more cell type labels until all cells have been classified. This type of self training approach might in fact be more generalizable to other datasets. Finally, a data integration approach based on integrative non-negative matrix factorization (NMF) was used by applying the previously published LIGER approach. By integrating both datasets in a similar subspace based on shared factors, cell type labels can be transferred using a nearest neighbor approach.

Challenge 2: determine signatures of cellular co-localization or spatial coordinates in non-spatial scRNA-seq

[suggestion 1]
How could one identify spatial patterns in the seqFISH data? This broad question can be divided into a number of specific tasks, such as detecting genes whose expression is spatially coherent, cell types whose spatial distribution is confined to distinct regions, recurrent multi-cell-type interaction clusters, etc, and the spatial scale may vary from subcellular all the way to tissue-wide organizations. While there have been abundant studies in the geo-spatial analysis domain, computational tools targeting specific spatial transcriptomic questions are still lacking. In this hackathon, one group tackled this challenge by aggregating gene expression data from neighboring cells followed by spatial clustering (Coulumb). Much more work in the future is need to further explore such information.

[suggestion 2]
Most analyses that were originally developed for scRNAseq data can be immediately applied to spatial transcriptomic datasets, however methods to extract sources of variation that originate from spatial factors are still sparse. To incorporate spatial information the cells from the seqFISH dataset were first connected through a spatial network based on Voronoi tessellation and then the expression of each individual cell was spatially smoothed by calculating the average gene expression levels over all the neighboring cells. This smoothened and aggregated data matrix was subsequently used to create a 2 dimensional UMAP from which clusters were identified through a density based clustering approach. The obtained cluster labels can then be mapped back to the original spatial locations for further visual inspection and analysis.

Spatial proteomics and cross-study analysis

Overview and biological question

Computational challenges

Challenge 1: address the lack of overlap between proteins across studies

Challenge 2: spatial protein expression analysis

scNMT-seq as a case-study for epigenetic regulation

Overview and biological question

Computational challenges

Challenge 1: defining genomic features

Challenge 2: DNA methylation imputation

Challenge 3: Linking epigenetic features / chromatin accessibility to gene expression

Commonalities between analytical multi-omics approaches for hackathons [Figure 5 + Table 1]

We summarize the common main challenges faces across all hackathons, and the common approaches adopted to analyse multi-omics single cell data.

Summary of hackathon study-specific methods

- **Table** describes method, foundation in the context of previous bulk and single cell literature, and technology dependence
  - Attempts to tweak existing methods and challenges associated in hackathons
  - List methods that are either technology dependent (e.g. spatial) vs universal and how to choose them

Dependence on pre-processing method and/or variable selection

- These steps are key and affect downstream analyses
  - Normalization / data transformation (seqFish), pre-processing, gene summaries (scNMT-seq) to variable selection (seqFish)
  - reproducibility difficult / no consensus. e.g. Alexis selected 19 genes whereas Zhu original paper based on 47 genes (difference in methods / processed data)
- Hackathon data pre-processed enable better comparisons across methods
- No consensus reached as those are emerging data with no ground truth nor established biological results

Approaches for partial overlap of information (cells / features) and how to predict (cell type, dataset) using another data set

- Overlap in each study
  - seqFish: same features but not cells; scProt: same proteins, not cells but similar patients; scNMT-seq: same cells but not features
  - How it was solved (Table)
- Anchoring information across datasets or studies is needed (Figure)
- Incorporation of existing biological knowledge

- ‘From discovery to detection’ (Meuleman + debrief), time is ripe to include more knowledge in our data driven approaches
- Challenge: Partial cell overlap (but no features matching) and No overlap were not addressed

Managing differences in scale and size for datasets that do not match cells or features

- Hackathons datasets did not match cells or features.
  - scNMTQ-seq: MOFA limitation when # features vary (and size of datasets).
  - seqFish: greedy approach to select the best gene subset (Alexis, size); consider batch effect removal method (Amrit, scale)
- Consensus on projection based methods, even if pre-processing was applied (Table)
- Additional weighting is needed (e.g. Arora, Abadi).

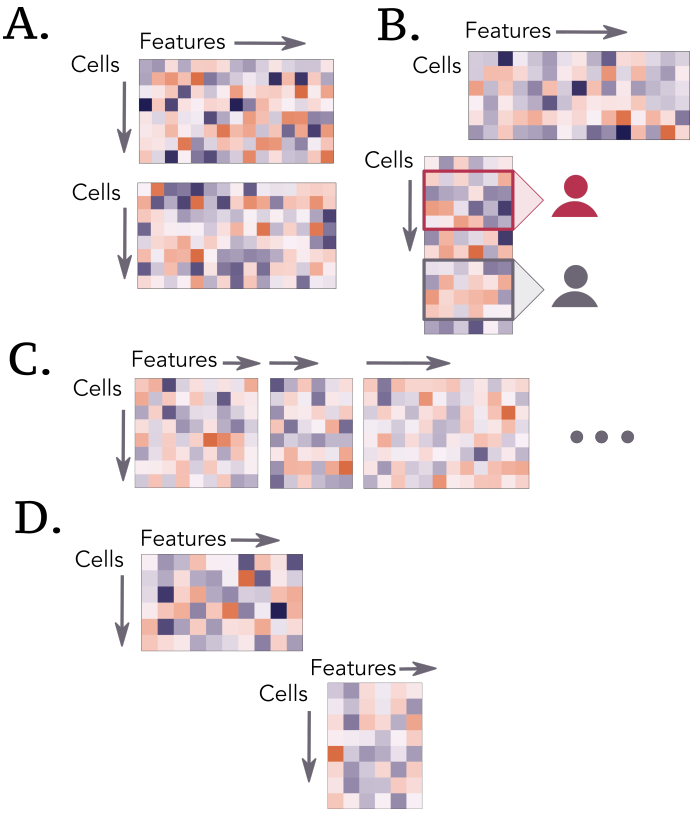


Figure caption: A) scSpatial: required overlap of features (genes), but cells do not overlap. Cell type prediction for seqFISH data was performed based on scRNA-seq (known) [credit: Amrit Singh / Kris S] B) scProteomics: a small number of features overlap (proteins) but patients and cells do not overlap. Data imputation (?), spatial co-localization or cell type prediction was performed [credit: Lauren Hsu and Pratheepan Jenagan / Kris S] C) scNMT-seq: cells are matching across assays but features do not overlap. Data integration was performed [credit: Al Abadi / Kris S] D) Nor cells nor features are matching [credit: Chen Meng / Kris S]

Table: Different methods were used in the hackathon. * indicates the method was not applied on the hackathon data. For some common challenges, ‘bulk’ indicates the method was originally developed for bulk omics, ‘sc’ indicates the method was specifically developed specifically for single cell data {#tbl:example-id}

Common challenges	Tasks	**seqFISH case study**	**Sc targeted proteomics**	**scNMT-seq**

Common challenges	Tasks	**seqFISH case study**	**Sc targeted proteomics**	**scNMT-seq**
	Normalisation, data transformation, pre-processing	Data distribution checks (Coullomb, Singh) HVG (Xu)	VSN (Meng) Arcsinh transformation (Jeganathan). Inverse transformation (Jenagan) Selection of patients (Jenagan)	Summaries of DNA measurements (data provided in hackathon)
Overlap	**Partial feature overlap** (cells not matching)		**Imputation**: Direct inversion with latent variables (Sankaran) Optimal transport to predict protein expression (Lin) KNN averaging (Jenathan*)* **No imputation:** Biological Network Interaction (Foster**)**	
	Partial cell overlap (no features matching)		MBPCA (Meng*)	
	No cell overlap (partial or complete feature overlap)	Averaging nearest neighbors in latent space to impute unmeasured expression values (Coullomb?)	Topic modelling to predict cell spatial co-location or spatial expression (Jenathan, partial feature overlap) Transfer cell type label with Random Forest (Hsu, complete feature overlap?)	LIGER - NMF (Welch, complete feature overlap)
	No overlap		RLQ (Chen*)	

Common challenges	Tasks	**seqFISH case study**	**Sc targeted proteomics**	**scNMT-seq**
Generic approaches	**Classification & feature selection**	Backward selection with SVM (Coullomb) self training ENet (Singh) Balanced error rate (Coullomb, Singh) Recursive Feature Elimination (Xu) (all bulk)		Supervised clustering MOSAIC (Arora) (bulk) Lasso in regression-type models (bulk)
	Cell type prediction	Projections and clustering (Sodicoff*) SVM (Coullomb, Xu) ssEnet (Singh) (all bulk)		
Study specific approaches	**Spatial analysis**	HMRF Voronoi tesselation (Coullomb) (bulk)	Spatial autocorrelation (Moran index, Hsu, Lin) Select spatial discriminative features: Moran Index, NN correlation, Cell type interaction composition, L function (Lin) (all bulk?)	
Managing differences in scale	**Data integration**	LIGER - NMF (Sodicoff*) (sc)* ComBat (Singh) Projection methods MFA, sGCCA (Singh*)* UMAP / tSNE (Sodicoff) (sc)	Multi-block PCA Weighting matrices based on their similarities: Data wise (STATIS, MFA) (Chen*) (bulk) Scale CyTOF and MIBI-TOF to the range of CyTOF values (Jenagan)	LIGER - NMF (Welch) (bulk) Projection to Latent Structures (Abadi) (bulk) MOSAIC as weighted approach (Arora) (bulk)

Common challenges	Tasks	**seqFISH case study**	**Sc targeted proteomics**	**scNMT-seq**
Inclusion of additional information			Survival prediction: Cox regression based on spatial features (Lin)	Include annotated DHS Index to anchor new/unseen data from DNase-seq, (sc)ATAC-seq, scNMT-seq, etc. for *De novo* peak calling(Meuleman*) (bulk)

Challenges for interpretation

There are many difficulties involved of the understanding and communication of results from such complex data sets and analyses as we have seen. Let's separate out the different challenges into different levels. The first is the communication within the data scientists, ie communicating methods to practitionners who do not have the same vocabulary or background.

Interpretation for data scientists reading the methods sections requires a good understanding of the building blocks

Communicating within the field: what approaches are we talking about? This requires agreement on a glossary which we have attempted to construct in (ref: Table1). Then comes a dichotomy of methods and their underlying properties. A simple delineation is available as some methods aim to predict a clearly defined outcome at the start of the project. This is the case in ref: crossref hackaton example on @ Supervised versus unsupervised methods. Visualization figures are useful for the mathematical and data science team in the Exploratory phase.

Interpretation for biologists:

Understanding the output from the analyses of the data is facilitated by the incorporation of contiguous information. Redundant biological knowledge and incorporation of information from databases are important in the workflow. Biological interpretations are facilitated by bridges to databases such as KEGG, Gene Ontology, Human Cell Atlas, Biomart and many other databases. Validation through complementary data and sequential experimental design.

Visualization tools for interpretation and communication to biologists

There are pitfalls in using sophisticated graphics which lead to over-interpretation or misinterpretation (size of clusters in tSNE related to sampling baselines rather than density, ...) Example of effective visual interpretation tools : brushing UMAP (Kris Sankaran).

Explaining results to biologists through generative models and simulations (ex: Factor Analysis).

Several difficulties arise when explaining summaries and conclusions, problems encountered include non-identifiability of models or non-sufficiency of summaries, simulations can often provide effective communication tools.

Issues of over-discretization, over-simplification

Example 1: The notion of cell-type is insufficient (Communication challenge with biologists about tradeoffs between focusing on rare cell types vs. more “continuous” view on cell types).

Reference the human cell atlas and the cell type discussion (ref:)

Problem with loss of information in the desire to simplify.

Counterexamples

Techniques and challenges for benchmarking methods

We must first define what we are benchmarking

- Often the goal in benchmarking is recovery of known cell types with processing of raw data, quantification, and clustering. The Adjusted Rand Index (ARI) or other metrics for partitions are used.
- One may also attempt to benchmark methods for their ability to discover known relationships between data modalities, e.g. gene regulatory relationships observed between chromatin accessibility and gene expression. However, this is made difficult by the fact that these relationships are not fully known at the single cell level.

Strategies for benchmarking

- First, we acknowledge that benchmarking multi-modal methods on typical multi-modal datasets is inherently difficult, as we rarely know the ground truth [1].

- Simulation is useful for having known truth, but it is difficult to simulate realistic covariance structure across features and across data modalities.

- Benchmarking datasets (add examples from Google Doc). Benchmark datasets for single cell studies have largely centered around measuring sequencing depth and diversity of cell types derived from a single assay of interest (e.g. scRNAseq). A benchmark dataset serves a few purposes:

    - Provides ground truth for the intended effect of exposure in a proposed study design.
    - Provides validation for a data integration task for which a new computational method may be proposed.

    For multi-modal assays, while the intended effects can vary based on the leading biological questions, one may abstract out common data integration tasks such as co-embedding, mapping or correlation, and inferring causal relationships. We distinguish data integration from further downstream analyses that may occur on integrated samples such as differential analysis of both assays with regard to to a certain exposure.

    Both the intended effects and data integration task rely on study design that takes into account:

    - Biological and technical variability via replicates, block design, and randomization.
    - Power analysis for the intended effect or data integration task.
    - Dependencies between modalities, for e.g. gene expression depending on gene regulatory element activity, requires that experiment design must also account for spatial and temporal elements in sampling for a given observation.

As such, no universal benchmark data scheme may suit every combination of modality, and benchmark datasets may be established for commonly used combinations of modalities or technologies, towards specific data integration tasks.

- Cross-validation within study can be performed. For example the following cross-validation analysis of the scNMT-seq dataset was performed using MOFA+.

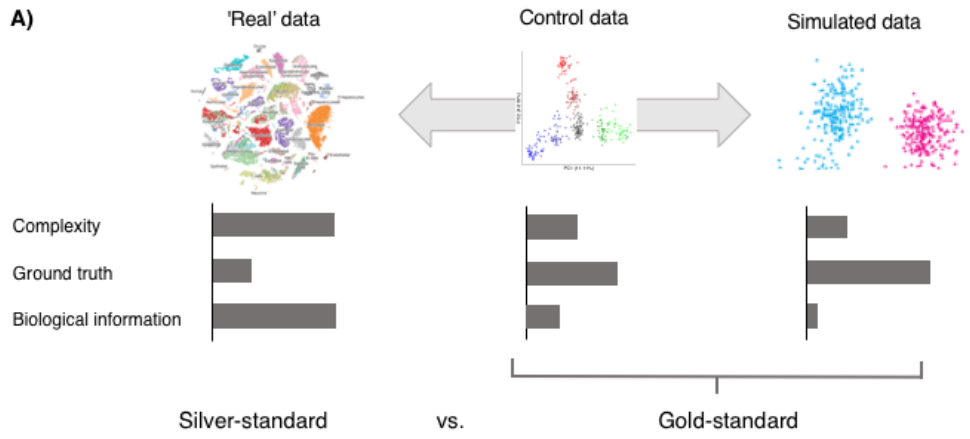
  Such an evaluation of methods using permutation or cross-validation has been performed previously, typically to optimize a tuning parameter or other aspects of model selection. Permutation has been used to create null datasets, either as demonstration that a method is not overfitting, or for tuning parameter selection, where the optimal parameter setting should produce an objective that is far from the null distribution [2,3,4]. Cross-validation using folds or leave-one-out has likewise been used in many multi-modal method development papers [5,6,7,8,9,10,11,12,13,14,15,16].

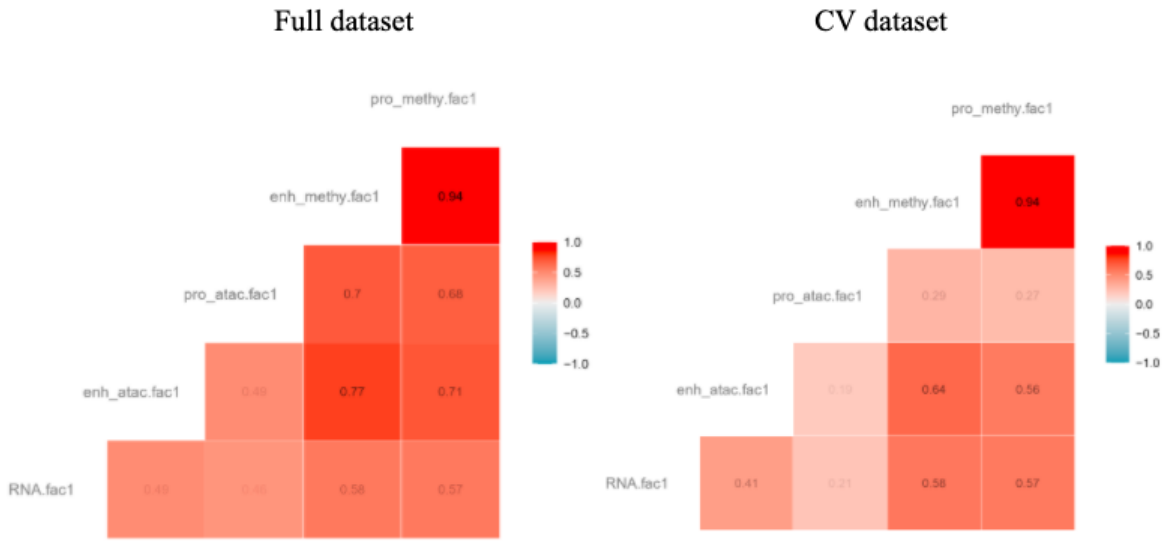
  A challenge with within study cross-validation is how to match dimensions of latent space across folds. Previous evaluations of multi-modal methods using cross-validation have focused on the top factor, swapping the sign of the project as needed to align the top latent factor across folds [17].

  Finally, we note that for assessing clustering, a number of papers have suggested to resampling or data-splitting strategies to determine prediction strength [18,19,20,21]. For clustering of cells into putative cell types or cell states, such previously developed techniques could be applied in a multi-modal setting.

- Cross-study validation would assess if relationships discovered in one dataset present in other datasets, potentially looking across single cell and bulk.

  Figure A) Silver standard: Svensson et al. (2017) Nat Methods; Wang et al. (2019) bioRxiv; Cole et al. (2019) Cell Systems; Zhang et al. (2017) bioRxiv; Soneson et al. (2018) Nat Methods; Saelens et al. (2019) Nat Biotechnol; Gold standard control data: Tian et al. (2019) Nat Meth; Freytag et al. (2018) F1000Res; Gold standard simulated data with the splatter R package appia et al. (2017) Genome Biol [credit: Matt Ritchie] **B)** scNMT-seq study: correlations with linear projections (MOFA+) evaluated with cross-validation.





Software strategies to enable analyses of multimodal single cell experiments

In this chapter we review the situation of scientists who create and use analytic software for visualization and inference in multimodal single-cell experiments. Our discussion is necessarily limited in scope, but we provide pointers to concrete details when relevant.

Basic aims

We take it for granted that **openness** is a *sine qua non* for computational tooling in this area. All components need to be accessible for full vetting by the community, so licensing in Creative Commons, Artistic, or GNU frameworks is expected. We also aim for a **coordinated approach**, so that duplication of effort between groups working on similar problems can be avoided. Finally, we seek solutions that are **efficient** and avoid **lock-in**. Real-time improvements to the tool-set should be feasible, respecting needs for stability, reliability, and continuity of access to evolving components.

These objectives are fluid and open to interpretation. Community engagement and communication are important to achieving desired goals in this domain.

Key questions

- How should multimodal single cell data be managed for interactive and batch analyses?
- What methods will help software developers create scalable solutions for multimodal single cell analysis?
- How can we ensure that visualization methods that are central to multimodal single cell analysis are usable by researchers with visual impairments?

These questions will ultimately be answered through the creation of a **software ecosystem**. As an example of an ecosystem of broad scope, we cite bioconductor.org. This project produces code in R for **data representation and data services** for many data modalities used in genome-scale experimentation. Bioconductor's resources for achieving **scalability**[**???**] include tools for analyzing massive data resources with tunable RAM footprints, and tooling for supporting fault-tolerant parallel distributed computing in various cluster and cloud contexts. Finally, Bioconductor supports *developers* who seek to build broad user bases by providing multiplatform/multistream **continuous integration/continuous delivery** of contributed packages, and *users* with different skill sets by articulating standards for documentation, and testing, and by hosting community forums and workshops.

Data management strategies

- Abstract data type: "multiassay experiment". This reflects the idea that each mode will be characterized by a different collection of features on possibly non-overlapping collections of samples. The metadata on features should be clearly and conventionally defined. For example, genes and transcripts are enumerated using Ensembl catalog identifiers; regions of accessibility are defined using genomic coordinates in a clearly specified reference build. Metadata on samples must include all relevant information on experimental conditions such as treatment, protocol, and date of technical processing.

(More fodder-AS)

Key points: 1) What do we want to store and share? Data object vs analysis object. How would the design change based on what is stored? 2) Do we need a flexible, universal framework (e.g. MAE) or an experiment class for every possible combination of modalities or technologies? 3) Do we have adequate data representation for all "assays"?

- Multi-modal single cell data may consist of multi-assay measurements from the same cell (e.g. CITE-seq, sci-CAR) or integration of multi-assay measurements from distinct cells from the same or distinct starting samples. A sample here refers to the biological specimen of origin (tissue A from individual X). A data container for a multi assay analysis must hold

1. Assay slots containing variables or features from multiple modalities (e.g. gene expression units from scRNA-seq and protein units from sc-proteomics). In some cases, the feature may be multidimensional (e.g. spatial coordinates, locations of eQTLs).
2. Observations or cell identities
3. Metadata for sample of origin for the individual cells, e.g. study, center, phenotype, perturbation.
4. A map between the different assays to enable analysis

- The MAE is such a Bioconductor container for overlapping observations, and may serve as a starting point for further expansion. Besides the primary data elements for storing "data objects", the summarizedExperiment class offers attributes and Methods for storing results of analysis, as an "analysis object".

- While common assays such as RNA-seq and ATAC-seq have well-defined data representations (e.g. transcript names), data representation need to be defined newer assays, which may need multiple dimensions for adequate definition (e.g. x, y, z coordinates for images).
- The observations of different modalities may not be directly comparable (e.g. RNA may be measured from individual cells but spatial transcriptomics may cover a few cells in the matched area).
- In the absence of universal standards, the metadata may vary from analysis to analysis.
- It is crucial that data containers use consistent assay access methods (possibly through methods inheritance. e.g. from `SummarizedExperiment`). This will ensure less redundancy in development process and allow powerful implementation strategies.

(Note, standard BioC container/class terms may not be correctly used. End of fodder - AS)

- Serializations and data access methods for
  - spatial transcriptomics
  - scNMT-seq ...

Scalability strategies

An overview of our suggested approach for compilation of the hackathon contributions

The contributed challenge analyses as well as the used datasets may be collated into software packages which include their specific dependencies. In such a setting, the analysis packages can simply use the corresponding dataset package(s) as a dependency. Additionally, if the challenge datasets have undergone preprocessing it is essential that all the preprocessing steps are outlined and made available in the dataset packages. This will facilitate transparency and analysis reproducibility, as well as allow Continuous Integration (CI) of the analyses and preprocessing changes and Continuous Delivery (CD) of the analysis reports. The CI/CD workflow may also be automated on a hosted server and containerized reports can be generated for enhanced efficiency and portability, respectively.

Reducing barriers to interpretable visualizations

Color is a powerful data visualization tool that helps representing the different dimensions of our increasingly complex and rich scientific data. Color vision deficiencies affect a substantial portion of the population. Therefore, it is desirable to aim towards presenting scientific information in a manner that is as accessible as possible for all readers. Color vision deficiency leads to difficulties in perceiving patterns (the basis for the Ishihara's color vision tests) in multi-colored figures. In rare cases, the perceived patterns; e.g. in heatmaps and reduced dimension plots, can differ between individuals with normal and color deficient vision.

One strategy to address these issues is to include colorblind friendly visualizations [22] as a default setting in our visualizations. Several colorblind-friendly palettes exist (e.g., see R packages viridis and dittoSeq) and can be integrated into data presentation as the default option. Even with these palettes in place, it is desirable to limit the number (about 8-10 at a maximum) of colors in visualizations. To reduce the dependence on colors, one solution would be to include additional visual cues to differentiate regions (hatched areas) or cells (point shapes). Overall, a broader discussion regarding the accessibility of our figures that is not just limited to color vision deficiencies would be greatly beneficial towards improving data accessibility. Perhaps one tool to address broader accessibility could be the inclusion an "accessibility caption" accompanying figures which "guide" the reader's perception of the images.

Reference 1: Color Coding

Reference 2: Points of View: Color Blindness

Viridis Color Palettes

An overview of the issues with impaired color perception

US Government tools for accessibility

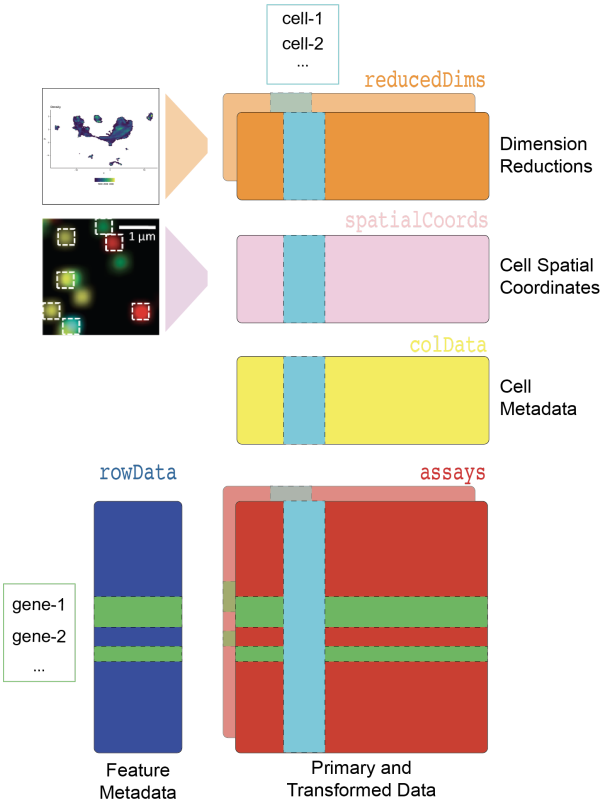
Details of working components – trimmed

you can interact with underlying data at google sheet

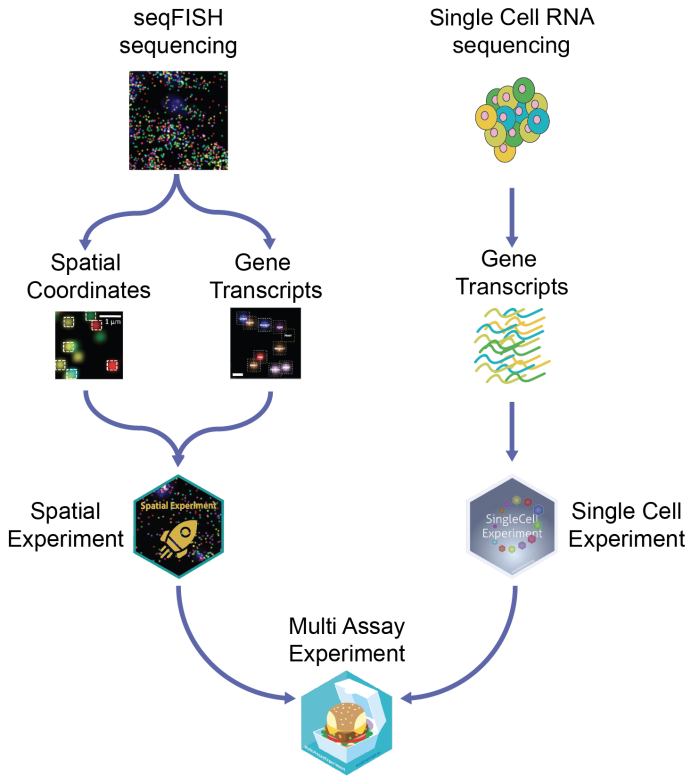
Type	Brief name (link)	Description
Matlab package	CytoMAP	CytoMAP: A Spatial Analysis Toolbox Reveals Features of Myeloid Cell Organization in Lymphoid Tissues
Matlab package	histoCAT	histoCAT: analysis of cell phenotypes and interactions in multiplex image cytometry data
Python library	PyTorch	General framework for deep learning
Python package	SpaCell	SpaCell: integrating tissue morphology and spatial gene expression to predict disease cells
Python package	Scanpy	Python package for single cell analysis
R data class	MultiAssayExperiment	unify multiple experiments
R data class	SpatialExperiment	SpatialExperiment: a collection of S4 classes for Spatial Data
R package	Giotto	Spatial transcriptomics
R package	cytomapper	cytomapper: Visualization of highly multiplexed imaging cytometry data in R
R package	Spaniel	Spaniel: analysis and interactive sharing of Spatial Transcriptomics data
R package	Seurat	R toolkit for single cell genomics
R package	SpatialLIBD	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex
R package	Cardinal	Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments
R package	CoGAPS	scCoGAPS learns biologically meaningful latent spaces from sparse scRNA-Seq data

Type	Brief name (link)	Description
R package	projectR	ProjectR is a transfer learning framework to rapidly explore latent spaces across independent datasets
R package	SingleCellMultiModal	Serves multiple datasets obtained from GEO and other sources and represents them as MultiAssayExperiment objects
R scripts	SpatialAnalysis	Scripts for SpatialExperiment usage
Self-contained GUI	ST viewer	ST viewer: a tool for analysis and visualization of spatial transcriptomics datasets
Shiny app	Dynverse	A comparison of single-cell trajectory inference methods: towards more accurate and robust tools
R package	mixOmics	R toolkit for multivariate analysis of multi-modal data
Python package	totalVI	A variational autoencoder (deep learning model) to integrate RNA and protein data from CITE-seq experiments
Python web application		ImJoy
Python package	napari	Interactive big multi-dimensional 3D image viewer
Software	QuPath	Multiplex whole slide image analysis
Python package	Cytokit	Multiplex whole slide image analysis
Python package	cmIF	Multiplex whole slide image analysis
Software	Facetto	Multiplex whole slide image analysis, not available yet
Software, Python based	CellProfiler	Image analysis

Here is the schematic of SpatialExperiment class from Dario Righelli.



Here is the schematic of how seqFISH data are stored in the SingleCellMultiModal package from Dario Righelli.



Discussion

Emerging analytical methods and technologies

Community needs for data structures, analysis methods, etc

Glossary

Table 1: Glossary of interchangeable terms in the field of single-cell and bulk multi-omics (multi-source) data analysis.

Consensus Term	Related Terms	Description	Citation
network	graph, adjacency matrix	A set of *nodes*, representing objects of interest, linked by *edges*, representing specific relationships between nodes.	?
node	vertex	Element of interest in a network and linked to other nodes. For example: people, cells, proteins or genes. Nodes can have several properties called *attributes* like cell type or position.	?
edge	link	The relationship between 2 nodes in a network. For example: friendship in social networks, cells in contact in a spatial network, or gene-gene interactions in a gene regulatory network.	?
concordant	concordant, coherent, consistent	?	17
contributions	variable weights, loadings, eigenvector, axis, direction, dimension, coefficients, slopes	Contributions of the original variables in constructing the components.	15, 23
latent factors	variates, scores, projections, components, latent/hidden/unobserved variables/factors	Weighted linear combinations of the original variables.	15, 23
multimodal	Multiview, multiway arrays, multimodal, multidomain, multiblock, multitable, multi-omics, multi-source data analysis methods, N-integration	Methods pertaining to the analysis of multiple data matrices for the same set of observations.	15, 24, 25
conjoint analysis	conjoint analysis, P-integration, meta-analysis, multigroup data analysis	Methods pertaining to the analysis of multiple data matrices for the same set of variables.	15, 23, 26
variable	feature, variable	A measurable quantity that describes an observation's attributes. Variables from different modalities include age, sex, gene or protein abundance, single nucleotide variants, operational taxonomic units, pixel intensity *etc.*	?

Consensus Term	Related Terms	Description	Citation
biomarker	marker, biomarker	A variable that is associated with normal or disease processes, or responses to exposures, or interventions. Any change in this variable is also associated with a change in the associated clinical outcome. These variables may be used for diagnostic, monitoring, Pharmacodynamic responses. Examples include LDL cholesterol, CD4 counts, hemoglobin A1C.	27
panel	biomarker panel, biomarker signature	A subset of the originally measured variables that are determined to be associated with the outcome or response variable. This may be determined using statistical inference, feature selection methods, or machine/statistical learning.	28, 29
observation	sample, observation, array	A single entity belonging to a larger grouping. Examples include patients, subjects, participants, cells, biological sample, usually the unit of observation on which the variables are measured *etc.*	?

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