MESSI : Multiomics Experiments with SyStematic Interrogation

A Nextflow pipeline for benchmarking multiomics integration methods

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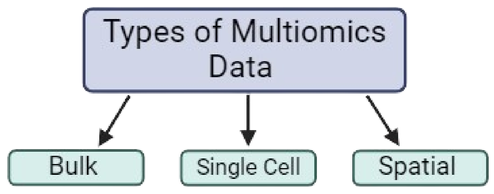
INTRODUCTION

- **Omics** is the comprehensive study of all molecules of a particular type within an organism (**e.g. proteins, metabolites, genes**)
- Multiomics compensates for missing or unreliable information in any single omics data



- Many integration methods: which to use?
- How to reproduce method and get same results?
- We introduce *Multiomics Experiments with SyStematic Interrogation* (MESSI).
- Tool to assist in the development and evaluation of new/existing multiomics integration methods.

METHODS

- Looking into multiview (3), DIABLO (4), RGCCA (5), MOFA (6), MOGONET (7)
- Using a **5-fold** cross validation (cv) with are under the curve (AUC) score as metric
- Validating with known ground truth data from **500+** simulated data with varying parameters
- Evaluate on 6 real world datasets

Dataset	# of subjects	Disease	Prop(Y=1)	Omics	# of predictors
GSE71669	33	Bladder cancer	0.424	mrna	5831
				cpg	8915
				cc	10
ROSMAP	351	Alzheimer Disease	0.519	epigenomics	58
				genomics	74
				transcriptomics	90
TCGA-BLCA	336	Bladder cancer	0.685	Methylation_HM450K	8072
				miRNA	285
				RPPA	44
				RNAseq_HiSeq	6376
TCGA-BRCA	109	Breast cancer	0.358	Methylation_HM450K	7985
				miRNA_GA	282
				RPPA	43
				RNAseq_HiSeq	6191
TCGA-KIPAN	123	Kidney cancer	0.520	Methylation_HM450K	7914
				miRNA_GA_miR	225
				RPPA	60
				RNAseq_HiSeq	6145
TCGA-THCA	217	Thyroid cancer	0.318	Methylation_HM450K	6367
				miRNA	256
				RPPA	25
				RNAseq_HiSeq	5692

Table1: Real world dataset description. Each dataset is a public source multiomics dataset that studies one disease. Prop(Y=1) represents the proportion of positive cases in the dataset. # of predictors are number of molecular measurements in individual omics. # of subjects represent the size of study performed.

RESULTS

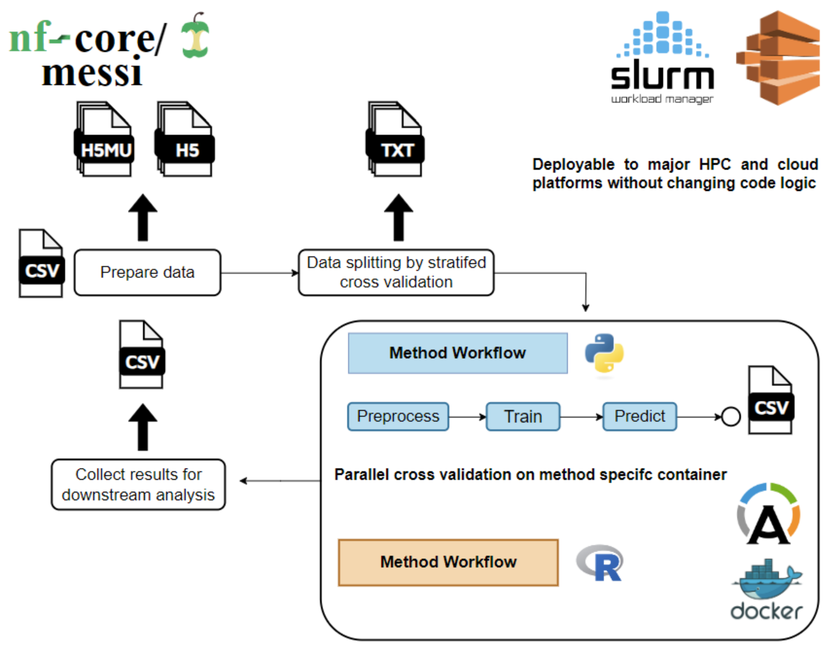


Figure 1: Overview of MESSI Workflow. Data are standardized into MuData and MultiAssayExperiemnt, then passed to methods for cross-validation in a parallel and fully isolated through processes and containers. Then each performance will be assessed by its task (classification or clustering) corresponding metrics.

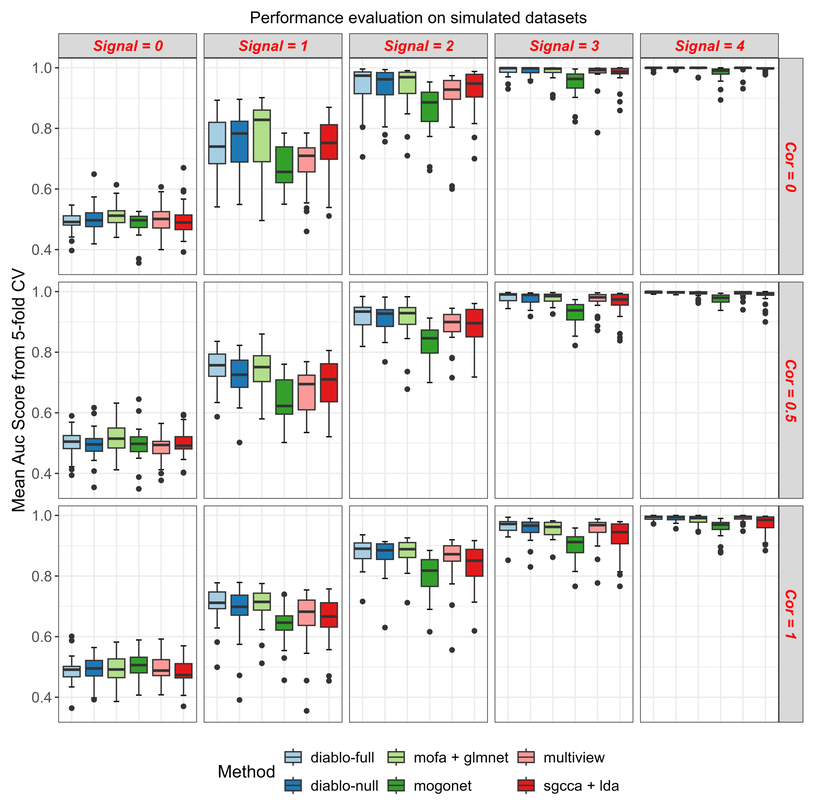


Figure 2: Evaluation of simulated datasets with varying parameters. Boxplot represents mean AUC score distributions from 5-fold CV, with controlled signal and correlation inside the datasets.

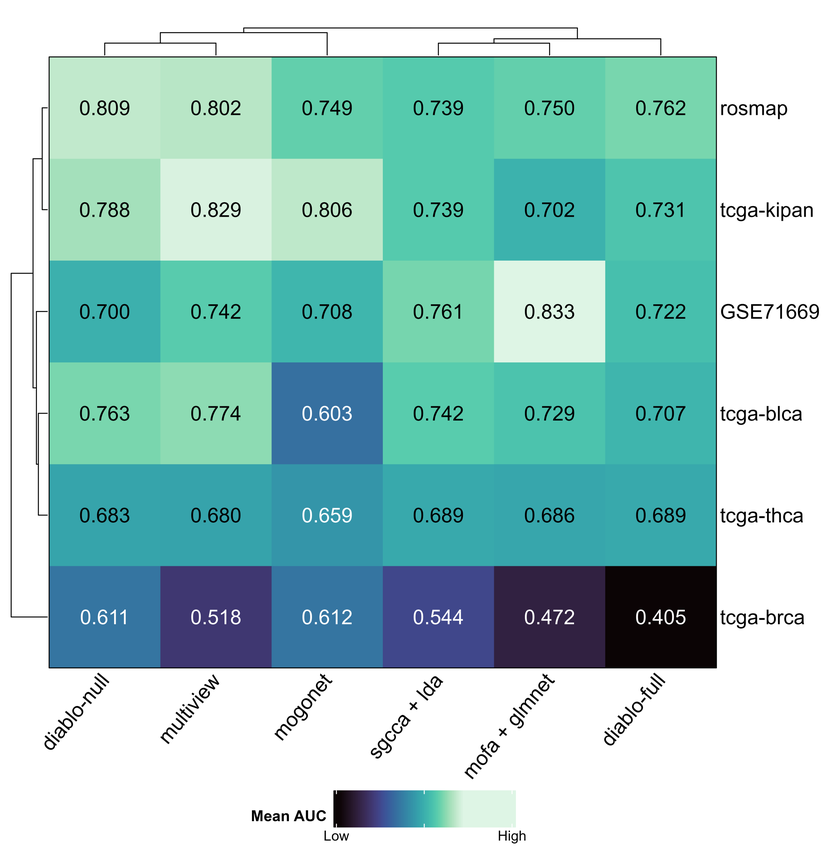


Figure 3: Performance of methods over real world datasets. Lighter color indicates better AUC score, numbers are exact score.

RESULTS

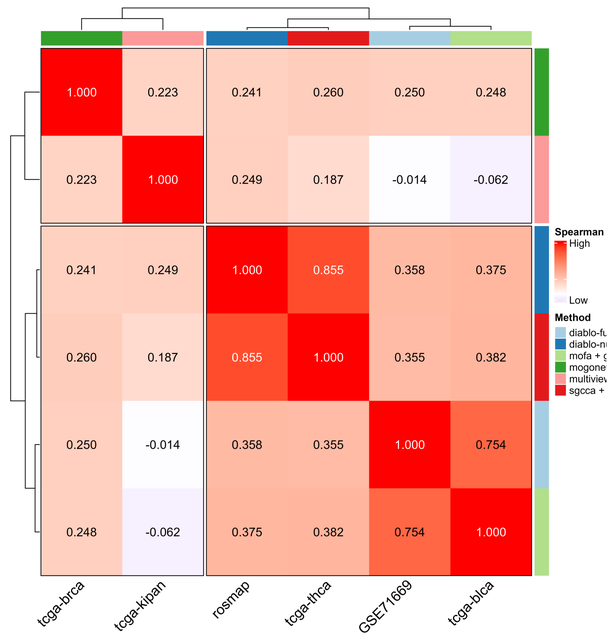


Figure 4: Spearman rank correlation on ranking biomarkers identified between methods. Darker color indicates higher similarity between the rankings of important biomarkers across method and dataset.

CONCLUSION

- **No method works** universally well on all datasets
- Pipeline proves way to reproducibly benchmark different aspects of integration methods
- GNN like **MOGONET,** overcomplicated yet low performance
- **DIABLO** is the best at moment
- Methods overall work better with higher effect, and less sensitive to correlation between omics
- Need to generalize for more datasets, at sc or spatial level
- Add in other methods (like bayesian, other DLs)

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