THE UNIVERSITY OF BRITISH COLUMBIA

Department of Anesthesiology, Pharmacology & Therapeutics
Faculty of Medicine

Centre for
Heart Lung Innovation
UBC and St. Paul's Hospital

CompBio Lab @ HLI

cbl-hli.med.ubc.ca/

MESSI: Multiomics Experiments with SyStematic Interrogation

A pipeline for benchmarking multi-omics integration methods on classification problems using Nextflow
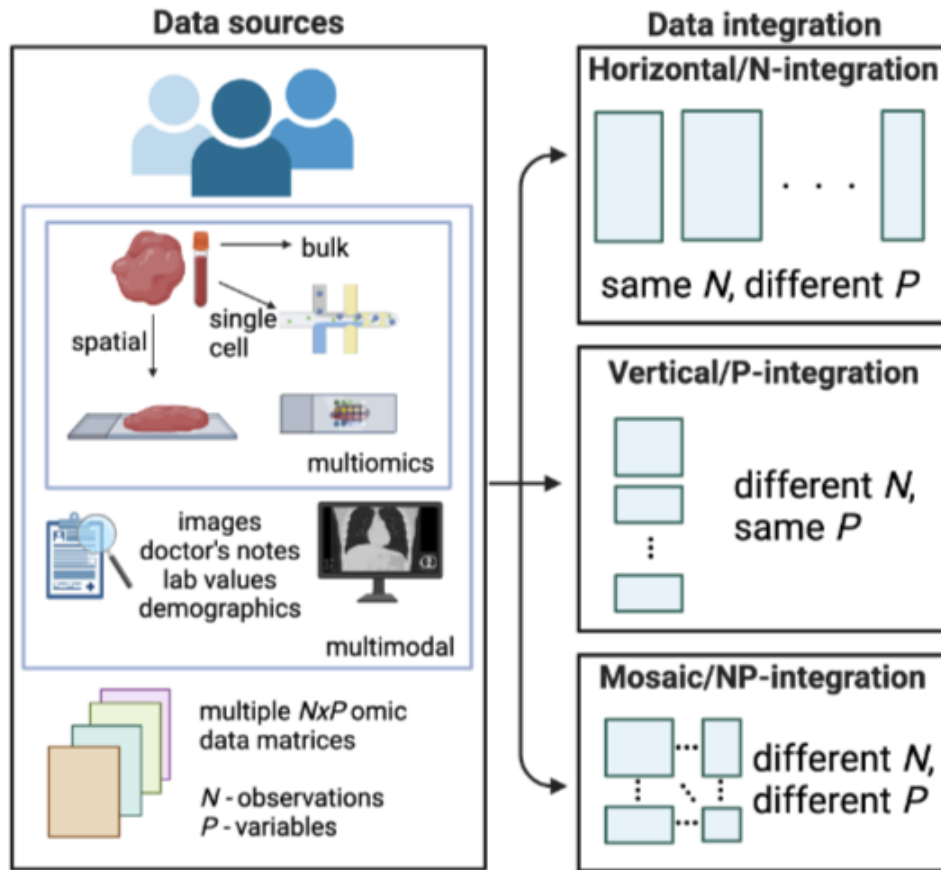
Chunqing Tony Liang

Msc student in Bioinformatics

Supervisor: Dr. Amrit Singh

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Multiomics data and analysis

Figure 1: Overview of multiomics data and integration [1]

Motivation

- Technological advancement and reduced costs –> studies with multiomics data

- Multiomics data –> bulk/single-cell/spatial data

- More generalized –> "multimodal data", other non-omics data

- Types of integrations: by sample (N), by omics (P), or both

1. Shannon et al., *Manuscript Under Revision*, 2024.

Multiomics data integration methods

Figure 2: Overview of multi-omics data integration tools [1]
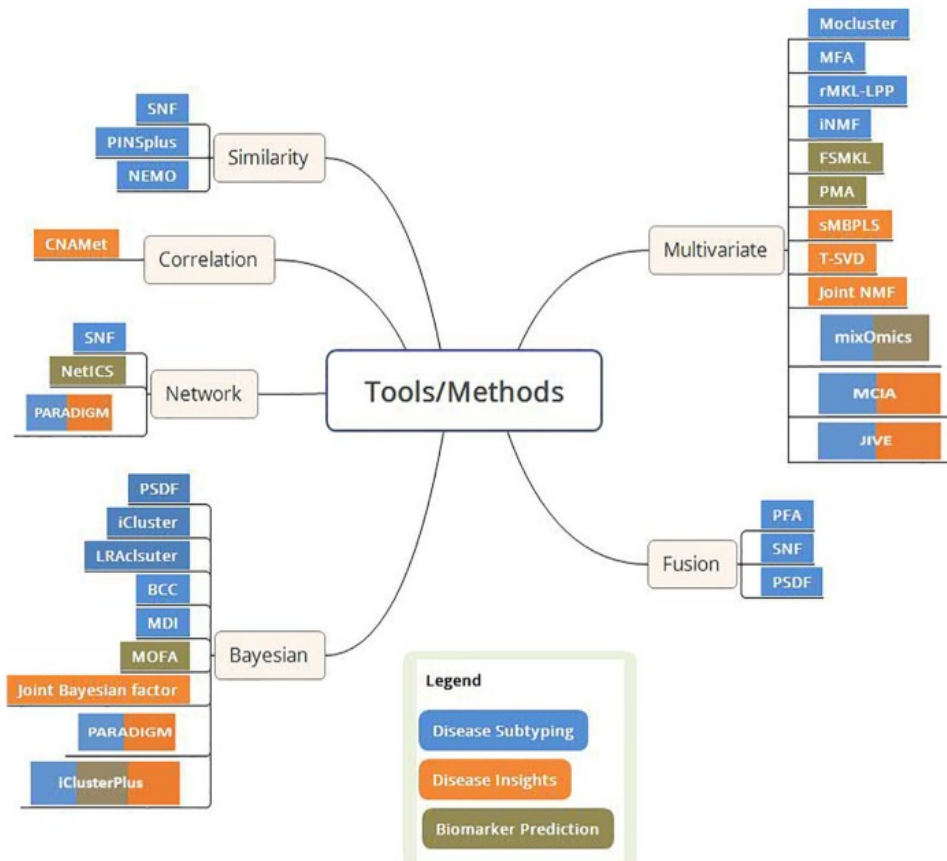
Question arises

- Many integration methods

  —> Which to use, how to choose them?

- Reproducibility crisis

  —> How to reproduce method and get reliable results?

- Existing benchmark studies are not 100% complete or all-encompassing

  —> Technical difficulty in implementation?

1. Indhupriya Subramanian et al., "Multi-Omics Data Integration, Interpretation, and Its Application," *Bioinformatics and Biology Insights* 14 (2020): 1177932219899051.
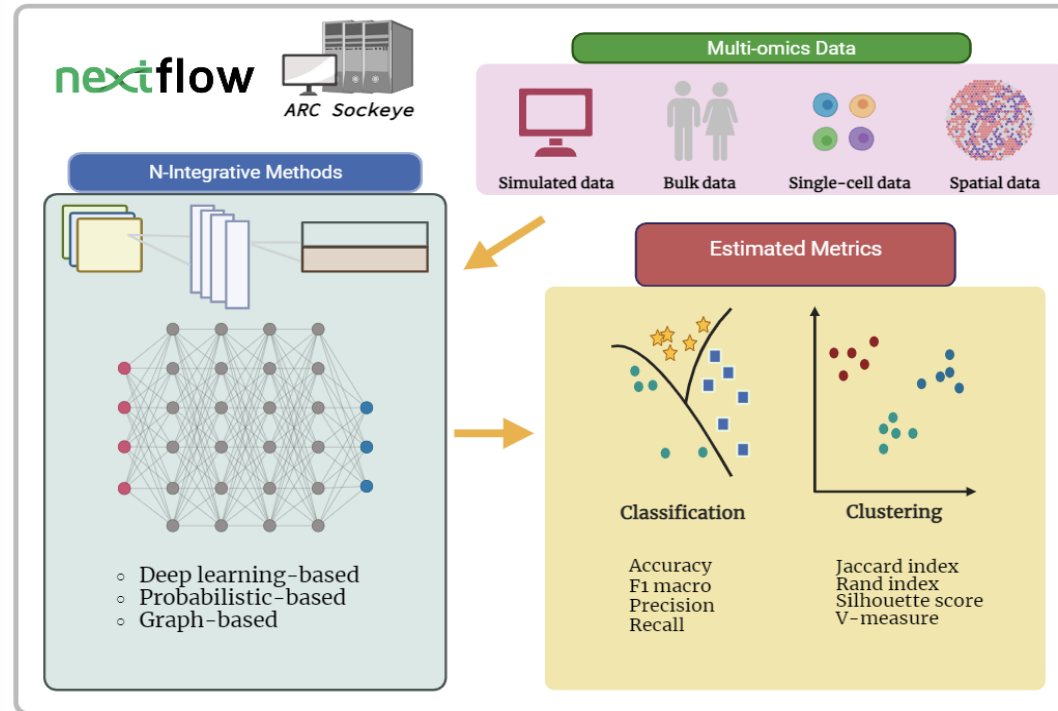
Overview of MESSI

Figure 3: Overview of MESSI workflow

- Generalizable for more integration methods
- Data transformable for Python or R based methods
- Reproducible workflow, results/findings

- Multiple data types (bulk, sc, spatial)
- Help to develop new integration method
- Compare large set of independent data at once

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