Project ATRACTion

Autoimmunity/Inflammation Through Rnaseq Analysis at single Cell level for Therapeutical Innovation

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Multi-Omics Data Integration

(collaborative project with diiP)

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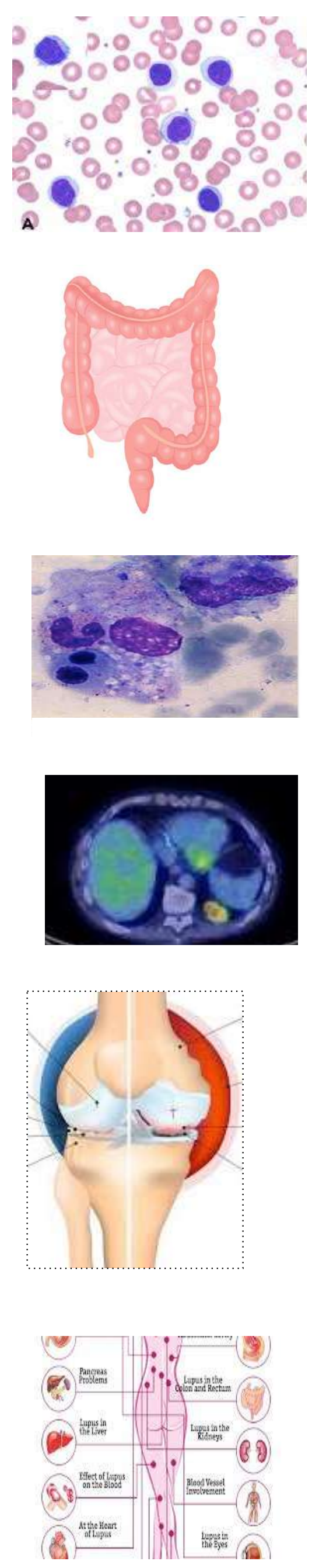
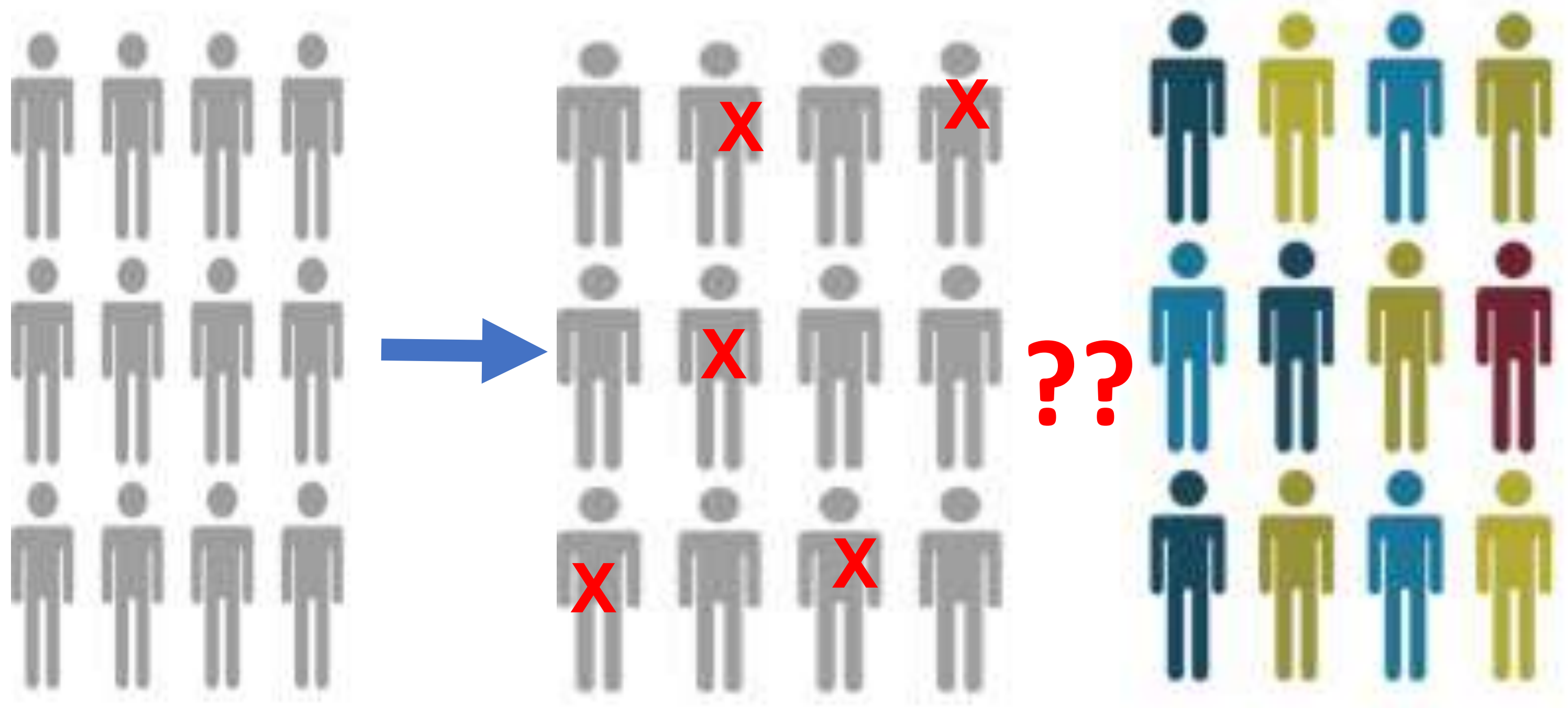
one presentation -> several genes
one gene -> several presentations



Autoimmune cytopenia	FOXP3, IL2RA
	RIL10
Enteropathy/ Colitis	CTLA4, LRBA, TIM3
	XIAP, FAS
Hemophagocytic syndrome	Perforin, Rab27 …
Lympho proliferation	JAK/STAT
	NLRP3, NLRC4
Arthritis SJA	TREX1, SAMHD1, RNAseH2, STING
	NFkB, RelA
Lupus	NADPH oxydases

Primary Immunodeficiencies



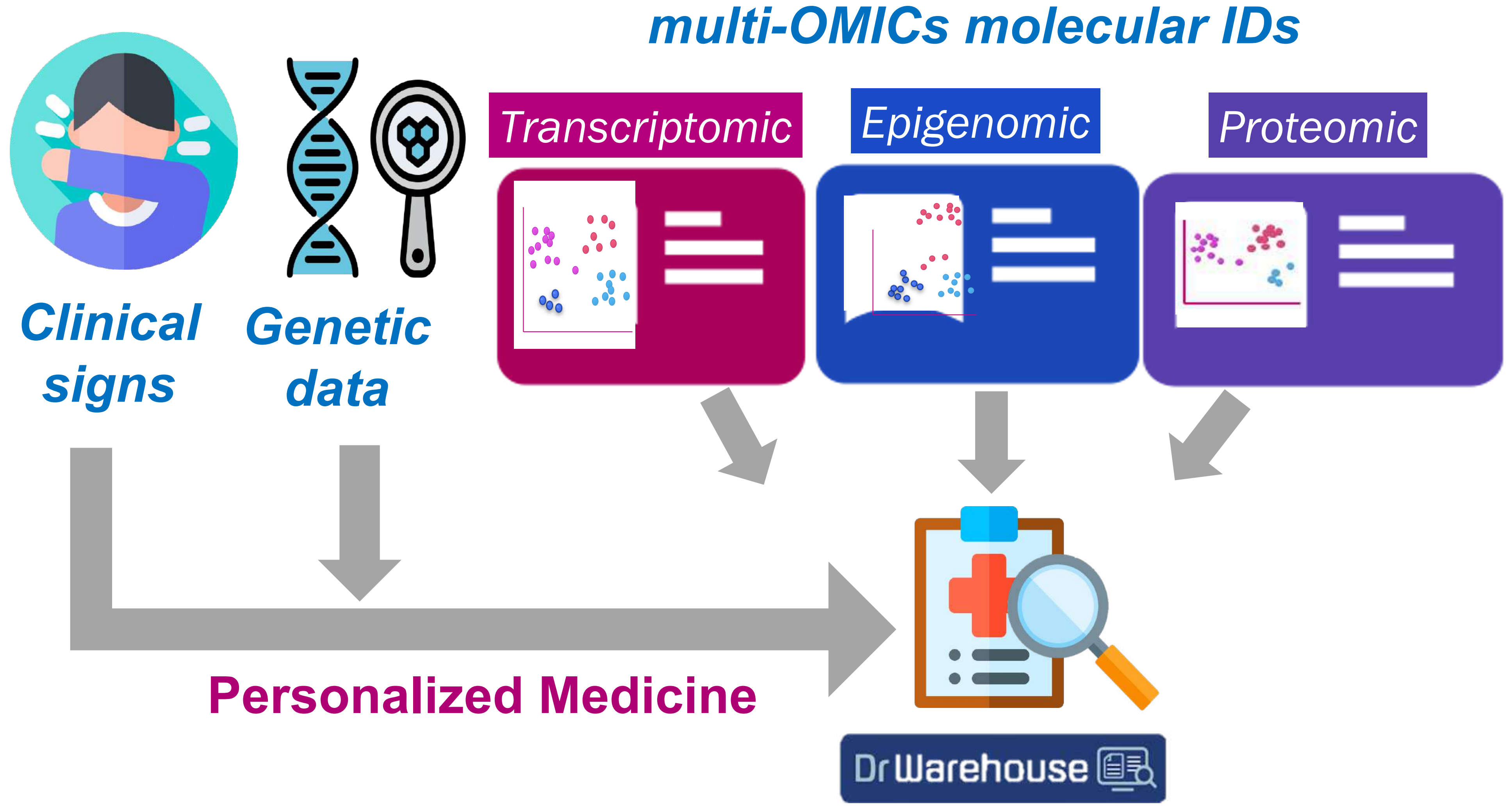
Treatment

??

Clinical signs

Molecular heterogeneity

Diagnosis and treatment wandering



multi-OMICs molecular IDs

Transcriptomic

Epigenomic

Proteomic

Clinical signs

Genetic data

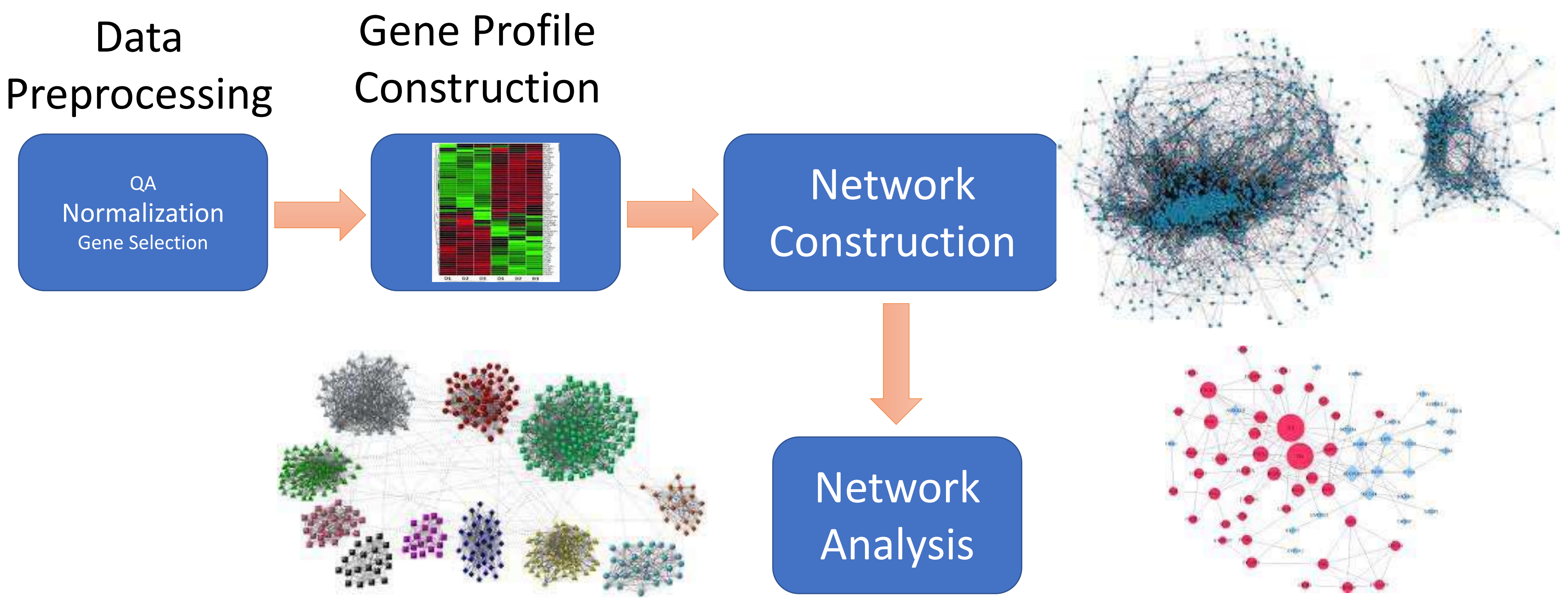
Personalized Medicine

Multi-omics Data Integration in Practice

- ***How to optimally integrate multi-omics data?***
  - ***Integrative ML/AI***
    - ***Sample clustering***
    - ***Network fusion***
    - ***Dimensionality Reduction***
  - ***ML/AI for data integration***
    - ***Heterogenous Network inference***
    - ***Correlation/regression based***
- ***Which specific algorithms to employ?***
  - ***Applicabilitu***
  - ***Accuracy***
  - ***Robustness***
  - ***Scalability***
- ***How to applicability of multi-omics integration?***

Preliminary work on Juveline Idiopathic Arthritis (JIA) dataset

Gene Network Inference using JIA data



Data Preprocessing

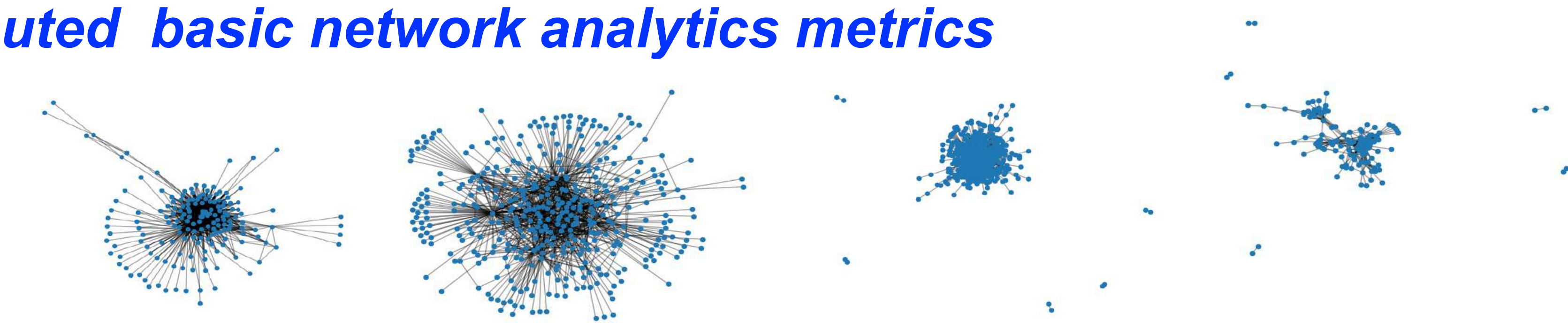
QA
Normalization
Gene Selection

Gene Profile Construction

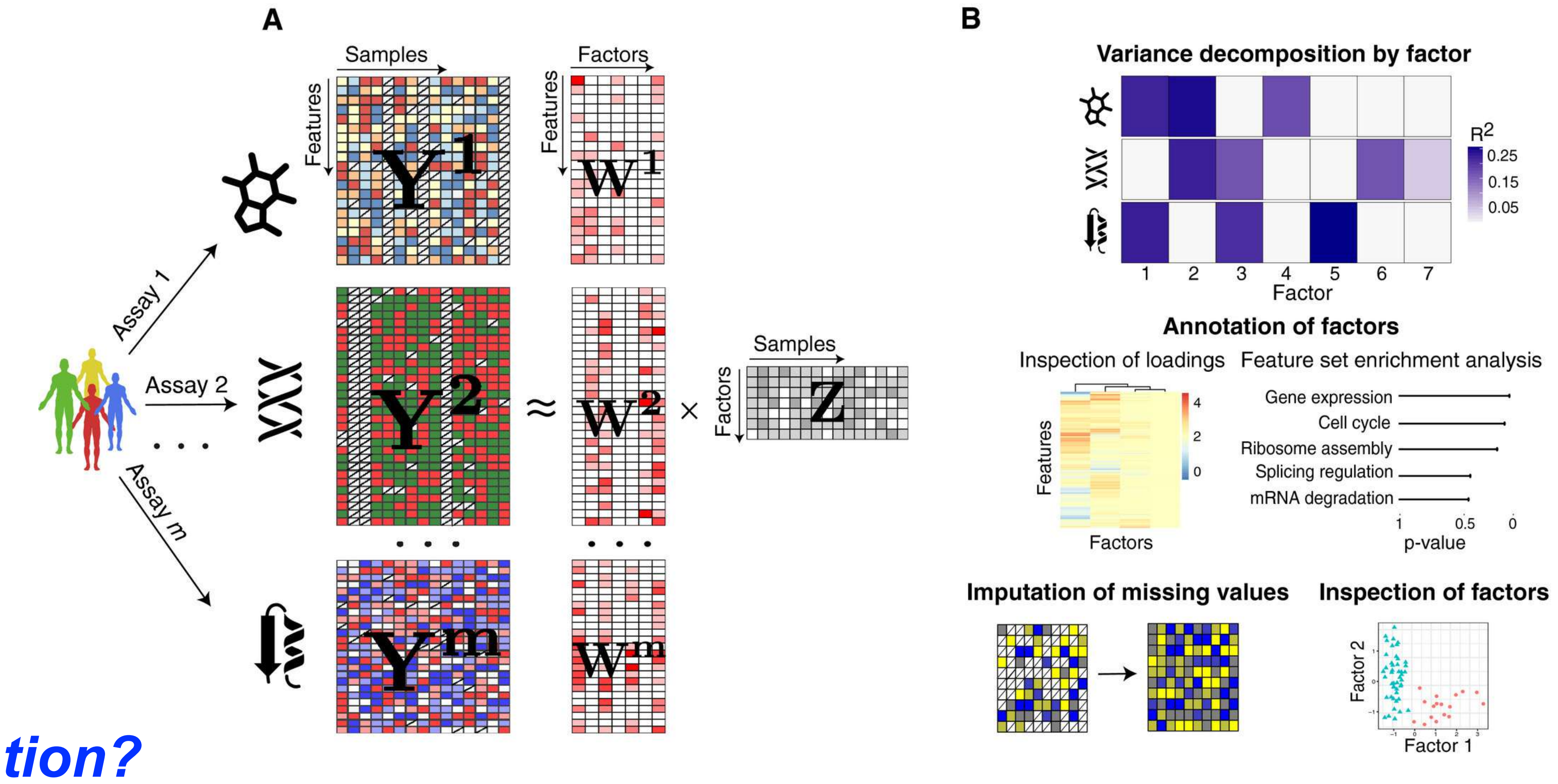
Network Construction

Network Analysis

- ***generated various co-expression networks over the entire cell population by varying:***
  - ***method of gene profile construction***
  - ***similarity measures (e.g., pearson, mutual information, cosine)***
  - ***number of top-k edges to maintain***
  - ***varying method of identification of top-k edges***
- ***computed basic network analytics metrics***



Dimensionality Reduction: Latent Factor Analysis



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