

MoReL: Multi-omics Relational Learning

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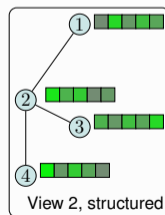
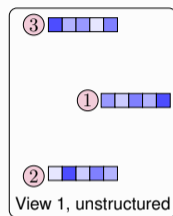
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Proposed method

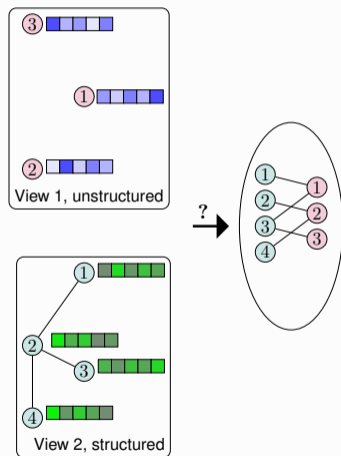
MoReL is a novel **Bayesian relational learning** method

- **Integrating** high-dimensional multi-omics data
- Taking advantage of *a priori known* relationships
 - ▶ modeled as a **graph at each corresponding view**
- Enabling **heterogeneous** multi-view learning
 - ▶ integrating **structured and unstructured views**
- Inferring the relational interactions as a **multipartite graph**
 - ▶ **no need to have** any pre-known interactions across views
 - ▶ novel **FGW-based decoder** for node distribution matching
⇒ handling **unpaired samples** and **missing samples**
- Exploiting **non-linear** and deep transformations of data
- Enabling **Bayesian interpretation**



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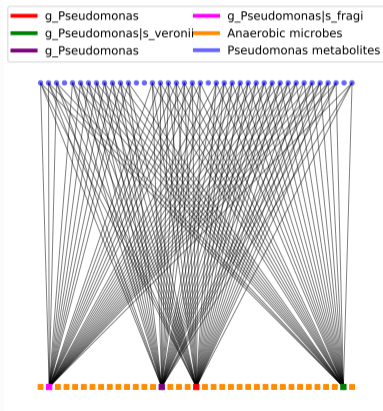
MoReL captures meaningful inter-relations across views:

- precision medicine in acute myeloid leukemia (AML)
- robust performance in prediction sensitivity

Avg. degree	0.10	0.15	0.20	0.25	0.30	0.40	0.50
SRCA	8.03	12.00	17.15	20.70	26.85	34.93	45.79
BCCA	9.65 ± 0.75	14.34 ± 0.06	18.96 ± 0.42	23.29 ± 0.52	28.22 ± 0.66	38.02 ± 2.15	46.88 ± 1.88
MoReL _{uu}	11.29 ± 0.16	15.74 ± 0.62	21.21 ± 0.81	26.20 ± 1.10	30.47 ± 1.07	39.05 ± 0.75	50.19 ± 0.19
MoReL _{us}	12.79 ± 0.39	17.51 ± 2.21	22.82 ± 1.01	29.58 ± 1.08	35.05 ± 1.27	45.74 ± 1.75	53.16 ± 0.96

MoReL captures meaningful inter-relations across views:

- microbiome-metabolome interactions in cystic fibrosis
- Test set: reported target molecules of *P. aeruginosa*



Thanks!

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