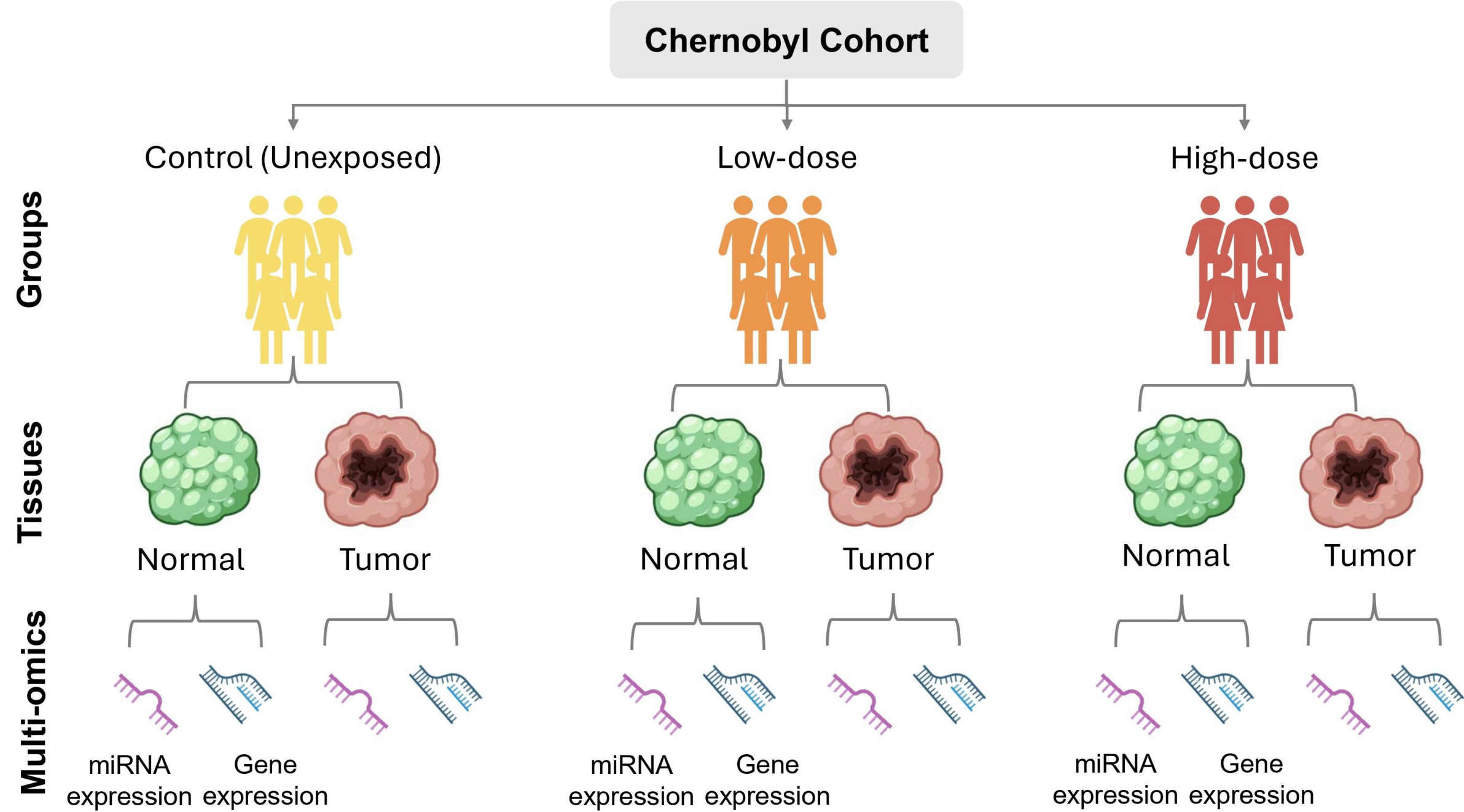


Latent Differential Graphical model for Multi-Tissue and Multi-Omics integration to model molecular interaction networks under multiple Radiation Exposure groups

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Background and challenges

- Exposure to ionizing radiation during childhood is associated with an increased risk of **papillary thyroid carcinoma**.
- Understanding the biological effects of **low-dose radiation exposure** remains a major challenge.
- High dimensional** data with **multiple modalities**: multiple radiation exposure groups, multiple biological tissues and multiple omics layers.



State-of-the-art in Network Inference

- Our previous study** identified radiation-associated molecular **signatures**.
- But** characterizing **low-dose** specific mechanisms using conventional integrative approaches such as **feature selection** is **challenging**.
- Sparse **Graphical models** enable the reconstruction of molecular networks.
- Existing graphical models do not **simultaneously** handle all these modalities.
- **Lack** a **unified framework** for jointly modeling **complex hierarchical structures**.

Method	Multi-omics	Multi-tissue	Multi-group	Latent
FGL ^[2]			X	
CoGLasso ^[3]	X			
Hetero-difgraph ^[4]			X	X
DIABLO ^[5]	X		X	X
multiSLICE ^[6]	X	X		X
Multi-DiffNet (our model)	X	X	X	X

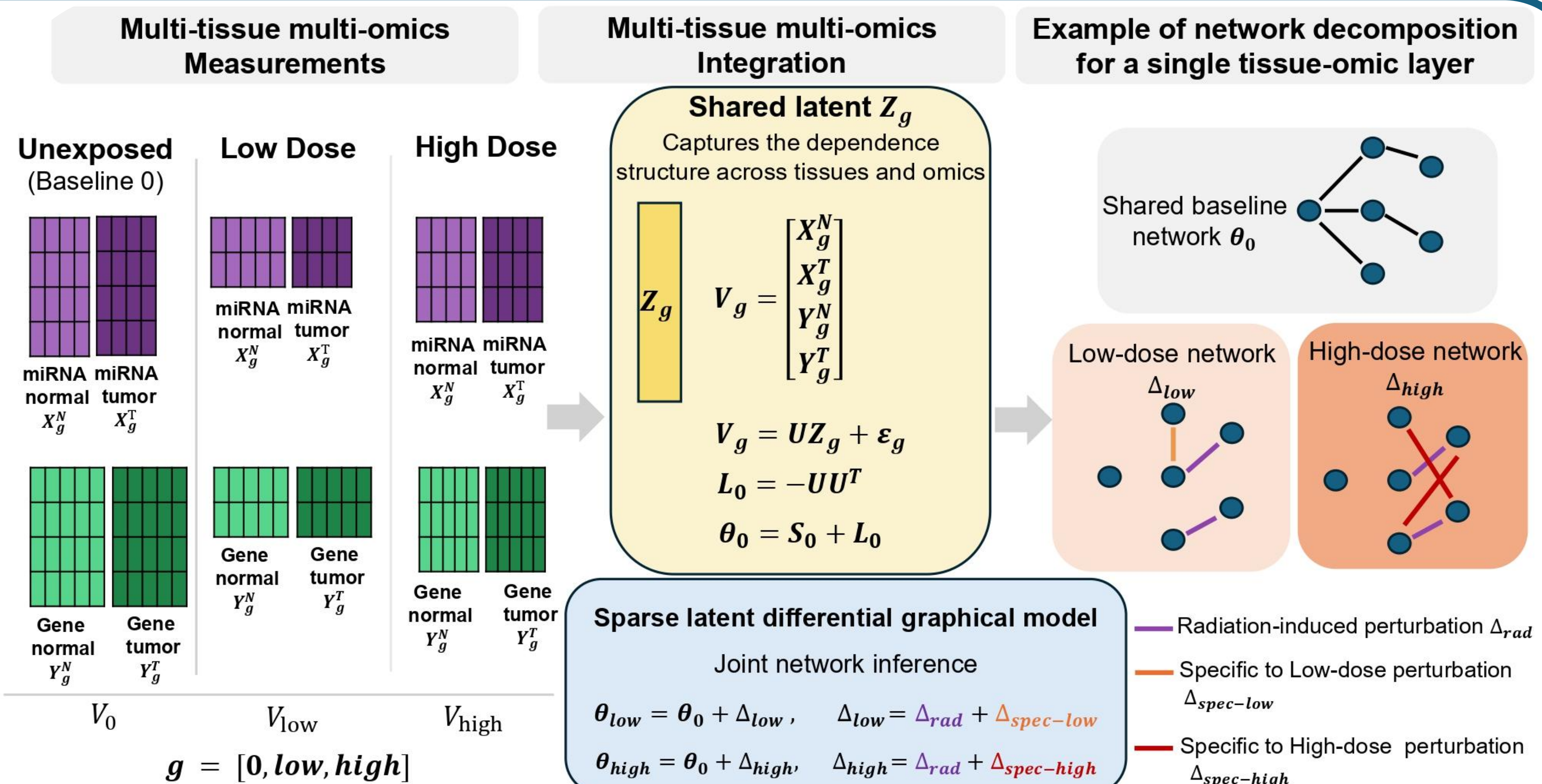
→ **Goal**: Develop an **integrative framework** based on graphical gaussian models for differential network inference across multiple omics, tissues, groups.

Contribution: Multi-DiffNet

Latent differential graphical model for multi-tissue and multi-omics network inference to identify **shared** and **exposure-specific (low and high)** interactions:

$$\mathcal{L}(S_0, L_0, \{\Delta_k\}) = n_0 [-\log \det(\Theta_0) + \text{Tr}(\widehat{\Sigma}_0 \Theta_0)] + \lambda_1 \|S_0\|_1 + \mu_0 \|L_0\|_* + \sum_{k \in \{\text{low, high}\}} n_k [-\log \det(\Theta_0 + \Delta_k) + \text{Tr}(\widehat{\Sigma}_k (\Theta_0 + \Delta_k))] + \sum_{k \in \{\text{low, high}\}} \lambda_2^{(k)} \|\Delta_k\|_1 + \lambda_3 \|\Delta_{\text{low}} - \Delta_{\text{high}}\|_1$$

- $\Theta_0 = S_0 - L_0$: baseline network with sparse (S_0) and latent (L_0) components.
- Δ_k : dose-specific differential network ($k \in \{\text{low, high}\}$)
- $\widehat{\Sigma}_0, \widehat{\Sigma}_k$: empirical covariance matrices.
- λ_1 : baseline sparsity penalty.
- $\lambda_2^{(k)}$: differential sparsity penalty.
- λ_3 : similarity penalty between differential networks.
- μ_0 : latent low-rank regularization parameter.



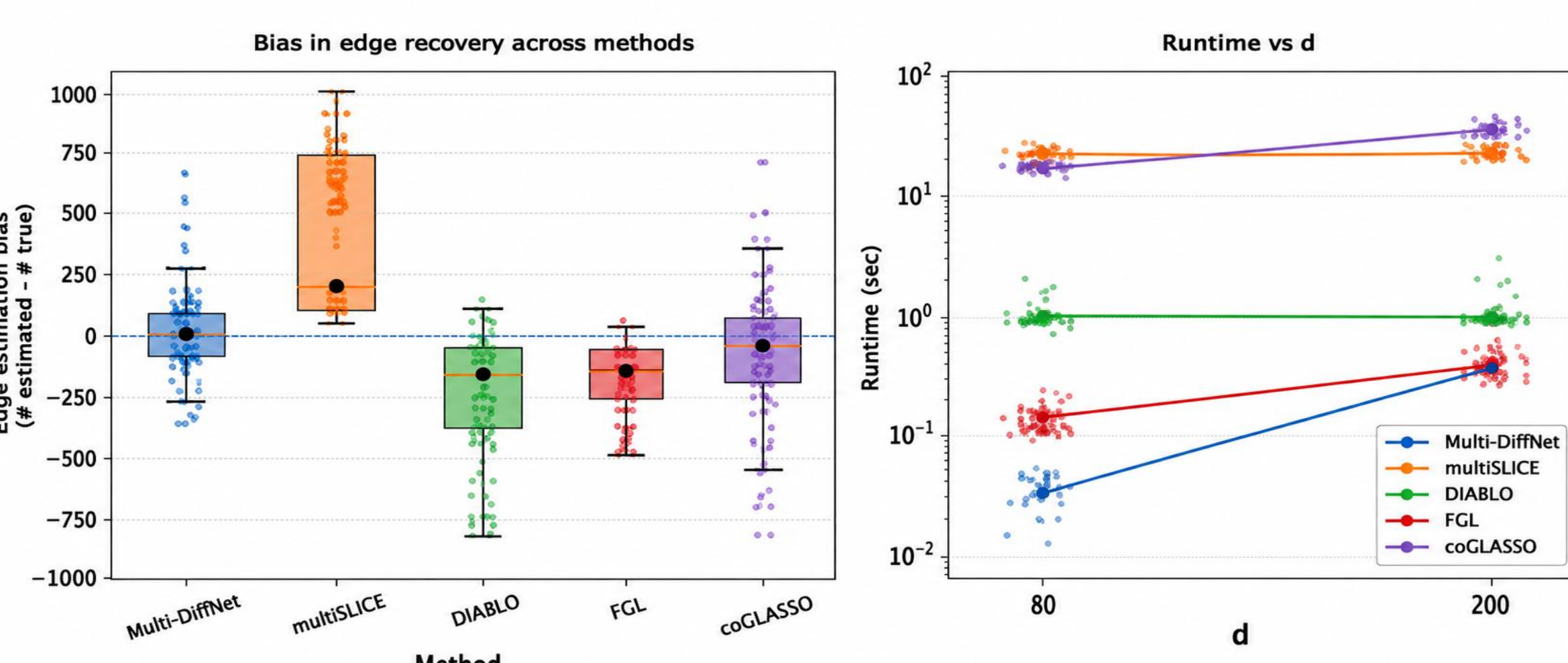
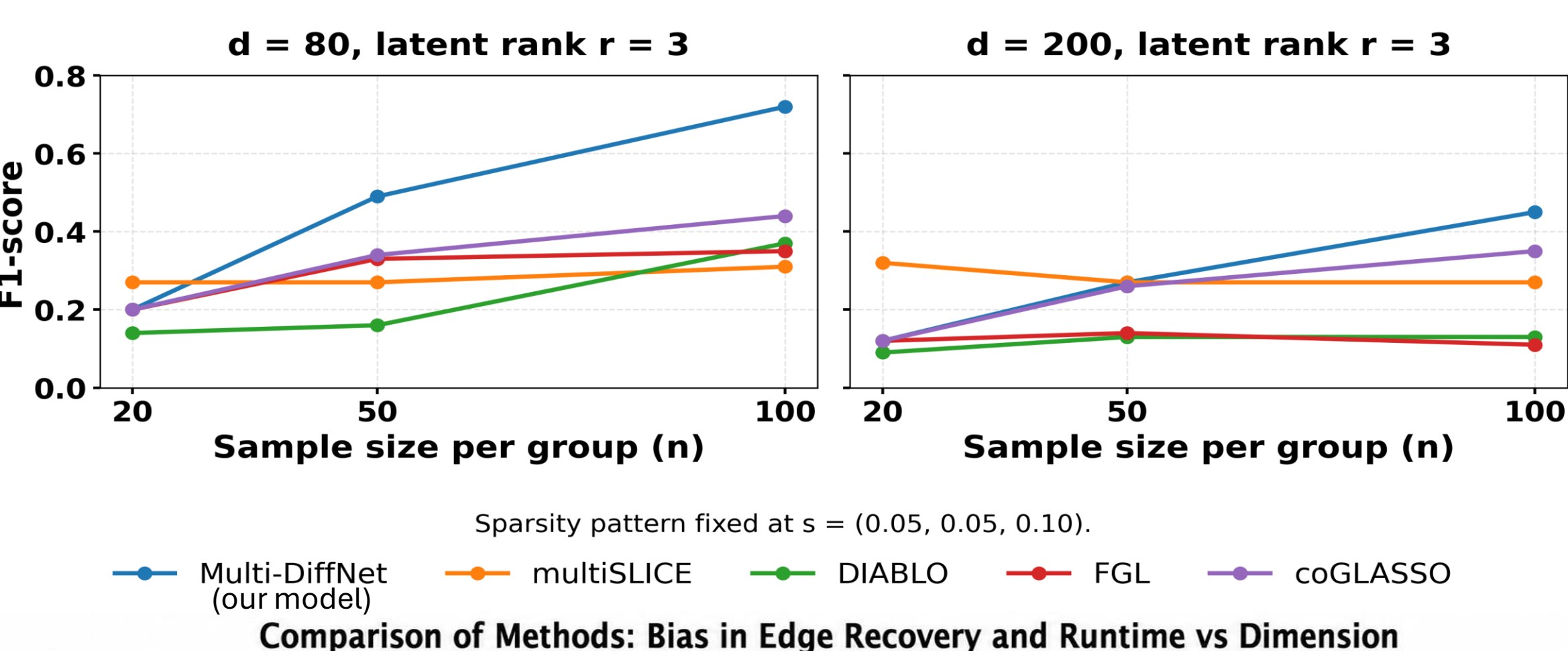
Simulated data

Multiple group Gaussian data (**unexposed, low-dose** and **high-dose**) with:

- a **shared latent structure** across tissues and omics
- a **sparse baseline network**
- sparse **exposure-specific** perturbations.

Scenarios: sample size ($n = 20, 50, 100$), dimension ($d = 80, 200$), latent rank ($r = 3, 10$).

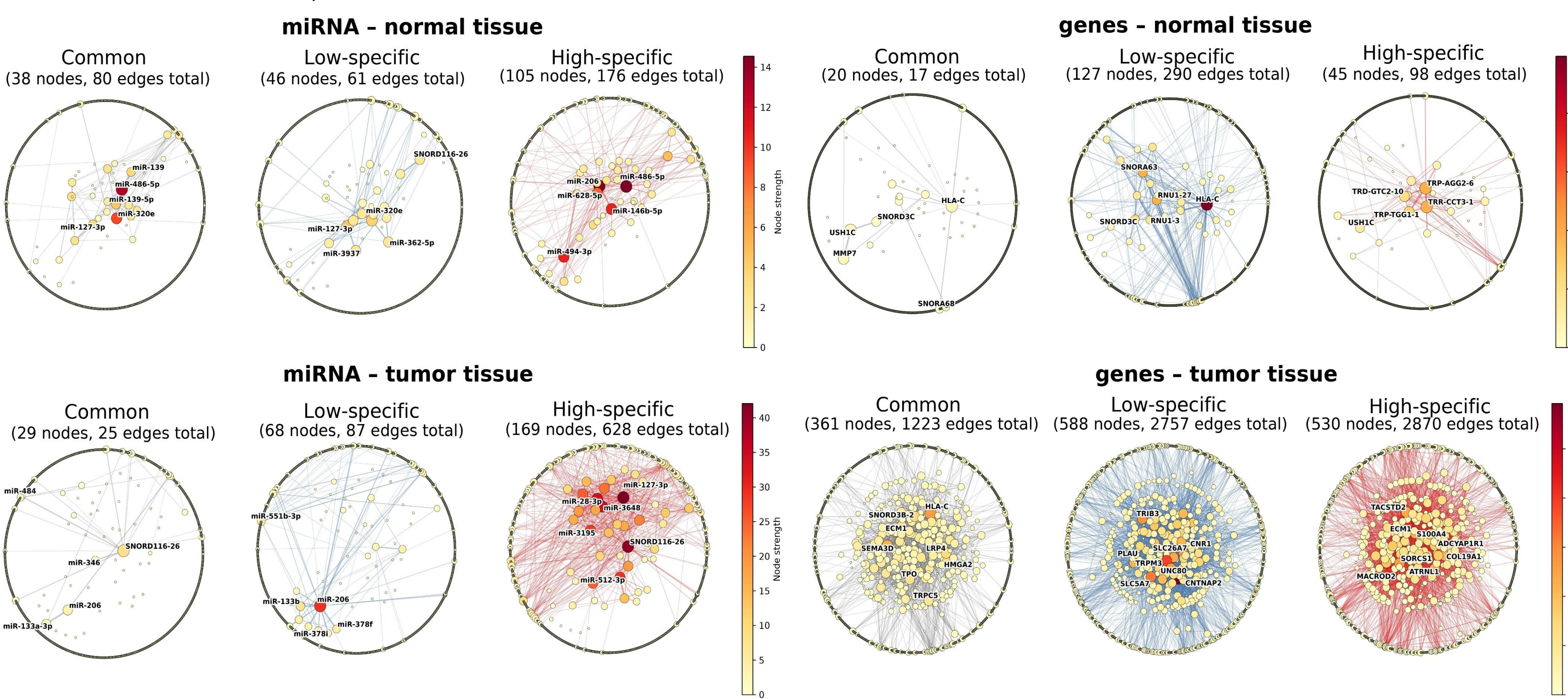
Multi-DiffNet improves edge recovery across simulation scenarios



→ **Multi-DiffNet** consistently **outperforms** competing methods in differential **edge recovery**, achieving the **highest F1-scores**, **reduced estimation bias**, and **competitive runtimes** across all simulation scenarios.

Chernobyl Tissue Bank (CTB) Thyroid Cancer Cohort [7]

- 47 individuals** (**28 unexposed**, **11 low-dose** (< 50 mGy), **8 high-dose** (> 500 mGy)).
- Features** retained after differential expression analysis: 1,571 miRNAs and 1,947 genes.
- Tissues**: Normal, Tumor.



→ **High-dose** irradiation group induces markedly **denser and more connected** differential networks than **low-dose** irradiation group, particularly in **tumor tissue**, across both miRNA and gene omics.

Network Inference interactions

- Inference of **intra-omics, cross-omics, intra-tissue** and **cross-tissue** interactions.
- Inference of **shared** and **dose-specific** radiation-associated networks.

References

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Multi-DiffNet Code