Réseaux de neurones pour graphe pour la prédiction de phénotype à partir de données transcriptomiques

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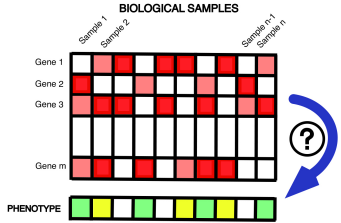
Outline

Objective

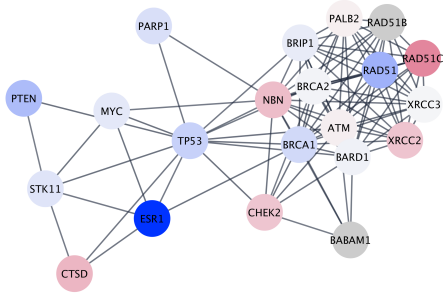
Prediction of phenotype from gene expressions



- Machine learning is increasingly used for transcriptomic-based predictions
  - Example: prediction of cancer type or the likelihood of a patient responding to a specific treatment
- Challenging due to the high dimensionality and small-to-moderate sample size

Objective

- Genes are organized into regulatory networks in cells
  → some works have used the **gene network information** to improve phenotype predictions



- Gene network: gene regulatory network, protein-protein interaction (PPI) network, co-expression network etc.

Earlier work in this field

Problem: predict y (numerical) from X (multivariate, dimension p) with a linear model:

$$y = X \times \beta + \epsilon$$

Examples:

- [Rapaport et al., 2007]: y is irradiated/not irradiated sample and X is gene expression. A network is given on the p genes based on KEGG metabolic pathways
- [Li and Li, 2008]: y is time to death (Glioblastoma) and X is gene expression. A network is given on the p genes based on KEGG metabolic pathways

Background and notations

We have a network (graph) $\mathcal{G}$, with p nodes $v_1, \ldots, v_p$ and edges between these nodes

An important matrix: the Laplacian

$$L_{ij}^{\mathcal{G}} = \begin{cases} -1 & \text{if } i \neq j \text{ and } v_i \text{ and } v_j \text{ are linked by an edge} \\ 0 & \text{if } i \neq j \text{ and } v_i \text{ and } v_j \text{ are not linked by an edge} \\ d_i & \text{if } i = j \end{cases}$$

with d_i the degree of nodes v_i

Eigendecomposition of the Laplacian

L is symmetric and positive so it can be decomposed into:

$$L = \sum_{i=1}^{p} \lambda_i e_i e_i^T$$

with λ_i the eigenvalues (in increasing order) and e_i the orthonormal eigenvectors in $\mathbb{R}^p$

To extract the most relevant information from the network, use the eigenvectors associated to the smallest eigenvalues:

- **low pass filter**: $F^{\mathcal{G}} = \sum_{i=1}^{r} \lambda_i e_i e_i^T$ for $r < p$
- **regularization**: $F^{\mathcal{G}} = \sum_{i=1}^{p} \phi(\lambda_i) e_i e_i^T$ with $\phi(\lambda_i) = e^{-\beta\lambda_i}$ or $\frac{1}{\lambda_i}$ for instance

[Rapaport et al., 2007]

- **Transformation of expression profiles**: spectral decomposition of gene expression profiles with respect to the eigenfunctions of the Laplacian

$$S_\phi(x_j) = \sum_{i=1}^{p} x_{ji}\phi(\lambda_i)e_i$$

- Optimization problem:

$$\min_{\beta\in\mathbb{R}^p} \sum_{i=1}^{n} \ell\left(\beta^t S_\phi(x_i), y_i\right) + C\|\beta\|^2$$

How to use L in prediction models ? [Li and Li, 2008]

Incorporate information on the gene network by using a **network constrained regularization**:

$$\arg \min_{\beta \in \mathbb{R}^p} \sum_{i=1}^{n} \left(\beta^t x_i - y_i\right)^2 + \lambda_1 \beta^T L \beta + \lambda_2 \|\beta\|_1$$

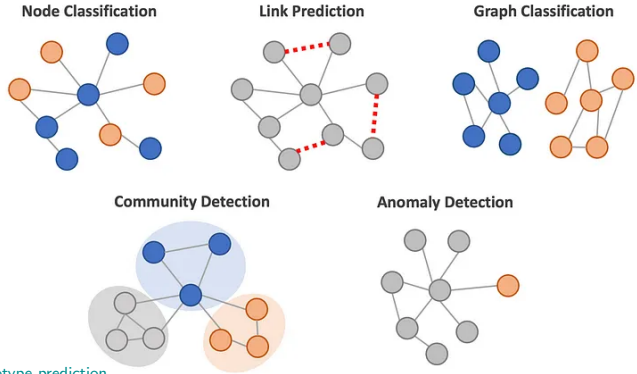
Motivation: genes that are linked on the network are expected to have similar functions and therefore smoothed regression coefficients

Implemented in R package glmgraph (not maintained, archived on CRAN)

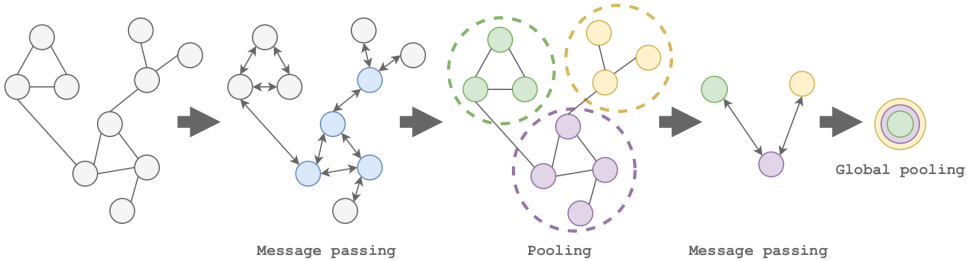
Outline

Graph Neural Networks

- Recently graph neural networks (GNN) were proposed for phenotype prediction
- Particular type of convolutional neural network:
  - a graph representing pairwise relationships between nodes is used to drive the convolution
- GNN can be used to solve different problems:



Overview of GNN



General idea: the representation of a node is computed from the representations of nodes in the neighborhood

The last layer is fed to a standard MLP for prediction

Message passing layers

Generalization of convolutional layers to graph data

The representation of node v_i is learned iteratively (layers $t = 1, \dots, T$) with:

$$h_{v_i}^0 = x_i$$
$$h_{v_i}^{t+1} = F\left(h_{v_i}^t, \square_{v_j \in \mathcal{N}(v_i)} \phi_t(h_{v_i}^t, h_{v_j}^t)\right)$$

- $\square$: differential permutation invariant function (mean, sum)
- F and ϕ_t: parameterized functions which parameters are learned during the training

GNN in practice

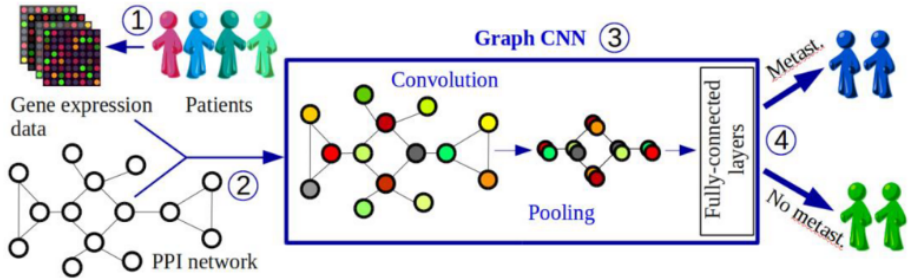
GNN libraries:

- **Spektral** [Grattarola and Alippi, 2020]
  - Python library for graph deep learning based on the Keras API and TensorFlow 2
- **PyTorch Geometric (PyG)** [Fey and Lenssen, 2019]
  - based on PyTorch
- also Graph Nets, Deep Graph Library

Graph Neural Networks for phenotype prediction

- Some authors have used GNNs for phenotype prediction
  - Example: metastatic event prediction
- They used biological knowledge on gene regulatory networks:
  - PPI networks or co-expression networks

Graph Neural Networks for phenotype prediction



Each patient is represented as a **graph signal**:

- the molecular network structures the genes and is the same for every patient
- patient's gene-expressions are assigned to the vertex of the network

Phenotype prediction is addressed as a **graph classification task**

Graph Neural Networks for phenotype prediction

- In other fields of applications, recent works tend to show that GNNs are frequently over-complex for the task
  [Errica et al., 2020, Böther et al., 2022, Santana et al., 2023]
- [Smith et al., 2020] even showed that classical ML methods often outperform deep learning for phenotype prediction
- $\Rightarrow$ simpler models can obtain comparable results
- Ratio between benefits and costs (in particular computational) of these methods ?

Outline

Benchmark

Comprehensive and reproducible benchmark comparing GNN to other ML methods for transcriptomic-based phenotype prediction

- We used previously published datasets and models
- Systematic comparison using a common ground methodology

Published works

- **BreastCancer** [Chereda et al., 2021]:
  - prediction of metastasis within the first 5 years in breast cancer
  - PPI network (HPRD)
- **CancerType** [Ramirez et al., 2020]:
  - classification of different tumor and non-tumor samples into 33 cancer types or as normal (data from TCGA)
  - PPI network and co-expression network

Published works

- **F1000** [McDermott et al., 2020]:
  - gene expression profiles over 76 cell lines, that are treated with bioactive small molecules or genetic perturbations (LINCS)
  - 3 classification tasks : prediction of primary site (tissue type), subtype, drug mechanism of action
  - 2 views of the dataset: full dataset over 76 cell lines and a dataset containing only samples from prostate tissue
  - network of transcription-factor and micro-RNA regulatory relationships from several external datasets (RegNetwork)

These 3 works used the model and the implementation of [Defferrard et al., 2016].
This model uses **Chebnets** as convolutional layer and **graph coarsening** as pooling.

Chebnets [Defferrard et al., 2016]

It is based on a **spectral decomposition of the graph**

$$y = g_\theta(L)x = \sum_{k=0}^{K} \theta_k T_k(\tilde{L})x$$

- $\tilde{L}$: scaled Laplacian
- T_k: Chebyshev polynomial of order k
- θ_k: layer's trainable parameters

It can capture information from a node's wider neighborhood by including higher-degree polynomials

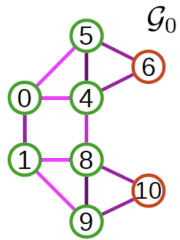
GCN [Kipf and Welling, 2017]

- More scalable approach by using a first-order approximation of spectral graph convolution
- A linear model w.r.t. L is considered by limiting K to 1.
- Using this model and a single parameter θ, the equation simplifies to:

$$y = \theta \left(I + D^{-\frac{1}{2}} A D^{-\frac{1}{2}} \right) x$$

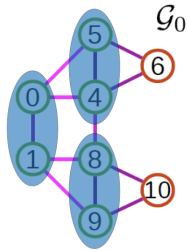
Graph coarsening [Defferrard et al., 2016]

- Multilevel clustering algorithm: each level produces a coarser graph
- The size of the graph is reduced by a factor 2 at each level



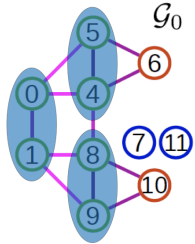
Graph coarsening [Defferrard et al., 2016]

At each level, a vertex i is matched to the neighbor j that maximizes $A_{ij}(\frac{1}{d_i} + \frac{1}{d_j})$

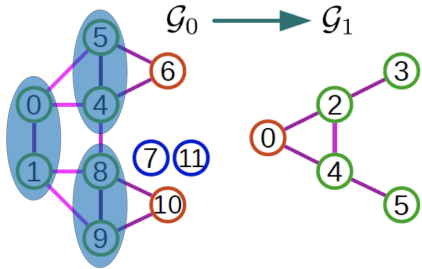


Graph coarsening [Defferrard et al., 2016]

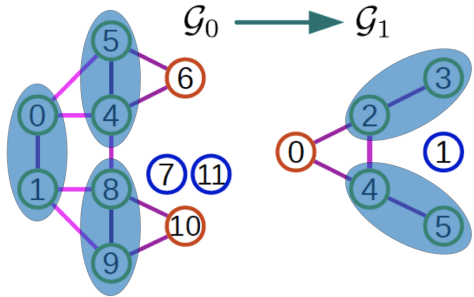
Artificial (disconnected) nodes are added to ensure two children for each vertex



Graph coarsening [Defferrard et al., 2016]

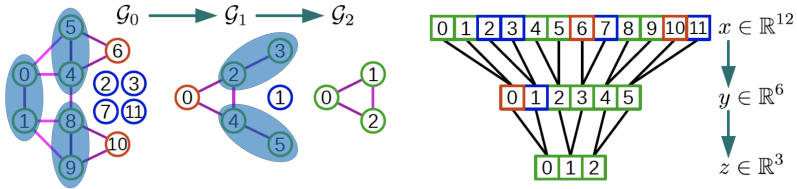


Graph coarsening [Defferrard et al., 2016]



Graph coarsening [Defferrard et al., 2016]

- Creation of a balanced binary tree: fake (disconnected) nodes are added to pair with singletons
- Vertices are arranged such that a graph pooling operation becomes as efficient as a 1D pooling



Defferrard et al. 2016

Outline

Datasets

Dataset	# nodes	# observations	Prediction type (# classes)	Gene network
BreastCancer [Chereda et al., 2021]	6,888	969	Classification (2)	PPI network (HPRD)
CancerType [Ramirez et al., 2020]	4,444	11,070	Classification (34)	PPI and co-expression networks
F1000 prostate [McDermott et al., 2020]	978	25,565	Classification (9)	Regulatory network
F1000 full [McDermott et al., 2020]	978	156,461	Classification (12, 14, 49)	Regulatory network

Comparison

Comparison with different approaches:

- Standard machine learning methods: **random forest**, **multilayer perceptron**, **SVM**
- **glmgraph**: graph-constrained regression model
- **GNN**
- **GNNo**: GNN based on convolution between observations rather than between features

We systematically used cross-validation

Implementations

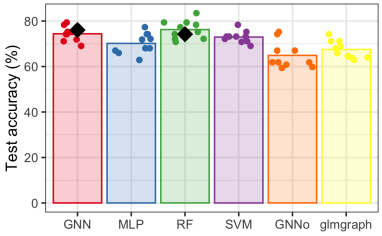
- **GNN**:
  - We kept the coarsening approach from [Defferrard et al., 2016]
  - We implemented the convolutional layer using the Spektral library and the neural network model in tensorflow/keras
  - The GNN model has to be adapted to take into account the different coarsened graphs
- **GNNo**: modification of the implementation of GNN from keras

Implementations

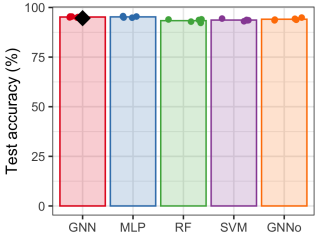
We also run the same methods with different implementations:

- **multilayer perceptron**: functions from the Python libraries scikit-learn and keras/tensorflow 2
- **SVM**: Python library scikit-learn and the R package **e1071**
- **random forests**: Python library scikit-learn and the R package **randomForest**

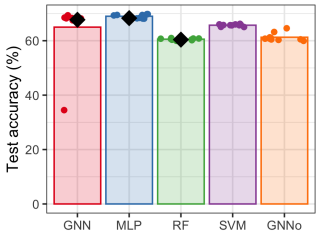
Results: test accuracy



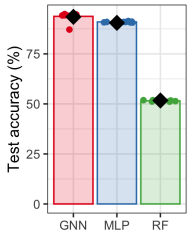
BreastCancer



CancerType



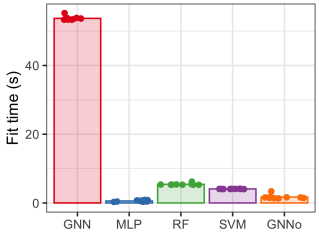
F1000 prostate

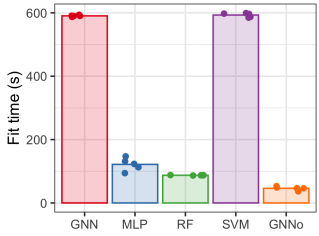


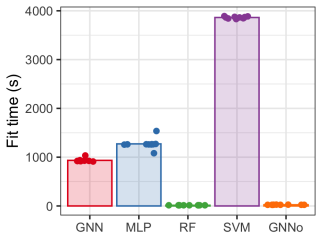
F1000 full (subtype)

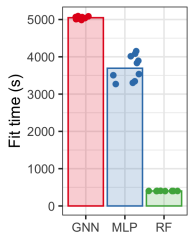
- Good reproducibility of published results
- Except in F1000 full, GNN is not the best method
- Unlike GNN, other methods (MLP, RF, SVM) were used with default hyperparameters
- No clear winner stands out
- GNN performs better than GNNo

Results: computational time



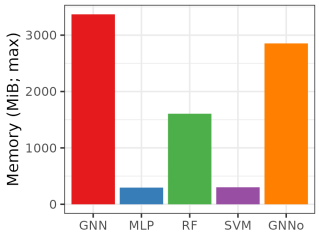




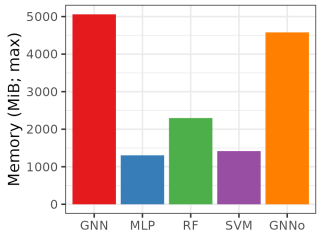


- glmgraph is the most computationally demanding method for BreastCancer (not represented for the sake of readability)
- SVM is strongly influenced by the number of samples and the number of classes
- GNN computational time is increased when both the number of samples and the number of genes are large

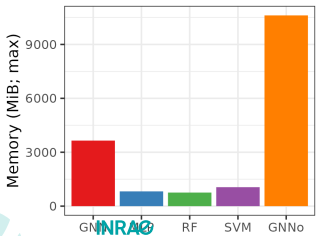
Results: maximum memory load for methods implemented in Python



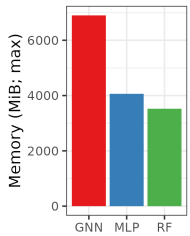
BreastCancer



CancerType



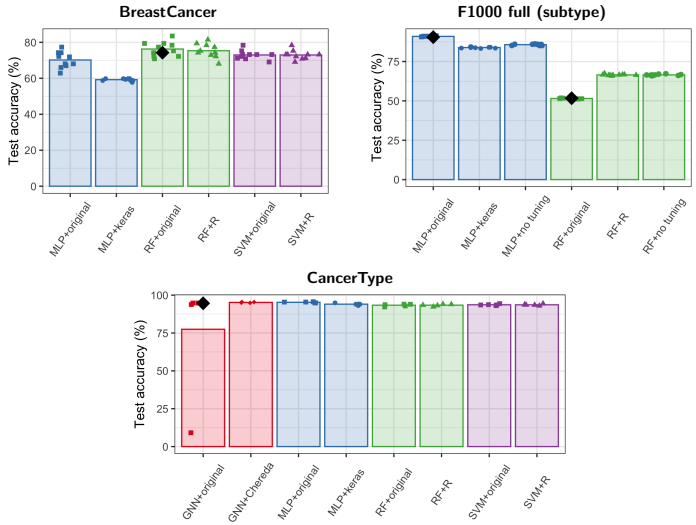
F1000 prostate



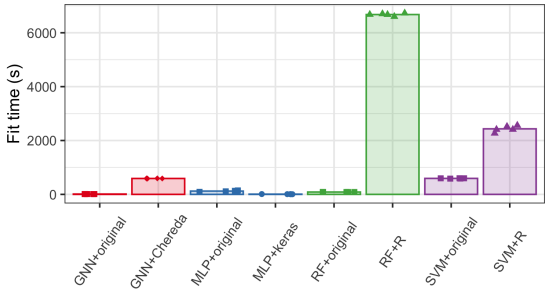
F1000 full (subtype)

GNN and GNNo are the most demanding methods, GNNo being again strongly impacted by the number of samples

Impact of the implementations: accuracy



Impact of the implementations: computational time



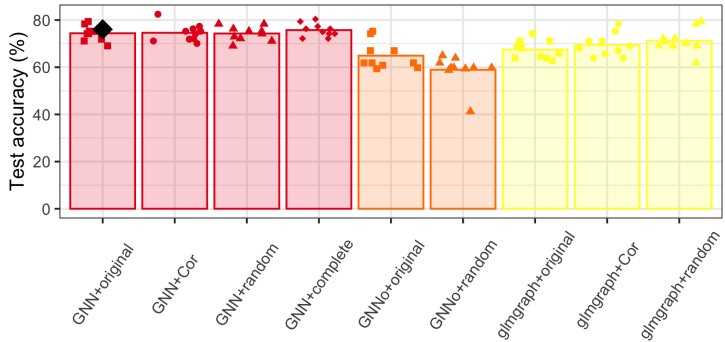
However, the improvements came sometimes at the cost of a larger computational time.

Impact of the input graph

In order to see the usefulness of the added information in graph based models, we also used these methods with naive graphs for the BreastCancer dataset:

- **Cor**: simple thresholding of the Pearson correlation matrix between genes
- **random**: random permutation between gene edges (to obtain random graph with same degree distribution)
- **complete**: complete graph

Impact of the input graph



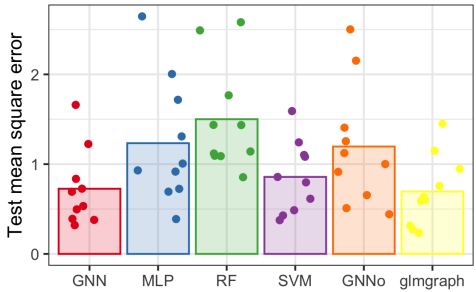
- The impact of the input network is not visible
- For GNN and glmgraph, the random and complete networks achieve better performance that networks based on biological knowledge

Simulated data

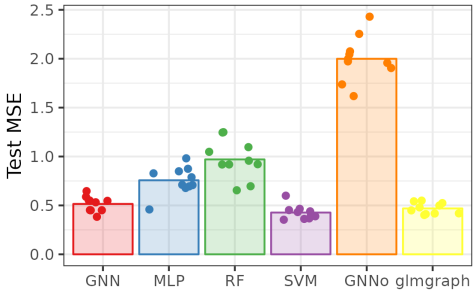
To better assess the impact of using a gene network for transcriptomic predictions, we relied on *in silico* expression data in which the network is part of the generation process

- Simulated:
  - Small well-controlled dataset generated with the simulation tool sismonr
  - This dataset was simulated from 20 genes and 200 times steps were simulated for 100 independent individuals
  - Prediction goal: prediction of one protein quantity at time t from mRNA quantities at time $t-1$
- DREAM5:
  - previously made available through the DREAM5 challenge on network inference
  - One gene was randomly chosen as the target gene expression to predict from the other gene expressions and the network

Results: simulated data



Simulated

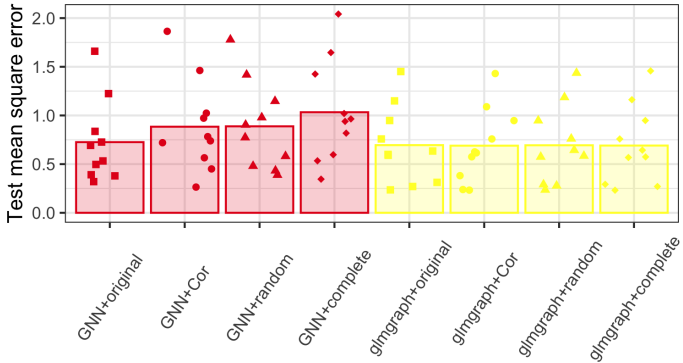


DREAM5

- Simulated: graph-based methods improve the prediction MSE, except for GNNo
- DREAM5: Similarly graph prediction methods perform among the best, only competing with SVM

Results: simulated data

Impact of using a non relevant network in the prediction for Simulated

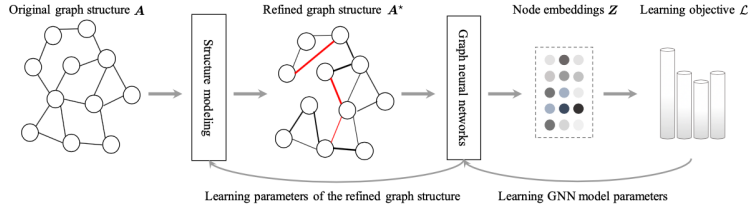


Discussion

- Standard ML methods, not explicitly accounting for the dependency structure between genes, frequently obtain better or comparable performance on the prediction task
- In addition, benchmarking with real expression datasets and irrelevant networks do not show decrease in performance compared to using a biologically relevant gene network
- When the network is perfectly known, better performances are obtained with GNN and glmgraph
- The lack of improvement for GNN with real data might be due to the low accuracy of available gene networks

Perspectives

Graph structure learning: learn simultaneously the relevant graph for the prediction task and the GNN's parameters



- Few existing hybrid approaches, and not always relevant for omics data
- Difficulty: learning a discrete structure while descent gradient is used for learning GNN's parameters

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Datasets

Table S1: Description of datasets.

Dataset	Gene network	Type of transcriptomic data	Prediction goal
BreastCancer	PPI network (HPRD)	microarray	Prediction of metastasis within the first five years in breast cancer.
CancerType	PPI network (STRING) and co-expression network based on Spearman correlation	RNA-seq data (TCGA)	Classification of different tumor and non-tumor samples into 33 cancer "types" (actually tissue in which the tumor has been found) or as normal.
F1000	Regulatory network (RegNetwork)	L1000 assay (measurement of a reduced representation of the transcriptome) on cell lines, profiled in different tissues and with different drugs	Prediction of primary site (tissue type), subtype (e.g., "malignant melanoma" or "myoblast", related to a disease state) and drug mechanism of action.
Simulated	Given network	Simulated data (obtained from the network and simulating from mRNA / protein quantities dynamic relations) by **sismonr**	Prediction of one protein quantity at time t from mRNA quantities at time $t-1$.
DREAM5	Given network	Simulated static expression data (obtained from the network)	Prediction of one gene expression based on the expression of the other genes.