

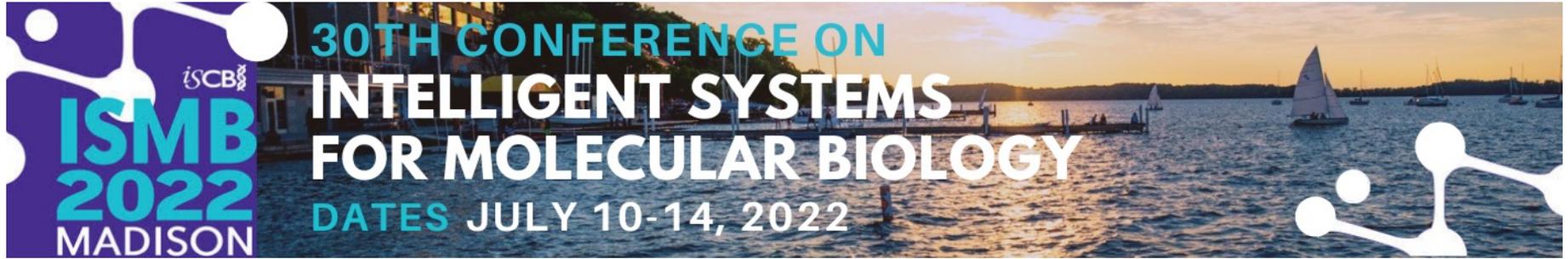
Towards Precision Medicine with Graph Representation Learning

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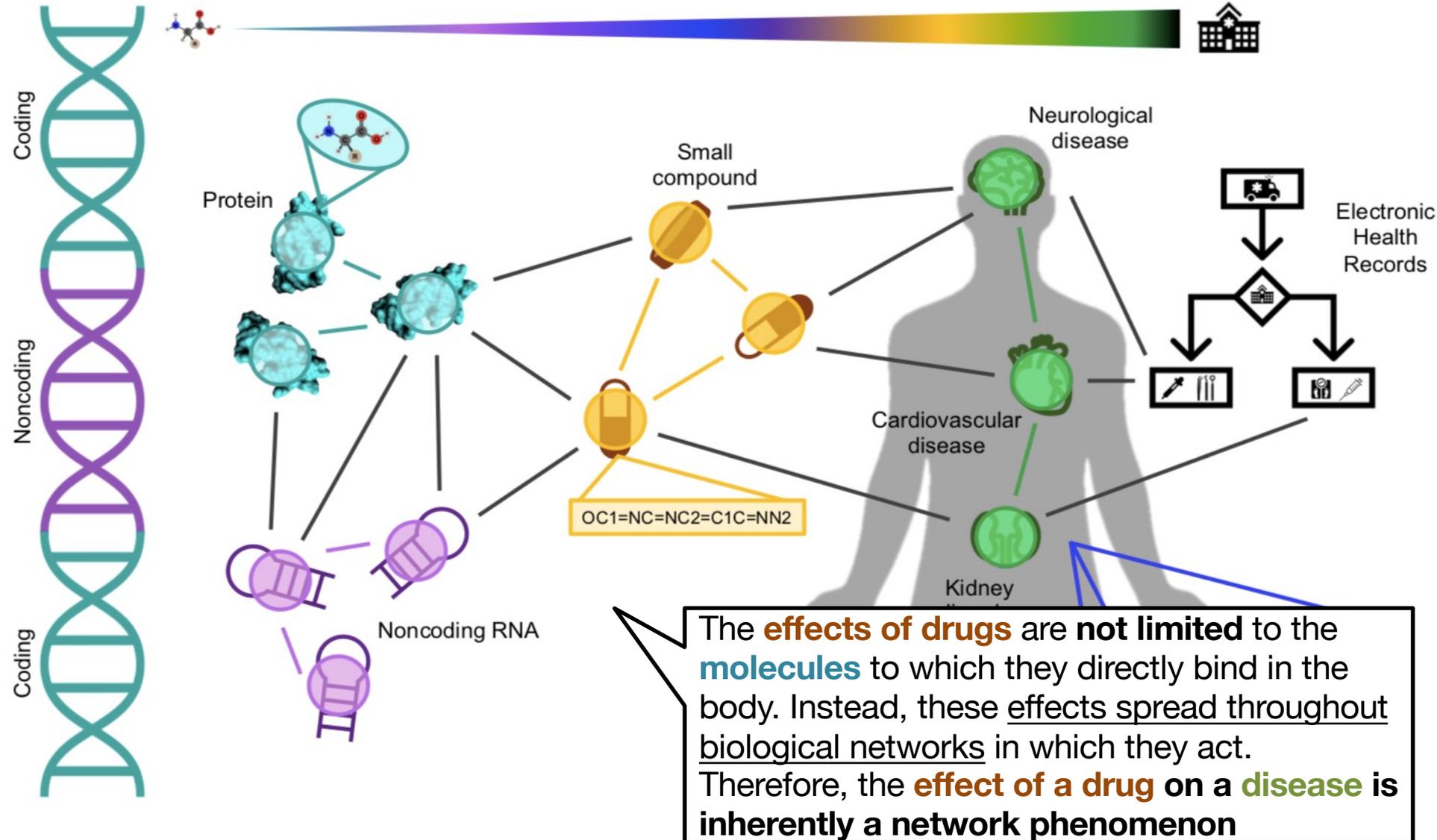
Tutorial VT4

July 7, 2022 at 9am – 1pm CDT

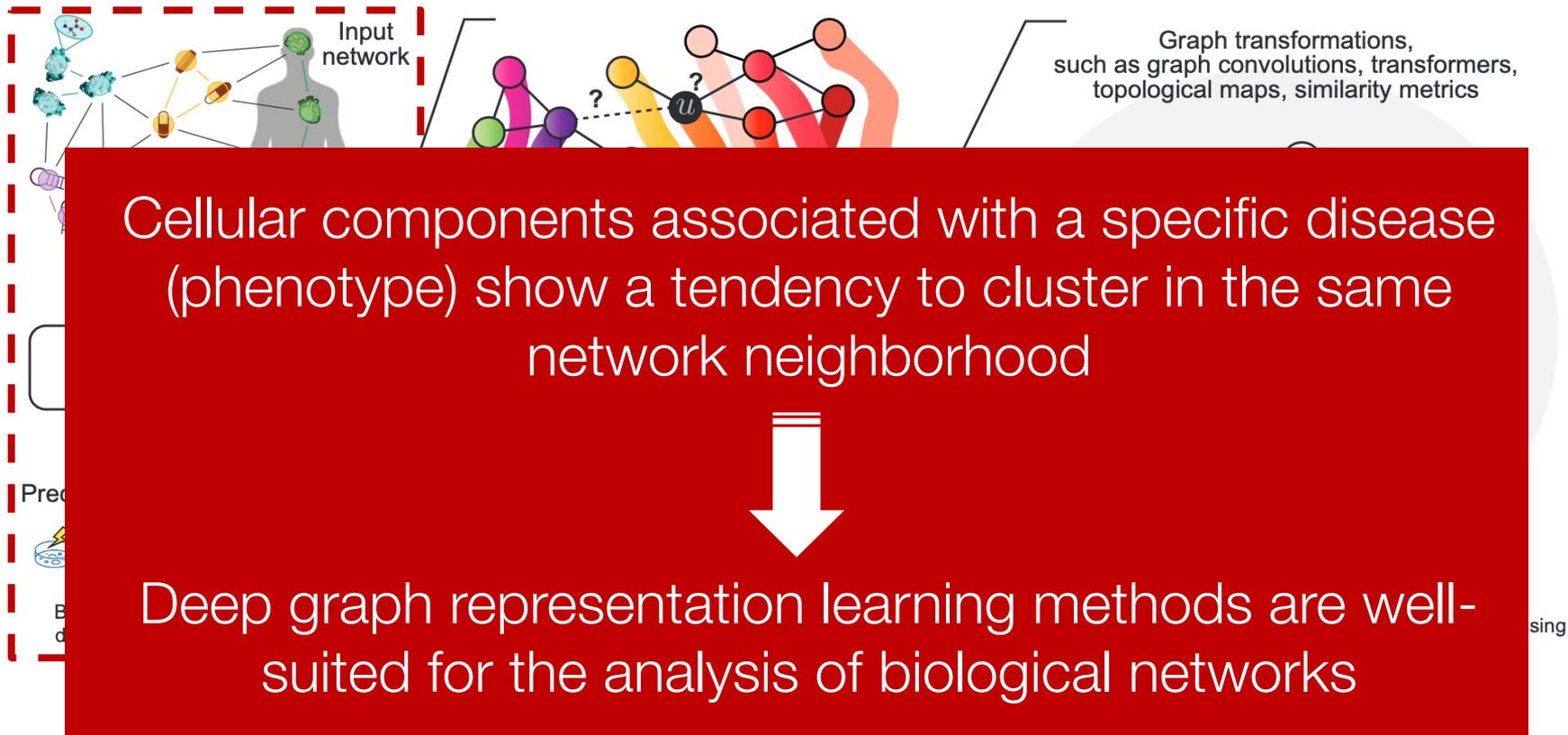


All tutorial materials are available at
zitniklab.hms.harvard.edu/biomedgraphml

Biology is interconnected



Graph representation learning realizes key network principles for data-rich biomedicine



This Tutorial

- ✓ 1. Methods: Network diffusion, shallow network embeddings, graph neural networks, equivariant neural networks
- ✓ 2. Applications: Fundamental biological discoveries and precision medicine
-  3. Hands-on exercises: Demos, implementation details, tools, and tips

Hands-on Exercises

[NeurIPS 2020 Demo] MolDesigner: Interactive Design of Efficacious Drugs with Deep Learning

|| Kexin Huang, Tianfan Fu, Vivian Hu, Dawood Khan, Ali Abid, Ali Abdalla, Abubakar Abid, Lucas M. Glass, Marinka Zitnik, Cao Xiao, Jimeng Sun || Demo: youtube.com/watch?v=PbyHP0iRoP8 || DeepPurpose: github.com/kexinhuang12345/DeepPurpose || TDC: github.com/mims-harvard/TDC || Gradio: github.com/gradio-app/gradio ||

AMINO ACID SEQUENCE

MOLECULE

Please refer to:
<http://deeppurpose.sunlab.org/>

AFFINITY PREDICTION MODEL TYPE
MPNN-CNN

ADMET PREDICTION MODEL TYPE
MPNN

CLEAR SUBMIT

Practical Advice & Tips

Network & machine learning packages

- **Data science & machine learning basics:** Numpy, pytorch, pandas, scipy, scikit-learn
- **Visualization basics:** Matplotlib, plotly, UMAP, seaborn
- **Network construction & analysis:** NetworkX, iGraph, Stanford Network Analysis Platform (SNAP)
- **Graph machine learning:** Pytorch Geometric (+ tutorials), Deep Graph Library (+ public slack channel), Pytorch Lightning

Developer tools for graphs & machine learning

- **Network visualization:** Gephi, Cytospace, GraphVis, Neo4j
- **Model visualization:** Weights & Biases, Neptune, TensorBoard, Comet, HiPlot, Gradio
- **Code profilers:** cProfile/profile for Python3
- **Making paper-ready figures:** draw.io, Adobe color wheel

Quick tip: New packages and software are released all the time, but there's no need to be overwhelmed! Stick with a few that you like and be proficient in them!

Practical Advice & Tips

Helpful tools for programming

- **Notebooks:** Google Colab (free GPUs), Jupyter Notebook
- **Version control:** GitHub
- **Environment management system:** Conda
- **Integrated Development Environment (IDE):** Visual Studio Code, PyCharm, Spyder
- **Terminal multiplexers:** Screen, tmux
- **Runtime:** tqdm
- Use debuggers and breakpoints (e.g., pdb package, built-in debuggers in IDEs)

Implementation tips

- Normalize by degree (e.g., node features, node weights)
- Apply batch and/or layer normalization
- Use minibatching (especially on large graphs)
- Experiment with the number of layers (deeper GNNs do not necessarily yield better performance)

Practical Advice & Tips

Training tips: Data & metrics

- Split dataset into train, validation, and test sets (avoid data leakage!)
- For self-supervised learning, carefully define negative samples
- Define metrics carefully (e.g., Is the data is balanced or imbalanced?)
 - Balanced: Receiver operating characteristic (ROC) curve
 - Imbalanced: Average precision (AP) score
- Start small (e.g., toy dataset) and then scale up
- Log everything (e.g., print statements, progress bars, model visualization software)

Training tips: Model evaluation

- Ensure that the model can overfit on training data (e.g., >90% ROC)
- Avoid over- or under-training the model (e.g., specify number of epochs, define early-stopping criteria)
- Evaluate hyperparameters on left-out validation set (e.g., grid search, random search) – *Don't be overwhelmed by all the possible parameters; start with learning rate! Consider using a learning rate scheduler.*
- Establish strong baseline models (e.g., consider domain-specific as well as classic machine learning models)
- Set a seed for code to ensure reproducibility
- Save models at critical points (e.g., new minimum loss, new maximum ROC)
- Make sure code *actually* works before requesting tons of resources (e.g., cluster)

Practical Advice & Tips

Common bugs in implementation

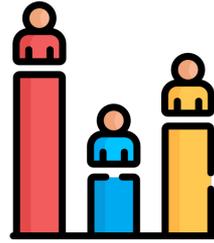
- Performance is random / opposite to what is expected
 - Edges are unintentionally shuffled during training
 - An imported function is re-indexing, and it is unaccounted for in our code
- Out-of-memory error on GPU
 - Implement minibatching or decrease batch size
 - Decrease model size (e.g., number of layers, number of attention heads)

Common model training issues

- Model has near-perfect performance on the validation/test set
 - Data leakage between train and validation/test set
- Model takes forever to start running
 - Minimize preprocessing steps done at launch
 - Consider loading only the necessary data (e.g., columns/rows in dataframe)
- Model takes a long time to converge
 - Increase learning rate
 - Apply normalization (e.g., batch norm, which allows us to increase learning rate too!)
- Model is overfitting
 - Apply dropout layer
 - Simplify model (e.g., remove layers)
 - Use early stopping

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Time for a poll question about...

OUR TUTORIAL

1. What is the most memorable thing about graph representation learning that you learned today?
Fill in the blank
2. What topic would you like us to cover in future iterations of this tutorial? *Fill in the blank*

ISMB 2022 Tutorial Feedback

Which tutorial did you attend? (If you attended more than one tutorial, you will * have the opportunity to submit a second survey)

- Tutorial IP1: Gene regulatory network inference from single-cell transcriptomics data
- Tutorial IP2: A practical introduction to the design, quantification, and analysis of

Please refer to:

docs.google.com/forms/d/e/1FAIpQLSftVbl5O-P6EidL-PBgmqjdVE9QX3SfsgGKqkX6DDxJzGvrfQ/viewform

- Tutorial VT1: Introduction to Python programming for bioscientists
- Tutorial VT2: Building Interactive Visualizations of Genomics Data with Gosling
- Tutorial VT3: Federated Learning in Biomedicine
- Tutorial VT4: Towards Precision Medicine with Graph Representation Learning
- Tutorial VT5: Computational analysis of antibody repertoires, with applications for therapeutic discovery
- Tutorial VT6: Online tools for visualizing RNA structure

Resources

■ Books & survey papers

- William Hamilton, *Graph Representation Learning* (morganclaypool.com/doi/abs/10.2200/S01045ED1V01Y202009AIM046)
- Li et al., Graph Representation Learning for Biomedicine (arxiv.org/abs/2104.04883)

■ Keynotes & seminars

- Michael Bronstein, “Geometric Deep Learning: The Erlangen Programme of ML” (ICLR 2021 keynote) (youtube.com/watch?v=w6Pw4MOzMuo)
- Broad Institute Models, Inference & Algorithms: Actionable machine learning for drug discovery; Primer on graph representation learning (youtube.com/watch?v=9YpTYdru0Rg)
- Stanford University (CS224W Lecture): Graph neural networks in computational biology (youtube.com/watch?v=_hy9AgZXhbQ)
- AI Cures Drug Discovery Conference (youtube.com/watch?v=wNXSkISMTw8)

■ Conferences & summer schools

- London Geometry and Machine Learning Summer School (logml.ai)
- Learning on Graphs Conference (logconference.github.io)

Resources

- **Software & packages**
 - PyTorch Geometric
 - NetworkX
 - Stanford Network Analysis Platform (SNAP)
- **Tutorials & code bases**
 - Pytorch Geometric Colab Notebooks (pytorch-geometric.readthedocs.io/en/latest/notes/colabs.html)
 - Zitnik Lab Graph ML Tutorials (github.com/mims-harvard/graphml-tutorials)
 - Stanford University's CS224 (web.stanford.edu/class/cs224w)
- **Datasets**
 - Precision Medicine Oriented Knowledge Graph (PrimeKG) (zitniklab.hms.harvard.edu/projects/PrimeKG)
 - Therapeutic Data Commons (TDC) (tdcommons.ai)
 - BioSNAP (snap.stanford.edu/biodata/)
 - Open Graph Benchmark (OGB) (ogb.stanford.edu)