Classification of Intestinal Gland Cell-Graphs Using Graph Neural Networks

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Why Graphs?

Pathologist consider morphological changes in tissue, spatial relationship between cell (sub-) types, density of certain cells etc.

→ Graphs are able to represent the geometrical and topological properties of colorectal glands

Graph Neural Networks (GNNs)

- **Message Passing (Graph Convolution):** Send message of features to all neighbors → update hidden state according to graph convolution type. More layers = larger neighborhood to collect information from
- **Read-out phase:** Compute vector representation of the whole graph v_G → used to perform classification

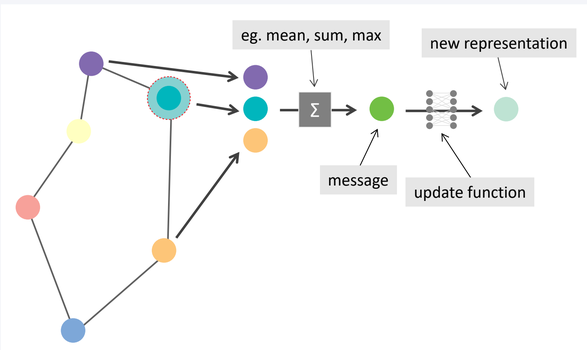

Fig. 1: Message passing phase

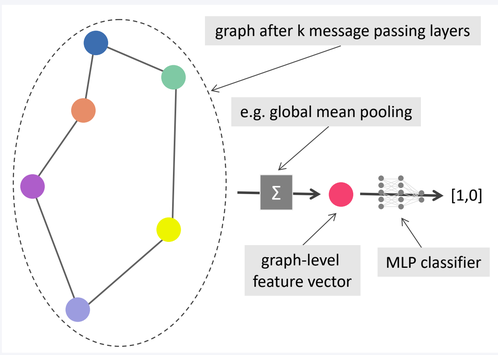

Fig. 2: Read-out and classification phase

Experimental Setup

- Graph convolutional layers: Graph Convolution Network (*GCN*), *GraphSAGE*, Graph Attention Networks (*GAT*), Edge Network (*enn*), Graph Isomorphism Network (*GIN*), 1-dimensional GNN (*1-GNN*)
- Compare two node feature sets: 4 features used by baseline versus full features set (33)
- 4-fold cross-validation
- Binary classification: normal or dysplastic gland

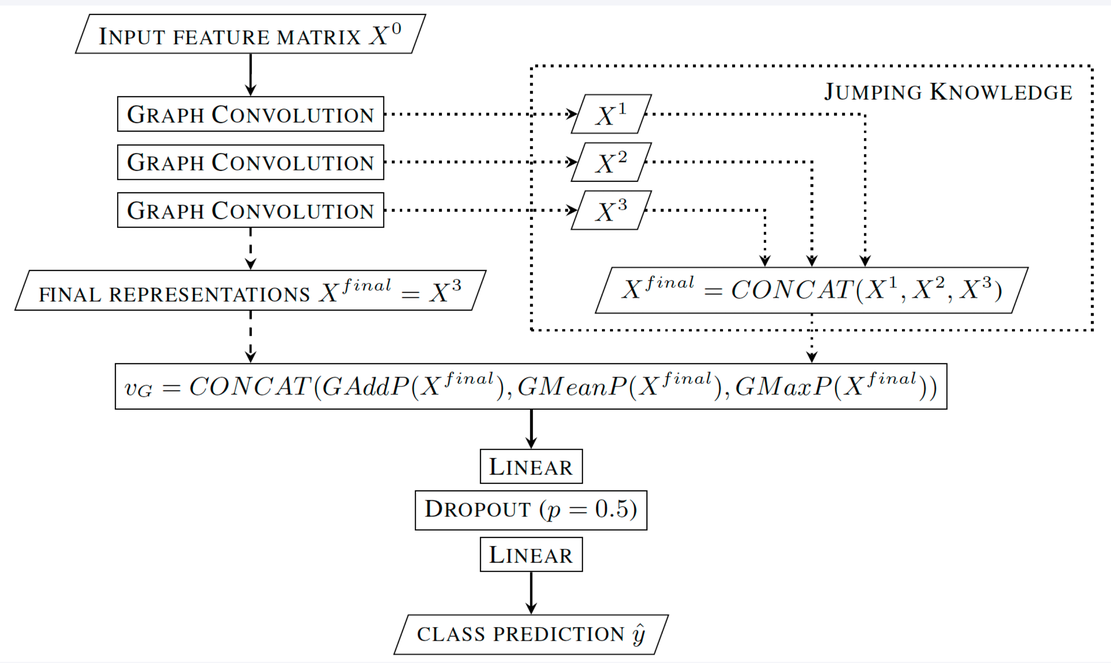

Fig. 3: Schematic overview of the used graph neural network architecture. The dotted arrows correspond to the setup with and without Jumping Knowledge, respectively.

pT1-Gland Graph Dataset

- 26 well-defined glands extracted from H&E stained images from 20 different patients (13 dysplastic, 13 normal) → 520 in total
- **Graph representations:** one node for each cell. Every node is connected to its spatially two closest neighbours.
- **33 node features** extracted using QuPath (based on the cytoplasm staining , cell, and nucleus)

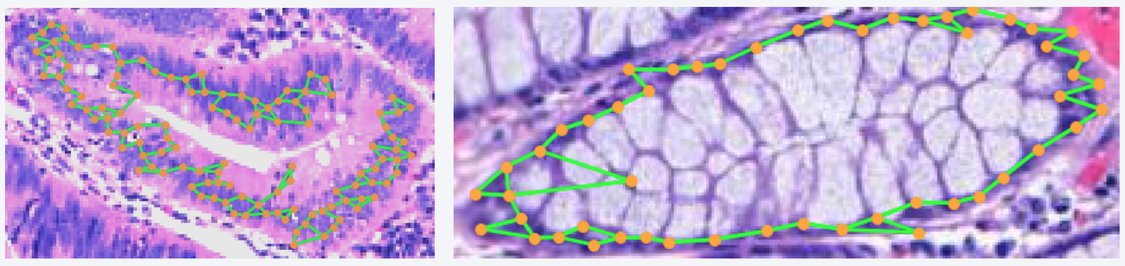

Fig. 2: Examples of cell-graphs in the pT1 Gland Graph dataset overlaid on the H&E image. Cells are represented as nodes in the graph (in orange) and are connected with edges (in green) based on the physical distance between them.

Results

Table 1: Average accuracy and standard deviation achieved by the different GNN architectures on the full and baseline node feature set, along with the Graph Edit Distance (GED) baseline and a additional CNN baseline (with and without image rotation data augmentation).

	# Node Features	
	4 (baseline)	33 (all)
1-GNN	**89.2 ± 3.8%**	94.6 ± 2.3%
GAT	85.5 ± 5.4%	94.3 ± 2.4%
GCN	85.5 ± 4.9%	94.5 ± 2.6%
GCN-JK	85.4 ± 4.5%	**94.8 ± 2.4%**
GIN	89.0 ± 4.1%	94.5 ± 2.6%
GraphSAGE	85.4 ± 4.5%	**94.8 ± 2.4%**
GraphSAGE-JK	85.1 ± 5.2%	94.7 ± 2.4%
enn	89.1 ± 3.7%	93.7 ± 3.0%
GED-Baseline[1]	83.3 ± 1.7%	n/a
CNN (VGG-16)	91.8 ± 5.5%	
CNN (VGG-16-Rotation)	92.0 ± 5.1%	

[1] Graph-based Classification of Intestinal Glands in Colorectal Cancer Tissue Images, Studer et. al., COMPAY workshop, MICCAI 2019

Conclusion

- Different types of GNNs achieve similarly good results
- GNNs can profit from the full 33 node feature set
- Beat SOTA results achieved with Graph Edit Distance (GED)

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github.com/waljan/GNNpT1

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