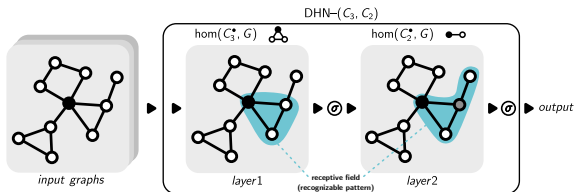


# Deep Homomorphism Network

Expressivity through stacking homomorphism layers

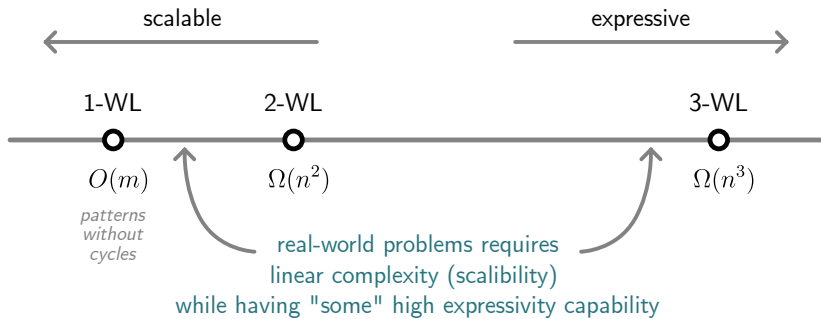


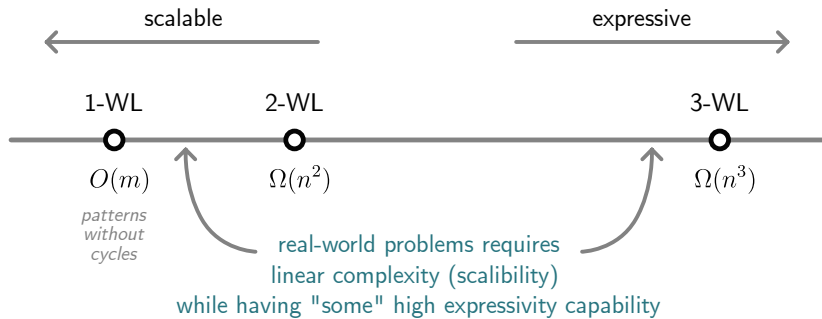
Takanori Maehara & Hoang NT

Roku & UTokyo

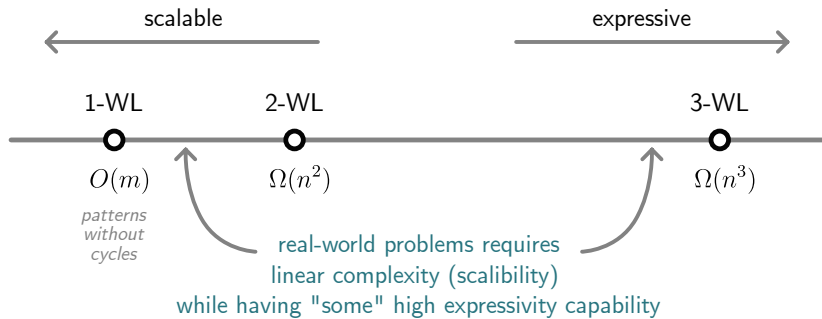
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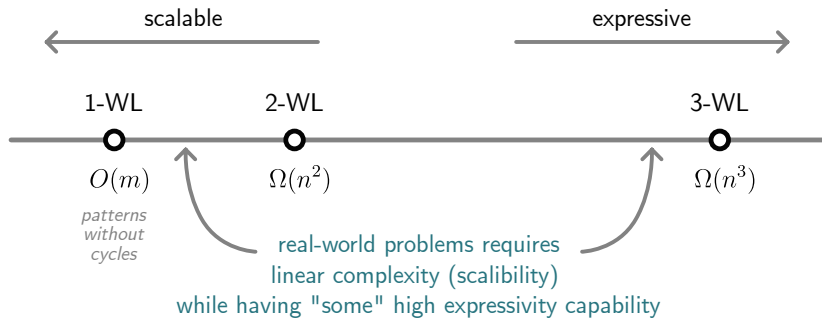




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  - ▶ Develop models that can detect patterns with cycles, but run in  $O(n)$  time on sparse graphs.
  - ▶ Analyze the expressivity of the multi-layers version of the proposed model.



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! Our proposal:

- ▶ Specify  $F$ 's collection of interest (cycles of lengths up to 6, cliques, etc.), then enumerate all these homomorphism mappings.
- ▶ Aggregate the transformed features along the mapping to get a single homomorphism convolution layer:

$$\text{hom}((F^\bullet, \mu), (G^\bullet, x)) = \sum_{\pi \in \text{Hom}(F^\bullet, G^\bullet)} \prod_{p \in V(F^\bullet)} \mu_p(x_{\pi(p)})$$



Let  $P^\ell$  be a series of patterns, and  $(G, x), (G', x')$  be inputs.

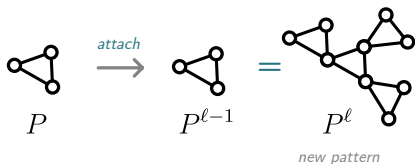
Theorem 1 (Main Theorem)

*$DHN(x) = DHN(x')$  iff  $\text{hom}(P^\ell, G) \neq \text{hom}(P^\ell, G')$ , where  $P^0$  is a singleton and  $P^\ell$  are patterns obtained by attaching  $P$  to  $P^{\ell-1}$ .*

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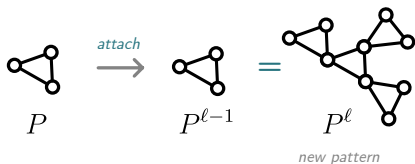




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- Stacking layers make the model *exponentially* expressive.
- DHN is a generalization of 1-WL when  $P$  is the single-edge.



- ! Complexity: DHN runs in the same time complexity as computing  $\text{hom}(P, G)$ , i.e.,  $O(n)$  if  $G$  is sparse and  $P$  is tree-like. This is true for real-world applications.

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- ! Implementation: Homomorphism mappings for each unit pattern can be precomputed and stored similar to edge list.

	#params	CSL	EXP	SR25	ENZYMES	PROTEINS
MPNN (4 layers)	27k	0	0	0	$54.6 \pm 4.5$	$72.0 \pm 4.0$
PPGN (4 layers)	96k	100	100	0	$58.2 \pm 5.7$	$77.2 \pm 3.7$
$\text{l}^2$ -GNN (4 layers)	143k	100	100	100	-	-
$\text{N}^2$ -GNN (4 layers)	355k	100	100	100	-	-
DHN- $(C_{2:4})$	5k	100	50	0	$64.3 \pm 5.5$	$76.5 \pm 3.0$
DHN- $(C_{2:5})$	7k	100	81	0	$63.7 \pm 5.4$	$77.0 \pm 3.2$
DHN- $(C_{2:10})$	27k	100	98	0	$58.0 \pm 5.3$	$78.5 \pm 2.5$
DHN- $(C_2K_{3:5})$	7k	100	50	53	$63.3 \pm 5.5$	$76.0 \pm 2.7$
DHN- $(C_{2:4}, C_2)$	8k	100	50	0	$64.4 \pm 5.9$	$77.1 \pm 2.8$
DHN- $(C_{2:5}, C_2)$	11k	100	99	0	$62.0 \pm 5.5$	$77.0 \pm 2.5$
DHN- $(C_{2:5}, C_{2:5})$	36k	100	99	0	$59.9 \pm 5.2$	$76.7 \pm 3.3$
DHN- $(C_{5:10}, C_2)$	27k	100	100	0	$63.5 \pm 6.1$	$78.2 \pm 3.3$
DHN- $(C_2K_{3:5}, C_2K_{3:5})$	36k	100	100	100	$57.5 \pm 6.6$	$77.4 \pm 3.4$

- ! Implication of our main theorem: Let  $k$  be the tree-width of pattern  $P$ . Then DHN is:
  - ▶ Strictly more expressive than 1-WL if  $P$  contains a single-edge pattern,
  - ▶ Incomparable with  $k'$ -WL for  $k' < k$ ,
  - ▶ Less expressive than  $k$ -WL
  - ▶ See our manuscript for comparison with other GNN models.
- ! Conclusion and future work:
  - ▶ Stacking homomorphism layers leads to powerful models
  - ▶ Future work will study how graph pooling and attention can help realizing the potential of DHN.

Thank you for listening!

