

Today: - what if my graph grows, what if too large?  
↳ graph limits: graphons

→ We understand the different ways a graph can be perturbed, and we know how to design stable GNNs.



- ↳ 1) but what if my graph grows?  
2) or, what if it is too large and I don't have enough resources to train on it?

(recall a GNN forward pass requires  $\Theta(LK|E|)$  complexity)

For 1): can we measure how close two large graphs are? <sup>b)</sup> If we can and if the GNN is continuous wrt this metric, then we are good. d)

what does it mean for graphs to be close?

↳ convergence to a common limit a)

For 2) can we sample a subgraph? c)

↳ random graph model

We have more questions than answers! Let's take them on one at a time.

a) What does it mean for graphs to be close?

We are statisticians/ probabilists; the prevailing perspective is that we consider graphs to be close if sampled subgraphs have similar distributions, or, equivalently, if they have similar subgraph counts

↳ can be measured using homomorphism densities

Recall from Lecture 11:

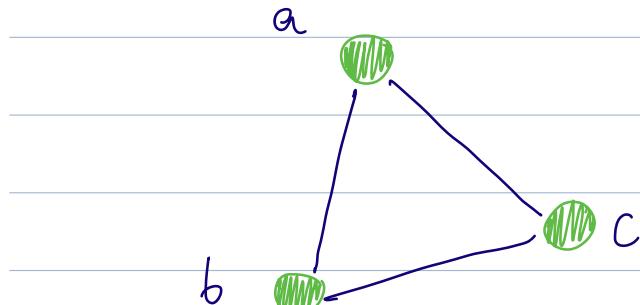
(DEF) Graph homomorphism: Let  $G = (V, E)$  &  $F = (V', E')$ . A homomorphism from  $F$  to  $G$  is a map  $\gamma: V' \rightarrow V$ :

$$(i, j) \in E' \Rightarrow (\gamma(i), \gamma(j)) \in E$$

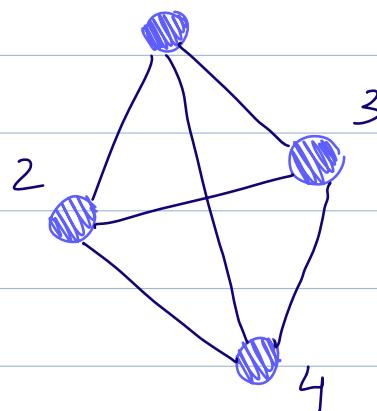
I.e., homomorphisms are adjacency preserving maps  
 $\text{of } F \hookrightarrow G$

E.g.:

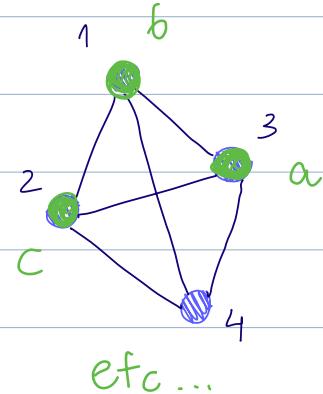
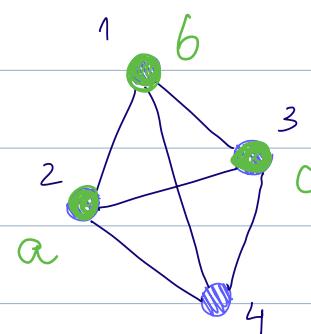
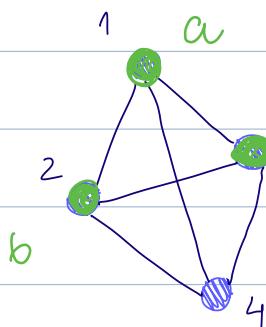
$F$



$1$        $G$



Homomorphisms from  $F$  to  $G$ :



etc...

1

2

a

3

b

c

4

...  
.

(6 in total)

(plus other permutations

of a,b,c) (6 total)

1 a

2

b

3

c

4

1 a

2

b

3

c

4

II

II

We will denote the total number of homomorphisms  
 from  $F$  to  $G$   $\text{hom}(F, G)$ . In the example,  
 $\text{hom}(F, G) = 24$

(DEF) Homomorphism density: the hom. density from  $F$  to  $G$ ,  
 denoted  $t(F, G)$  is:

$$t(F, G) = \frac{\text{hom}(F, G)}{|V|^{|V'|}}$$

$$\text{In the example, } t(F, G_1) = \frac{24}{4^3} = \frac{3}{8}$$

$\Rightarrow$  For now, we will say two graphs  $G_1$  &  $G_2$  are close if, for all motifs  $F$  (undirected, unweighted graphs, w/ one edge per node pair & no self loops),  $t(F, G_1) \approx t(F, G_2)$

$\rightarrow$  Convergent graph sequences & graphons (Lovász, Chayes, Borgs, Vesztergombi)  $\cup$  2008 onwards

(DEF) Let  $(G_n)_n$  be a graph sequence such that  $\lim_{n \rightarrow \infty} t(F, G_n)$  exists for all motifs  $F$ .

Then, this sequence is convergent and its limit is given a graphon.

(DEF) A graphon is a symmetric, bounded, measurable function  $w: [0, 1]^2 \rightarrow [0, 1]$   
 $([0, 1] \times [0, 1])$

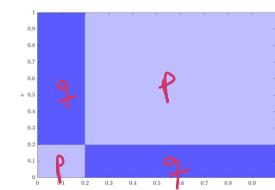
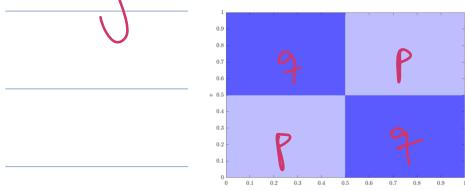
I.e., it is a bounded kernel

Obs. 1: A more general definition is  $w: \mathcal{L} \times \mathcal{L} \rightarrow [0, 1]$  where  $\mathcal{L}$  is some sample space endowed with some probability measure  $f$ . But, since we can always map  $\mathcal{L}$  into  $[0, 1]$  using a measure-preserving map (as long as CDF of  $f$  is strictly monotone  $\rightarrow$  exercise to verify), we'll stick with  $[0, 1]$  as our node sample space.

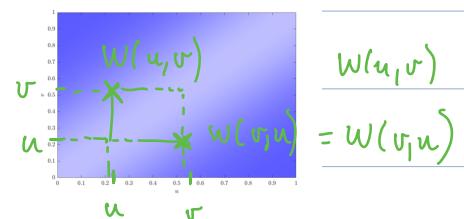
Obs. 2: The codomain of  $w$  may be  $[0, B]$ ,  $B < +\infty$ , but it is typical to have  $B = 1$  since  $w(x, y)$  often represents a probability.

The easiest way to think of a graphon is as a graph with an uncountable number of nodes  $u \in [0, 1]$ , and edges  $(u, v)$  with weights  $w(u, v)$ .

E.g.



$$w(u, v) = \exp\left(\frac{(u-v)^2}{\sigma^2}\right)$$



## (DEF) Graphon homomorphism density

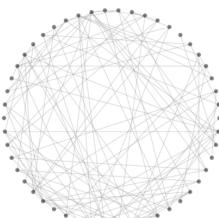
The density of homomorphisms from a graph motif  $F = (V', E')$  to a graphon  $W$  is denoted  $t(F, W)$  and defined as:

$$t(F, W) = \iint_{[0,1]^{|V'|} \times [0,1]^{|E'|}} \prod_{(i,j) \in E'} W(u_i, u_j) \prod_{i \in V'} du_i.$$

If  $W(u_i, v) < 1 \wedge u_i, v$ ,  $t(F, W)$  can be interpreted as the probability of sampling the motif  $F$  from the graphon  $W$ .

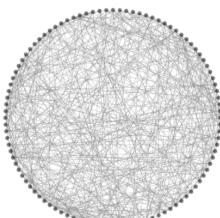
$n \rightarrow \infty$        $(G_n)_n$  is a conv.  
 $t(F, G_n) \rightarrow t(F, W) \iff$  graph sequence w/  
 $\forall F$       limit  $W$

E.g.:  $G_{50}$



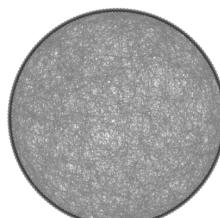
(a) 50 nodes

$G_{100}$



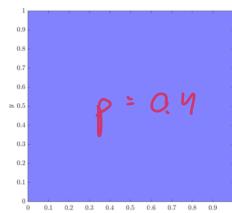
(b) 100 nodes

$G_{200}$



(c) 200 nodes

$W$



(d) Graphon

This notion of convergence is called left convergence as it deals with left homomorphisms  $t(F, G_n)$ ,  $t(F, w)$

This is not the only way to define/identify (dense) convergent graph sequences. Another definition based on the convergence of min-cuts (micro-canonical ground state energy in physics) exists, based on right homomorphisms ( $t(G_n, F)$ ,  $t(w, F)$ ). For dense graphs, left & right convergence are equivalent.

b) Can we measure how close two large graphs are?

While  $t(F, G)$  gives us a way to define convergence, it is difficult to use it to measure the distance between graphs, as we'd have to compute  $t(F, G_1)$  &  $t(F, G_2)$  for all motifs  $F$ .

## ► Cut distance for graphs

① Graphs  $G$  &  $G'$  with same  $n$  & same node sets  $V, V'$  (i.e., same node labeling)

We define two distances:

$L_1$  norm or edit distance:  $d_1(G, G') = \|A - A'\|_1$ ,

where  $A, A'$  are the (unweighted) adjacencies of  $G, G'$

Cut distance:  $d_{\square} = \|A - A'\|_{\square}$ ,

where  $\|\cdot\|_{\square}$  is the cut norm:

$$\|B\|_{\square} = \max_{S \subseteq [n], T \subseteq [n]} \left| \sum_{s \in S, t \in T} B_{ts} \right|$$

I.e., given a (graph) matrix  $B$ ,  $\|B\|_{\square}$  is "the size" (total number of edges, or sum of edge weights) of the max cut.

② graphs  $G$  &  $G'$  with the same number of nodes:

Cut distance:  $\hat{\delta}_\square(G, G') = \min_{P \in P} \|A - P^T A' P\|_\square$

I.e., we must look at all possible permutations of the nodes of  $G'$  (while fixing the node labels in  $G$ )

③ Graphs  $G_n$  &  $G_m$  with  $\neq$  number of nodes ( $n \neq m$ )

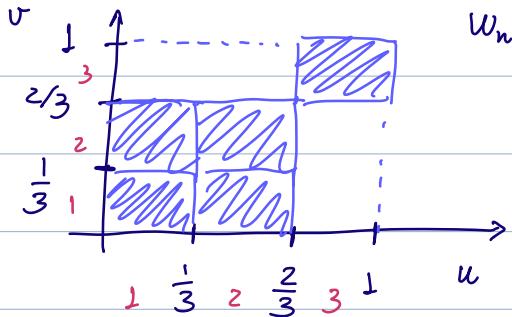
Define  $W_n(u, v) = \sum_{i=1}^n \sum_{j=1}^m A_{ij} I(u \in I_i) I(v \in I_j)$

where  $I$  is the indicator function and  $I_j$  is defined as:

$$I_j = \begin{cases} \left[ \frac{j-1}{n}, \frac{j}{n} \right], & 1 \leq j \leq n-1 \\ \left[ \frac{n-1}{n}, 1 \right], & j = n \end{cases}$$

E.g.:

$$A_n = \begin{bmatrix} 1 & 1 & 3 \\ 1 & 1 & 0 \\ 3 & 0 & 0 \end{bmatrix}$$



w<sub>n</sub> is called the graphon induced by A<sub>n</sub>.

Back to the cut distance:

Using transformation (\*), we can represent both  $A_n$  and  $G_m$  as kernels on  $[0,1]^2$ , so they are compatible objects. But now we need a notion of cut norm for kernels.

Cut norm: Let  $w$  be a kernel in  $[0,1]^2$ .

Its cut norm is defined as:

$$\|w\|_{\square} = \sup_{S,T \subseteq [0,1]} \left| \iint_{S \times T} w(u,v) du dv \right|$$

We're not done yet! We need to take into account "node relabelings" (permutations of  $I_1, I_2, \dots$ ).

So far two Kernels (graphons), we define the cut metric:

$$S_{\square}(w, w') = \inf_{\phi} \|w^{\phi} - w'\|_{\square}$$

where  $w^{\phi}(u, v) = w(\phi(u), \phi(v))$  and  $\phi$  are measure-preserving bijections.