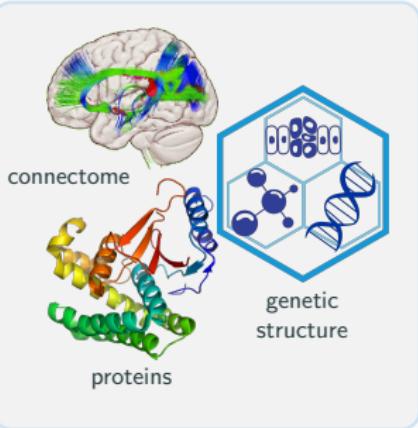


SUSAN: The Structural Similarity Random Walk Kernel

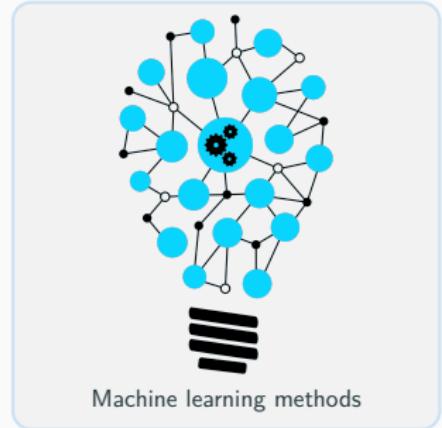
Janis Kalofolias, Pascal Welke, Jilles Vreeken



Comparing graphs

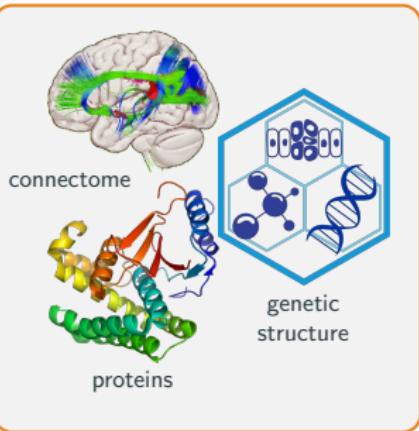


Applications



Standard Tools

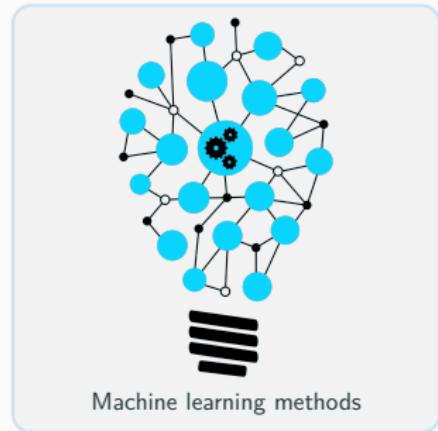
Comparing graphs



Applications

Classification, Regression,
Clustering, Dim. Reduction

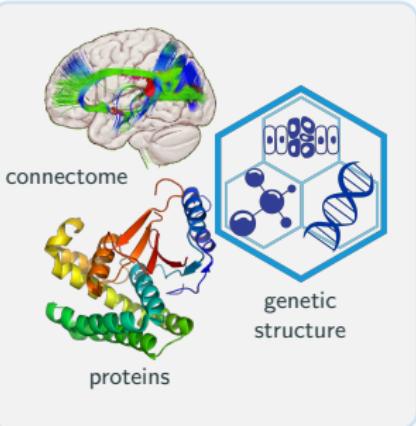
...



Machine learning methods

Standard Tools

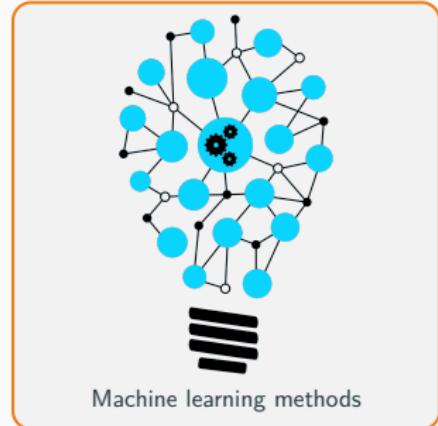
Comparing graphs



Applications

Classification, Regression,
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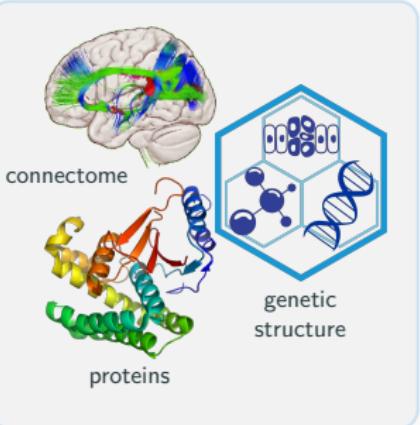


Standard Tools

SVM, Logistic,
K-Means, PCR

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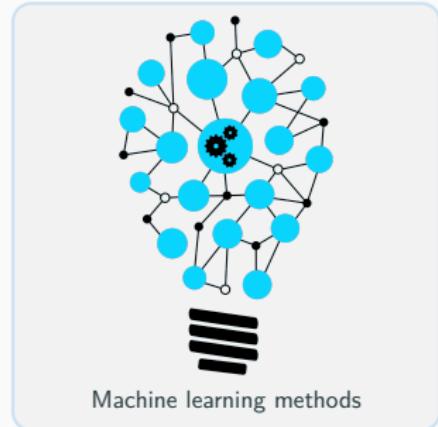
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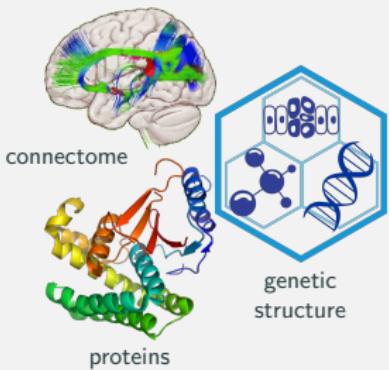
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...

Can we apply standard tools on graphs?

Comparing graphs



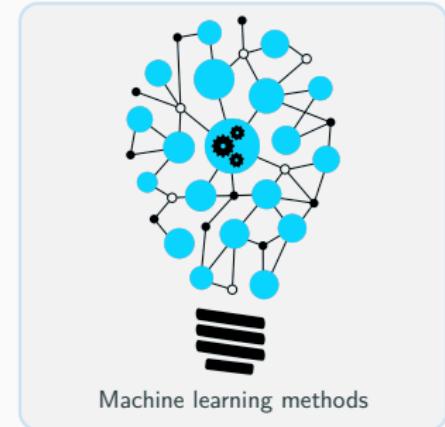
Applications

Classification, Regression,
Clustering, Dim. Reduction

...

Non-vectorial data

Can we apply standard tools on graphs?



Machine learning methods

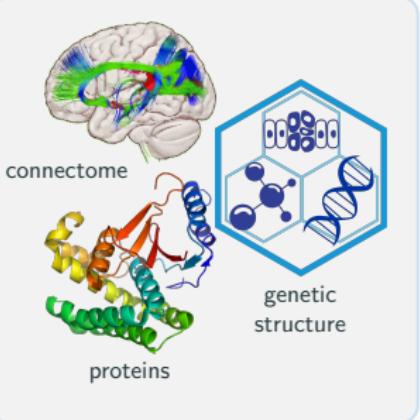
Standard Tools

SVM, Logistic,
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...

Need vector data

Comparing graphs



Applications

Classification, Regression,
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Non-vectorial data



Standard Tools

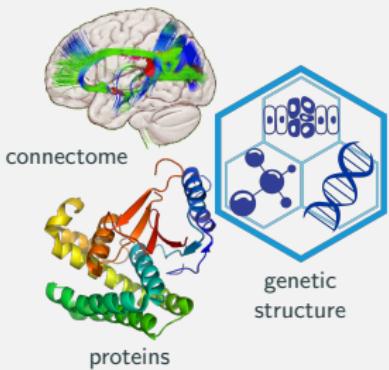
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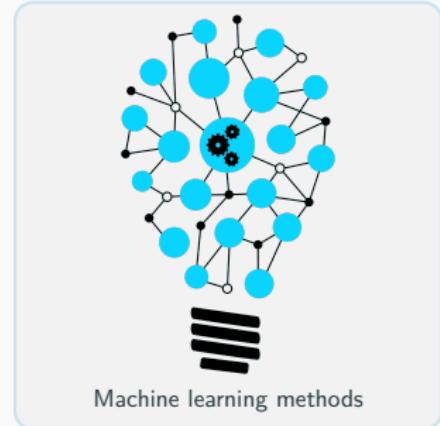
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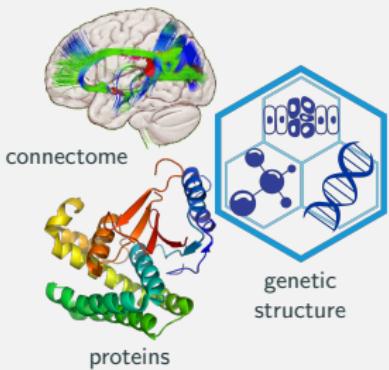
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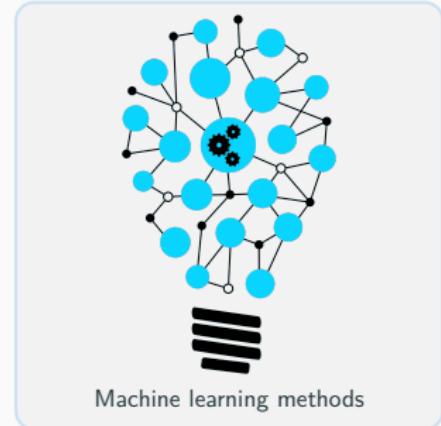
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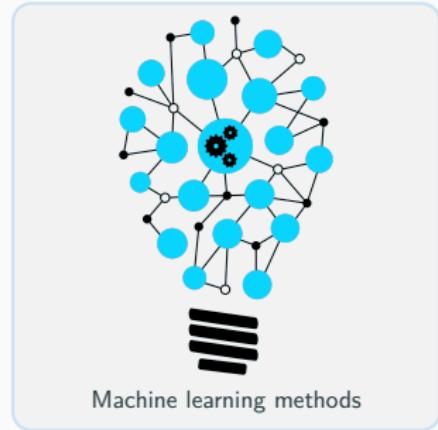
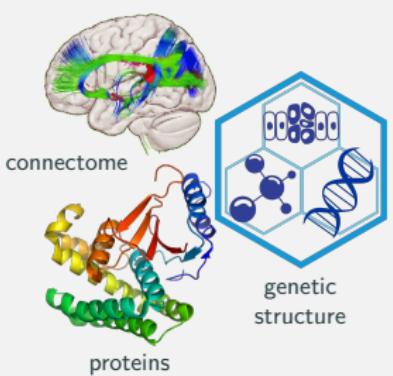
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...

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Can we apply standard tools on graphs?

⇒ Use a kernel on graphs

How do kernels compare graphs?



How do kernels compare graphs?



Goal: Can we define something like $\langle G_1, G_2 \rangle$?



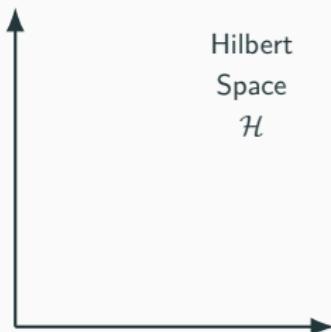
How do kernels compare graphs?



Goal: Can we define something like $\langle G_1, G_2 \rangle$?



Kernels define a space \mathcal{H}
with $\langle \cdot, \cdot \rangle$ and mapping function ϕ



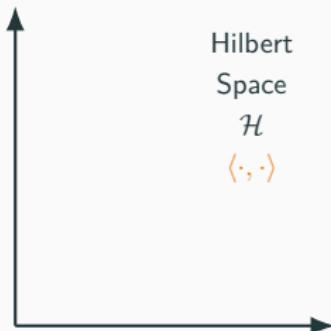
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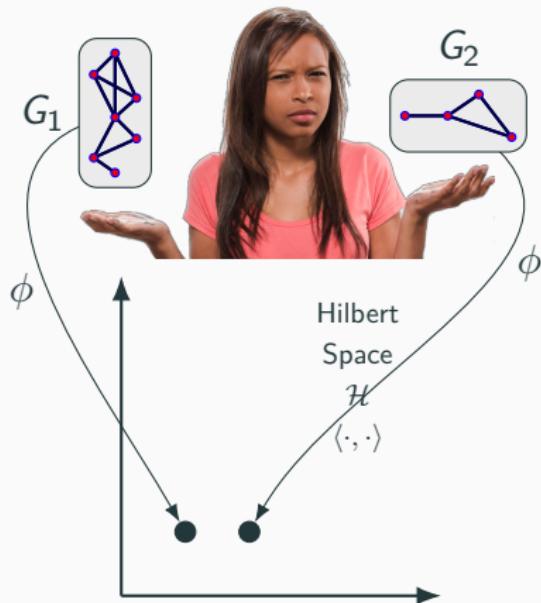
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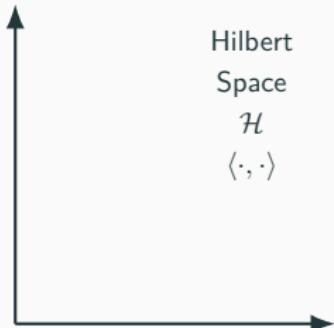


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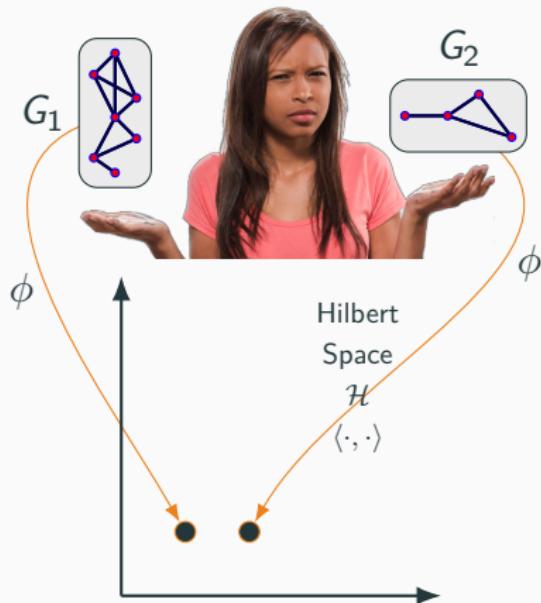
Kernels define a space \mathcal{H}
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⇒ Use as graph similarity
 G_1 , G_2

How do kernels compare graphs?



Goal: Can we define something like $\langle G_1, G_2 \rangle$?



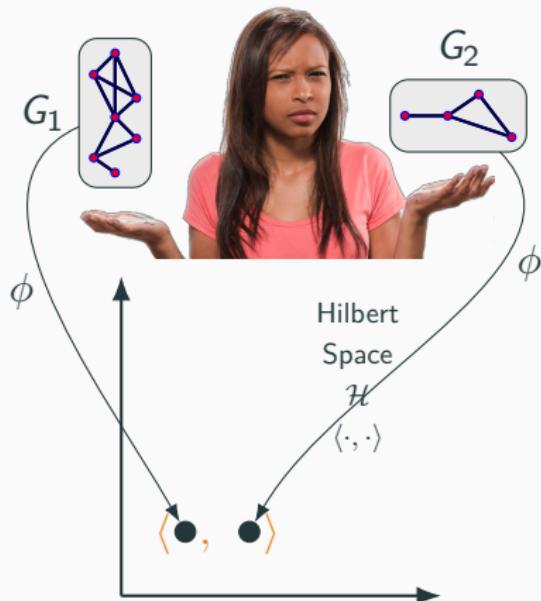
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⇒ Use as graph similarity
 $\phi(G_1), \phi(G_2)$

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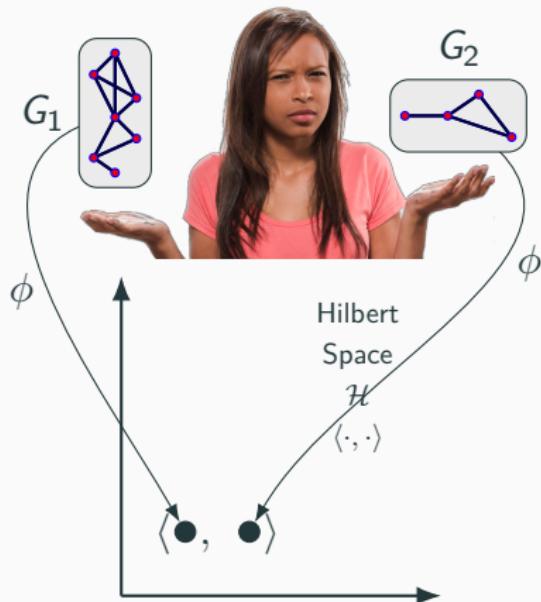
⇒ Use as graph similarity

$$\langle \phi(G_1), \phi(G_2) \rangle_{\mathcal{H}}$$

How do kernels compare graphs?



Goal: Can we define something like $\langle G_1, G_2 \rangle$?



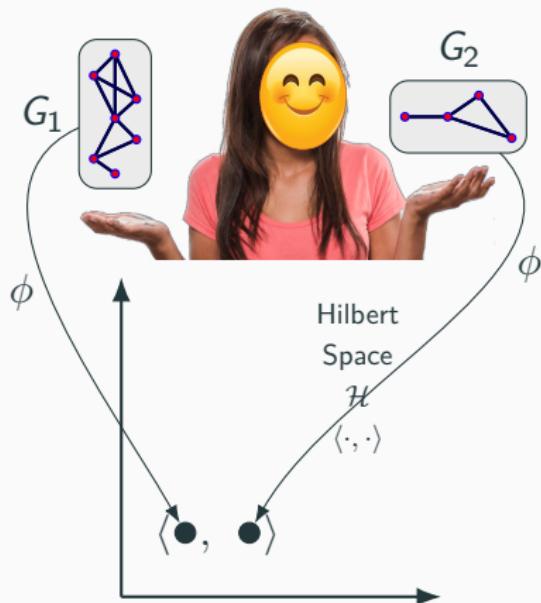
Kernels define a space \mathcal{H}
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⇒ Use as graph similarity
 $k(G_1, G_2) := \langle \phi(G_1), \phi(G_2) \rangle_{\mathcal{H}}$

How do kernels compare graphs?



Goal: Can we define something like $\langle G_1, G_2 \rangle$?



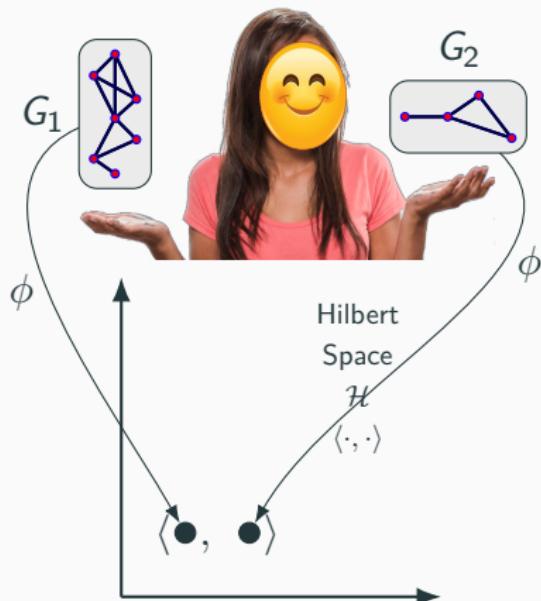
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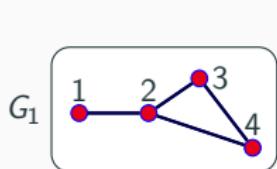
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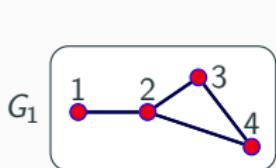
We focus on Random Walk kernels

Random Walk (Reproducing) Kernels

[Gärtner et al., 2003]

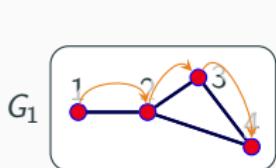


Goal: Count graph walks



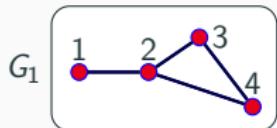
Goal: Count graph walks

ex: 3-step walk: (1, 2, 3, 4)



Goal: Count graph walks

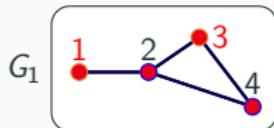
ex: 3-step walk: $(1, 2, 3, 4)$



Goal: Count graph walks

1-step walks from 1, 3?

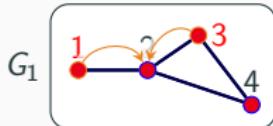
$$\underbrace{\begin{bmatrix} 0 \\ 2 \\ 0 \\ 1 \end{bmatrix}}_{x_1} = \underbrace{\begin{bmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 1 & 1 & 0 \end{bmatrix}}_A \underbrace{\begin{bmatrix} 1 \\ 0 \\ 1 \\ 0 \end{bmatrix}}_{x_0}$$



Goal: Count graph walks

1-step walks from 1, 3?

$$\underbrace{\begin{bmatrix} 0 \\ 2 \\ 0 \\ 1 \end{bmatrix}}_{x_1} = \underbrace{\begin{bmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 1 & 1 & 0 \end{bmatrix}}_A \underbrace{\begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix}}_{x_0}$$



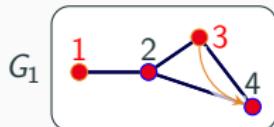
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1-step walks from 1, 3?

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Random Walk (Reproducing) Kernels

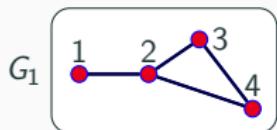
[Gärtner et al., 2003]



Goal: Count graph walks

1-step walks from 1, 3?

$$\underbrace{\begin{bmatrix} 0 \\ 2 \\ 0 \\ \textcolor{orange}{1} \end{bmatrix}}_{x_1} = \underbrace{\begin{bmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 1 & \textcolor{orange}{1} & 0 \end{bmatrix}}_A \underbrace{\begin{bmatrix} 1 \\ 0 \\ 1 \\ 0 \end{bmatrix}}_{x_0}$$



Goal: Count graph walks

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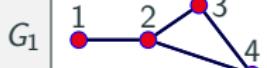
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k -step walks from x_0 ?

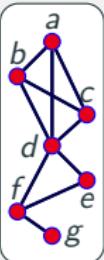
$$x_k = A^k x_0$$



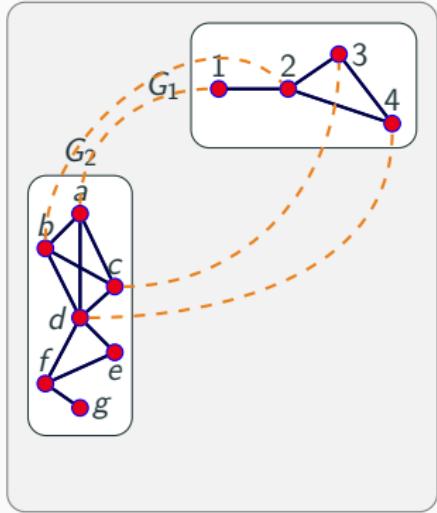
Goal: Count graph walks



G_2



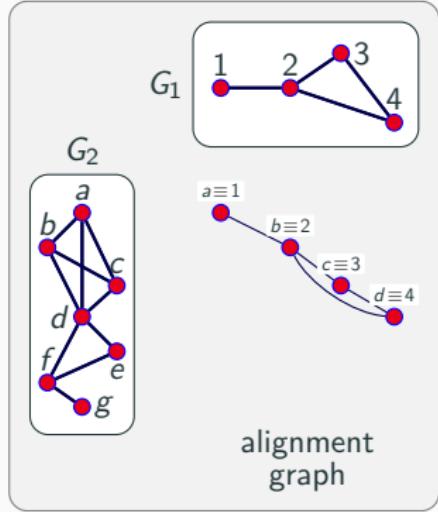
But: in 2 graphs?



Goal: Count common walks

But: in 2 graphs?

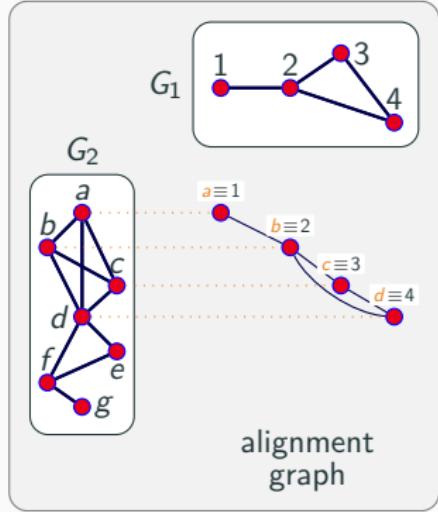
- Assume vertex alignment
e.g.: $a \equiv 1, b \equiv 2, c \equiv 3, d \equiv 4$



Goal: Count common walks

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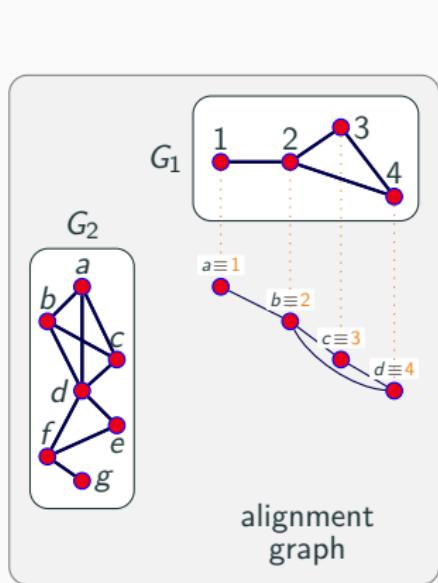
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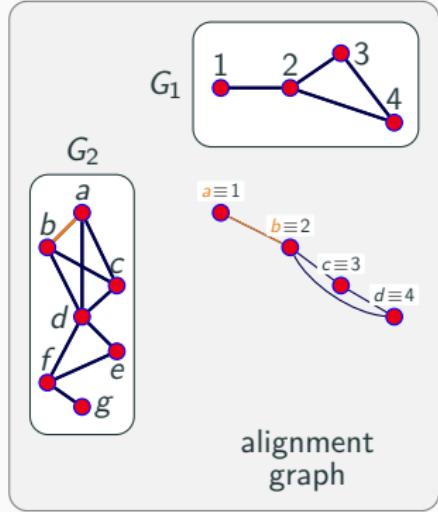
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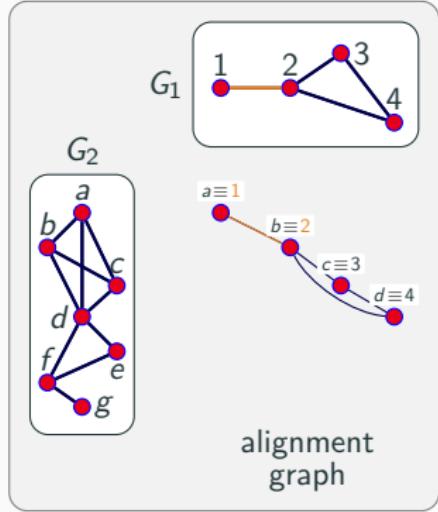
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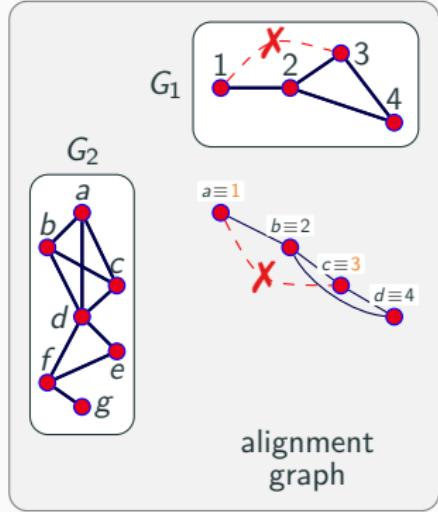
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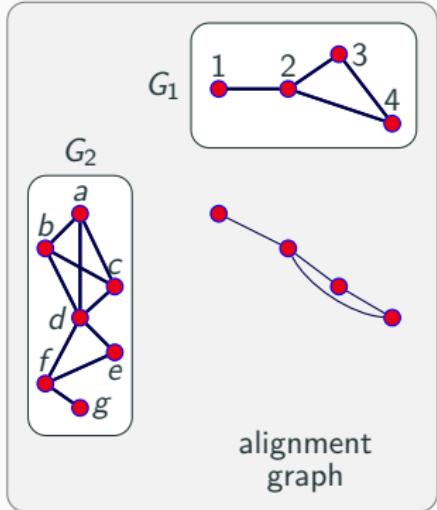
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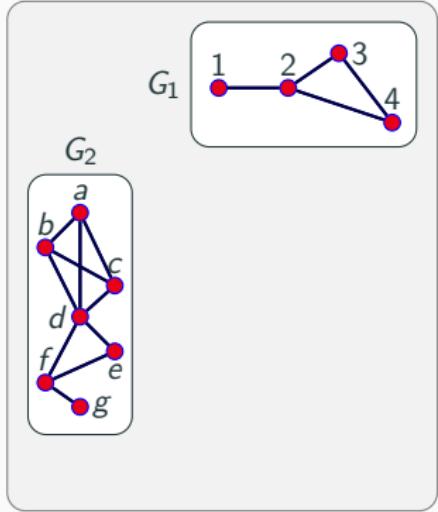
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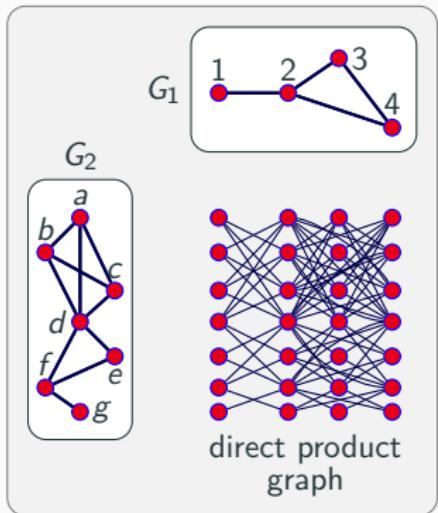


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But: Alignments are rarely available

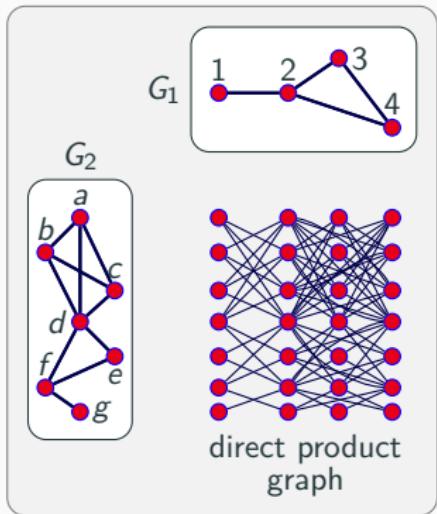


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⇒ Use all possible alignments



Direct product graph:

$$A_x = A \otimes A'$$

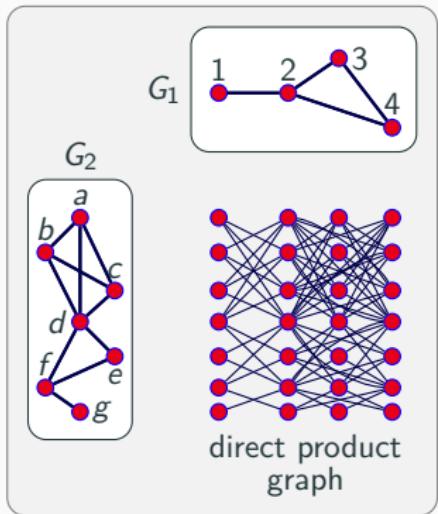


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Direct product graph:

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$$A_x x_x = (Ax) \otimes (A'x')$$

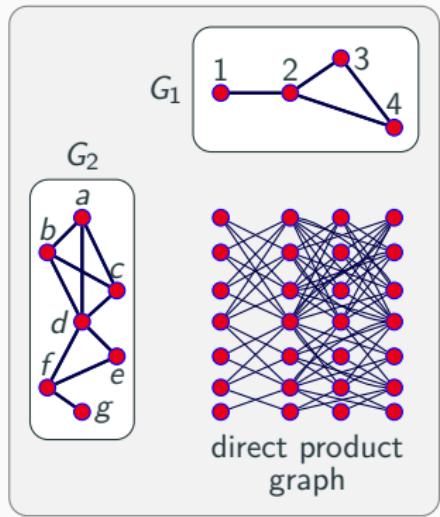


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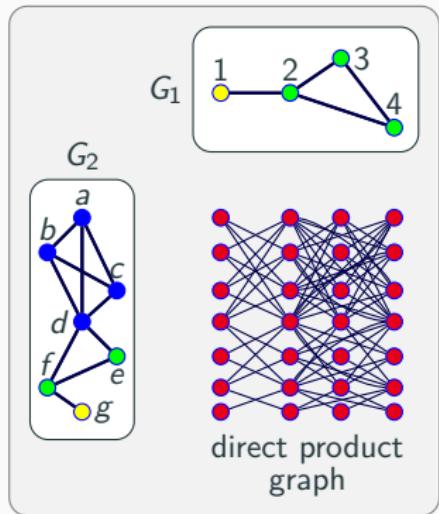
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Goal: Count common walks

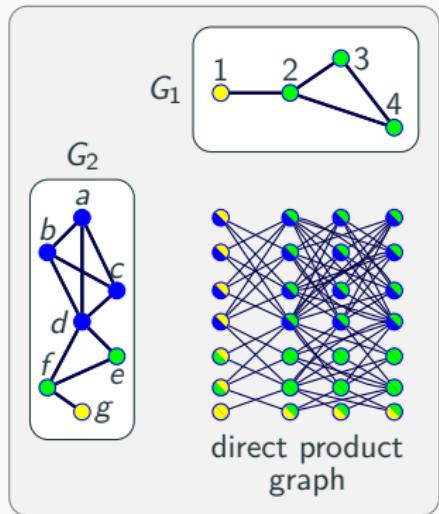
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But: Alignments are rarely available

⇒ Use all possible alignments

But: If vertices are not similar?

⇒ Not all alignments equally good

Are all vertex alignments equally good?

- Dissimilar vertices can be noisy
- Do not contribute to similarity

Are all vertex alignments equally good?

- Dissimilar vertices can be noisy \implies Only match similar vertices
- Do not contribute to similarity

Are all vertex alignments equally good?

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Labeled vertices



✓ same label ⇒ similar vertices

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- ✓ same label ⇒ similar vertices
- ✗ G_2 has no O. What now?
- ✗ How close is C to H?

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Labeled vertices



- ✓ same label ⇒ similar vertices
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Unlabeled graphs

- ✓ many similarity measures
- ✗ not always clear or easy

Are all vertex alignments equally good?

- Dissimilar vertices can be noisy
 - Do not contribute to similarity
- ⇒ Only match similar vertices

Labeled vertices



- ✓ same label ⇒ similar vertices
- ✗ G_2 has no O . What now?
- ✗ How close is C to H ?

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We seek a vertex partitioning

- structurally aware
- efficient to compute
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We propose to use
⇒ core decomposition

Core decomposition

Definition (k -core of graph G)

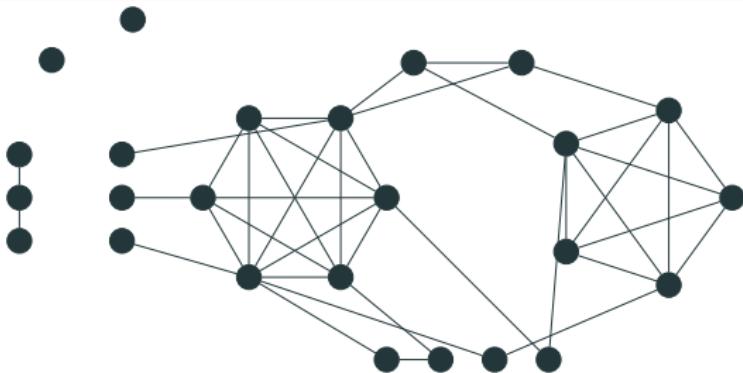
A maximal subgraph with vertices of degree at least k .

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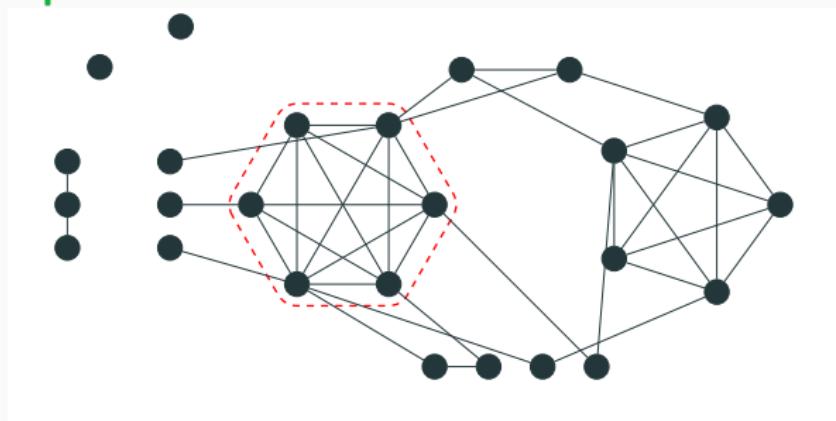


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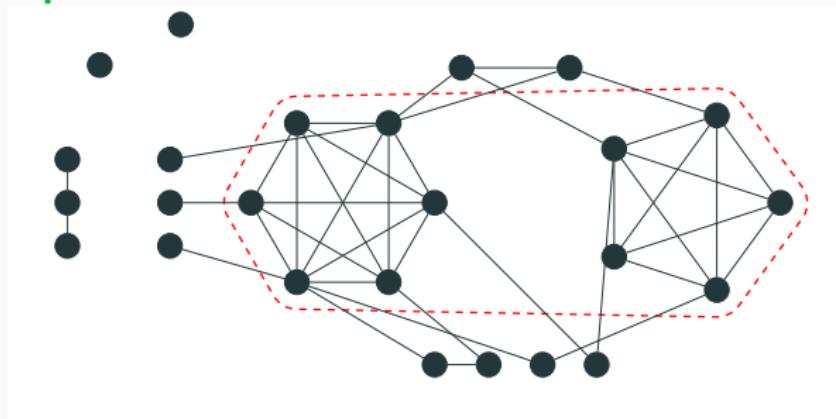


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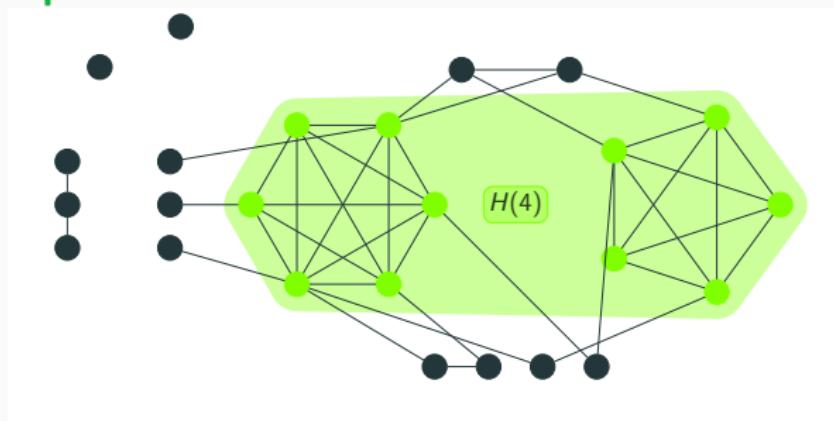


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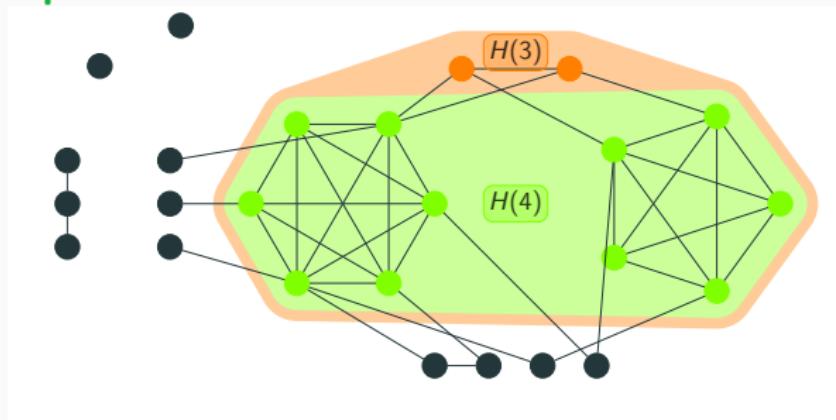


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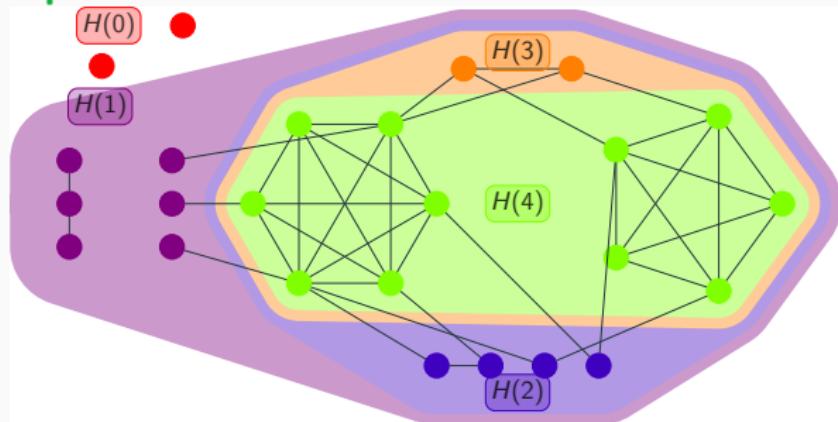


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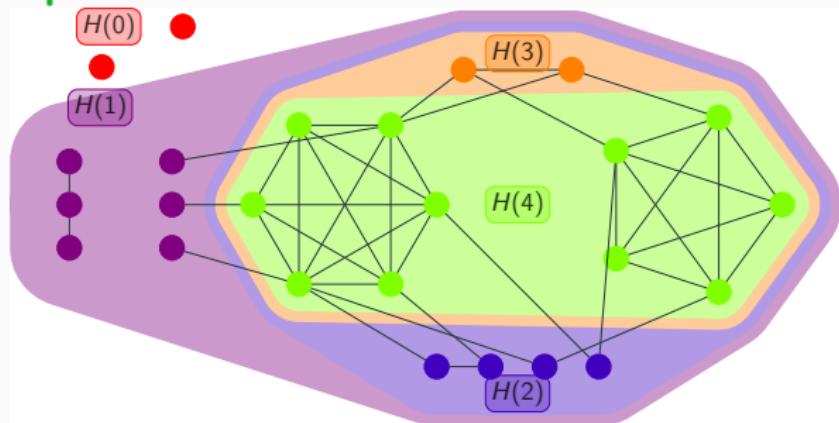


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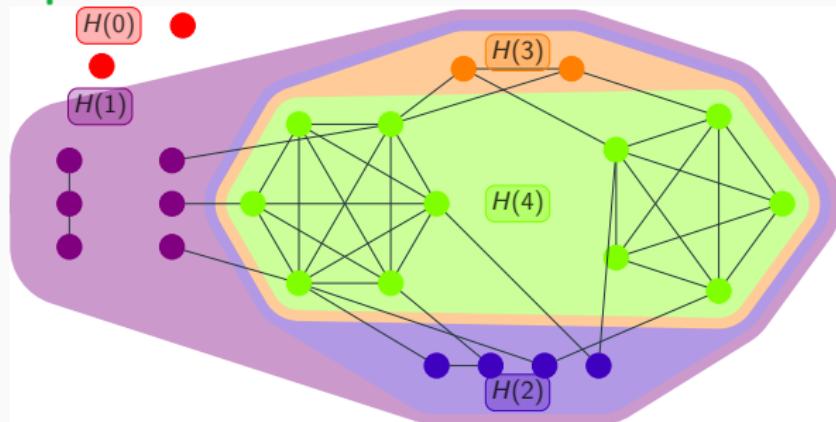
Decomposition: $\kappa : V \rightarrow \mathbb{N}$

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Definition (vertex coreness)

$$\kappa(u) := \max_{u \in H(k)} k$$

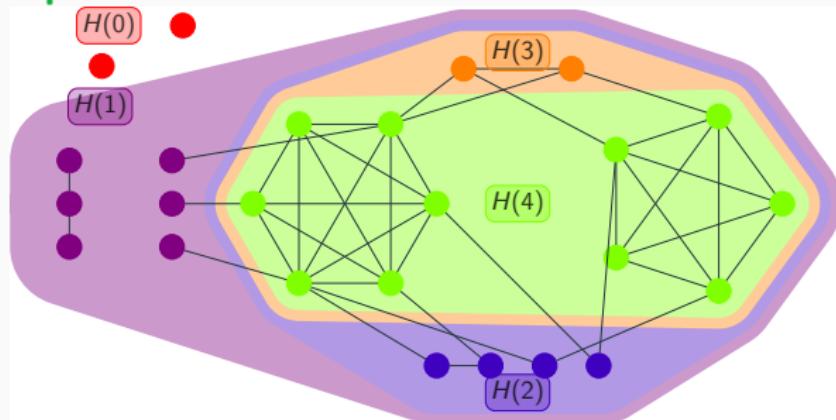
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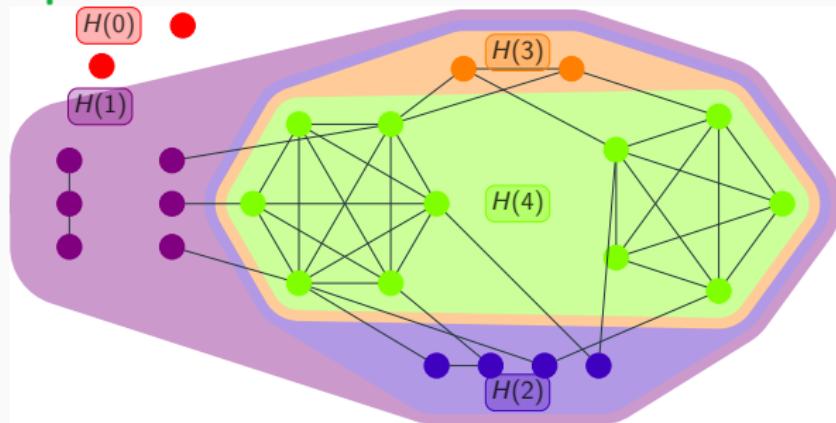
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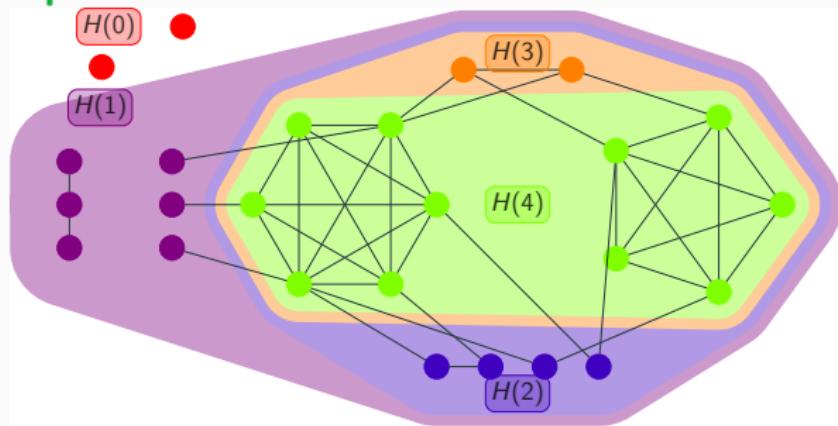
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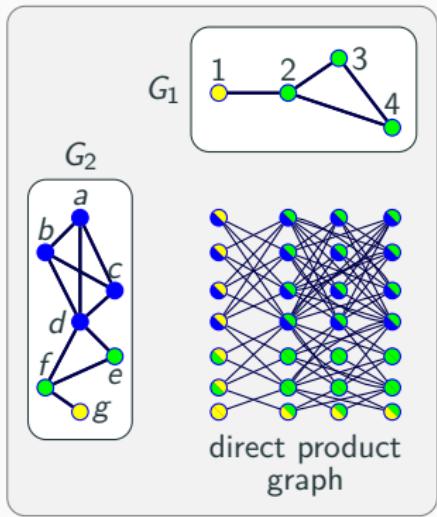
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- Needs only $O(n)$. [Batagelj and Zaversnik, 2003]
- Intuitive comparison between labels

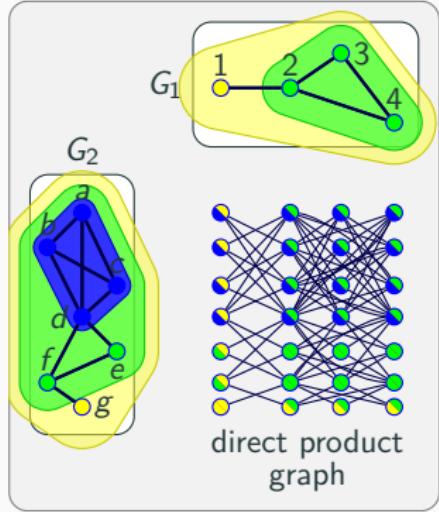
Random Walk (Reproducing) Kernels

[Gärtner et al., 2003]



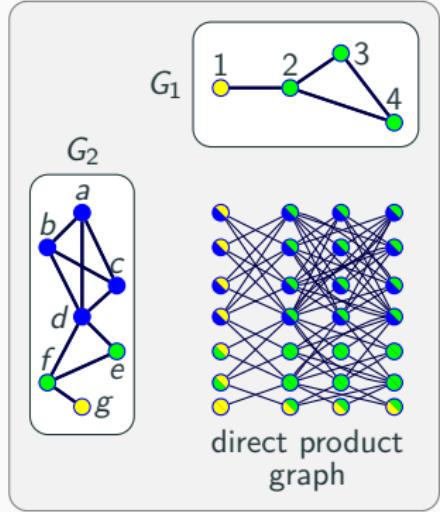
Goal: Count **similar** walks





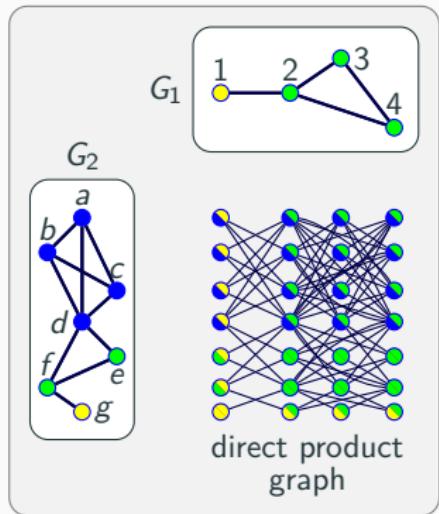
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and/or existing labels



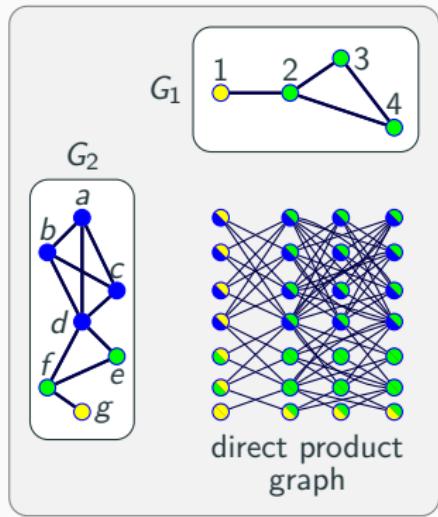
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Goal: Count similar walks

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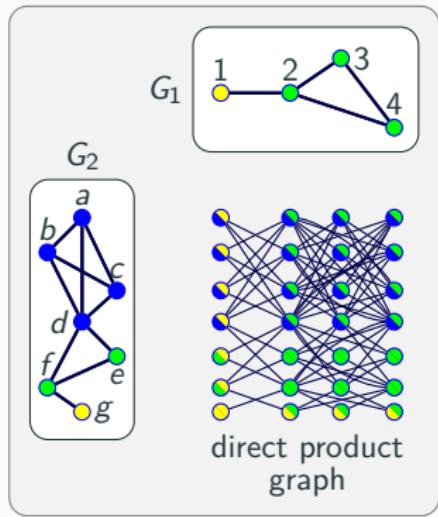
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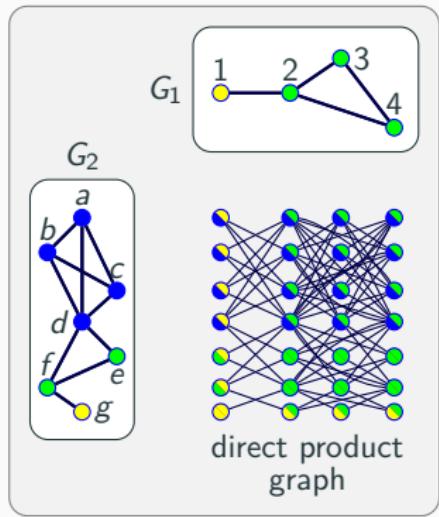
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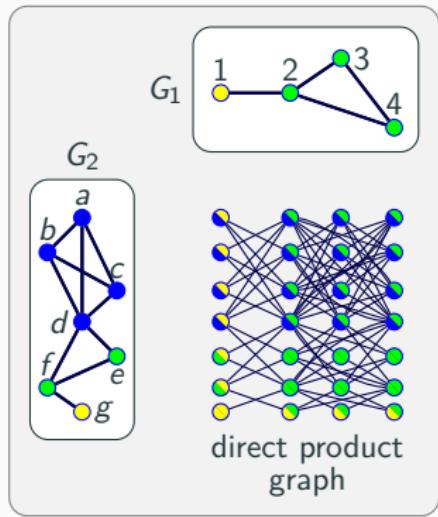


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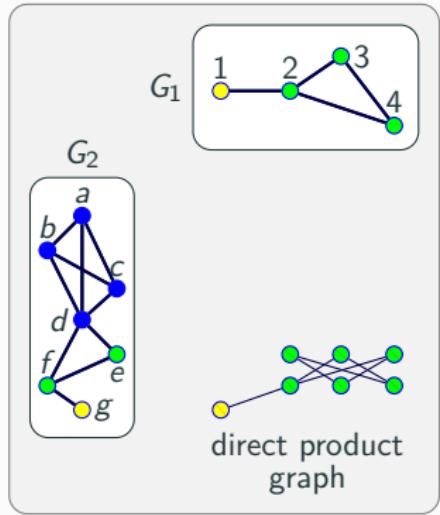
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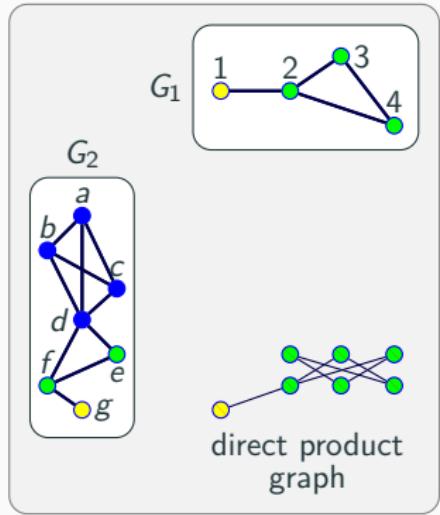
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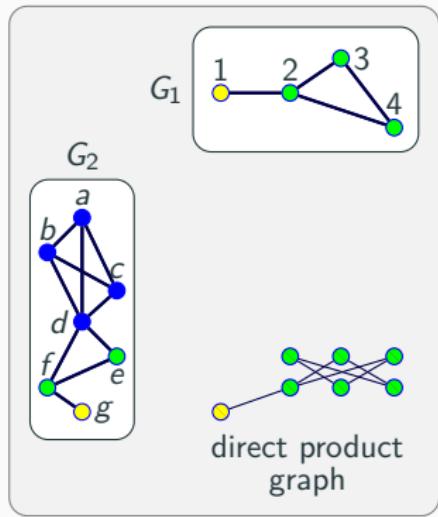


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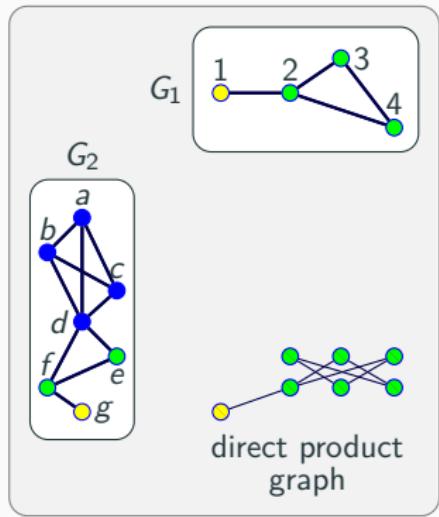


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e.g.: 0,0.5,1,1.5,2



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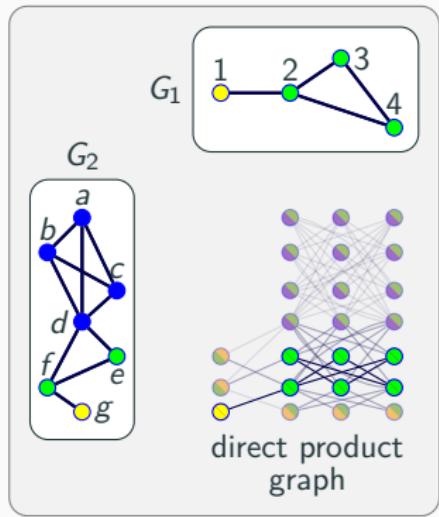


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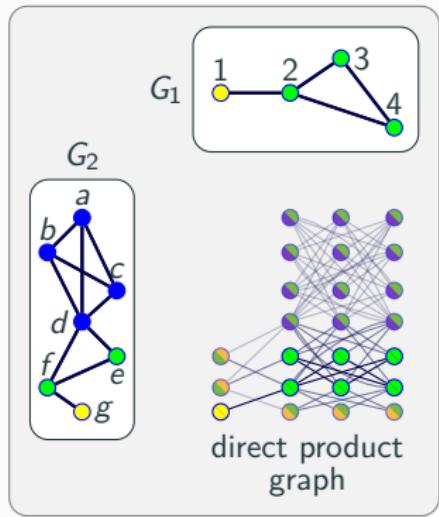


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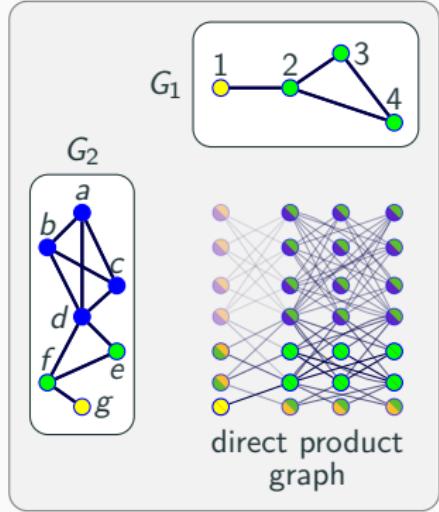
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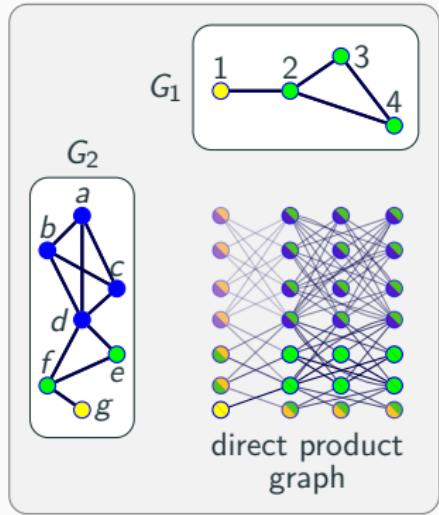
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Computing the Kernel II

Finally: sum # common walks:

- of any # steps (with weight μ_n)
- from each vertex to every other

$$k(G_1, G_2) = \mathbf{e}^\top \underbrace{\sum_{n=0}^{\infty} \mu_n \mathbf{A}_x^n}_{\mathbf{e}} \mathbf{e}$$

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But: How do we compute the MV operations efficiently?

To compute SUSAN efficiently

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Lemma

The MV operator for SUSAN with bandwidth δ is computable as

$$\mathbf{A}_x x = \mathbf{T} \odot (\mathbf{A}''(\mathbf{T} \odot \mathbf{X})\mathbf{A}'^\top)$$

for \mathbf{T} block banded with constant blocks and bandwidth δ , time

$$O((\delta + 1)(n' + n'')b^2)$$

for b the largest core size and n' , n'' the vertex numbers of G' , G'' .

To compute SUSAN efficiently

- we decompose the contribution of each graph

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- and reduce computational complexity.

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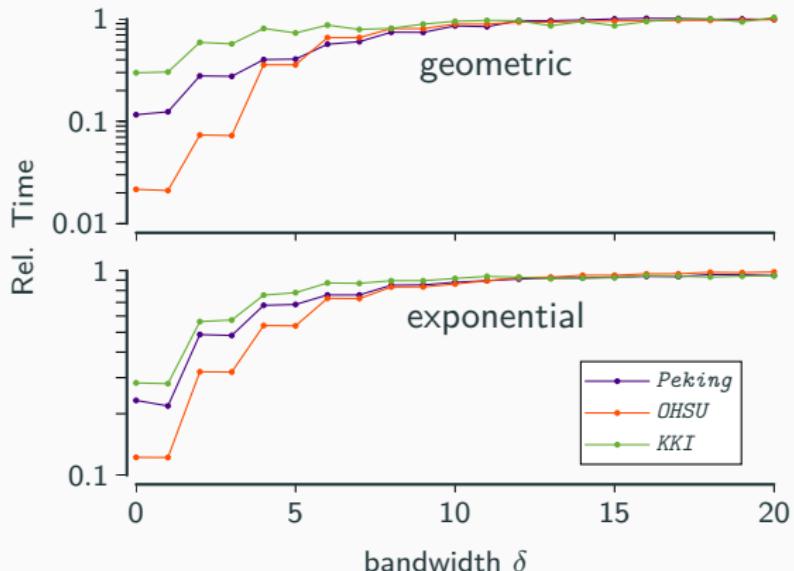
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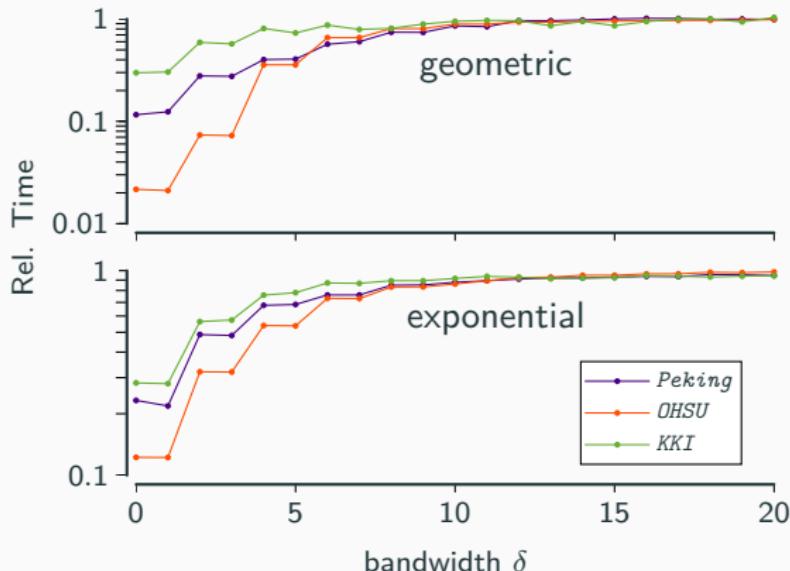
Results

Time comparison



Relative wall-clock time
(SUSAN vs. naïve)

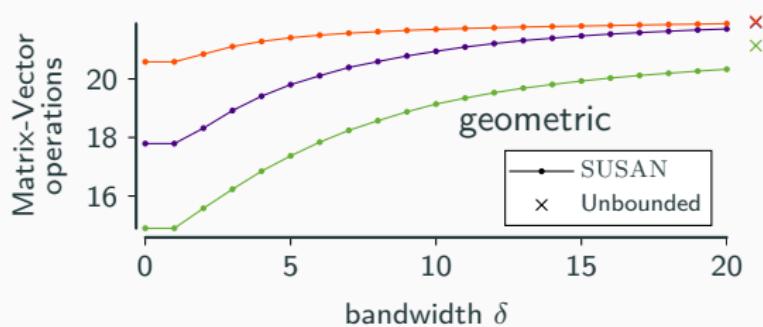
Time comparison



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- outperforms naive computation, especially for small δ .

Time comparison

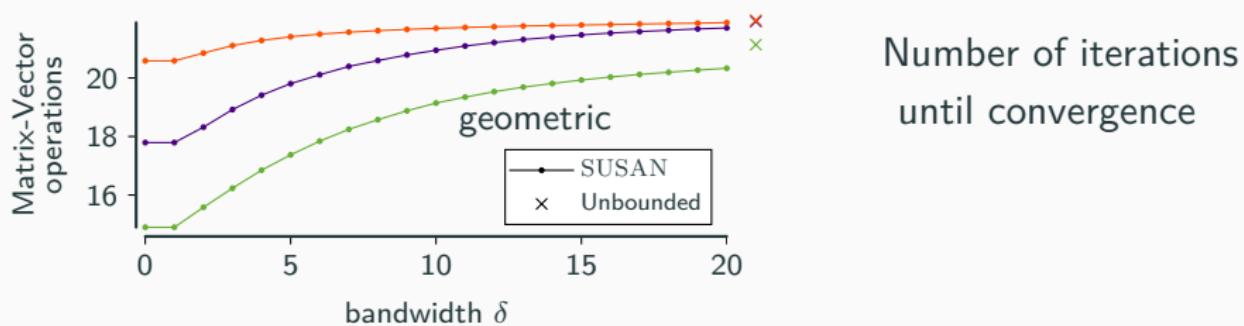


Number of iterations
until convergence

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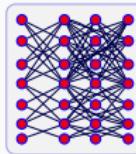
SUSAN

- outperforms naive computation, especially for small δ .
- (geometric) converges faster for smaller δ .

Conclusion

We study

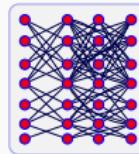
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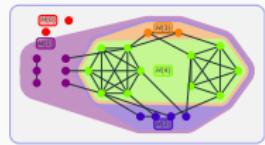
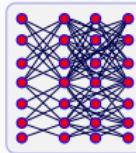


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- coreness as structurally-aware vertex labels

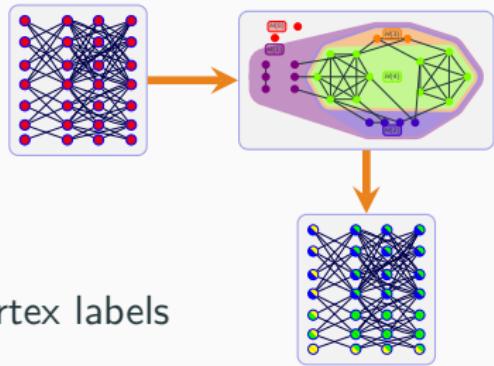
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- induce **intuitive vertex similarity**



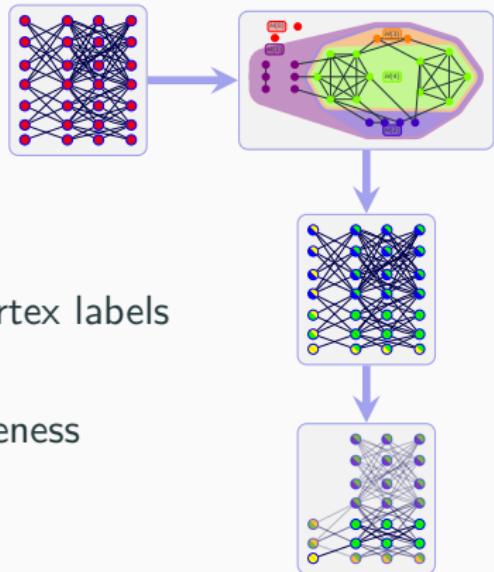
Conclusion

We study

- random walk graph kernels
- weighted vertex alignments

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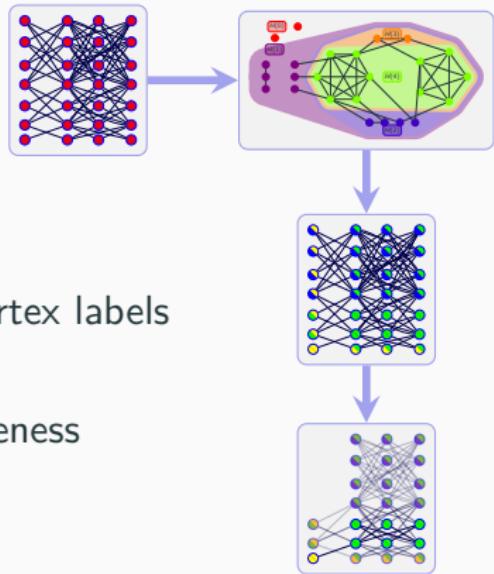
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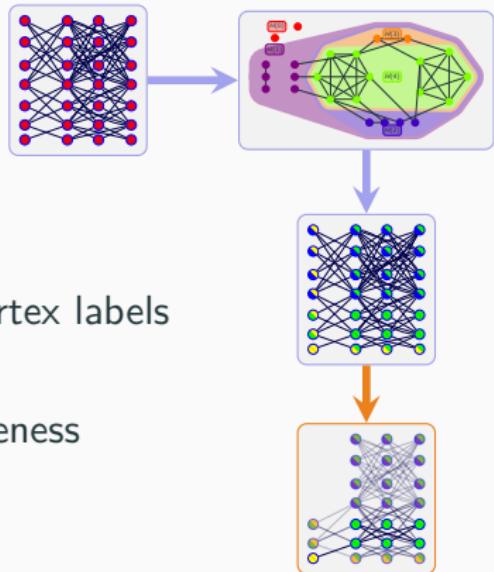
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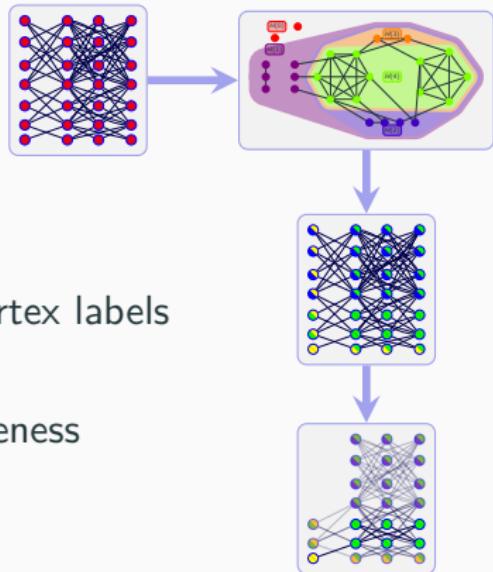
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- **close the gap** between loose and strict alignment constraints

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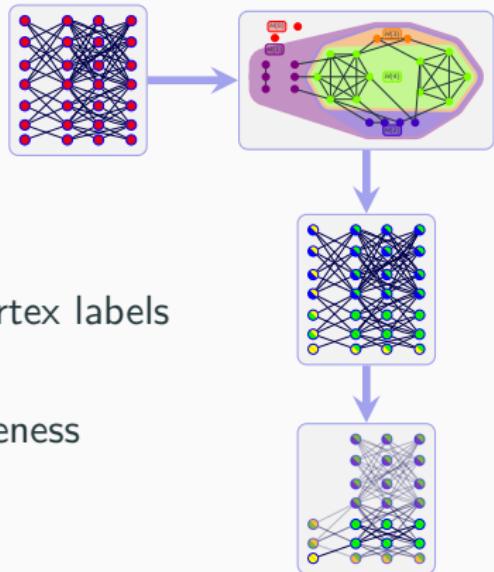
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We study

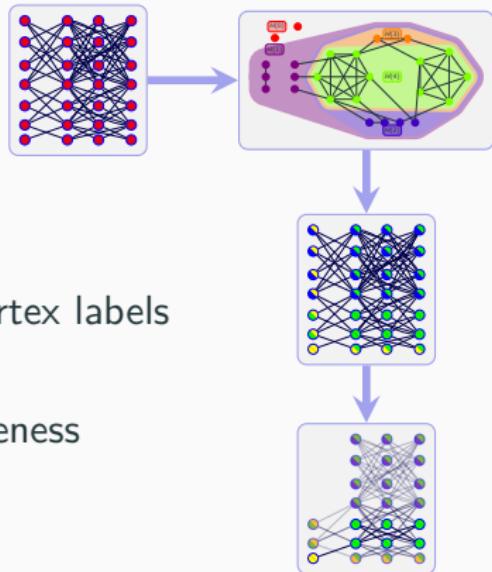
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