Persistent Spectral Theory Nick Sale - Swansea TDA Seminar - 14/04/20

- Zhenyu Meng and Kelin Xia, Persistent spectral based machine learning (PerSpect ML) for drug design, 2020, <u>https://arxiv.org/abs/2002.00582</u>
- Rui Wang, Duc Duy Nguyen and Guo-Wei Wei, Persistent spectral graph, 2019, <u>https://arxiv.org/abs/1912.04135</u>

Spectral Graph Theory

Consider a graphG = (V, E)Definition:Adjacency matrix $A_{i,j} = \begin{cases} 1 & \text{if } (v_i, v_j) \in E \\ 0 & \text{otherwise} \end{cases}$ Definition:Graph Laplacian $L_{i,j} = \begin{cases} deg(v_i) & \text{if } i = j \\ -1 & \text{if } (v_i, v_j) \in E \\ 0 & \text{otherwise} \end{cases}$

Note that $deg(v_i) = \sum_j A_{i,j}$, and we can also write L = D - A where $D = diag(\{v\}_{v \in V})$

Properties of the Laplacian

Consider $f: V \to \mathbb{R}$ as a vector in \mathbb{R}^n with components f_i

Proposition:
$$f^T L f = \sum_{(v_i,v_j) \in E} (f_i - f_j)^2$$

<u>Corollary</u>: *L* is positive semi-definite, so all its eigenvalues are non-negative

Since L is symmetric, the spectral theorem also tells us it has n linearlyindependent eigenvectors with eigenvalues $0 \le \lambda_1 \le \lambda_2 \le \ldots \le \lambda_n$

<u>Proposition</u>: $dim(kerL) = \beta_0$ (# of connected components)

Hence *G* is connected iff $\lambda_2 \ge 0$. In fact, λ_2 gives a "measure of connectedness"

Example: What can the other eigenvalues tell us?

<u>Definition</u>: Cheeger constant (also Isoperimetric ratio)

$$h(G) = \min_{A\subseteq V, \; |A|\leq rac{1}{2}|V|} rac{|\partial A|}{|A|}$$

where
$$\partial A = \{(v,w) \in E \mid v \in A, \; w
ot \in A \}$$

<u>Theorem</u>: (Cheeger-Alon-Milman) Let d_{max} be the maximum degree of any vertex. Then

$$rac{\lambda_2}{2} \leq h(G) \leq \sqrt{2d_{max}\lambda_2}$$



Extension to Simplicial Complexes

Consider a chain complex (C_i, ∂_i)

<u>Definition</u>: k-th Combinatorial Laplacian $L_k = \partial_k^T \partial_k + \partial_{k+1} \partial_{k+1}^T$

Note that when k = 0 we obtain the same definition as before

<u>Proposition</u>: $dim(kerL_k) = \beta_k$

We can also relate the combinatorial Laplacian to random walks on simplicial complexes (see *Random walks on simplicial complexes and the normalized Hodge 1-Laplacian* by Shaub et al.)



Persistent Spectral Theory

Idea: PerSpect (Persistent spectral based machine learning (PerSpect ML) for drug design)

$$\begin{array}{ll} K^{1} \subseteq K^{2} \subseteq \ldots \subseteq K^{n} & \text{filtration of a simplicial complex} \\ & & \downarrow \\ & & \downarrow \\ L_{k}^{1}, L_{k}^{2}, \ldots, L_{k}^{n} & \text{k-th combinatorial Laplacians} \\ & & \downarrow \\ & & \downarrow \\ \{\lambda_{2}^{1}, \sum_{i} \lambda_{i}^{1}, \sum_{i} |\lambda_{i}^{1} - \overline{\lambda^{1}}|, \ldots\}, \ldots, \{\lambda_{2}^{n}, \sum_{i} \lambda_{i}^{n}, \sum_{i} |\lambda_{i}^{n} - \overline{\lambda^{n}}|, \ldots\} \end{array}$$

Biomolecular Topological Modeling

<u>Model</u>: Element-specific (ES) modelling

Given the spatial configuration of a molecule, consider separate point clouds for each element







Modelling Interactions

In drug design we want to look at the interaction between two molecules: a <u>protein</u> and a <u>ligand</u>. In particular, we might want to predict the <u>binding affinity</u>

Take element point clouds R_P , R_L from the protein and ligand

Definition: ES interactive distance

$$d(x,y) = egin{cases} \|x-y\| & ext{if } x \in R_P, y \in R_L ext{ or } y \in R_P, x \in R_L \ \infty & ext{otherwise} \end{cases}$$

<u>Definition</u>: ES interactive electrostatic distance

$$d_E(x,y) = egin{cases} (1+exp(rac{cq_xq_y}{\|x-y\|}))^{-1} & ext{if } x\in R_P, y\in R_L ext{ or } y\in R_P, x\in R_L \ \infty & ext{otherwise} \end{cases}$$



Predicting Binding Affinity

Given protein P and ligand L

We have 4 protein element point clouds C, N, O, S

And 9 ligand element point clouds C, N, O, S, P, F, Cl, Br, I

Giving 4*9 = 36 Vietoris-Rips filtrations $VR_d(C_P \cup$

 $VR_d(C_P\cup C_L),\ VR_d(C_P\cup N_L),\ \dots$

11*250*36 = 99,000 features computed (11 features at 250 filtration values)



Similarly, 11*100*50 = 55,000 features are computed using d_E

Spectral Features

- 1. Betti 0
- 2. Betti 1
- 3. Mean
- 4. Standard deviation

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- 5. Maximum
- 6. Minimum

- 7. Laplacian graph energy
- 8. Generalized mean graph energy
- 9. Spectral moment (second order)
- 10. Quasi-Wiener index
- 11. Spanning tree number

$$WI(G) = \sum_{\lambda
eq 0} rac{|\{\lambda
eq 0\}|+1}{\lambda} \qquad \qquad ST(G) = lg(rac{1}{|\{\lambda
eq 0\}|+1} \prod_{\lambda
eq 0} \lambda)$$

Performance

Trained using Gradient Boost Trees on data from the PDBbind-2007, PDBbind-2013 and PDBbind-2016 databases



Persistent Laplacians

Similar to ideas in the presentation *Persistent harmonic forms* by André Lieutier (<u>https://project.inria.fr/gudhi/files/2014/10/Per</u> <u>sistent-Harmonic-Forms.pdf</u>)

Idea: (Persistent spectral graph) Consider a filtration of chain complexes

$$\cdots C_{q+1}^{1} \xrightarrow{\partial_{q+1}^{1}} C_{q}^{1} \xrightarrow{\partial_{q}^{1}} \cdots \xrightarrow{\partial_{3}^{1}} C_{2}^{1} \xrightarrow{\partial_{2}^{1}} C_{1}^{1} \xrightarrow{\partial_{1}^{1}} C_{0}^{1} \xrightarrow{\partial_{0}^{1}} C_{1}^{1} \xrightarrow{\partial_{0}^{1}} \cdots \xrightarrow{\partial_{0}^{1}} C_{1}^{1} \xrightarrow{\partial_{0}^{1}} \xrightarrow{\partial_{0}^{1}} \xrightarrow{\partial_{0}^{1}} \xrightarrow{\partial_{0}^{1}} \xrightarrow{\partial_{0}^{1}} \cdots \xrightarrow{\partial_{0}^{1}} \xrightarrow{\partial_{0}^{1$$

<u>Definition</u>: p-persistent k-th Laplacian $L_{k}^{t+p} = \overline{\partial}_{k+1}^{t+p} (\overline{\partial}_{k+1}^{t+p})^{T} + (\partial_{k}^{t})^{T} \partial_{k}^{t}$

$$\text{ where } \quad A_k^{t+p} = \{ \sigma \in C_k^{t+p} \mid \partial \sigma \in C_{k-1}^t \} \qquad \quad \overline{\partial}_k^{t+p} = \partial_k^{t+p}|_{A_k^{t+p}}$$

<u>Proposition</u>: $dim(kerL_k^{t+p}) = \beta_k^{t+p}$

Questions

- What level of stability do we have for these spectral features?
- If none, how much do we actually miss it in applications like these?
- Aren't these spectral features very expensive to compute lots of times? What methods for computing these faster for filtrations might there be>

Image URLs

- <u>https://courses.lumenlearning.com/introchem/chapter/molecules/</u>
- <u>https://www.creative-proteomics.com/services/protein-ligand-binding-site-prediction-service.htm</u>