

## Signal Processing on Graphs

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Graph Signals

Graph Laplacian

Graph Fourier Transform (GFT)

Ordering of frequencies

Inverse graph Fourier transform (iGFT)

**Graph Filters** 

Application: Gene Network

Information sciences at ESE

### The support of one dimensional signals



- We have studied one-dimensional signals, image processing, PCA
- It is time to understand them in a more unified way
- Consider the support of one-dimensional signals
- There is an underlying graph structure
  - $\Rightarrow$  Each node represents discrete time instants (e.g. hours in a day)
  - $\Rightarrow$  Edges are unweighted and directed



Spring day in Philadelphia



- Similarly, images also have an underlying graph structure
- Each node represents a single pixel
- Edges denote neighborhoods of pixels
  - $\Rightarrow$  Unweighted and undirected





## PCA uses another underlying graph



- The previous underlying graph assumes a structure between pixels (neighbors in lattice) a priori of seeing the images
- PCA considers images as defined on a different graph
- Each node represents a single pixel
- Edges denote covariance between pairs of pixels in the realizations
  - $\Rightarrow$  A posteriori after seeing the images
  - $\Rightarrow$  Undirected and weighted, including self loops



## Graphs



- Formally, a graph (or a network) is a triplet  $(\mathcal{V}, \mathcal{E}, W)$
- $\mathcal{V} = \{1, 2, \dots, N\}$  is a finite set of N nodes or vertices
- $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$  is a set of edges defined as order pairs (n, m)
  - $\Rightarrow$  Write  $\mathcal{N}(n) = \{m \in \mathcal{V} : (m, n) \in \mathcal{E}\}$  as the in-neighbors of n
- W: E → R is a map from the set of edges to scalar values, w<sub>nm</sub>
  ⇒ Represents the level of relationship from n to m
  ⇒ Unweighted graphs ⇒ w<sub>nm</sub> ∈ {0,1}, for all (n, m) ∈ E
  ⇒ Undirected graphs ⇒ (n, m) ∈ E if and only if (m, n) ∈ E and
  - $w_{nm} = w_{mn}$ , for all  $(n, m) \in \mathcal{E}$

 $\Rightarrow$  In-neighbors are neighbors

 $\Rightarrow$  More often weights are strictly positive,  $\mathcal{W}:\mathcal{E}\rightarrow\mathbb{R}_{++}$ 

## Graphs – examples





- ► Unweighted and directed graphs  $\Rightarrow \mathcal{V} = \{0, 1, \dots, 23\}$   $\Rightarrow \mathcal{E} = \{(0, 1), (1, 2), \dots, (22, 23), (23, 0)\}$   $\Rightarrow W : (n, m) \mapsto 1, \text{ for all } (n, m) \in \mathcal{E}$
- ► Unweighted and undirected graphs  $\Rightarrow \mathcal{V} = \{1, 2, 3, \dots, 9\}$   $\Rightarrow \mathcal{E} = \{(1, 2), (2, 3), \dots, (8, 9), (1, 4), \dots, (6, 9)\}$   $\Rightarrow W : (n, m) \mapsto 1, \text{ for all } (n, m) \in \mathcal{E}$





► Weighted and undirected graphs  $\Rightarrow \mathcal{V} = \{p_1, p_2, p_3, p_4\}$   $\Rightarrow \mathcal{E} = \{(p_1, p_1), (p_1, p_2), \dots, (p_4, p_4)\} = \mathcal{V} \times \mathcal{V}$   $\Rightarrow W : (n, m) \mapsto \Sigma_{nm} = \Sigma_{mn}, \text{ for all } (n, m)$ 



- Given a graph  $G = (\mathcal{V}, \mathcal{E}, W)$  of N vertices,
- Its adjacency matrix  $\mathbf{A} \in \mathbb{R}^{N \times N}$  is defined as

$$egin{aligned} \mathcal{A}_{nm} &= egin{cases} w_{nm}, & ext{if}(n,m) \in \mathcal{E} \ 0, & ext{otherwise} \end{aligned}$$

A matrix representation incorporating all information about G
 ⇒ For unweighted graphs, positive entries represent connected pairs
 ⇒ For weighted graphs, also denote proximities between pairs

Inherently defines an ordering of vertices

 $\Rightarrow$  same ordering as in graph signals that we will see soon

## Adjacency matrices – examples





# Graph signals



- Graph signals are mappings  $x : \mathcal{V} \to \mathbb{R}$
- Defined on the vertices of the graph
- May be represented as a vector  $\mathbf{x} \in \mathbb{R}^N$
- $x_n$  represents the signal value at the *n*th vertex in  $\mathcal{V}$
- Inherently utilizes an ordering of vertices

⇒ same ordering as in adjacency matrices





- Graphs representing gene-gene interactions
  - $\Rightarrow$  Each node denotes a single gene (loosely speaking)
  - $\Rightarrow$  Connected if their coded proteins participate in same metobolism



A sample network

### Graph signals - Genetic profiles



Genetic profiles for each patient can be considered as a graph signal
 ⇒ Signal on each node is 1 if mutated and 0 otherwise





- ► We are going to derive following concepts for graph signal processing
  - $\Rightarrow$  Total variations
  - $\Rightarrow$  Frequency
  - $\Rightarrow$  the notion of high or low frequency will be less obvious
  - $\Rightarrow$  DFT and iDFT for graph signals
  - $\Rightarrow$  Graph filtering
- And apply graph signal processing to gene mutation dataset



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- The degree of a node is the sum of the weights of its incident edges
- Given a weighted and undirected graph  $G = (\mathcal{V}, \mathcal{E}, W)$
- ► The degree of node *i*, deg(*i*) is defined as deg(*i*) =  $\sum_{j \in \mathcal{N}(i)} w_{ij}$ ⇒ where  $\mathcal{N}(i)$  is the neighborhood of node *i*

Equivalently, in terms of the adjacency matrix A

- $\Rightarrow \operatorname{deg}(i) = \sum_{i} A_{ij} = \sum_{i} A_{ji}$
- ▶ The degree matrix  $\mathbf{D} \in \mathbb{R}^{N \times N}$  is a diagonal matrix s.t.  $D_{ii} = deg(i)$
- In directed graphs, each node has an out-degree and an in-degree
  Weights in outgoing and incoming edges need not coincide

Penn

Given a graph G with adjacency matrix A and degree matrix D

▶ We define the Laplacian matrix  $\mathbf{L} \in \mathbb{R}^{N \times N}$  as

### $\bm{L}=\bm{D}-\bm{A}$

Equivalently, L can be defined element-wise as

$$L_{ij} = \begin{cases} \deg(i) = \sum_{j \in \mathcal{N}(i)} w_{ij} & \text{if } i = j \\ -w_{ij} & \text{if } j \in \mathcal{N}_i \\ 0 & \text{otherwise} \end{cases}$$

- We assume undirected  $G \Rightarrow \deg(i)$  is well-defined
- ► The normalized Laplacian can be obtained as L = D<sup>-1/2</sup>LD<sup>-1/2</sup> ⇒ We will mainly focus on the unnormalized version



Consider the weighted and undirected graph and its Laplacian



Diagonal elements are strictly positive since no node is isolated
 ⇒ Every node has a non-zero degree
 Off-diagonal elements are non-positive

### Multiplication by the Laplacian



- Consider a graph G with Laplacian L and a graph signal x on G
- Signal y = Lx results from multiplying x with the Laplacian
- Component  $y_i$  of **y** is (matrix product definition, separate j = i)

$$y_i = \sum_j L_{ij} x_j = L_{ii} x_i + \sum_{j \neq i} L_{ij} x_j$$

▶ We know  $L_{ij} = 0$  when  $j \notin N_i$  and  $L_{ij} = -w_{ij}$  when  $j \in N_i$ . Then

$$y_i = L_{ii}x_i - \sum_{j \in \mathcal{N}_i} w_{ij}x_j$$

• We also know that  $L_{ii} = \deg(i) = \sum_{j \in \mathcal{N}_i} w_{ij}$ . Therefore

$$y_i = \sum_{j \in \mathcal{N}_i} w_{ij} x_i - \sum_{j \in \mathcal{N}_i} w_{ij} x_j = \sum_{j \in \mathcal{N}_i} w_{ij} (x_i - x_j)$$

Replaces x<sub>i</sub> by weighted average of difference with neighbors



• Multiplying by the Laplcian yields 
$$\Rightarrow y_i = \sum_{j \in \mathcal{N}_i} w_{ij}(x_i - x_j)$$

 $\blacktriangleright$  y<sub>i</sub> measures the difference between **x** at a node and its neighborhood

- We say the signal diffuses through the graph. Like heat diffuses
- Temperature at i is averaged with neighbor's temperatures
- Further Laplacian multiplications continue diffusion process
  ⇒ L<sup>2</sup>x brings in energy from 2-hop neighborhood
  ⇒ L<sup>3</sup>x brings in energy from 3-hop neighborhood
  ⇒ ... L<sup>k</sup>x brings in energy from k-hop neighborhood



- The Laplacian quadratic form of graph signal  $\mathbf{x}$  is  $\Rightarrow \mathbf{x}^T \mathbf{L} \mathbf{x}$
- Quadratic form is a number: row vector  $\times$  matrix  $\times$  column vector

#### Theorem

The Laplacian quadratic form of signal  $\textbf{x} = [x_0, x_1, \dots, x_N]$  is explicitly given by

$$\mathbf{x}^{\mathsf{T}} \mathbf{L} \mathbf{x} = \frac{1}{2} \sum_{i} \sum_{j \in \mathcal{N}_i} w_{ij} (x_i - x_j)^2 = \frac{1}{2} \sum_{(i,j) \in \mathcal{E}} w_{ij} (x_i - x_j)^2$$

x<sup>T</sup>Lx quantifies the local variation of signal x
 ⇒ signals can be ordered depending on how much they vary
 ⇒ will be important to order frequencies



### Proof.

• We already know the result of the product  $\mathbf{y} = \mathbf{L}\mathbf{x}$ . Components are:

$$y_i = \sum_{j \in \mathcal{N}_i} w_{ij}(x_i - x_j)$$

• Use explicit form of the product  $\mathbf{x}^T \mathbf{y} = \sum_i x_i y_i$  to write

$$\mathbf{x}^T \mathbf{y} = \sum_i x_i y_i = \sum_i \sum_{j \in \mathcal{N}_i} x_i w_{ij} (x_i - x_j)$$

▶ The term  $x_i w_{ij}(x_i - x_j)$  has a symmetric  $x_j w_{ji}(x_j - x_i)$ . Group them

$$\mathbf{x}^{\mathsf{T}}\mathbf{y} = \frac{1}{2}\sum_{i} x_{i} w_{ij}(x_{i} - x_{j}) + x_{j} w_{ji}(x_{j} - x_{i})$$

But the terms in the sum are now simply

$$x_i w_{ij}(x_i - x_j) + x_j w_{ji}(x_j - x_i) = w_{ij}(x_i - x_j)^2$$



- Denote by  $\lambda_i$  and  $\mathbf{v}_i$  the eigenvalues and eigenvectors of L
- Since  $\mathbf{x}^T \mathbf{L} \mathbf{x} > 0$  for  $\mathbf{x} \neq 0$ ,  $\mathbf{L}$  is positive semi-definite
  - $\Rightarrow$  All eigenvalues are nonnegative, i.e.  $\lambda_i \ge 0$  for all i
- ► A constant vector **1** is an eigenvector of **L** with eigenvalue 0

$$[\mathsf{L}\mathbf{1}]_i = \sum_{j \in \mathcal{N}(i)} w_{ij}(1-1) = 0$$

▶ Thus,  $\lambda_1 = 0$  and  $\mathbf{v}_1 = 1/N \ \mathbf{1}$ 

 $\Rightarrow$  In connected graphs  $\lambda_i > 0$  for  $i = 2, \ldots, n$ 

 $\Rightarrow$  Multiplicity of  $\lambda = 0$  equals the nr. of connected components



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Application: Gene Network

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- Given an arbitrary graph  $G = (\mathcal{V}, \mathcal{E}, W)$
- ► A graph-shift operator  $\mathbf{S} \in \mathbb{R}^{N \times N}$  of graph *G* ia a matrix satisfying  $\Rightarrow S_{ij} = 0$  for  $i \neq j$  and  $(i, j) \notin \mathcal{E}$
- **S** can take nonzero values in the edges of G or in its diagonal
- We have already seen some possible graph-shift operators
  - $\Rightarrow$  Adjacency **A**, Degree **D** and Laplacian **L** matrices
- We restrict our attention to normal shifts S = V∧V<sup>H</sup>
  ⇒ Columns of V = [v<sub>1</sub>v<sub>2</sub>...v<sub>N</sub>] correspond to the eigenvectors of S
  ⇒ Λ is a diagonal matrix containing the eigenvalues of S



- Given a graph G and a graph signal x ∈ ℝ<sup>N</sup> defined on G
  ⇒ Consider a normal graph-shift S = VΛV<sup>H</sup>
- ► The Graph Fourier Transform (GFT) of **x** is defined as

$$\tilde{\mathbf{x}}(k) = \langle \mathbf{x}, \mathbf{v}_k \rangle = \sum_{n=1}^N \mathbf{x}(n) \mathbf{v}_k^*(n)$$

- ► In matrix form,  $\tilde{\mathbf{x}} = \mathbf{V}^H \mathbf{x}$
- Given that the columns of V are the eigenvectors v<sub>i</sub> of S
  ⇒ x̃(k) = v<sub>k</sub><sup>H</sup>x is the inner product between v<sub>k</sub> and x
  ⇒ x̃(k) is how similar x is to v<sub>k</sub>
  ⇒ In particular, GFT ≡ DFT when V<sup>H</sup> = F, i.e. v<sub>k</sub> = e<sub>kN</sub>

# DFT and PCA as particular cases of GFT





For the directed cycle graph, GFT ≡ DFT
 ⇒ if S = A or
 ⇒ if S = L for symmetrized graph
 ⇒ then V<sup>H</sup> = F

For the covariance graph, GFT  $\equiv$  PCA  $\Rightarrow$  if **S** = **A**, then **V**<sup>H</sup> = **P**<sup>H</sup>





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## Ordering of frequencies



Recall in conventional DFT, the kth DFT component can be written

$$X(\mathbf{k}) = \langle \mathbf{x}, \mathbf{e}_{\mathbf{k}N} \rangle = \frac{1}{\sqrt{N}} \sum_{n=0}^{N-1} x(n) e^{-j2\pi \mathbf{k}n/N}$$

► We say X(k) the component for higher frequency given higher k ⇒ There exists a natural ordering of frequencies ⇒ Higher k ⇒ higher oscillations





- We want to quantify the qualitative intuition of 'high oscillations'
- Classical zero crossings # of places signals change signs

$$ZC(\mathbf{x}) = \sum_{n} \mathbf{1} \{ x_n x_{n-1} < 0 \}$$

▶ Graph zero crossings – # of edges signals on two ends differ in signs



### Quantifying oscillations - Total variations



Classical total variations – sum of squared differences in consecutive signal samples

$$TV(\mathbf{x}) = \sum_{n} (x_n - x_{n-1})^2$$

Graph total variations – sum of squared differences between signals on two ends of edges multiplied by the corresponding edge weights

 $\Rightarrow$  Also known as Laplacian quadratic form





- ► The Laplacian eigenvalues can be interpreted as frequencies
- ► Larger eigenvalues ⇒ Higher frequencies
- The eigenvectors associated with large eigenvalues oscillate rapidly ⇒ Dissimilar values on vertices connected by edges with high weight
- ► The eigenvectors associated with small eigenvalues vary slowly
  - $\Rightarrow$  Similar values on vertices connected by edges with high weight
- Eigenvector associated with eigenvalue 0 is constant

 $\Rightarrow$  for connected graph



Three graph Laplacian eigenvectors for the gene networks





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- Recall the graph Fourier transform x
  - $\Rightarrow$  of any signal  $\mathbf{x} \in \mathbb{R}^N$  on the vertices of graph G
  - $\Rightarrow$  is the expansion of  ${\bf x}$  of the eigenvectors of the Laplacian

$$\tilde{\mathbf{x}}(\mathbf{k}) = \langle \mathbf{x}, \mathbf{v}_{\mathbf{k}} \rangle = \sum_{n=1}^{N} x(n) v_{\mathbf{k}}^{*}(n)$$

- ► In matrix form,  $\tilde{\mathbf{x}} = \mathbf{V}^H \mathbf{x}$
- ► The inverse graph Fourier transform is

$$\mathbf{x}(n) = \sum_{k=0}^{N-1} \tilde{\mathbf{x}}(k) v_k(n)$$

ln matrix form,  $\mathbf{x} = \mathbf{V}\tilde{\mathbf{x}}$ 



▶ Recap in proving theorems we have monkey steps and one smart step ⇒ That was orthonormality ⇒  $V^H$  is Hermitian ⇒  $VV^H = I$ 

### Theorem

The inverse graph Fourier transform (iGFT) is, indeed, the inverse of the GFT.

### Proof.

▶ Write  $\mathbf{x} = \mathbf{V}\tilde{\mathbf{x}}$  and  $\tilde{\mathbf{x}} = \mathbf{V}^{H}\mathbf{x}$  and exploit fact that  $\mathbf{V}$  is Hermitian

$$\mathbf{x} = \mathbf{V}\tilde{\mathbf{x}} = \mathbf{V}\mathbf{V}^{H}\mathbf{x} = \mathbf{I}\mathbf{x} = \mathbf{x}$$

This is the last inverse theorem we will see...

#### Theorem

The GFT preserves energy  $\,\Rightarrow\, \|\bm{x}\|^2 = \bm{x}^H \bm{x} = \tilde{\bm{x}}^H \tilde{\bm{x}} = \|\tilde{\bm{x}}\|^2$ 

### Proof.

► Use GFT to write  $\tilde{\mathbf{x}} = \mathbf{V}^H \mathbf{x}$  and the fact that  $\mathbf{V}$  is Hermitian  $\|\tilde{\mathbf{x}}\|^2 = \tilde{\mathbf{x}}^H \tilde{\mathbf{x}} = (\mathbf{V}^H \mathbf{x})^H \mathbf{V}^H \mathbf{x} = \mathbf{x}^H \mathbf{V} \mathbf{V}^H \mathbf{x} = \mathbf{x}^H \mathbf{x} = \|\mathbf{x}\|^2$ 

This is the last energy conservation theorem we will see...

### Graph signal representations in two domains



Graph signals can be equivalently represented in two domains
 The vertex domain and the graph spectral domain



Sample patient 1 with subtype 2



Spectral representation for patient 2 with subtype 1



Spectral representation for patient 1 with subtype 2





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- A graph filter  $f : \mathbb{R}^N \to \mathbb{R}^N$  is a map between graph signals
  - $\Rightarrow$  Given a graph signal  $\mathbf{x} \in \mathbb{R}^N$ , its filtered version is  $\mathbf{y} = \mathbf{f}(\mathbf{x})$
- We will focus on filters f that are linear and shift-invariant
- ► A linear filter *f* is one that satisfies

$$\mathbf{y}_1 = \mathbf{f}(\mathbf{x}_1), \quad \mathbf{y}_2 = \mathbf{f}(\mathbf{x}_2) \implies \alpha_1 \mathbf{y}_1 + \alpha_2 \mathbf{y}_2 = \mathbf{f}(\alpha_1 \mathbf{x}_1 + \alpha_2 \mathbf{x}_2)$$

A shift-invariant filter f satisfies

$$f(\mathbf{S}\mathbf{x}) = \mathbf{S}f(\mathbf{x})$$

where  $\mathbf{S}$  is the graph-shift operator of the graph where  $\mathbf{x}$  is defined

Shift-invariance is the graph analog of time invariance in classical SP



- Given a graph G and a graph-shift operator  $\mathbf{S} \in \mathbb{R}^{N \times N}$  on G
- ► We define the graph filter **H** as

$$\mathbf{H} := h_0 \mathbf{S}^0 + h_1 \mathbf{S}^1 + h_2 \mathbf{S}^2 + \ldots = \sum_{\ell=0}^{L} h_\ell \mathbf{S}^\ell$$

- ► **H** is a polynomial on the graph-shift operator **S** with coefficients  $h_i$  $\Rightarrow$  *L* is the degree of the filter
- ► Filter **H** acts on a graph signal  $\mathbf{x} \in \mathbb{R}^N$  to generate  $\mathbf{y} = \mathbf{H}\mathbf{x}$ ⇒ If we define  $\mathbf{x}^{(\ell)} := \mathbf{S}^{\ell}\mathbf{x} = \mathbf{S}\mathbf{x}^{(\ell-1)}$

$$\mathbf{y} = \sum_{\ell=0}^L h_\ell \mathbf{x}^{(\ell)}$$

Why is H defined as a polynomial on S?



### Proposition

The graph filter  $\mathbf{H} = \sum_{\ell=0}^{L} h_{\ell} \mathbf{S}^{\ell}$  is linear and shift-invariant. Proof.

Since H is a matrix, linearity is trivial

$$\mathbf{y}_1 = \mathbf{H}\mathbf{x}_1, \quad \mathbf{y}_2 = \mathbf{H}\mathbf{x}_2 \implies \alpha_1\mathbf{y}_1 + \alpha_2\mathbf{y}_2 = \mathbf{H}(\alpha_1\mathbf{x}_1 + \alpha_2\mathbf{x}_2)$$

For shift-invariance, note that S commutes with S<sup>i</sup> for all i

$$\mathbf{H}(\mathbf{S}\mathbf{x}) = \left(\sum_{\ell=0}^{L} h_{\ell} \mathbf{S}^{\ell}\right) \mathbf{S}\mathbf{x} = \mathbf{S}\left(\sum_{\ell=0}^{L} h_{\ell} \mathbf{S}^{\ell}\right) \mathbf{x} = \mathbf{S}(\mathbf{H}\mathbf{x})$$

In fact, no other formulation of  ${\rm H}$  is linear and shift-invariant  $\Rightarrow$  We will not show this





Consider the particular case where S = A<sub>dc</sub>
 Adjacency matrix of a directed cycle

Focus on a signal x defined on a cyclic graph with 6 nodes



• Consider the output signal y = Hx

$$\mathbf{y} = h_0 \mathbf{x} + h_1 \mathbf{S}^1 \mathbf{x} + h_2 \mathbf{S}^2 \mathbf{x} + h_3 \mathbf{S}^3 \mathbf{x} + h_4 \mathbf{S}^4 \mathbf{x} + h_5 \mathbf{S}^5 \mathbf{x}$$



Let's focus on the first component of signal y

$$y_1 = h_0 [\mathbf{S}^0 \mathbf{x}]_1 + h_1 [\mathbf{S}^1 \mathbf{x}]_1 + h_2 [\mathbf{S}^2 \mathbf{x}]_1 + h_3 [\mathbf{S}^3 \mathbf{x}]_1 + h_4 [\mathbf{S}^4 \mathbf{x}]_1 + h_5 [\mathbf{S}^5 \mathbf{x}]_1$$
  
=  $h_0 x_1 + h_1 x_6 + h_2 x_5 + h_3 x_4 + h_4 x_3 + h_5 x_2$ 

ln general, for element  $y_n$  of y, exploiting the fact that x is cyclic

$$y_n = \sum_{l=0}^{N-1} h_l x_{n-l}$$

• Defining  $\mathbf{h} := [h_0, h_1, \dots, h_5]^T$  we may write

 $\mathbf{y} = \mathbf{h} * \mathbf{x}$ 

Thus, for the particular case where S = A<sub>dc</sub>
 ⇒ h recovers the impulse response of the filter



• Recalling that  $\mathbf{S} = \mathbf{V} \wedge \mathbf{V}^H$ , we may write

$$\mathbf{H} = \sum_{\ell=0}^{L} h_{\ell} \mathbf{S}^{\ell} = \mathbf{V} \left( \sum_{\ell=0}^{L} h_{\ell} \Lambda^{\ell} \right) \mathbf{V}^{H}$$

- ► The application **H**x of filter **H** to x can be split into three parts ⇒ **V**<sup>*H*</sup> takes signal x to the graph frequency domain  $\tilde{\mathbf{x}}$ ⇒  $\hat{\mathbf{H}} := \sum_{\ell=0}^{L} h_{\ell} \wedge^{\ell}$  modifies the frequency coefficients to obtain  $\tilde{\mathbf{y}}$ ⇒ **V** brings the signal  $\tilde{\mathbf{y}}$  back to the graph domain y
- Since Ĥ is diagonal, define Ĥ =: diag(ĥ)
  ⇒ ĥ is the frequency response of the filter H
  ⇒ Output at frequency i depends only on input at frequency i

$$\tilde{y}_i = \widehat{h}_i \tilde{x}_i$$

# Frequency response and filter coefficients



► In order to design a graph with a particular frequency response  $\hat{\mathbf{h}}$  $\Rightarrow$  Need to know the relation between  $\hat{\mathbf{h}}$  and the filter coefficients  $\mathbf{h}$ 

• Define the matrix 
$$\Psi := \begin{pmatrix} 1 & \lambda_1 & \dots & \lambda_1^{L-1} \\ \vdots & \vdots & & \vdots \\ 1 & \lambda_N & \dots & \lambda_N^{L-1} \end{pmatrix}$$

### Proposition

The frequency response  $\hat{\mathbf{h}}$  of a graph filter with coefficients  $\mathbf{h}$  is given by

 $\widehat{\mathbf{h}} = \Psi \mathbf{h}$ 

Proof.

- Since  $\hat{\mathbf{h}} := \operatorname{diag}(\sum_{\ell=0}^{L} h_{\ell} \wedge^{\ell})$  we have that  $\hat{h}_{i} = \sum_{\ell=0}^{L} h_{\ell} \lambda_{i}^{\ell}$
- Defining  $\lambda_i = [\lambda_i^0, \lambda_i^1, \dots, \lambda_i^{L-1}]^T$  we have that  $\hat{h}_i = \lambda_i^T \mathbf{h}$
- Stacking the values for all  $\hat{h}_i$ , the result follows

### Graph filter design



• Given the desired frequency response  $\hat{\mathbf{h}}$  of the graph filter  $\Rightarrow$  We can find the graph coefficients  $\mathbf{h}$  as

$$\mathbf{h} = \mathbf{\Psi}^{-1} \widehat{\mathbf{h}}$$

- ► Since **Ψ** is Vandermonde
  - $\Rightarrow$   $\Psi$  is invertible as long as  $\lambda_i \neq \lambda_j$  for  $i \neq j$
- ▶ For the particular case when  $S = A_{dc}$ , we have that  $\lambda_i = e^{-j\frac{2\pi}{N}(i-1)}$

$$\Psi = \begin{pmatrix} 1 & 1 & \dots & 1 \\ 1 & e^{-j\frac{2\pi(1)(1)}{N}} & \dots & e^{-j\frac{2\pi(1)(N-1)}{N}} \\ \vdots & \vdots & & \vdots \\ 1 & e^{-j\frac{2\pi(N-1)(1)}{N}} & \dots & e^{-j\frac{2\pi(N-1)(N01)}{N}} \end{pmatrix} = \mathsf{F}$$

 $\Rightarrow$  The frequency response is the DFT of the impulse response

$$\widehat{\mathbf{h}} = \mathbf{F}\mathbf{h}$$



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- Patients diagnosed with same disease exhibit different behaviors
- Each patient has a genetic profile describing gene mutations
- Would be beneficial to infer phenotypes from genotypes
  - $\Rightarrow$  Targeted treatments, more suitable suggestions, etc.
- Traditional approaches consider different genes to be independent
  Not so ideal, as different genes may affect same metabolism
- Alternatively, consider genetic network
  - $\Rightarrow$  Genetic profiles becomes graph signals on genetic network
  - $\Rightarrow$  We will see how this consideration improves subtype classification

### Genetic network



- Undirected and unweighted graph with 2458 nodes
  - ⇒ Describes gene-to-gene interactions
- Each node represents a gene in human DNA related to breast cancer
- An edge between two genes represents interaction
  - $\Rightarrow$  Proteins encoded participate in the same metabolism process
- Adjacency matrix of the gene network



## Genetic profiles



- Genetic profile of 240 women with breast cancer
  ⇒ 44 with serous subtype and 196 with endometrioid subtype
  ⇒ Patient *i* has an associated profile x<sub>i</sub> ∈ {0,1}<sup>2458</sup>
- Mutations are very varied across patients
  - $\Rightarrow$  Some patients present a lot of mutations
  - $\Rightarrow$  Some genes are consistently mutated across patients



Can we use the genetic profile to classify patients across subtypes?



• Quantify the distance between genetic profiles  $\Rightarrow d(i, j) = ||\mathbf{x}_i - \mathbf{x}_i||_2$ 

Given a patient *i* to classify, all other patients' subtypes are known
 Find the *k* most similar profiles, i.e. *j* such that *d(i,j)* is minimized
 Assign to *i* the most common subtype among these *k* neighbors

- Compare estimated with real subtype y for all patients
- We obtain the following error rates

 $k = 3 \Rightarrow 13.3\%$ ,  $k = 5 \Rightarrow 12.9\%$ ,  $k = 7 \Rightarrow 14.6\%$ 

Can we do any better using graph signal processing?



Each genetic profile **x**<sub>i</sub> can be seen as a graph signal

- $\Rightarrow$  On the genetic network
- We can look at the frequency components  $\tilde{\mathbf{x}}_i$  using the GFT
  - $\Rightarrow$  Use as shift operator  $\boldsymbol{S}$  the Laplacian of the genetic network

Example of signal  $\mathbf{x}_i$ 







### **Distinguishing Power**



• Define the distinguishing power of frequency  $\mathbf{v}_k$  as

$$DP(\mathbf{v}_{k}) = \left| \frac{\sum_{i:y_{i}=1} \tilde{\mathbf{x}}_{i}(k)}{\sum_{i} \mathbf{1} \{y_{i}=1\}} - \frac{\sum_{i:y_{i}=2} \tilde{\mathbf{x}}_{i}(k)}{\sum_{i} \mathbf{1} \{y_{i}=2\}} \right| / \sum_{i} |\tilde{\mathbf{x}}_{i}(k)|,$$

Normalized difference between the mean GFT coefficient for v<sub>k</sub> ⇒ Among patients with serous and endometrioid subtypes
 Distinguishing power is not equal across frequencies





### The distribution of discriminating power



Most frequencies have weak distinguishing power

 $\Rightarrow$  A few frequencies have strong differentiating power

- $\Rightarrow$  The most powerful frequency outperforms others significantly
- The distinguishing power defined is one of many proper heuristics

### Increasing accuracy via graph filters



- Keeps only information in the most distinguishable frequency
- For the genetic profile  $\mathbf{x}_i$  with its frequency representation  $\tilde{\mathbf{x}}_i$
- Multiply  $\tilde{\mathbf{x}}_i$  with graph filter  $H_1$  having the frequency response

$$H_1(k) = egin{cases} 1, & ext{if } k = ext{argmax}_k \ egin{matrix} DP(\mathbf{v}_k); \ 0, & ext{otherwise}. \end{cases}$$

• Then perform inverse GFT to get the filtered graph signals  $\hat{\mathbf{x}}_i$ 



### Increasing accuracy via another graph filters



- Keeps information in frequencies with higher distinguishing power
- Multiply  $\tilde{\mathbf{x}}_i$  with graph filter  $H_p$  having the frequency response

 $H_p(k) = \begin{cases} 1, & \text{if } DP(\mathbf{v}_k) \ge p \text{-th percentile of the distribution of } DP; \\ 0, & \text{otherwise,} \end{cases}$ 





Graph Signals

Graph Laplacian

Graph Fourier Transform (GFT)

Ordering of frequencies

Inverse graph Fourier transform (iGFT)

**Graph Filters** 

Application: Gene Network

Information sciences at ESE



- Transforms, PCA mostly, are the brain of data analysis
  But you still need a heart.
- Transforms concentrates information in a space of lower dimensionality
  ⇒ But you still have to extract that information
  ⇒ We did that with minimal sophistication (nearest neighbors)
- ► If you think you want to learn more about this, follow the DS sequence ⇒ ESE224: Signal and Information Processing
  - $\Rightarrow$  ESE305: Foundations of Data Science (V. Preciado)
  - $\Rightarrow$  ESE545: Data Mining: Learning From Massive Datasets (H. Hassani)
- Penn is also starting a masters of data science. Consider sub-matriculating



- ► To follow up on what we did on the first half of the course you can ...
  - $\Rightarrow$  Follow up literally by digging deeper intro signal processing
  - $\Rightarrow$  Follow up philosophically by studying systems
- Signal Processing sequence
  - ⇒ ESE224: Signal and Information Processing
  - $\Rightarrow$  ESE325: Fourier Analysis and Applications
  - $\Rightarrow$  ESE531: Digital Signal Processing
- Systems analysis and design
  - $\Rightarrow$  ESE210: Introduction to Dynamic Systems (R. Ghrist)
  - ⇒ ESE224: Signal and Information Processing
  - $\Rightarrow$  ESE303: Stochastic Systems Analysis and Simulation



- Once you have information you may want to something with it
- Controlling the state of a system
  - $\Rightarrow$  ESE406: Control of Systems
  - $\Rightarrow$  ESE500: Linear Systems Theory
- Making decisions that are good in some sense (optimal)
  - $\Rightarrow$  ESE204: Decision Models
  - $\Rightarrow$  ESE304: Optimization of Systems
  - $\Rightarrow$  ESE504: Introduction to Optimization Theory
  - $\Rightarrow$  ESE605: Modern Convex Optimization



At some point, you want to use what you've learned to do something
 ⇒ ESE290: Introduction to ESE Research Methodology
 ⇒ ESE350: Embedded Systems/Microcontroller Laboratory



- ▶ It has been my pleasure. I am very happy abut how things turned out
- If you need my help at some point in the next 30 years, let me know
- I will be retired after that