



## Block 10: Inference of network processes

### ELEC 573: Network Science and Analytics

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Fall 2021



Wk.	Date	Topic	HW	Project
1	23-Aug	Introduction to course	HW0 out	
2	30-Aug	Graph theory	HW0 solutions posted	
3	6-Sep	LABOR DAY (no class)	HW1 out	
4	13-Sep	Centrality measures / Community detection		
5	20-Sep	Community detection		
6	27-Sep	Signal Processing and Deep learning for graphs	HW1 due	
7	4-Oct	Signal Processing and Deep learning for graphs	HW2 out	
8	11-Oct	FALL BREAK (no class)		
9	18-Oct	Network models	HW2 due	
10	25-Oct	Network models	HW3 out	Project proposal due
11	1-Nov	Inference of network topologies and features		
12	8-Nov	Inference of network topologies and features	HW3 due	
13	15-Nov	Inference of network topologies and features		
14	22-Nov	Epidemics		Project progress report
15	29-Nov	Inference of network processes		

13-Dec Project presentation (video recording) and final report due



Nearest-neighbor prediction

Markov random fields

Kernel regression on graphs

Case study: Predicting protein function



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  - ▶ So far studied graphs as representations of these systems
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- ▶ Quantities **may be influenced** by the interactions among elements
  - 1) Behaviors and beliefs influenced by social interactions
  - 2) Functional roles of proteins influenced by their sequence similarity
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  - 1) Behaviors and beliefs influenced by social interactions
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  - 3) Spread of epidemics influenced by proximity of individuals
- ▶ Can think of these quantities as **random processes defined on graphs**
  - ▶ Static  $\{X_i\}_{i \in V}$  and dynamic processes  $\{X_i(t)\}_{i \in V}$  for  $t \in \mathbb{N}$  or  $\mathbb{R}_+$



- ▶ Consider prediction of a static process  $\mathbf{X} := \{X_i\}_{i \in V}$  on a graph
  - ▶ Process may be truly static, or a snapshot of a dynamic process

## Static network process prediction

Predict  $X_i$ , given observations of the adjacency matrix  $\mathbf{Y} = \mathbf{y}$  and of all attributes  $\mathbf{X}^{(-i)} = \mathbf{x}^{(-i)}$  but  $X_i$ .



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- ▶ **Idea:** exploit the network structure in  $\mathbf{y}$  for prediction
- ▶ For binary  $X_i \in \{0, 1\}$ , say, simple **nearest-neighbor method** predicts

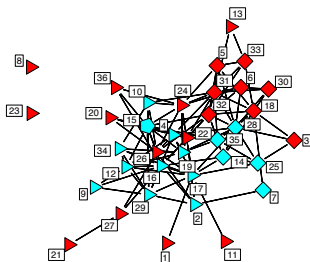
$$\hat{X}_i = \mathbb{I} \left\{ \frac{\sum_{j \in \mathcal{N}_i} x_j}{|\mathcal{N}_i|} > \tau \right\}$$

- ⇒ Average of the observed process in the neighborhood of  $i$
- ⇒ Called ‘guilt-by-association’ or graph-smoothing method





- ▶ Network  $G^{obs}$  of working relationships among lawyers [Lazega'01]
  - ▶ Nodes are  $N_v = 36$  partners, edges indicate partners worked together



- ▶ Data includes various node-level attributes  $\{X_i\}_{i \in V}$  including
  - ⇒ Type of practice, i.e., litigation (red) and corporate (cyan)
- ▶ Suspect lawyers collaborate more with peers in same legal practice
  - ⇒ Knowledge of collaboration useful in predicting type of practice



- ▶ Q: In predicting practice  $X_i$ , how useful is the value of **one neighbor**?
  - ⇒ Breakdown of 115 edges based on practice of incident lawyers

	Litigation	Corporate
Litigation	29	43
Corporate	43	43

- ▶ Looking at the rows in this table
  - ▶ Litigation lawyers collaborators are 40% litigation, 60% corporate
  - ▶ Collaborations of corporate lawyers are evenly split
  - ⇒ Suggests using a single neighbor has little predictive power



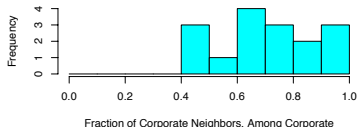
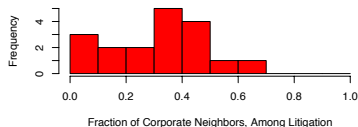
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- ▶ But 60% ( $29+43=72$ ) of edges join lawyers with common practice  
⇒ Suggests on aggregate knowledge of collaboration informative



- ▶ Incorporate information of all collaborators as in nearest-neighbors
  - ▶ Let  $X_i = 0$  if lawyer  $i$  practices litigation, and  $X_i = 1$  for corporate



- ▶ Nearest-neighbor prediction rule

$$\hat{X}_i = \mathbb{I} \left\{ \frac{\sum_{j \in \mathcal{N}_i} x_j}{|\mathcal{N}_i|} > 0.5 \right\}$$

- ⇒ Infers correctly 13 of the 16 corporate lawyers (i.e., 81%)
- ⇒ Infers correctly 16 of the 18 litigation lawyers (i.e., 89%)
- ⇒ Overall error rate is just under 15%



- ▶ Nearest-neighbor methods may seem rather informal and simple  
⇒ But competitive with more formal, model-based approaches
- ▶ Still, **model-based methods** have certain potential advantages:
  - a) Probabilistically rigorous predictive statements;
  - b) Formal inference for model parameters; and
  - c) Natural mechanisms for handling missing data



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  - a) Probabilistically rigorous predictive statements;
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  - c) Natural mechanisms for handling missing data
- ▶ Model the process  $\mathbf{X} := \{X_i\}_{i \in V}$  given an observed graph  $\mathbf{Y} = \mathbf{y}$ 
  - ⇒ Markov random field (MRF) models
  - ⇒ Kernel-regression models using graph kernels



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- ▶ Consider a graph  $G(V, E)$  with given adjacency matrix  $\mathbf{A}$ 
  - ⇒ Collection of discrete RVs  $\mathbf{X} = [X_1, \dots, X_{N_v}]^T$  defined on  $V$





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- ▶ **Def:** process  $\mathbf{X}$  is a **Markov random field (MRF)** on  $G$  if

$$P[X_i = x_i \mid \mathbf{X}^{(-i)} = \mathbf{x}^{(-i)}] = P[X_i = x_i \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}], \quad i \in V$$

- ▶  $X_i$  conditionally independent of other  $X_k$ , given neighbors values
- ▶ ‘Spatial’ Markov property, generalizing Markov chains in time
- ▶  $G$  defines neighborhoods  $\mathcal{N}_i$ , hence dependencies



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- ▶ Roots in statistical mechanics, Ising model of ferromagnetism [Ising '25]  
⇒ MRFs used extensively in spatial statistics and image analysis



- MRFs equivalent to **Gibbs random fields**  $\mathbf{X}$ , having joint distribution

$$P[\mathbf{X} = \mathbf{x}] = \left( \frac{1}{\kappa} \right) \exp\{U(\mathbf{x})\}$$

⇒ Energy function  $U(\cdot)$ , partition function  $\kappa = \sum_{\mathbf{x}} \exp\{U(\mathbf{x})\}$

⇒ Equivalence follows from the **Hammersley-Clifford theorem**



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- ▶ Energy function decomposable over the cliques in  $G$

$$U(\mathbf{x}) = \sum_{c \in \mathcal{C}} U_c(\mathbf{x})$$

⇒ Defined clique potentials  $U_c(\cdot)$ , set  $\mathcal{C}$  of cliques in  $G$

- ▶ Can show  $P[X_i | \mathbf{X}^{(-i)}]$  depends only on cliques involving vertex  $i$



- ▶ May specify MRFs through choice of clique potentials  $U_c(\cdot)$
- ▶ Ex: Class of **auto models** are defined through the constraints:
  - (i) Only cliques  $c \in \mathcal{C}$  of size one and two have  $U_c \neq 0$
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- ▶ For binary RVs  $X_i \in \{0, 1\}$ , the energy function takes the form

$$U(\mathbf{x}) = \sum_{i \in V} \alpha_i x_i + \sum_{(i,j) \in E} \beta_{ij} x_i x_j$$



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- ▶ Resulting MRF is known as **auto-logistic model**, because

$$P[X_i = 1 | \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}] = \frac{\exp\{\alpha_i + \sum_{j \in \mathcal{N}_i} \beta_{ij} x_j\}}{1 + \exp\{\alpha_i + \sum_{j \in \mathcal{N}_i} \beta_{ij} x_j\}}$$

⇒ Logistic regression of  $x_i$  on its neighboring  $x_j$ 's

⇒ Ising model a special case, when  $G$  is a regular lattice



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- ▶ **Ex:** Specifying  $\alpha_i = \alpha$  and  $\beta_{ij} = \beta$  yields conditional log-odds

$$\log \left[ \frac{P[X_i = 1 \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}]}{P[X_i = 0 \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}]} \right] = \alpha + \beta \sum_{j \in \mathcal{N}_i} x_j$$

⇒ Linear in the number of neighbors  $j$  of  $i$  with  $X_j = 1$



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- ▶ **Ex:** Specifying  $\alpha_i = \alpha + |\mathcal{N}_i|\beta_2$  and  $\beta_{ij} = \beta_1 - \beta_2$  yields

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⇒ Linear also in the number of neighbors  $j$  of  $i$  with  $X_j = 0$



- ▶ **MRFs with continuous RVs:** replace pmfs/sums with pdfs/integrals  
⇒ Gaussian distribution common for analytical tractability



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⇒ Gaussian distribution common for analytical tractability
- ▶ **Ex:** auto-Gaussian model specifies Gaussian  $X_i \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}$ , with

$$\mathbb{E} [X_i \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}] = \alpha_i + \sum_{j \in \mathcal{N}_i} \beta_{ij} (x_j - \alpha_j)$$
$$\text{var} [X_i \mid \mathbf{X}_{\mathcal{N}_i} = \mathbf{x}_{\mathcal{N}_i}] = \sigma^2$$

⇒ Values  $X_i$  modeled as weighted combinations of  $i$ 's neighbors



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⇒ Values  $X_i$  modeled as weighted combinations of  $i$ 's neighbors

- ▶ Let  $\boldsymbol{\mu} = [\alpha_1, \dots, \alpha_{N_v}]^\top$  and  $\boldsymbol{\Sigma} = \sigma^2(\mathbf{I} - \mathbf{B})^{-1}$ , where  $\mathbf{B} = [\beta_{ij}]$   
⇒ Under  $\beta_{ii} = 0$  and  $\beta_{ij} = \beta_{ji} \rightarrow \mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$

- ▶ **Homogeneity** assumptions can be imposed, simplifying expressions  
⇒ Further set  $\alpha_i = \alpha$  and  $\beta_{ij} = \beta \rightarrow \mathbf{X} \sim \mathcal{N}(\alpha \mathbf{1}, \sigma^2(\mathbf{I} - \beta \mathbf{A})^{-1})$



- ▶ In studying process  $\mathbf{X} = \{X_i\}_{i \in V}$  of interest to **predict some or all of  $\mathbf{X}$**
- ▶ MRF models we have seen for this purpose are of the form

$$P_{\theta}(\mathbf{X} = \mathbf{x}) = \left( \frac{1}{\kappa(\theta)} \right) \exp\{U(\mathbf{x}; \theta)\}$$

$\Rightarrow$  Parameter  $\theta$  low-dimensional, e.g.,  $\theta = [\alpha, \beta]$  in auto-models



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⇒ Parameter  $\theta$  low-dimensional, e.g.,  $\theta = [\alpha, \beta]$  in auto-models

- ▶ Predictions can be generated based on the distribution  $P_{\theta}(\cdot)$ 
  - ⇒ Knowledge of  $\theta$  is necessary, and typically  $\theta$  is unknown
- ▶ Unlike nearest-neighbors prediction, MRFs requires inference of  $\theta$  first



- ▶ Estimation of  $\theta$  most naturally approached via **maximum-likelihood**
- ▶ Even though the log-likelihood function takes a simple form

$$\ell(\theta) = \log P_{\theta}(\mathbf{X} = \mathbf{x}) = U(\mathbf{x}; \theta) - \log \kappa(\theta)$$

⇒ Computing  $\kappa(\theta) = \sum_{\mathbf{x}} \exp\{U(\mathbf{x}; \theta)\}$  often **intractable**





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- ▶ Popular alternative is **maximum pseudo-likelihood**, i.e., maximize

$$\sum_{i \in V} \log P_{\theta} \left( X_i = x_i \mid \mathbf{X}^{(-i)} = \mathbf{x}^{(-i)} \right)$$

- ⇒ Ignores dependencies beyond the neighborhood of each  $X_i$
- ⇒ Probabilities depend on clique potentials  $U_c$ , not on  $\kappa(\theta)$



- ▶ Given a value of  $\theta$ , consider predicting some or all of  $\mathbf{X}$  from  $P_{\theta}(\cdot)$ 
  - ⇒ Computing  $P_{\theta}(\cdot)$  hard, can **draw from it using a Gibbs sampler**



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⇒ Computing  $P_\theta(\cdot)$  hard, can **draw from it using a Gibbs sampler**
- ▶ Gibbs sampler exploits  $P_\theta(X_i | \mathbf{X}^{(-i)} = \mathbf{x}^{(-i)})$  in simple closed form
  - ▶ New value  $\mathbf{X}_{(k)}$  obtained from  $\mathbf{X}_{(k-1)} = \mathbf{x}_{(k-1)}$  by drawing

$$\begin{aligned} X_{1,(k)} & \text{ from } P_\theta(X_1 | \mathbf{X}^{(-1)} = \mathbf{x}_{(k-1)}^{(-1)}) \\ & \vdots \\ X_{N_v,(k)} & \text{ from } P_\theta(X_{N_v} | \mathbf{X}^{(-N_v)} = \mathbf{x}_{(k-1)}^{(-N_v)}) \end{aligned}$$

⇒ Generated sequence  $\mathbf{X}_{(1)}, \mathbf{X}_{(2)}, \dots$  forms a Markov chain

- ▶ Under appropriate conditions, stationary distribution equals  $P_\theta(\cdot)$



- ▶ Given large sample from  $P_\theta(\cdot)$ , predict  $\mathbf{X}$  using empirical distributions  
Ex: for binary  $\mathbf{X}$  use empirical marginal frequencies to predict  $X_i$ , i.e.,

$$\hat{X}_i = \mathbb{I} \left\{ \frac{1}{n} \sum_{k=m+1}^{m+n} X_{i,(k)} > 0.5 \right\} \text{ for large } m, n$$



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- ▶ Suppose we observe some elements  $\mathbf{X}^{obs} = \mathbf{x}^{obs}$ , and wish to predict  $\mathbf{X}^{miss}$   
 $\Rightarrow$  Draw from the relevant  $P_\theta(\mathbf{X}^{miss} \mid \mathbf{X}^{obs} = \mathbf{x}^{obs})$  as

$$X_{i,(k)} \text{ from } P_\theta \left( X_i \mid \mathbf{X}^{obs} = \mathbf{x}^{obs}, \mathbf{X}^{(-i),miss} = \mathbf{x}_{(k-1)}^{(-i),miss} \right)$$

$\Rightarrow$  Prediction from empirical distributions analogous

- ▶ Prior inference of  $\theta$  based on limited data  $\mathbf{X}^{obs} = \mathbf{x}^{obs}$  non-trivial

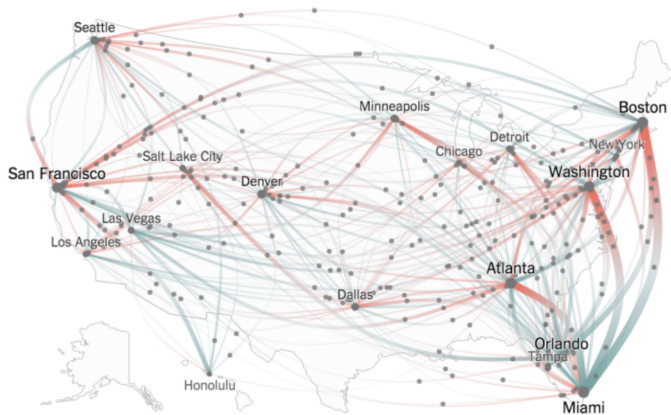
# Network of the week (the last one!)





- ▶ Collaborators of Paul Erdős
- ▶ Character co-appearance in Les Miserables
- ▶ Zachary's karate club
- ▶ Blogosphere of US 2014 elections
- ▶ C. elegans neuronal connectome
- ▶ Internet has no Achilles heel
- ▶ Collaboration between network scientists
- ▶ Coloring problem on human subjects
- ▶ Co-citation network in particle physics
- ▶ Ebola epidemics on Africa

# Network of the week (the last one!)





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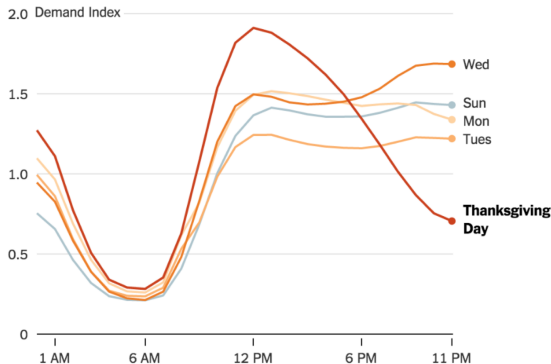
- ▶ Additional flight demand (Google flights) for Thanksgiving
- ▶ Origins in red and destinations in blue (New York Times, 2015)
- ▶ Boston and Seattle vs. Miami and Las Vegas

# Network of the week (the last one!)



## ► Times of flight also tell a story

When People Fly for Thanksgiving

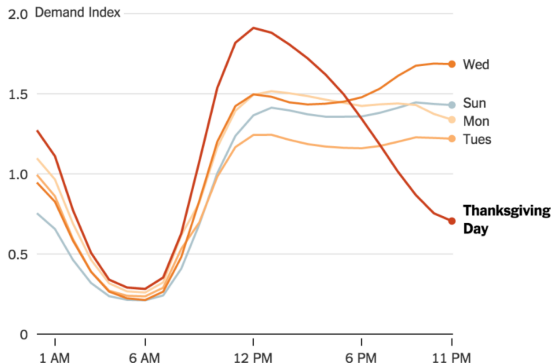


# Network of the week (the last one!)



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When People Fly for Thanksgiving



## ► Take the week off or leave late (Tuesday uncommon)



Nearest-neighbor prediction

Markov random fields

Kernel regression on graphs

Case study: Predicting protein function



- ▶ MRFs specify precise dependency structures in  $\mathbf{X}$ , given the graph  $G$
- ▶ **Q1:** Can we just **learn a function** relating the vertices to their attributes?  
**A1:** Yes! A regression-based approach on  $G$  is in order



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**A1:** Yes! A regression-based approach on  $G$  is in order
- ▶ Methods such as LS regression relate data in Euclidean space
- ▶ **Q2:** Can these methods be tuned to accommodate **graph-indexed data**?  
**A2:** Yes! Kernel methods consisting of:
  - 1) Generalized predictor variables (i.e., encoded using a kernel)
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- ▶ **Key innovation here is the construction of graph kernels**



- ▶ Let  $G(V, E)$  be a graph and  $\mathbf{X} = \{X_i\}_{i \in V}$  a vertex attribute process
  - ⇒ Suppose we observe  $X_i = x_i$  for  $i \in V^{obs} \subset V$ , with  $n = |V^{obs}|$

## Regression on graphs

Learn  $\hat{h} : V \mapsto \mathbb{R}$  describing how attributes vary across vertices.





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Learn  $\hat{h} : V \mapsto \mathbb{R}$  describing how attributes vary across vertices.

- ▶ Graph-indexed data not Euclidean  $\Rightarrow$  **kernel regression methods**
- ▶ **Def:** A function  $K : V \times V \mapsto \mathbb{R}$  is called a **kernel** if for each  $m = 1, \dots, N_v$  and subset of vertices  $\{i_1, \dots, i_m\} \subseteq V$ , matrix

$\mathbf{K}^{(m)} = [K(i_j, i_{j'})] \in \mathbb{R}^{m \times m}$  is symmetric and positive semi-definite



- ▶ Let  $G(V, E)$  be a graph and  $\mathbf{X} = \{X_i\}_{i \in V}$  a vertex attribute process  
⇒ Suppose we observe  $X_i = x_i$  for  $i \in V^{obs} \subset V$ , with  $n = |V^{obs}|$

## Regression on graphs

Learn  $\hat{h} : V \mapsto \mathbb{R}$  describing how attributes vary across vertices.

- ▶ Graph-indexed data not Euclidean ⇒ **kernel regression methods**
- ▶ **Def:** A function  $K : V \times V \mapsto \mathbb{R}$  is called a **kernel** if for each  $m = 1, \dots, N_v$  and subset of vertices  $\{i_1, \dots, i_m\} \subseteq V$ , matrix  $\mathbf{K}^{(m)} = [K(i_j, i_{j'})] \in \mathbb{R}^{m \times m}$  is symmetric and positive semi-definite
- ▶ Think of kernels as functions that produce similarity matrices  
⇒ Kernel regression builds predictors from such similarities  
⇒ Need to also decide on the space  $\mathcal{H}$  where to search for  $\hat{h}$



- ▶ Since  $V$  is finite, represent functions  $h$  on  $V$  as vectors  $\mathbf{h} \in \mathbb{R}^{N_v}$ 
  - ⇒ Form  $\mathbf{K}^{(N_v)} \in \mathbb{R}^{N_v \times N_v}$  by evaluating  $K$  in all pairs  $(i, j) \in V^{(2)}$
  - ⇒ Suppose  $\mathbf{K}^{(N_v)}$  admits an eigendecomposition

$$\mathbf{K}^{(N_v)} = \mathbf{\Phi} \mathbf{\Delta} \mathbf{\Phi}^T$$



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## Kernel regression

Given kernel  $K$  and data  $\mathbf{x}^{obs}$ , kernel regression seeks  $\hat{\mathbf{h}}$  from the class

$$\mathcal{H}_K = \{\mathbf{h} \in \mathbb{R}^{N_v} : \mathbf{h} = \mathbf{\Phi} \boldsymbol{\beta} \text{ and } \boldsymbol{\beta}^\top \mathbf{\Delta}^{-1} \boldsymbol{\beta} < \infty\}$$

- ▶  $\mathcal{H}_K$  is the **reproducing-kernel Hilbert space** induced by  $K$ 
  - ⇒ Members  $\mathbf{h} \in \mathcal{H}_K$  are linear combinations of eigenvectors of  $\mathbf{K}^{(N_v)}$
  - ⇒ Constrained to finite norm  $\|\mathbf{h}\|_{\mathcal{H}} = \|\mathbf{\Phi} \boldsymbol{\beta}\|_{\mathcal{H}} := \boldsymbol{\beta}^\top \mathbf{\Delta}^{-1} \boldsymbol{\beta} < \infty$



- ▶ Choose appropriate  $\hat{\mathbf{h}} \in \mathcal{H}_K$  using **penalized kernel regression**
- ▶ **Q:** Appropriate? Data fidelity and small norm (i.e., low complexity)

$$\hat{\mathbf{h}} = \Phi \hat{\beta}, \text{ where } \hat{\beta} = \arg \min_{\beta} \left[ \sum_{i \in V^{obs}} C(x_i, [\Phi \beta]_i) + \lambda \beta^\top \Delta^{-1} \beta \right]$$

- ▶ Convex loss  $C(\cdot, \cdot)$  encourages goodness of fit to  $\mathbf{x}^{obs}$
  - ▶ The term  $\|\mathbf{h}\|_{\mathcal{H}} = \beta^\top \Delta^{-1} \beta$  penalizes excessive complexity
  - ▶ Tuning parameter  $\lambda$  trades off data fidelity and complexity
- ▶ **Generalized ridge-regression with columns of  $\Phi$  as predictors**  
⇒ Eigenvectors with small eigenvalues penalized more harshly



- ▶ Need to compute the entire  $\Phi$  to find the regression function  $\hat{h}$ 
  - ⇒ Complex to evaluate  $K$  for all vertex pairs  $V^{(2)}$  and find  $\Phi$



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- ▶ Consider instead evaluating  $K$  in  $V \times V^{obs}$ , yielding  $\mathbf{K}^{(N_v, n)} \in \mathbb{R}^{N_v \times n}$   
 $\Rightarrow$  The Representer theorem asserts that  $\hat{\mathbf{h}}$  equivalently given by

$$\hat{\mathbf{h}} = \mathbf{K}^{(N_v, n)} \hat{\alpha}, \text{ where } \hat{\alpha} = \arg \min_{\alpha} \left[ \sum_{i \in V^{obs}} C(x_i, [\mathbf{K}^{(n)} \alpha]_i) + \lambda \alpha^\top \mathbf{K}^{(n)} \alpha \right]$$

- ▶ Just need to evaluate  $K$  in  $V^{obs} \times V^{obs}$  to form  $\mathbf{K}^{(n)}$   
 $\Rightarrow$  Complexity scales with the number of observations  $n$ , not  $N_v$



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- ▶ Just need to evaluate  $K$  in  $V^{obs} \times V^{obs}$  to form  $\mathbf{K}^{(n)}$   
 $\Rightarrow$  Complexity scales with the number of observations  $n$ , not  $N_v$
- ▶ Because  $\hat{\mathbf{h}} = \mathbf{K}^{(N_v, n)} \hat{\alpha}$ , can predict value in  $i \in V^{miss}$  via

$$\hat{h}_i = \sum_{j \in V^{obs}} \hat{\alpha}_j K(i, j)$$





- ▶ Let the  $X_i$  be continuous and the loss quadratic, i.e.,  $C(x, a) = (x - a)^2$
- ▶ The optimization problem defining  $\hat{\alpha}$  thus specializes to

$$\min_{\alpha} \left[ \|\mathbf{x}^{obs} - \mathbf{K}^{(n)}\alpha\|_2^2 + \lambda \alpha^\top \mathbf{K}^{(n)}\alpha \right]$$

⇒ Particular method known as **kernel ridge regression**. Intuition?



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- ▶ Define  $\boldsymbol{\theta} := (\mathbf{K}^{(n)})^{1/2}\alpha$  and  $\mathbf{M} := (\mathbf{K}^{(n)})^{1/2}$ . An equivalent problem is

$$\min_{\boldsymbol{\theta}} \left[ \|\mathbf{x}^{obs} - \mathbf{M}\boldsymbol{\theta}\|_2^2 + \lambda\boldsymbol{\theta}^\top \boldsymbol{\theta} \right]$$

- ▶ **Standard ridge regression** with solution  $\hat{\boldsymbol{\theta}} = (\mathbf{M}^\top \mathbf{M} + \lambda \mathbf{I})^{-1} \mathbf{M}^\top \mathbf{x}^{obs}$   
⇒ The kernel regression function is  $\hat{\mathbf{h}} = \mathbf{K}^{(N_v, n)} (\mathbf{K}^{(n)})^{-1/2} \hat{\boldsymbol{\theta}}$



- ▶ Let binary  $X_i \in \{-1, 1\}$  indicate class membership, for two classes
- ▶ A natural choice in this context is the **logistic loss**, given by

$$C(x, a) = \ln(1 + e^{-xa})$$

⇒ Corresponds to the negative log-likelihood of a Bernoulli RV



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⇒ No closed-form solution for  $\hat{\alpha}$ , need iterative algorithms

- ▶ Given  $\hat{\mathbf{h}} = \mathbf{K}^{(N_v, n)} \hat{\alpha}$ , prediction of  $X_i$  for  $i \in V^{miss}$  based on

$$\hat{P}(X_i = 1 \mid \mathbf{X}^{obs} = \mathbf{x}^{obs}) = \frac{e^{\hat{h}_i}}{1 + e^{\hat{h}_i}}$$



- ▶ In designing a kernel  $K$  on a graph  $G$ , desired properties are:
  - P1)  $\mathbf{K}^{(N_v)}$  is symmetric and positive semi-definite
  - P2)  $K$  captures suspected similarity among vertices in  $V$
- ▶ **Presumption:** proximity of vertices in  $G$  already indicative of similarity
  - $\Rightarrow$  Most kernels proposed are related to the topology of  $G$



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⇒ Most kernels proposed are related to the topology of  $G$
- ▶ **Ex:** the Laplacian kernel is  $\mathbf{K}^{(N_v)} := \mathbf{L}^\dagger$ , where  $^\dagger$  denotes pseudo-inverse  
⇒ Penalty term  $\|\mathbf{h}\|_{\mathcal{H}} = \beta^\top \mathbf{\Delta}^{-1} \beta$  takes the form

$$\begin{aligned}\beta^\top \mathbf{\Delta}^{-1} \beta &= \beta^\top \Phi^\top \Phi \mathbf{\Delta}^{-1} \Phi^\top \Phi \beta \\ &= \mathbf{h}^\top \mathbf{K}^\dagger \mathbf{h} = \mathbf{h}^\top \mathbf{L} \mathbf{h} \\ &= \sum_{(i,j) \in E} (h_i - h_j)^2\end{aligned}$$

- ▶ Kernel regression seeks smooth  $\hat{\mathbf{h}}$  with respect to the topology of  $G$



- ▶ Laplacian kernel  $\mathbf{K} = \mathbf{L}^\dagger$  encodes similarity among vertices through  $\mathbf{A}$ 
  - ⇒ Can encode similarity through paths, powers of  $\mathbf{A}$  and  $\mathbf{L}$





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- ▶ Popular choice incorporating all powers of  $\mathbf{L}$  is the diffusion kernel

$$\mathbf{K} = e^{-\zeta \mathbf{L}} := \sum_{m=0}^{\infty} \frac{(-\zeta)^m}{m!} \mathbf{L}^m$$

- ▶ Decay factor  $0 < \zeta < 1$  controls similarity assigned to longer paths
- ▶ Defined in terms of the matrix exponential  $e^{-\zeta \mathbf{L}}$



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- ▶ Decay factor  $0 < \zeta < 1$  controls similarity assigned to longer paths
- ▶ Defined in terms of the **matrix exponential**  $e^{-\zeta \mathbf{L}}$
- ▶ Treating  $\mathbf{K}$  as a function of  $\zeta$  yields the differential equation

$$\frac{\partial \mathbf{K}}{\partial \zeta} = -\mathbf{L} \mathbf{K}$$

⇒ Parallels the heat equation in physics, motivating its name



- ▶ Let  $\mathbf{L} = \mathbf{\Phi}\mathbf{\Gamma}\mathbf{\Phi}^\top$ , with  $\mathbf{\Gamma} = [\gamma_1, \dots, \gamma_{N_v}]^\top$  and  $\mathbf{\Phi} = [\phi_1, \dots, \phi_{N_v}]$
- ▶ Laplacian and diffusion kernels within class of **regularization kernels**

$$\mathbf{K} = \sum_{i=1}^{N_v} r^{-1}(\gamma_i) \phi_i \phi_i^\top$$

$\Rightarrow \mathbf{K}$  is the inverse of the **regularized Laplacian**  $r(\mathbf{L}) := \mathbf{\Phi}r(\mathbf{\Gamma})\mathbf{\Phi}^\top$



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- ▶ Regularization function  $r(\cdot) \geq 0$  is increasing, including:

Ex: Identity function  $r(\gamma) = \gamma$

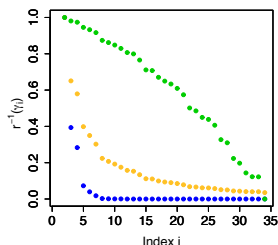
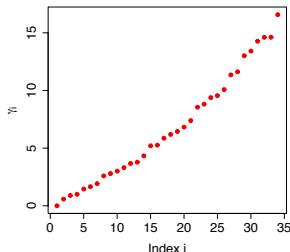
Ex: Exponential function  $r(\gamma) = \exp(\zeta \gamma)$

Ex: Linear inverse function  $r(\gamma) = (1 - \frac{\gamma}{\gamma_{\max}})^{-1}$

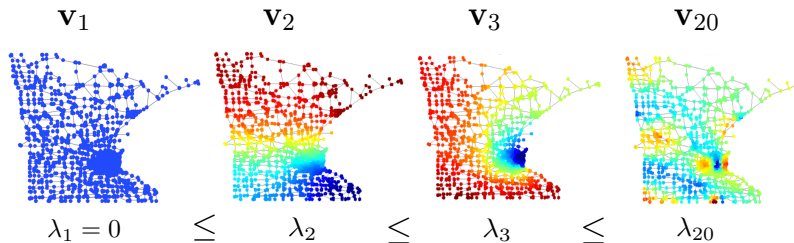
- ▶ All  $\mathbf{K}$  have identical eigenvectors, just vary the eigenvalues  $r^{-1}(\gamma_i)$   
 $\Rightarrow$  **Same predictors in the kernel regression, different penalty**



- ▶ Network of lawyer collaboration, connected component with  $N_v = 34$



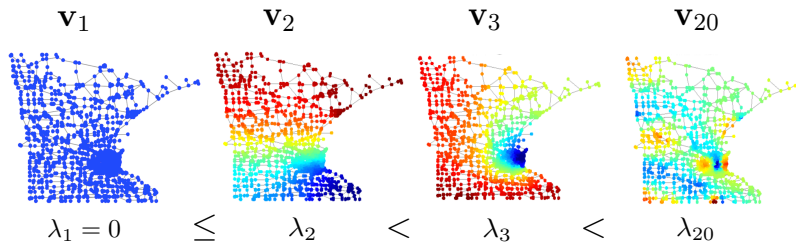
- ▶ Left figure shows eigenvalues  $\gamma_1, \dots, \gamma_{34}$  of  $\mathbf{L}$ , recall  $\gamma_1 = 0$
- ▶ Right figure shows values of  $r^{-1}(\gamma_i)$ , for  $i = 2, \dots, 34$
- ▶ Regularizers: **identity**, **exponential**, and **linear inverse** functions
  - ⇒ First two damp most eigenvalues, only few  $\phi_i$  affect  $\mathbf{K}$
  - ⇒ Small decay in the last, all  $\phi_i$  play a substantial role in  $\mathbf{K}$



- Early eigenvectors have entries relatively more uniform color  
⇒ Eigenvectors become less 'smooth' with increasing eigenvalue



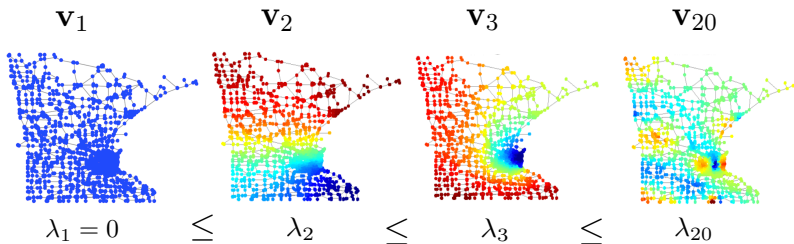
$$\mathbf{v}_k^T \mathbf{L} \mathbf{v}_k = \sum_{(i,j) \in \mathcal{E}} A_{ij} ([\mathbf{v}_k]_i - [\mathbf{v}_k]_j)^2 = \text{TV}(\mathbf{v}_k)$$



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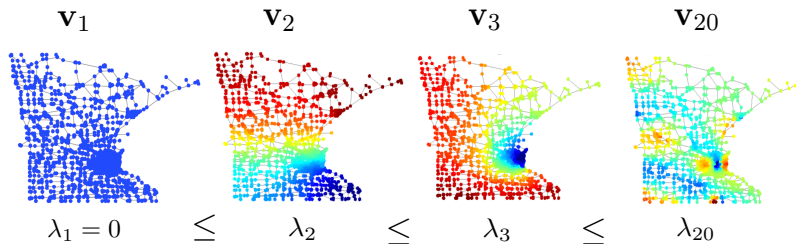


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Nearest-neighbor prediction

Markov random fields

Kernel regression on graphs

Case study: Predicting protein function



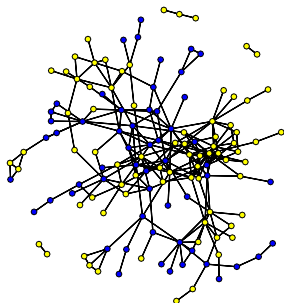
- ▶ Proteins integral to complex biochemical processes within organisms
  - ⇒ Understanding their **function** is critical in biology and medicine
- ▶ But  $\sim 70\%$  of genes code for proteins with unknown function
  - ⇒ Prediction of protein function a task of great importance



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  - ⇒ Understanding their **function** is critical in biology and medicine
- ▶ But  $\sim 70\%$  of genes code for proteins with unknown function
  - ⇒ Prediction of protein function a task of great importance
- ▶ Methodologies explored so far:
  - (i) Traditional experiment-intensive approaches
  - (ii) Methods based on sequence-similarity, protein structure
  - (iii) Network-based methods
- ▶ **Networks of protein-protein interactions** natural in the latter

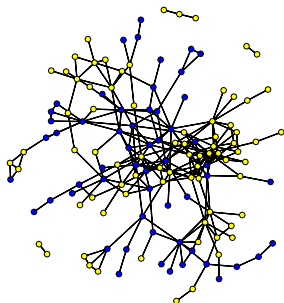


- ▶ Baker's yeast data, formally known as *Saccharomyces cerevisiae*
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- ▶ Predict functional annotation **intracellular signaling cascade (ICSC)**
  - ⇒ Signal transduction, how cells react to the environment
- ▶ Let  $\mathbf{X} = \{X_i\}_{i \in V}$  denote the vertex process of the annotation ICSC
  - ▶  $X_i = 1$  if protein  $i$  annotated ICSC (**yellow**),  $X_i = 0$  otherwise (**blue**)



**Method 1:** nearest-neighbor (NN) prediction with varying threshold  $\tau$

**Method 2:** MRF with predictors counting nodes with and without ICSC

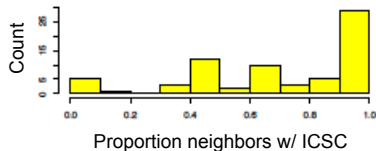
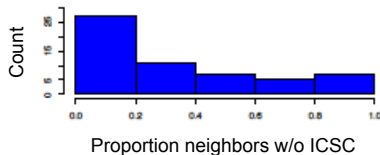
- ▶ Parameters  $(\alpha, \beta_1, \beta_2)$  estimated via maximum pseudo-likelihood
- ▶ Drew 1,000 samples of vertex annotations using a Gibbs sampler
- ▶ Predictions based on empirical estimates of  $P[X_i = 1 \mid \mathbf{X}^{obs} = \mathbf{x}^{obs}]$

**Method 3:** kernel logistic regression (KLR) with  $\mathbf{K} = \mathbf{L}^\dagger$  and  $\lambda = 0.01$

- ▶ In all cases predictions generated using 10-fold cross validation
  - ⇒ 90% of the labels used to train the prediction methods
  - ⇒ Remaining 10% used to test obtained predictors



- Empirical proportions of neighbors with and without ICSC



⇒ Classes less-well separated than for the lawyer data

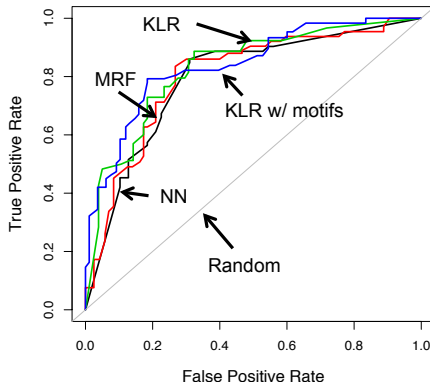
- Recall nearest-neighbor prediction rule for  $\tau = 0.5$  is

$$\hat{X}_i = \mathbb{I} \left\{ \frac{\sum_{j \in \mathcal{N}_i} x_j}{|\mathcal{N}_i|} > 0.5 \right\}$$

⇒ Yields a decent missclassification rate of roughly 23%



- ROC curves depict predictive performance



- All methods performed comparably. Area under the curve values:  
NN - 0.80, MRF - 0.82, KLR - 0.83, KLR w/ motifs - 0.85



- ▶ Not surprising that **all three methods performed similarly**
  - ⇒ NN and MRF use same statistics  $\sum_{j \in \mathcal{N}_i} x_j$  and  $\sum_{j \in \mathcal{N}_i} (1 - x_j)$
  - ⇒ **L** key to many graph partitioning algorithms



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  - ⇒ **L** key to many graph partitioning algorithms
- ▶ Simple NN prediction comparable to sophisticated classification methods
  - ⇒ **MRF and kernels flexible to incorporate information beyond G**
- ▶ **Ex:** certain DNA sequence motifs useful for function prediction
  - ▶ 114 out of 134 proteins associated with one or more of 154 motifs
  - ▶ Encode associations in  $\mathbf{M} \in \{0, 1\}^{134 \times 154}$ , construct kernel  $\bar{\mathbf{K}} = \mathbf{M}\mathbf{M}^T$
  - ⇒ **Improvement in performance with the combined kernel**

$$\mathbf{K} = 0.5 \times \mathbf{L}^\dagger + 0.5 \times \mathbf{M}\mathbf{M}^T$$



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- ▶ We did not go into too much detail within each topic
- ▶ Act as trigger for future exploration and inspiration for project
- ▶ Feel free to contact me (even after this semester) if you want to discuss