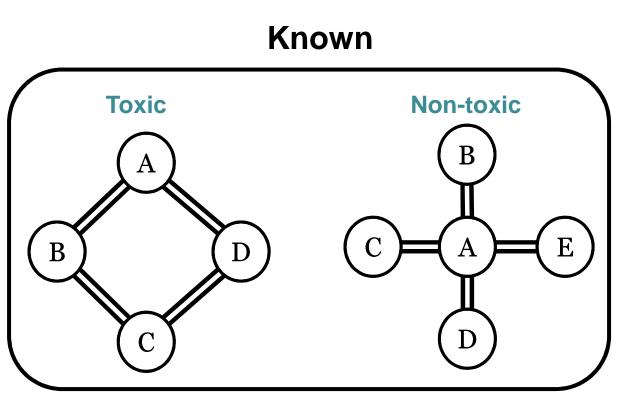
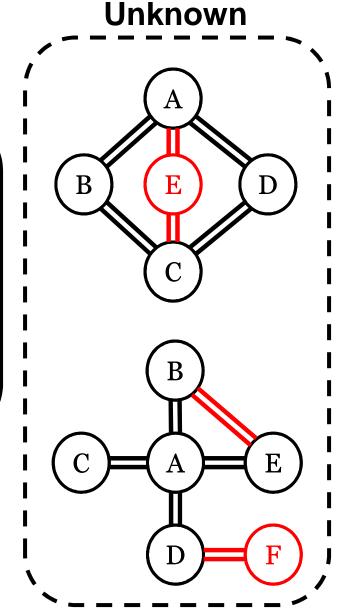
Graph Classification

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 - WEBKB example dataset
- Related Works

Example: Molecular Structures

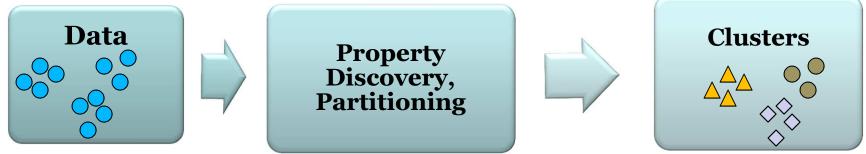


Task: predict whether molecules are toxic, given set of known examples

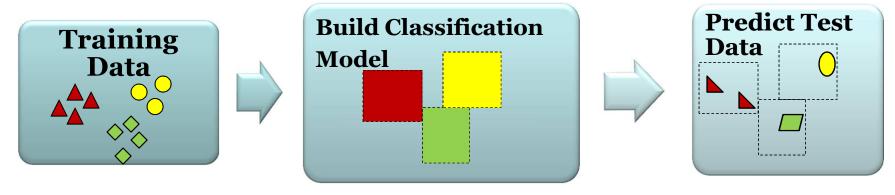


Solution: Machine Learning

- Computationally discover and/or predict properties of interest of a set of data
- Two Flavors:
 - Unsupervised: discover discriminating properties among groups of data (Example: Clustering)

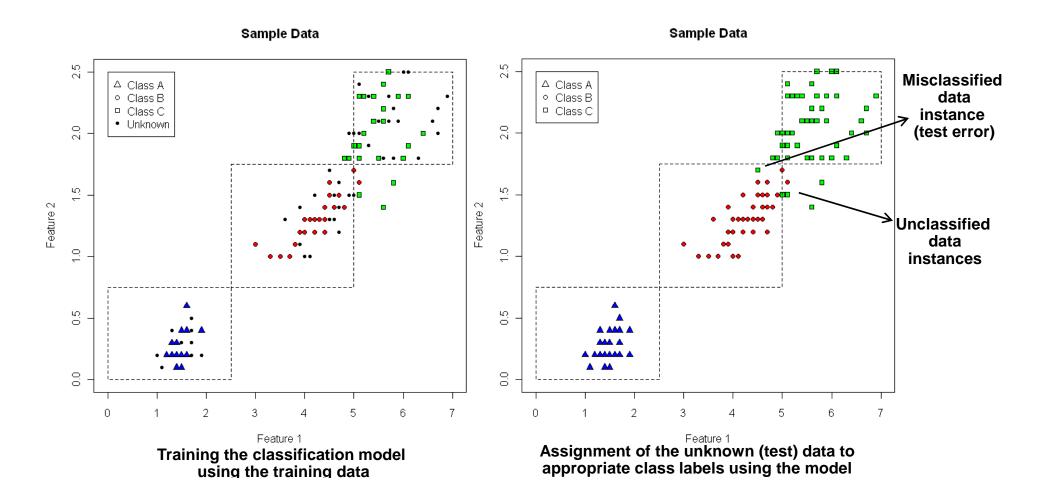


 Supervised: known properties, categorize data with unknown properties (Example: Classification)



Classification

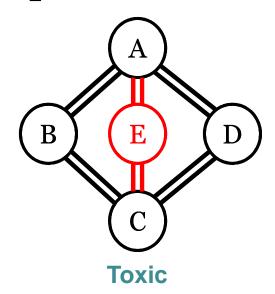
- Classification: The task of assigning class labels in a discrete class label set Y to input instances in an input space X
- Ex: Y = { toxic, non-toxic }, X = {valid molecular structures}



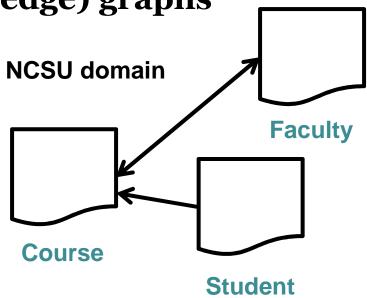
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Classification with Graph Structures

- Graph classification (between-graph)
 - Each full graph is assigned a class label
- Example: Molecular graphs



- Vertex classification (within-graph)
 - Within a single graph,
 each vertex is assigned
 a class label
- Example: Webpage (vertex) / hyperlink (edge) graphs



Relating Graph Structures to Classes?

Frequent Subgraph Mining (Chapter 7)

Associate frequently occurring subgraphs with classes

Anomaly Detection (Chapter 11)

Associate anomalous graph features with classes

*Kernel-based methods (Chapter 4)

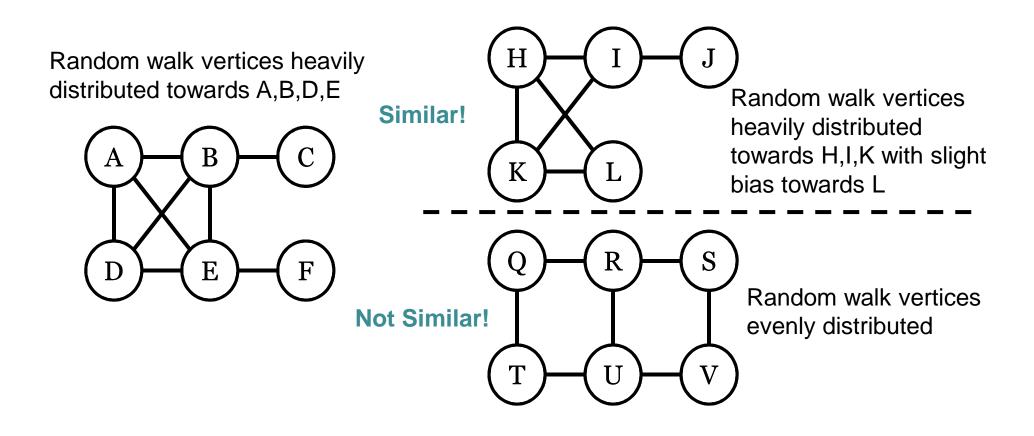
 Devise kernel function capturing graph similarity, use vectorbased classification via the *kernel trick*

Relating Graph Structures to Classes?

- This chapter focuses on kernel-based classification.
- Two step process:
 - Devise kernel that captures property of interest
 - Apply kernelized classification algorithm, using the kernel function.
- Two type of graph classification looked at
 - Classification of Graphs
 - Direct Product Kernel
 - Classification of Vertices
 - Laplacian Kernel
- See Supplemental slides for *support vector machines* (SVM), one of the more well-known kernelized classification techniques.

Walk-based similarity (Kernels Chapter)

• Intuition – two graphs are similar if they exhibit similar patterns when performing random walks



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Direct Product Graph – Formal Definition

Input Graphs

$$G_1 = (V_1, E_1)$$

 $G_2 = (V_2, E_2)$

Direct Product Notation

$$G_X = G_1 \times G_2$$

Intuition

Vertex set: each vertex of V_1 paired with *every* vertex of V_2

Edge set: Edges exist only if both pairs of vertices in the respective graphs contain an edge

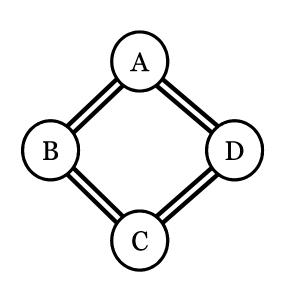
Direct Product Vertices

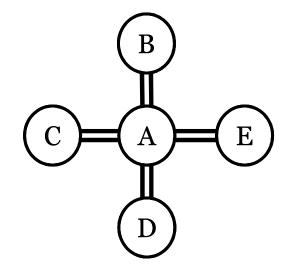
$$V(G_{\mathcal{X}}) = \{(a,b) \in V_1 \times V_2\}$$

Direct Product Edges

$$E(G_x) = \{((a,b),(c,d)) | (a,c) \in E_1 \text{ and } (b,d) \in E_2\}$$

Direct Product Graph - example





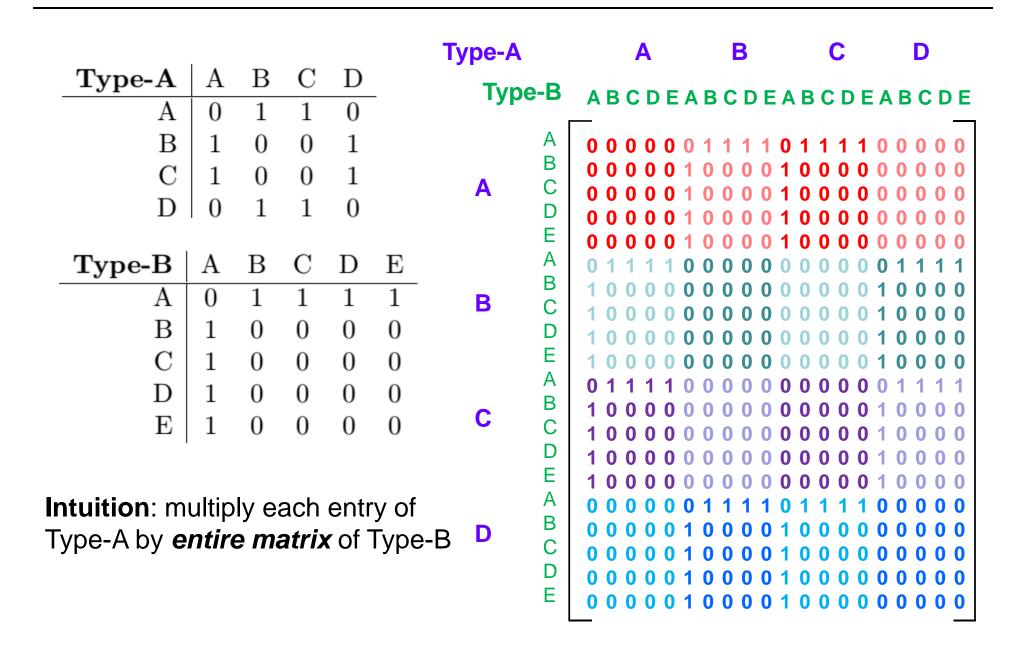
Type-A

Type-B

Type-A	A	В	\mathbf{C}	D
A	0	1	1	0
В	1	0	0	1
\mathbf{C}	1	0	0	1
D	0	1	1 0 0 1	0

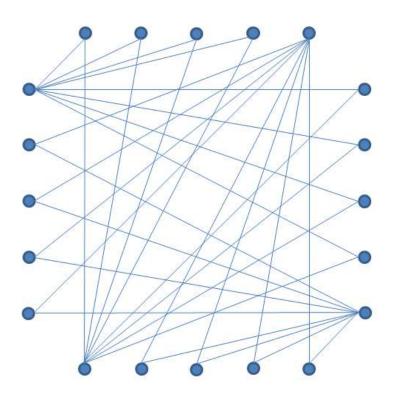
Туре-В А В С D Е	A	В	\mathbf{C}	D	\mathbf{E}
A	0	1	1	1	1
В	1	0	0	0	0
$^{\mathrm{C}}$	1	0	0	0	0
D	1	0	0	0	0
\mathbf{E}	1	0	0	0	0

Direct Product Graph Example



Direct Product Kernel (see Kernel Chapter)

- 1. Compute direct product graph G_x
- 2. Compute the maximum inand out-degrees of *Gx*, *di* and *do*.
- 3. Compute the decay constant γ < 1 / min(di, do)
- 4. Compute the infinite weighted geometric series of walks (array A).
- 5. Sum over all vertex pairs.



Direct Product Graph of Type-A and Type-B

$$k(G_1, G_2) = \sum_{i,j} (I - \frac{A_{ij}}{\gamma})^{-1}$$

Kernel Matrix

$$K(G_1, G_1), K(G_1, G_2), ..., K(G_1, G_n)$$

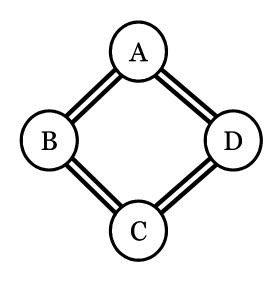
 $K(G_2, G_1), K(G_2, G_2), ..., K(G_2, G_n)$
...
 $K(G_n, G_1), K(G_n, G_2), ..., K(G_n, G_n)$

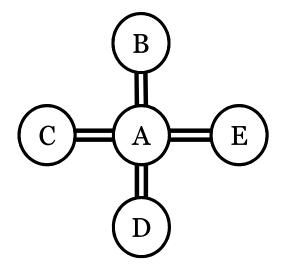
- Compute direct product kernel for all pairs of graphs in the set of known examples.
- This matrix is used as input to SVM function to create the classification model.
 - *** Or any other kernelized data mining method!!!

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Predictive Toxicology (PTC) dataset

- The PTC dataset is a collection of molecules that have been tested positive or negative for toxicity.
- 1. # R code to create the SVM model
- 2. data("PTCData") # graph data
- 3. data("PTCLabels") # toxicity information
- 4. # select 5 molecules to build model on
- 5. sTrain = sample(1:length(PTCData),5)
- 6. PTCDataSmall <- PTCData[sTrain]
- 7. PTCLabelsSmall <- PTCLabels[sTrain]
- 8. # generate kernel matrix
- K = generateKernelMatrix (PTCDataSmall, PTCDataSmall)
- 10. # create SVM model
- 11. model =ksvm(K, PTCLabelsSmall, kernel='matrix')





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Kernels for Vertex Classification

- von Neumann kernel
 - (Chapter 6)

$$K = \sum_{i=1}^{\infty} \gamma^{i-1} (B^T B)^i$$

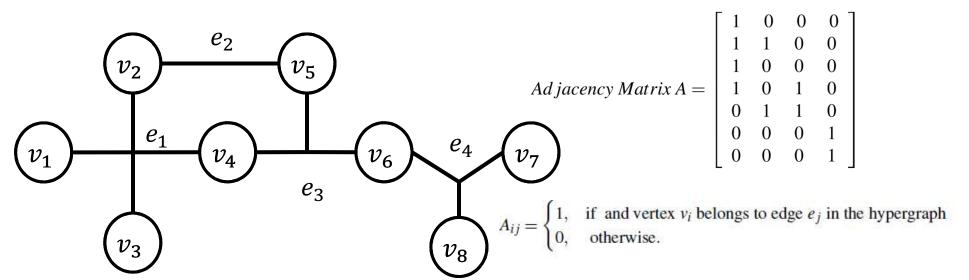
- Regularized Laplacian
 - (This chapter)

$$K = \sum_{i=1}^{\infty} \gamma^{i} (-L)^{i}$$

Example: Hypergraphs

- A hypergraph is a generalization of a graph, where an edge can connect any number of vertices
- I.e., each edge is a subset of the vertex set.

- Example: word-webpage graph
 - Vertex webpage
 - Edge set of pages containing same word



"Flattening" a Hypergraph

- Given hypergraph matrix A, $A \times A^T$ represents "similarity matrix"
- Rows, columns represent vertices
- (i, j) entry number of
- Problem: some "similar" as 1 and 2)

$$Adjacency\ Matrix\ A = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

Laplacian Matrix

- In the mathematical field of graph theory the Laplacian matrix (L), is a matrix representation of a graph.
- L = D M
 - M adjacency matrix of graph (e.g., A*A^T from hypergraph flattening)
 - D degree matrix (diagonal matrix where each (i,i) entry is vertex i's [weighted] degree)
- Laplacian used in many contexts (e.g., spectral graph theory)

$$AA^{T} = \begin{bmatrix} 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ 1 & 2 & 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 \end{bmatrix}$$

$$D = \sum_{j} [AA^{T}]_{ij}$$

$$D = \begin{bmatrix} 4 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 6 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 6 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 2 \end{bmatrix}$$

$$L = D - AA^{T}$$

$$L = \begin{bmatrix} 3 & -1 & -1 & -1 & 0 & 0 & 0 \\ -1 & 4 & -1 & -1 & -1 & 0 & 0 \\ -1 & -1 & 3 & -1 & 0 & 0 & 0 \\ -1 & -1 & -1 & 4 & -1 & 0 & 0 \\ 0 & -1 & 0 & -1 & 2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 0 & 0 & -1 & 1 \end{bmatrix}$$

Normalized Laplacian Matrix

 Normalizing the matrix helps eliminate bias in matrix toward high-degree vertices

Original L

$$L = \begin{bmatrix} 3 & -1 & -1 & -1 & 0 & 0 & 0 \\ -1 & 4 & -1 & -1 & -1 & 0 & 0 & 0 \\ -1 & -1 & 3 & -1 & 0 & 0 & 0 & 0 \\ -1 & -1 & -1 & 4 & -1 & 0 & 0 & 0 \\ 0 & -1 & 0 & -1 & 2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Regularized L

$$L = \begin{bmatrix} 3 & -1 & -1 & -1 & 0 & 0 & 0 \\ -1 & 4 & -1 & -1 & -1 & 0 & 0 \\ -1 & -1 & 3 & -1 & 0 & 0 & 0 \\ 0 & -1 & -1 & -1 & 4 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 0 & 0 & -1 & 1 \end{bmatrix} \quad L = \begin{bmatrix} 1.0 & -0.20 & -0.3 & -0.2 & 0.0 & 0.0 & 0.0 \\ -0.2 & 1.0 & -0.2 & -0.2 & -0.2 & 0.0 & 0.0 & 0.0 \\ -0.3 & -0.2 & 1.0 & -0.2 & 0.0 & 0.0 & 0.0 & 0.0 \\ -0.2 & -0.2 & -0.2 & -0.2 & 1.0 & -0.2 & 0.0 & 0.0 & 0.0 \\ 0.0 & -0.2 & 0.0 & -0.2 & 1.0 & -0.2 & 0.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1.0 & -0.5 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & -0.5 & 1.0 & 0.0 & 0.0 & 0.0 \end{bmatrix}$$

Laplacian Kernel

- Uses walk-based geometric series, only applied to regularized Laplacian matrix
- Decay constant NOT degree-based – instead tunable parameter < 1

$$K = \sum_{i=1}^{\infty} \gamma^{i} (-L)^{i}$$

$$K = (I + \gamma L)^{-1}$$

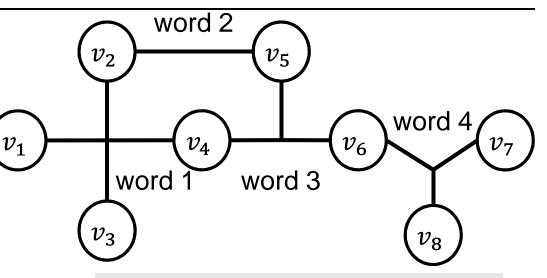
$$L = \begin{bmatrix} 1.0 & -0.20 & -0.3 & -0.2 & 0.0 & 0.0 & 0.0 \\ -0.2 & 1.0 & -0.2 & -0.2 & -0.2 & 0.0 & 0.0 \\ -0.3 & -0.2 & 1.0 & -0.2 & 0.0 & 0.0 & 0.0 \\ -0.2 & -0.2 & -0.2 & 1.0 & -0.2 & 0.0 & 0.0 \\ 0.0 & -0.2 & 0.0 & -0.2 & 1.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1.0 & -0.5 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & -0.5 & 1.0 \end{bmatrix}$$

Regularized L

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WEBKB dataset

- The WEBKB dataset is a collection of web pages that include samples from four universities website.
- The web pages are assigned into five distinct classes according to their contents namely course, faculty, student, project and staff.
- The web pages are searched for the most commonly used words. There are 1073 words that are encountered at least with a frequency of 10.



- 1. # R code to create the SVM model
- 2. data(WEBKB)
- 3. # generate kernel matrix
- 4. K = generateKernelMatrixWithinGraph(WEBKB)
- 5. # create sample set for testing
- 6. holdout <- sample (1:ncol(K), 20)
- 7. # create SVM model
- B. model =ksvm(K[-holdout,-holdout], y, kernel='matrix')

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- Kernel-based vector classification Support Vector Machines
- Related Works

Related Work - Classification on Graphs

Graph mining chapters:

- Frequent Subgraph Mining (Ch. 7)
- Anomaly Detection (Ch. 11)
- Kernel chapter (Ch. 4) discusses in detail alternatives to the direct product and other "walk-based" kernels.

gBoost – extension of "boosting" for graphs

- Progressively collects "informative" frequent patterns to use as features for classification / regression.
- Also considered a frequent subgraph mining technique (similar to gSpan in Frequent Subgraph Chapter).
- Tree kernels similarity of graphs that are trees.

Related Work – Traditional Classification

Decision Trees

- Classification model → tree of conditionals on variables, where leaves represent class labels
- Input space is typically a set of discrete variables

Bayesian belief networks

- Produces directed acyclic graph structure using Bayesian inference to generate edges.
- Each vertex (a variable/class) associated with a probability table indicating likelihood of event or value occurring, given the value of the determined dependent variables.

Support Vector Machines

- Traditionally used in classification of real-valued vector data.
- See Kernels chapter for kernel functions working on vectors.

Related Work – Ensemble Classification

 Ensemble learning: algorithms that build multiple models to enhance stability and reduce selection bias.

Some examples:

- Bagging: Generate multiple models using samples of input set (with replacement), evaluate by averaging / voting with the models.
- Boosting: Generate multiple *weak* models, weight evaluation by some measure of model accuracy.

Related Work – Evaluating, Comparing Classifiers

- This is the subject of Chapter 12, Performance Metrics
- A very brief, "typical" classification workflow:
 - 1. Partition data into *training*, *test* sets.
 - 2. Build classification model using only the training set.
 - 3. Evaluate accuracy of model using only the test set.
- Modifications to the basic workflow:
 - Multiple rounds of training, testing (cross-validation)
 - Multiple classification models built (bagging, boosting)
 - More sophisticated sampling (all)

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