

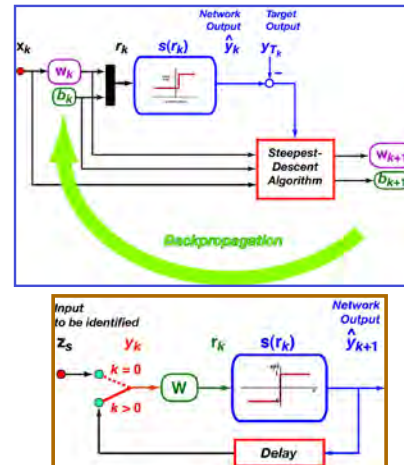
# Neural Networks

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Robotics and Intelligent Systems, MAE 345,  
Princeton University, 2015

## Learning Objectives

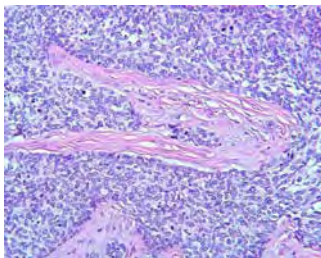
- Associative/recurrent networks
  - Hopfield network
  - Adaptive resonance theory network
- Unsupervised training
  - k-means clustering
  - Self-organizing map
- Deep learning
  - Restricted Boltzmann machine
  - Semi-supervised learning



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<http://www.princeton.edu/~stengel/MAE345.html>

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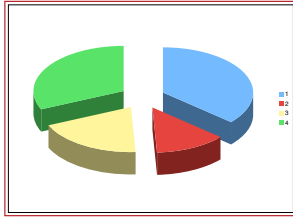
## Small, Round Blue-Cell Tumor Classification Example



Desmoplastic small,  
round blue-cell tumors

- Childhood cancers, including
  - Ewing's sarcoma (EWS)
  - Burkitt's Lymphoma (BL)
  - Neuroblastoma (NB)
  - Rhabdomyosarcoma (RMS)
- cDNA microarray analysis presented by J. Khan, *et al.*, *Nature Medicine*, 2001, 673-679.
  - 96 transcripts chosen from 2,308 probes for training
  - 63 EWS, BL, NB, and RMS training samples
- Source of data for my analysis

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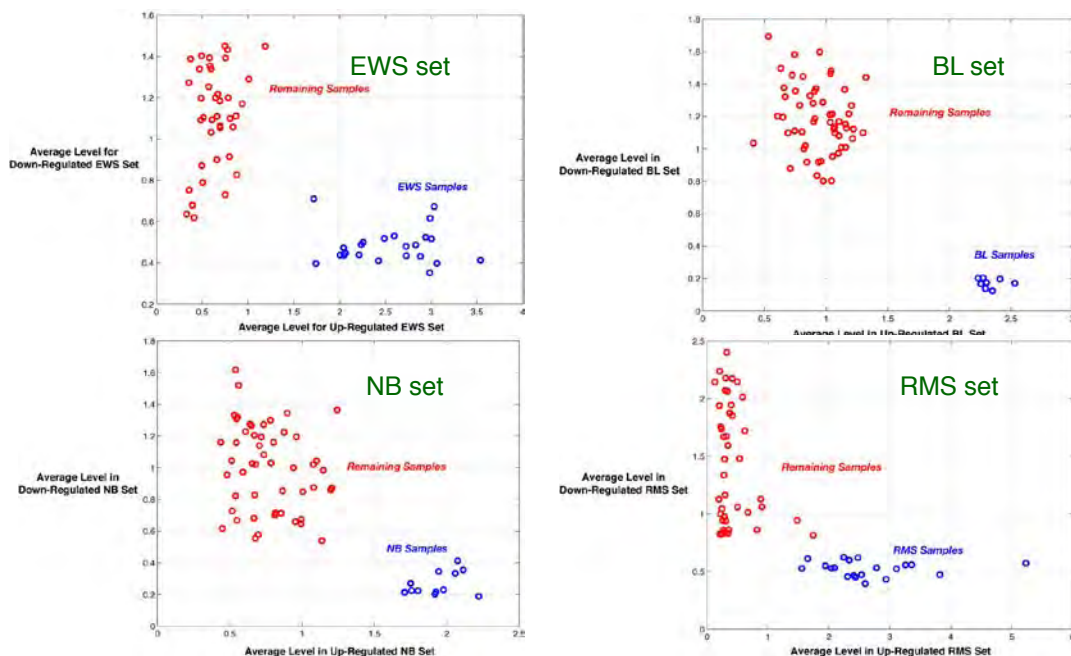


## Overview of Present SRBCT Analysis

- **Transcript selection by  $t$  test**
  - 96 transcripts, 12 highest and lowest  $t$  values for each class
  - Overlap with Khan set: 32 transcripts
- **Ensemble averaging of genes with highest and lowest  $t$  values in each class**
  - Cross-plot of ensemble averages
- **Classification by sigmoidal neural network**
  - Validation of neural network
    - Novel set simulation
    - Leave-one-out simulation

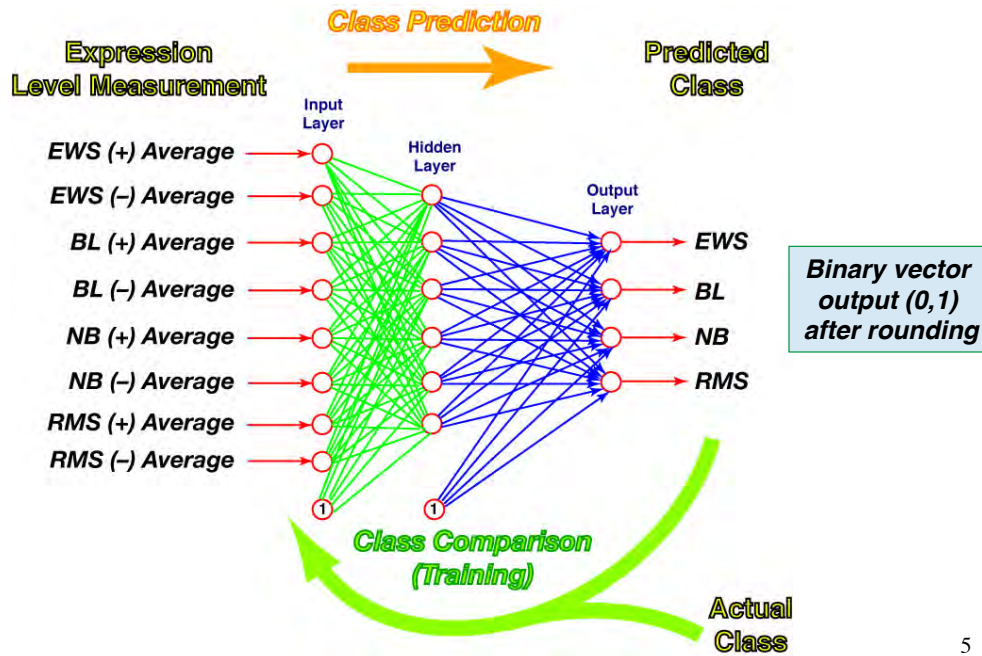
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## Clustering of SRBCT Ensemble Averages



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# SRBCT Neural Network



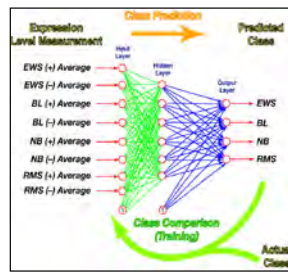
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## Neural Network Training Set

Each input row is an **ensemble average** for a transcript set, normalized in  $(-1,+1)$

Identifier	Sample 1	Sample 2	Sample 3	...	Sample 62	Sample 63
Target Output	EWS	EWS	EWS	...	RMS	RMS
Transcript Training Set	EWS(+) <i>Average</i>	EWS(+) <i>Average</i>	EWS(+) <i>Average</i>	...	EWS(+) <i>Average</i>	EWS(+) <i>Average</i>
	EWS(-) <i>Average</i>	EWS(-) <i>Average</i>	EWS(-) <i>Average</i>	...	EWS(-) <i>Average</i>	EWS(-) <i>Average</i>
	BL(+) <i>Average</i>	BL(+) <i>Average</i>	BL(+) <i>Average</i>	...	BL(+) <i>Average</i>	BL(+) <i>Average</i>
	BL(-) <i>Average</i>	BL(-) <i>Average</i>	BL(-) <i>Average</i>	...	BL(-) <i>Average</i>	BL(-) <i>Average</i>
	NB(+) <i>Average</i>	NB(+) <i>Average</i>	NB(+) <i>Average</i>	...	NB(+) <i>Average</i>	NB(+) <i>Average</i>
	NB(-) <i>Average</i>	NB(-) <i>Average</i>	NB(-) <i>Average</i>	...	NB(-) <i>Average</i>	NB(-) <i>Average</i>
	RMS(+) <i>Average</i>	RMS(+) <i>Average</i>	RMS(+) <i>Average</i>	...	RMS(+) <i>Average</i>	RMS(+) <i>Average</i>
	RMS(-) <i>Average</i>	RMS(-) <i>Average</i>	RMS(-) <i>Average</i>	...	RMS(-) <i>Average</i>	RMS(-) <i>Average</i>

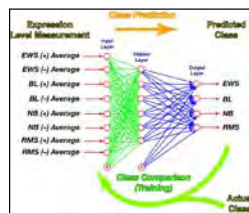
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## SRBCT Neural Network Training

- **Neural network**
  - 8 ensemble-average inputs
  - various # of sigmoidal neurons
    - 4 linear output neurons
    - 4 outputs
- **Training accuracy**
  - Train on all 63 samples
  - Test on all 63 samples
- **100% accuracy**

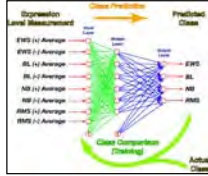
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## Leave-One-Out Validation of SRBCT Neural Network

- **Remove a single sample**
  - Train on remaining samples (125 times)
  - Evaluate class of the removed sample
    - Repeat for each of 63 samples
- **6 sigmoids: 99.96% accuracy (3 errors in 7,875 trials)**
- **12 sigmoids: 99.99% accuracy (1 error in 7,875 trials)**

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## Novel-Set Validation of SRBCT Neural Network

- Network always chooses one of four classes (i.e., “unknown” is not an option)
- Test on 25 novel samples (400 times each)
  - 5 EWS
  - 5 BL
  - 5 NB
  - 5 RMS
- 5 samples of unknown class
- 99.96% accuracy on first 20 novel samples (3 errors in 8,000 trials)
  - 0% accuracy on unknown classes

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## Observations of SRBCT Classification using Ensemble Averages

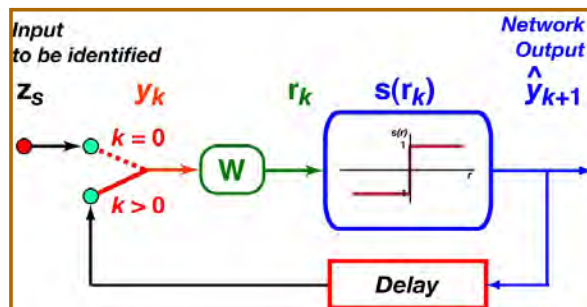
- *t* test identified strong features for classification in this data set
- Neural networks easily classified the four data types
  - **Caveat:** Small, round blue-cell tumors occur in different tissue types
    - Ewing’s sarcoma: Bone tissue
    - Burkitt’s Lymphoma: Lymph nodes
    - Neuroblastoma: Nerve tissue
    - Rhabdomyosarcoma: Soft tissue

Gene expression (i.e., mRNA) level is linked to tissue difference as well as tumor genetics

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# Recurrent Networks

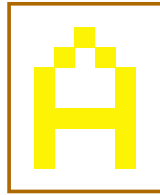
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## Recurrent Networks

- **Recursion to identify an unknown object**
  - Network is given a single, fixed input, and it iterates to a solution
- **Convergence and stability of the network are critical issues**
- **Single network may have many stable states**
  - Classified outputs of the map
  - Pattern recognition with noisy data

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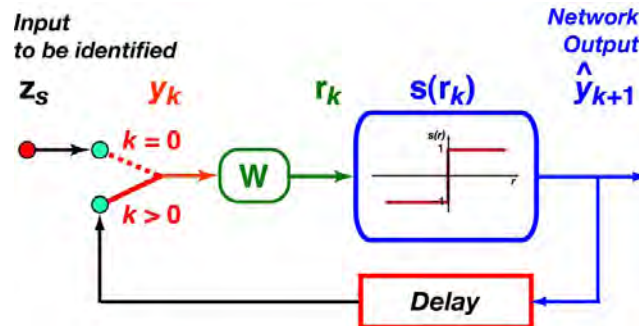


## Hopfield Network

- **Bipolar**  $(-1,1)$  inputs and outputs
  - $\dim(y) = n \times 1$
- **Supervised training with perfect exemplar outputs**
- **Noisy measurement of an exemplar as input to be identified**
- **Network operation**

$$\hat{y}_0 = z_s$$

- **Iterate to convergence**



$$z_s = y_s + n_s$$

$$\hat{y}_{k+1} = s(r_k) = s(W \hat{y}_k)$$

$$\hat{y}_{i,k+1} = \begin{cases} 1, & r_{i,k} > 0 \\ \text{Unchanged}, & r_{i,k} = 0 \\ -1, & r_{i,k} < 0 \end{cases}, i = 1 \text{ to } n$$

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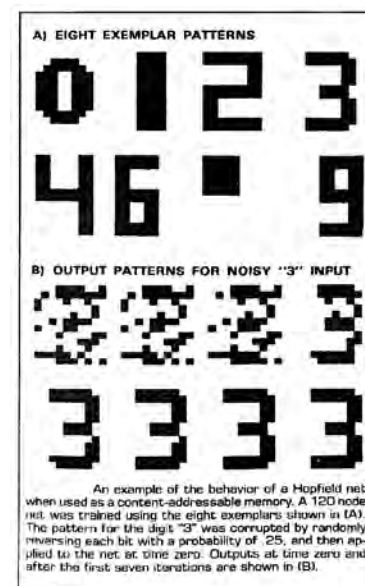
## Training a Hopfield Network

- **Network training**
  - Given  $M$  exemplars,  $y_s$  ( $n \times 1$ )
  - Each exemplar is a character represented by  $n$  pixels
  - Batch calculation of weighting matrix

$$W = \sum_{s=1}^M (y_s y_s^T - I_n)$$

$$= \begin{bmatrix} y_1^2 - 1 & y_1 y_2 & \dots \\ y_1 y_2 & y_2^2 - 1 & \dots \\ \dots & \dots & \dots \end{bmatrix}$$

- **No iterations to define weights**
- **Large number of weights**
- **Limited number of exemplars** ( $< 0.15 n$ )
- **Similar exemplars pose a problem**



$$n = 120; \quad M = 8$$

$$\# \text{ weights} = n^2 = 14,400$$

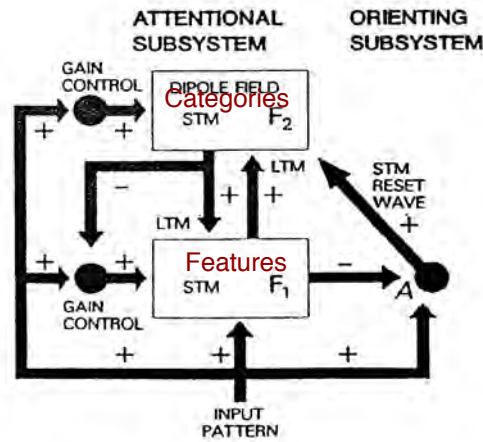
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# Adaptive Resonance Theory Network

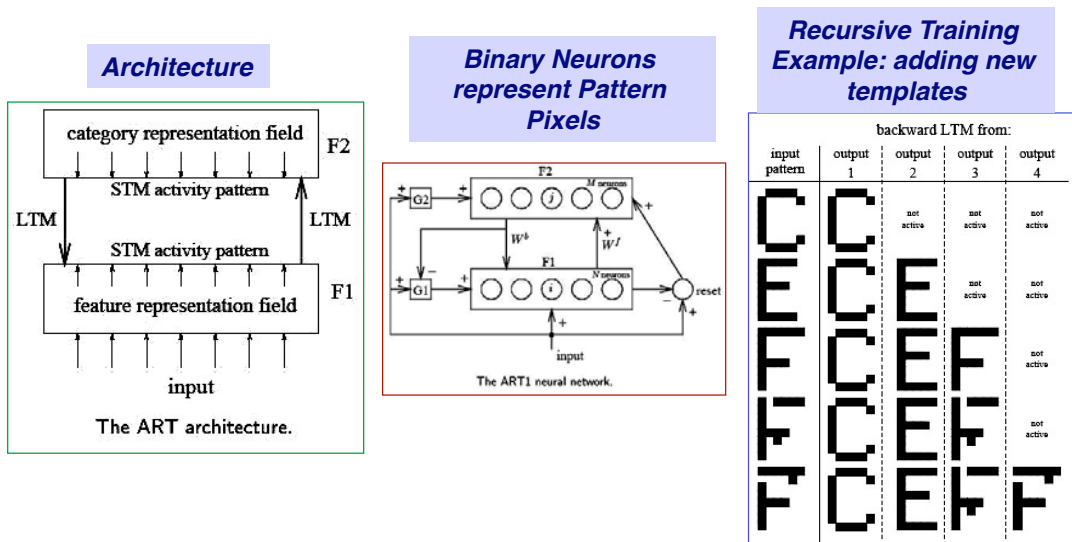
(Grossberg, Carpenter, 1976)

- Self-organizing and self-stabilizing network for **binary pattern recognition (ART-1)**
- Subjective evolution through “Fuzzy ART”
- Learns new patterns when it discerns sufficient mismatch from old patterns
  - Long-Term Memory
  - Short-Term Memory
  - Stability and plasticity
  - Unsupervised and supervised learning
  - “Bottom-up” input
  - “Top-down” priming
  - Pre-cursor to “deep learning”



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# Adaptive Resonance Theory Network



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# Neural Networks with Unsupervised Learning

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## Self-Organizing Map (Kohonen, 1981)



- **Competitive, unsupervised learning**
- **Premise:** input signal patterns that are close produce outputs that are close
- Ordered inputs produce a spacial distribution, i.e., a map
- Cells of the map are likened to the cell structure of the cerebral cortex

- **$x$ :**  $(n \times 1)$  input vector characterizes features (attributes) of a signal
- **$m$ :**  $(n \times 1)$  weight vector of a cell that represents an output class

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# Competition in the Self-Organizing Map



- Competition is based on minimizing distance from  $x$  to  $m$

$$\text{Cost} = \text{distance} = \|x - m_i\|$$

$$\min \text{Cost} = \min_{m_i} \|x - m\|$$

- $m$  **encodes** the output classes
- Semantic net **decodes** the output to identify classes

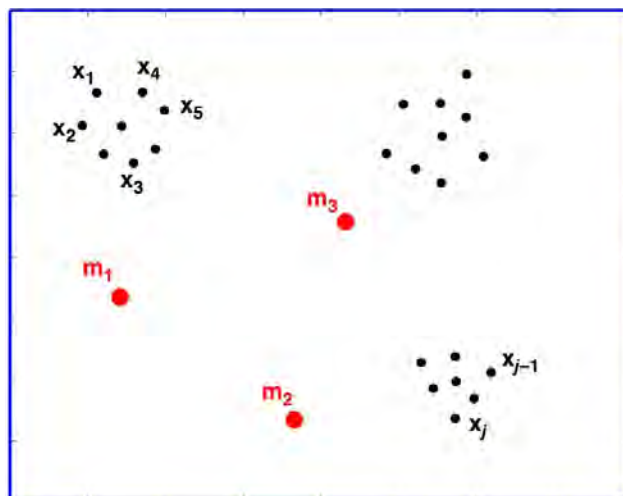
$$m_1 = \begin{bmatrix} 0 \\ 1 \\ 3 \end{bmatrix} \rightarrow \text{Class A}; \quad m_2 = \begin{bmatrix} 1 \\ 0 \\ 1 \end{bmatrix} \rightarrow \text{Class B}$$

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## Goal of the Self-Organizing Map

- Given:**
  - $I$  output classes
  - Input training set,  $x_j, j = 1$  to  $J$
- Find:** Cell weights,  $m_i, i = 1$  to  $I$  that best cluster the data (i.e., with minimum norm)
- Initialize the cell weights,  $m_i$ , randomly in the space of  $x$

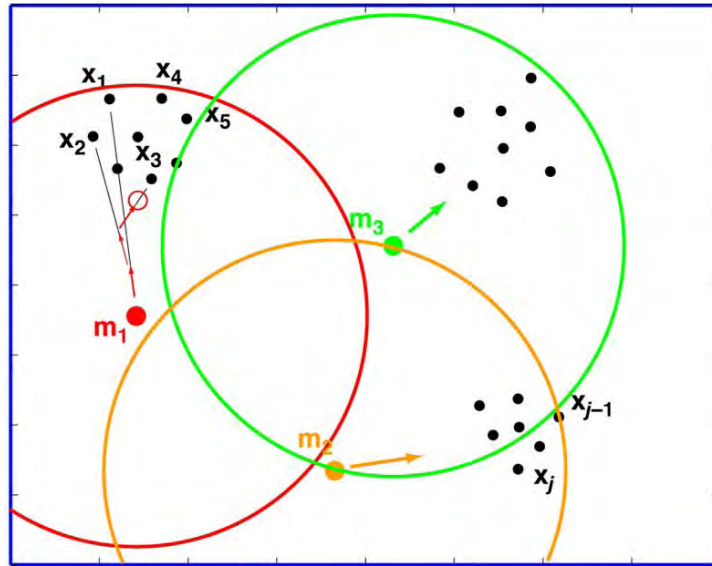


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## Training the Self-Organizing Map

- Define a neighborhood set within a radius of  $N_c$  around each cell,  $m_i$ 
  - Choose  $N_c$  to overlap with neighboring cells
- Find the best cell-weight match,  $m_{best}$ , (i.e., the closest  $m_i$ ) to the 1<sup>st</sup> training sample,  $x_1$

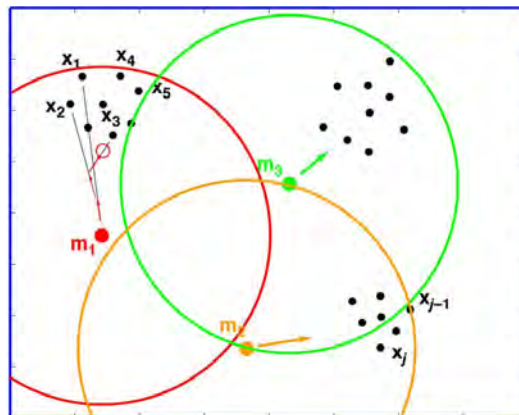


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## Cell Weight Updates

$$m_i(k+1) = \begin{cases} m_i(k) + \alpha_k [x_1 - m_i(k)], & m_i \in N_c \\ m_i(k), & m_i \notin N_c \end{cases}$$

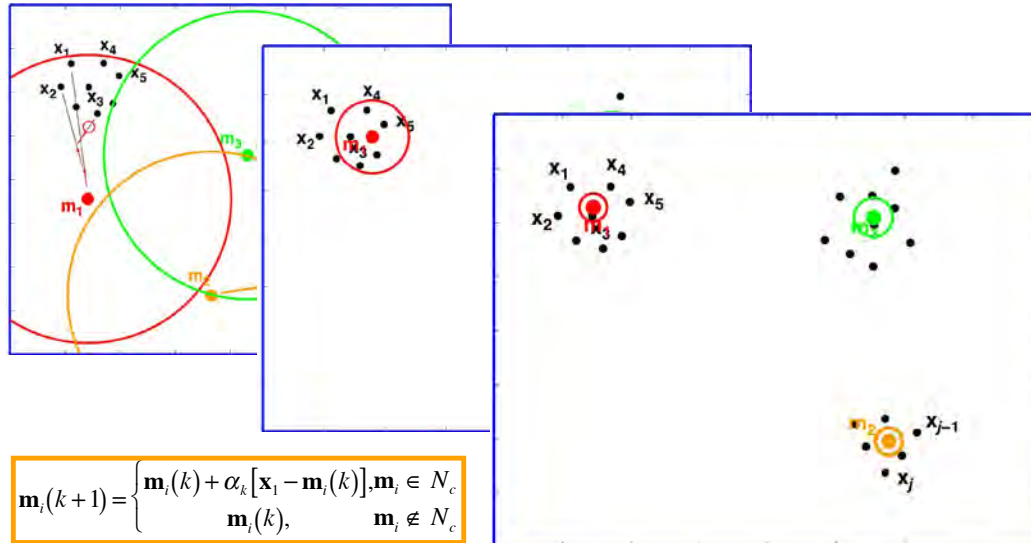
- Update cell weights for all cells in the neighborhood set,  $N_c$ , of  $m_{best}$ 
  - $\alpha_k$  = adaptation gain or learning rate
- Repeat for
  - $x_2$  to  $x_J$
  - $m_1$  to  $m_I$



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# Convergence of Cell Weights

Repeat entire process with decreasing  $N_c$  radius until convergence occurs



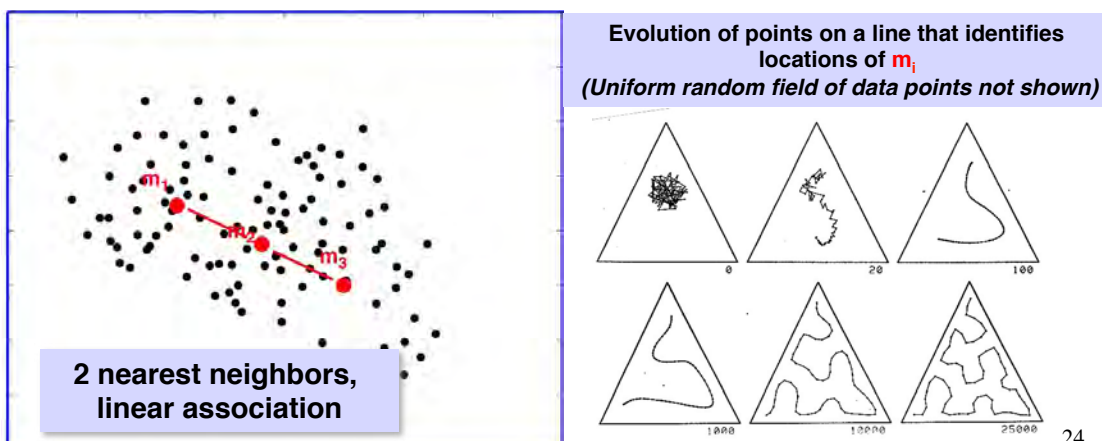
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## Semantic Map



- Representation of abstract or categorical information
- Contextual information used to generate map of symbols
- Dimensionality and # of nearest neighbors affects final map

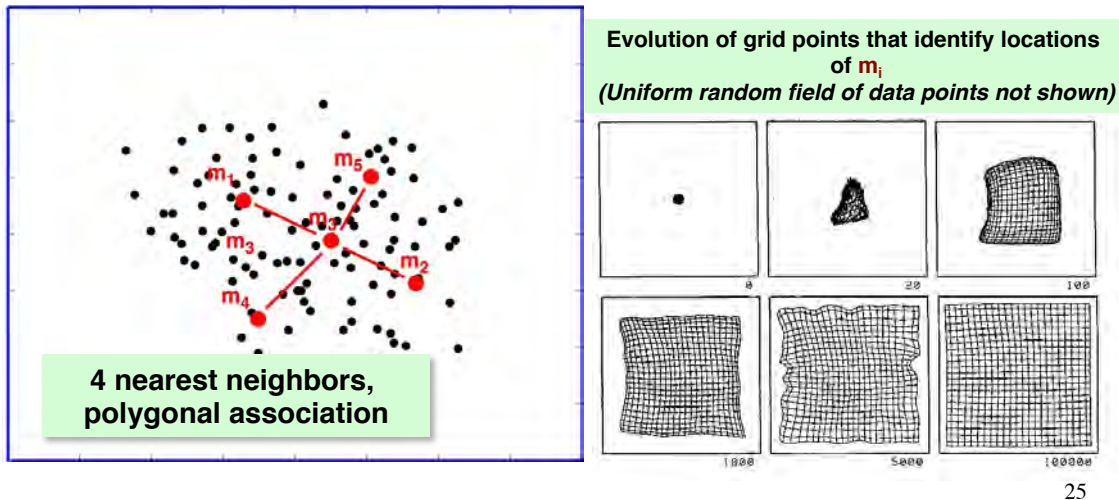
**Example: linear association of cell weights**  
Points for cell-weight update chosen randomly



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# Choice of Neighborhood Architecture

**Example:** Map is assumed to represent a grid of associated points  
 Number of cell weights specified  
 Random starting locations for training

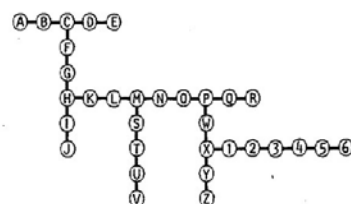


## Minimum Spanning Tree

**Example of hexagonal map association identification**  
 32 points with 5 attributes that may take six values  
 (0, 1, 2, 3, 4, 5)

Input Data Matrix																																	
		Item																															
Attribute	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	1	2	3	4	5	6	
	$a_1$	1	2	3	4	5	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
	$a_2$	0	0	0	0	0	1	2	3	4	5	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
	$a_3$	0	0	0	0	0	0	0	0	0	0	1	2	3	4	5	6	7	8	3	3	3	3	6	6	6	6	6	6	6	6	6	6
	$a_4$	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3	4	1	2	3	4	2	2	2	2	2	2
	$a_5$	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3	4	5	6

**Minimum spanning tree:**  
 smallest total edge length



Minimal spanning tree corresponding to Table

**Hexagonal lattice of grid points**  
 that identify locations of  $m_i$

	B	C	D	E	*	Q	R	*	Y	Z
A	*	*	*	*	*	P	*	*	X	*
	*	F	*	N	O	*	W	*	*	1
	*	G	*	M	*	*	*	*	*	2
	H	K	L	*	T	U	*	3	*	*
	*	I	*	*	*	*	*	*	4	*
	*	J	*	S	*	*	V	*	5	6

Self-organized map of the data matrix of Table

**Each item for training has symbolic expression and context**  
**Categories: noun, verb, adverb**

water meat bread dog horse

beer little cat

fast seldom Bob

slowly often much Jim Mary

well works eats

poorly speaks buys phones

runs sells visits

drinks walks hates likes

"Semantic map" obtained on a network of  $10 \times 15$  cells after 2000 presentations of word-context-pairs derived from 10 000 random sentences of the kind shown in Fig. 10(c). Nouns, verbs, and adverbs are segregated into different domains. Within each domain a further grouping according to aspects of meaning is discernible.

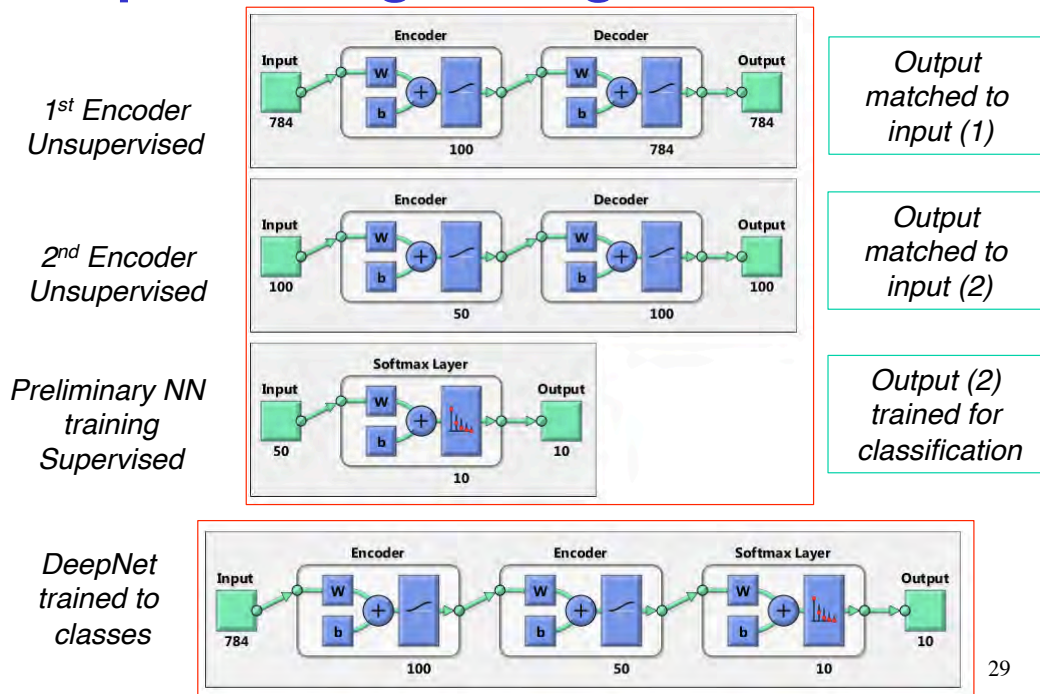
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# Deep Learning



# MATLAB Example

## Deep Learning for Digit Classification



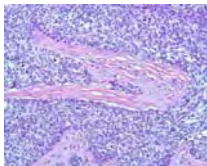
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**Next Time:**  
**Communication, Information,**  
**and Machine Learning**



# SUPPLEMENTAL MATERIAL

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## Comparison of Present SRBCT Set with Khan Top 10

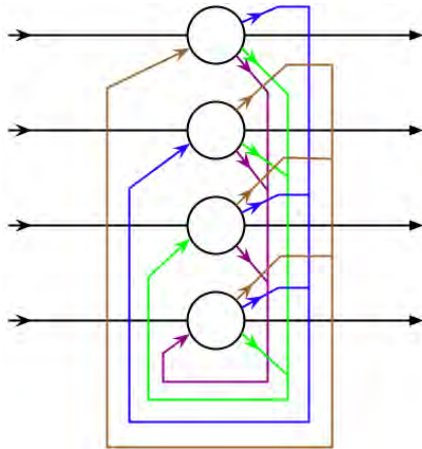
Image ID	Gene Description	EWS Student t Value	BL Student t Value	NB Student t Value	RMS Student t Value	Most Significant t Value	Khan Gene Class
296448	insulin-like growth factor 2 (somatomedin A)	-4.789	-5.226	-1.185	5.998	RMS	RMS
207274	Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF	-4.377	-5.424	-1.639	5.708	RMS	RMS
841641	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	6.841	-9.932	0.565	-4.300	BL (-)	EWS/NB
365826	growth arrest-specific 1	3.551	-8.438	-6.995	1.583	BL (-)	EWS/RMS
486787	calponin 3, acidic	-4.335	-6.354	2.446	2.605	BL (-)	RMS/NB
770394	Fc fragment of IgG, receptor, transporter, alpha	12.037	-6.673	-6.173	-4.792	EWS	EWS
244618	ESTs	-4.174	-4.822	-3.484	5.986	RMS	RMS
233721	insulin-like growth factor binding protein 2 (36kD)	0.058	-7.487	-1.599	2.184	BL (-)	Not BL
43733	glycogenin 2	4.715	-4.576	-3.834	-3.524	EWS	EWS
295985	ESTs	-9.260	-0.133	3.237	2.948	EWS (-)	Not EWS

- Red: both sets
- Black: Khan set only

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# Hopfield Network

Alternative plot of 4-node network



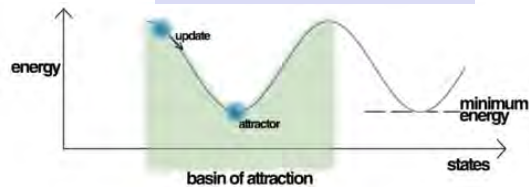
Novel Image



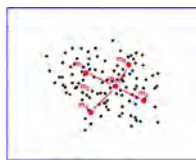
Exemplar



"Energy Landscape"



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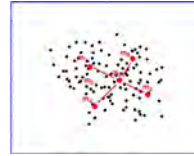


## Linear Vector Quantization

- Incorporation of supervised learning
- Classification of groups of outputs
- Type 1
  - Addition of codebook vectors,  $\mathbf{m}_c$ , with known meaning

$$\mathbf{m}_c(k+1) = \begin{cases} \mathbf{m}_c(k) + \alpha_k [\mathbf{x}_k - \mathbf{m}_c(k)], & \text{if classified correctly} \\ \mathbf{m}_c(k) - \alpha_k [\mathbf{x}_k - \mathbf{m}_c(k)], & \text{if classified incorrectly} \end{cases}$$

# Linear Vector Quantization



## ■ Type 2

- **Inhibition** of nearest neighbor whose class is known to be different, e.g.,
  - $\mathbf{x}$  belongs to class of  $\mathbf{m}_j$  but is closer to  $\mathbf{m}_i$

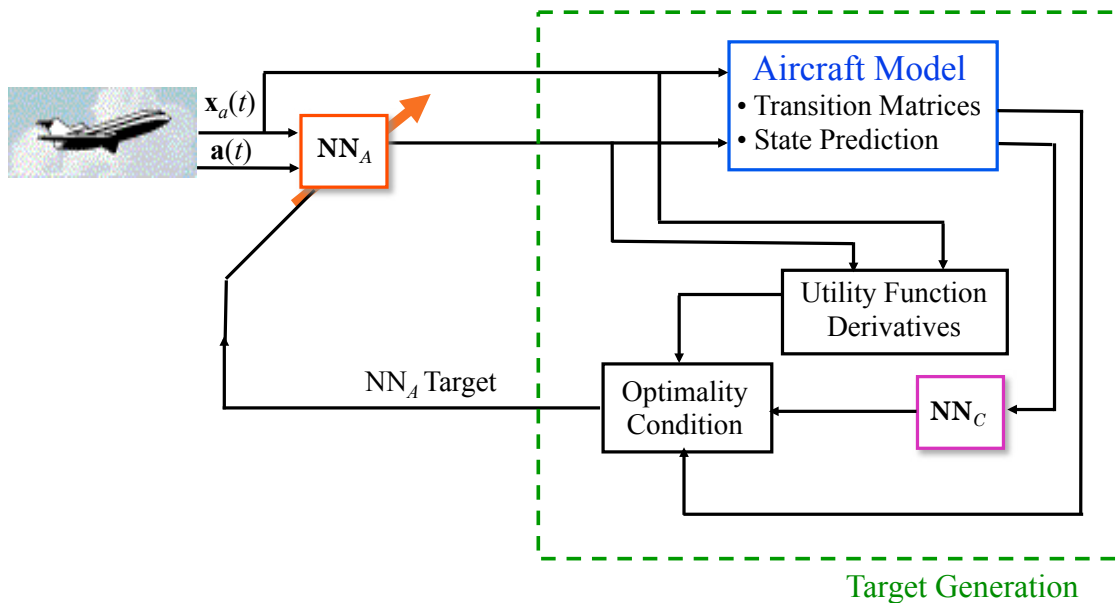
$$\mathbf{m}_i(k+1) = \mathbf{m}_i(k) - \alpha_k [\mathbf{x}_k - \mathbf{m}_i(k)]$$

$$\mathbf{m}_j(k+1) = \mathbf{m}_j(k) + \alpha_k [\mathbf{x}_k - \mathbf{m}_j(k)]$$

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## Adaptive Critic Proportional-Integral Neural Network Controller

### Adaptation of Control Network



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# Adaptive Critic Proportional-Integral Neural Network Controller

## Adaptation of Critic Network

