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ASSOCIATIVE MEMORY
BIOLOGICAL AND MATHEMATICAL ASPECTS

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ABSTRACT

A tutorial is presented encompassing both biological and mathematical aspects of associative memory for pattern processing. A systems viewpoint is adopted whereby biological associative memory is viewed as a system of adaptive filters, with the free parameters of the filter corresponding to the strengths of the biological neural connections. Certainly such viewpoint is not intended to accurately depict the true mechanisms underlying the extraordinary capabilities of biological associative memory — fast pattern recognition and apparently infinite memory capacity. For such mechanisms will unlikely be discovered in the absence of tools allowing the observance of collective behavior over systems of neurons. However, the viewpoint does serve to integrate both mathematics and biology on a general level.

Of most significance is perhaps the systematic treatment of mathematical associative memory. In the adaptive filter framework, associative memory is described and compared to traditional statistical techniques. Also, new insight into the generalization capability of associative memory is expressed. Conditions are presented to ensure both correct memory recall and significant generalization. *Keywords: optical processing, artificial intelligence*

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1. INTRODUCTION

The recent interest in associative memory can perhaps be attributed to the increasing awareness of the extraordinary, yet subtle, capabilities of biological associative memory. With only finite number of components and degrees of freedom ($10^{11} - 10^{12}$ neurons with average 10^3 connections per neuron) humans can store and recall seemingly infinite memories. In contrast, classical computer systems utilizing address memory can only store memories which increase linearly with the number of components. Moreover, correct computer memory recall requires exact address specification. Yet the biological memory implements recall by association. That is, a stored memory pattern can be recalled by mere association with an incomplete excitation pattern (key.) Thus by association, inexact information often results in correct memory recall, and thereby constitutes a robust memory recall mechanism.

Further astonishing is the physical realization of biological associative memory with slow and apparently inaccurate components. For example, the biological signal channels (axons) are several orders of magnitude slower and more passive that the analogous computer circuitry. Specifically the resistance of one meter of nerve fiber is approximately the resistance of 10^{10} miles of 22 gauge copper wire. And at a snail's pace (100 m/sec) the signals are propagated through the axon, compared to the blazing speed of light achieved by electrical signaling in computers. Yet the time required to recall a stored memory (or equivalently recognize a pattern) by association is only approximately 100 msec for biological memory, while the conventional digital computer (with nanosecond processors capable of performing tens of millions of instructions per second) requires minutes to perform the same task.

So how does biological memory, characterized by seemingly infinite memory capacity and quick recollection emerge from slow, noisy, and imprecise biomass circuitry?

Such question has driven research activity for decades. And even today, the question remains largely unanswered.

However physiological experiments have revealed fundamental differences between biological and computer memory, which are likely to contribute to the vast processing gap. Perhaps the most apparent contrast is that biological memory, in addition to being associative, is distributive. That is, the memory function and hence pattern recognition is spatially distributed over numerous neurons, rather than confined to a single location as in computer memory. This distributed phenomenon is believed to be responsible for the inherent fault-tolerance properties, in which memory often remains intact after minor damage. Furthermore the distribution of the processing over numerous neurons provides a parallel processing capability, thought to underly the quick system response times achieved with relatively slow circuitry.

Consequently, in building robust pattern recognition systems with increased memory capacity, distributed associative memories patterned after biological neural networks are subject of much investigation. The purpose of this chapter is to provide a tutorial encompassing both biological and mathematical aspects of associative memory. The nature is systematic and follows the work of Kohonen [1]. First, a brief section on biological associative memory is included to provide a perspective on neural circuitry involved in memory; certainly not an explanation of the true mechanisms underlying human memory. Next associative memory is defined mathematically with various models presented and characterized. Then criteria are defined for assisting in the evaluation of such models. Concluding, possible future research activity is mentioned regarding the development of systems much more characteristic of their biological counterparts.

2. BIOLOGICAL ASSOCIATIVE MEMORY

Although many theories of biological memory exist, scientists continue to seek a true understanding of the mechanisms which underlie the extraordinary capabilities of human associative memory. Here a systems viewpoint of biological memory is adopted, due in part to the physiological evidence and admittedly, the author's engineering background.

As with any large system, overall or collective behavior arises from the various functional components; and to understand the collective system behavior, the components must first be somewhat understood. Therefore, the discussion begins with describing the functional components of biological memory. These functional components are viewed as adaptive filters, whose adaptive elements are represented biologically by synapses (variable connections between brain cells (neurons)). Then, the physical organization of biological memory is discussed within such context.

2.1 System Viewpoint of Biological Memory

Increasing evidence suggests the extreme complexity of the brain is not due to randomness, but instead, arises from highly ordered design [2] ; a design which couples many distinct neural regions, each being tuned for specific stimuli processing. These distinct neural regions include the visual cortex for vision and the somatosensory cortex for tactile sensing. Within such regions there exists smaller subregions, again for specific function. In all, the brain can be considered as being composed of thousands of distinct specialized regions, each containing thousands of subregions. Consequently these subregions, composed of 10 to 1000 neurons, may be interpreted as the functional building blocks or components of the overall system.

Certainly through experimentation, biological memory has been established as a collective phenomenon, distributed over many such neural regions. This is confirmed by experiments where lesions are made in different brain localities, and observing the resulting impairment being a function of the severity of the lesion, and not so much the location [3,4]. Thus biological memory is a system, composed of numerous neural regions which act collectively to yield an associative memory with extraordinary capabilities.

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Subsequently, these neural regions comprising memory can be considered as adaptive filters, whose adaptive elements give rise to the distinct properties characteristic of each region (see Fig. 1.). And the role of biological memory, or analogously the system of adaptive filters, is to create an internal model to represent sensory environmental history.
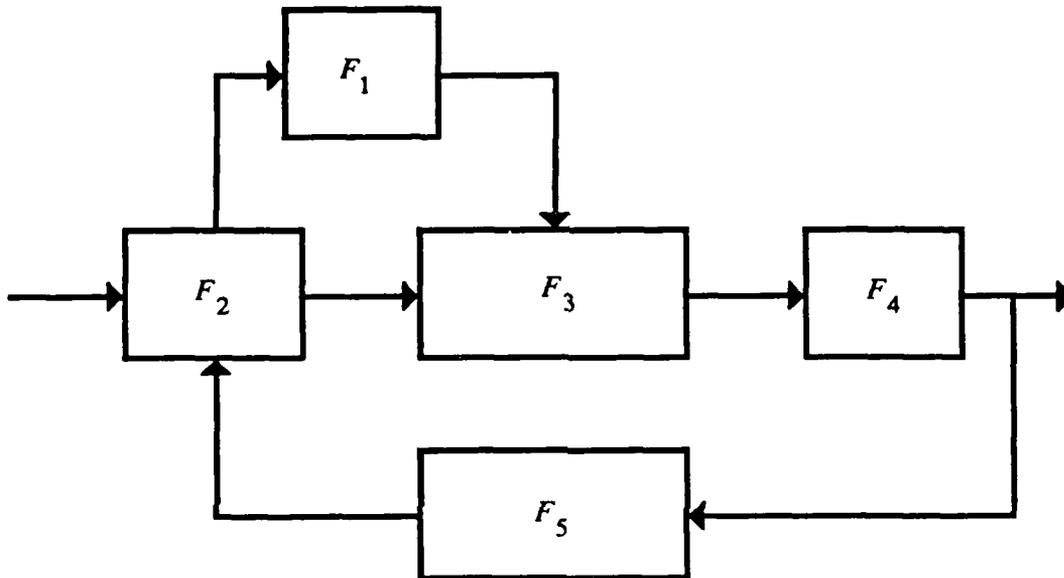
Fig. 1. Simple system of adaptive filters.

Since a sensory event consists of thousands of activation patterns from possibly many sensors, a good deal of preprocessing is presumed to facilitate the storage of apparently infinite events. The preprocessing in turn yields higher level information or features. The features comprising this feature set or map are then believed to be encoded through association. Thus instead of memorizing the explicit feature patterns, rather the associations between the features are preserved, likely by the neural synapses. Therefore if an input key representing only a portion of the feature set is presented to the system, through association the complete memory event is recalled [1]. Now given the analogy of biological memory with a system of adaptive filters for extracting and associating key features, the adaptive filter is discussed within the biological context.

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2.2 Adaptive Filter Paradigm

The adaptive filter representing a subregion of neurons is shown in Fig. 2. The amount of neurons represented by each filter coincides with the amount of neurons necessary to comprise a neural subregion with observable collective behavior, and hence likely to be a functional entity. The inputs and outputs are multidimensional signals derived from action potentials of nearby neurons. Most of the signal information is conveyed by the frequency of the impulse train (# impulses/sec) [5] and the location of the filter in which the signal terminates. Almost no information is contained in the amplitude of the impulses, for the amplitude is fairly constant throughout many animal species. The signal origination and destination is of extreme importance in semantic interpretation. This is demonstrated by realizing that the same electrical impulse train directed to the visual cortex and the auditory cortex produces profoundly different meaning.
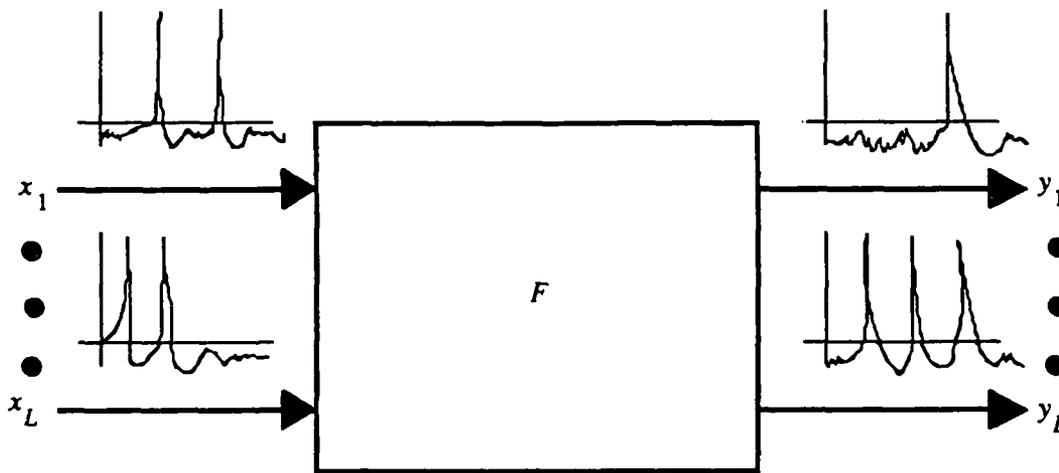
Fig. 2. Adaptive filter with transfer function F.

The filter itself is represented mathematically by a transfer function F relating the outputs to the inputs. The function can be dependent upon the inputs, outputs, and the adaptive filter elements. The nature of the adaptive filter, and hence the neural network, is the subject of the Mathematical Associative Memory section. As with any adaptive filter, the specification of the adaptive elements or parameters gives rise to the filter's identity. Correspondingly, the next subsection investigates the biological equivalents to the adaptive elements, the synapses.

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2.3 Adaptive Filter Elements - The Synapses

Many neurobiologists believe the unique character of individual human beings, including disposition, learning, and memory resides in the geometry and specific strengths (weights) of the neural interconnections or synapses [6]. The modification of these synapses is believed to be of primary importance both in learning and associative memory, and their strengths are viewed as the adaptive elements of the filters (see Fig. 3.)
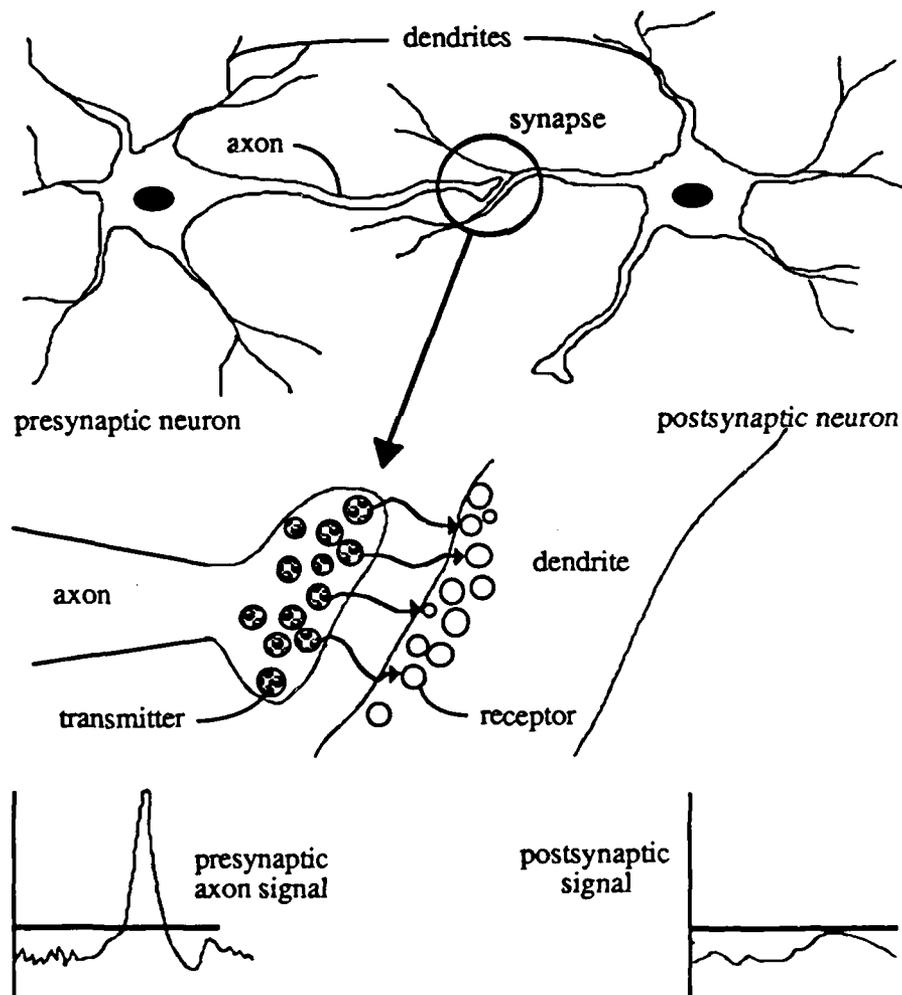
Fig. 3.a) Neural connection, b) signal transmission across synaptic channel c) transmitted and received signals.

Typically, modifications in connection geometry, such as sprouting new output channels (axons), occur at an early stage of development. While in the adult stage, most interconnection modifications for memory and learning are conducted by varying the synaptic strength. This change in synaptic strength alters the transmission of the action potential from the presynaptic neuron through the transmission channel to the postsynaptic neuron. The transmission channel between the communicating neurons supports chemical signaling. Specifically, at the arrival of an action potential, molecules of chemical transmitter from the presynaptic neuron are released into the channel and received by the receptor molecules residing in the postsynaptic neuron. Much debate arises concerning whether the presynaptic or postsynaptic neuron (or both) is physically responsible for the change in synaptic strength.

Nevertheless, the synaptic strengths, analogous to the adaptive filter elements, are adapted during both learning and memorization. And each synapse with a specific strength performs a weighting of the respective input signal to the postsynaptic neuron (see Fig. 3c.) Thus the neuron is often modeled as a device which first performs a weighted summation over the input signals (where weight w_{ji} designates the synaptic strength from neuron i to neuron j) then passes the result through a threshold function [7] (see Fig. 4.). Upon specifying a rule for synaptic modification (adaptive filter algorithm) and geometry, the simplified biological model becomes complete.

$$y = g\left(\sum_i w_{ji} x_i\right)$$

t (threshold)
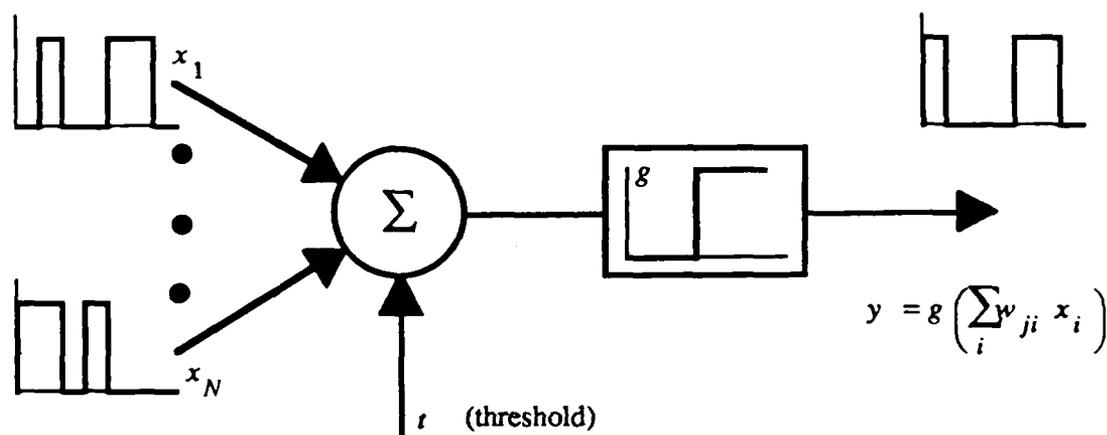
Fig. 4. Simple neuron model.

A well recognized synaptic modification rule basically states that the synaptic strength changes in proportion to the correlation of the activity of the presynaptic and postsynaptic neurons [8]. Mathematically, the rule is expressed

$$\frac{d}{dt} E \left\{ {^w}_{ji} \right\} \propto E \left\{ {^{yx}}_i \right\}$$

Two types of synapses are distinguished. The excitatory synapse promotes the firing of the postsynaptic cell ($w_{ji} > 0$) while the inhibitory synapse reduces the chance of firing ($w_{ji} < 0$).

The time constants for these biological adaptive elements are surprisingly fast. Experimental results have shown that brief periods (seconds) of stimulation to neural regions known to be involved in memory alters the synaptic strength for a substantial amount of time, thereby supporting the notion of memory being correlated with synaptic modification. These results imply that only moderate training is needed to produce lasting synaptic modification to support learning and memory [6,9]. The implication being, as you read this article your synapses are being modified accordingly (depending upon your attention level.)

2.4   Biological Memory Organization

As mentioned, the brain is a highly organized system. Signal processing for memory, as well as other functions, is often conducted in a layered fashion. In some cases, these layers are distributed in planar arrays, each layer being a neural subregion with observable collective behavior (thus comprising a functional entity) as illustrated in Fig. 5. The distinct functionality of the layers is demonstrated by electrophysiological recordings, whereby neurons in the same layer respond similarly and have similar receptive fields (areas which influence the activity of a given neuron.) The classical results of Hubel and Wiesel [10] clearly demonstrates this layered processing phenomenon, specifically from the retina to the visual cortex. Here the processing progresses from detecting light to detecting complex geometries.

Particularly for associative memory, many portions of the brain contribute in the overall processing. However from lesion experiments, memory is believed to be decomposable into various stages. Such physiological evidence suggests that for memory storage, both an encoder and physical storage medium (likely the synapses) are involved (see Fig. 6.).

| layer 1 | layer 2 | layer N |
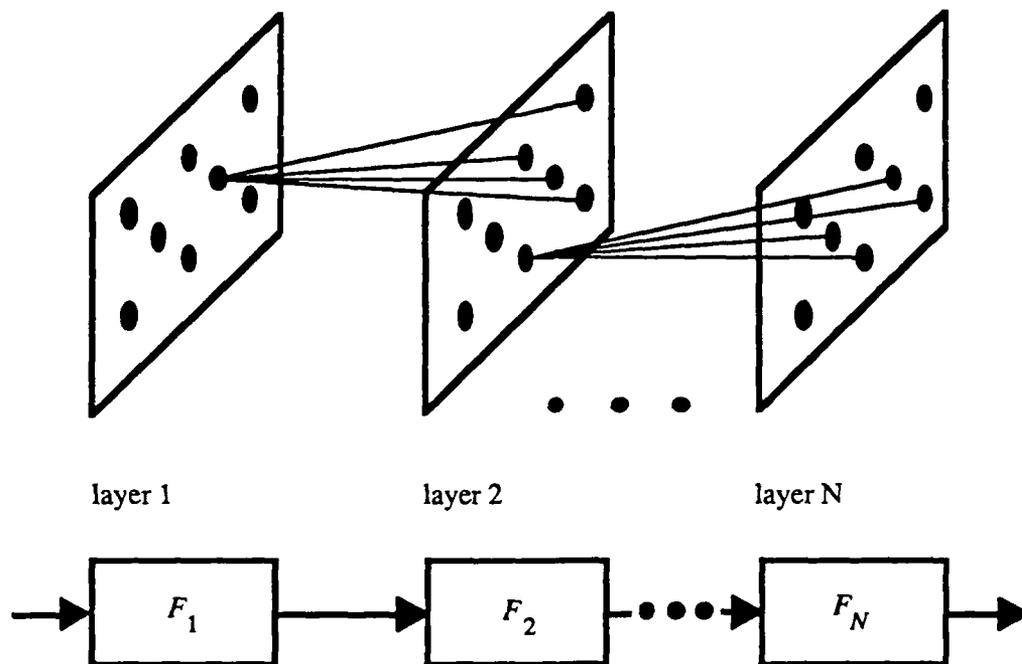
Fig. 5. Layers of neural subregions and corresponding adaptive filter system.

The encoder is deemed necessary to reduce the redundancy from the overwhelming number of patterns to be associatively stored. Evidence to support the source encoder theory is provided through brain surgery, originally in an attempt to correct epileptic seizures. The corrective surgery involved removing the temporal lobes, which included the hippocampus and amygdala. Although the epilepsy was cured, the patient now without a hippocampus, was unable to store new information in long term memory. Yet previous long term memory (stored prior to the surgery) remained intact [11]. Thus theories describing the hippocampus as a source encoder necessary for long term storage received credibility.

In fact some have theorized that the hippocampus may actually be a self-organizing source encoder which maximizes mutual information between the inputs (ensuring transformation invertibility) while also minimizing the mutual information between the output channels (ensuring minimally redundant output signals) [12,13]. Here the processing is fairly localized and layered, composed of a minimal three layers.

Although the encoding may be fairly localized, the actual storage is much more distributed. The storage is believed to be distributed amongst the synaptic connections throughout the cerebral neocortex, which amounts to 70% of the human brain. Furthermore, the incredible capability of human memory, being vastly superior to any other animal, is believed due to the substantially larger human cerebrum.

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  ──────▶   ENCODER   ────▶   STORAGE
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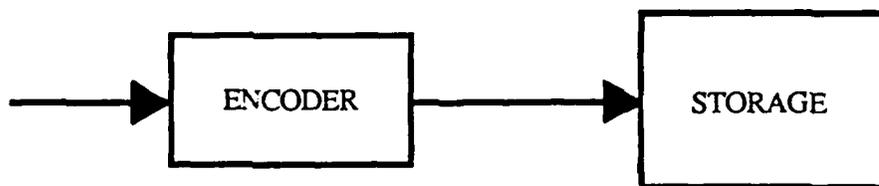
Fig. 6. Components of memory storage

With regard to the biological mechanisms of associative memory recall, much less is known and no attempt is made here to postulate a theory .

3. MATHEMATICAL ASSOCIATIVE MEMORY

Recall the particular system viewpoint of biological memory envisions the memory process being distributed over numerous regions of neurons, each region in turn composed of subregions represented by adaptive filters whose elements are adaptively chosen. With such viewpoint, the adaptive filter is thus seen as the system level building block. And the purpose of this section is to mathematically describe some of these building blocks.

3.1 Definition

A single adaptive filter for modeling associative memory is shown in Fig. 7. The input vector $\bar{x}_i \in \mathfrak{R}^N$ represents a prototypical key, while the output vector $\bar{y}_i \in \mathfrak{R}^L$ is the corresponding memory. Note the input and output vectors of finite dimension can also represent continuous time processes, since any finite energy signal $x(t)$ can be expanded by orthogonal functions yielding

$$x(t) = \sum_{i=1}^{N} x_i \varnothing_i(t) \quad .$$

(1)

The filter is characterized by the transfer function F, dependent upon both the input and the filter parameters or elements. The filter is designated adaptive if the matrix of elements remains dependent upon the data, that is

$$\bar{T}\left(\{\bar{x}_i, \bar{y}_i\}_{i=1}^{M}\right) \quad .$$

(2)

However for brevity, the notation below is adopted to signify the adaptive filter transfer function

$$\bar{y} = F\left(\bar{x}_i, \bar{T}\left(\{\bar{x}_i, \bar{y}_i\}_{i=1}^{M}\right)\right) = F(\bar{x}_i) \quad .$$

(3)

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$$\bar{y}_i = F(\bar{x}_i, T)$$
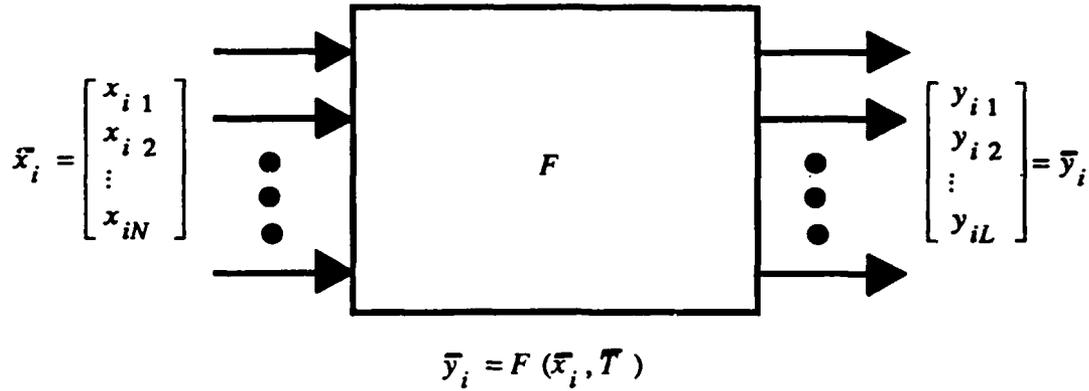
Fig. 7. Adaptive filter with transfer function F.

3.2 Objective

The ideal objective of mathematical associative memory by adaptive filtering is to construct a transfer function in an adaptive (often recursive or iterative) manner such that

(i) $\quad F(\bar{x}_i) = \bar{y}_i \qquad i = 1, 2, \dots M \qquad\qquad$ - perfect recall $\qquad$ (4)

(ii) $\quad F(\bar{x}_i + \bar{n}) = \bar{y}_i \qquad\quad (\bar{n} = \text{perturbation})\quad$ - generalization $\quad$ (5)

given a set of M arbitrary paired associations

$$\{(\bar{x}_1, \bar{y}_1), (\bar{x}_2, \bar{y}_2), \dots, (\bar{x}_M, \bar{y}_M)\} . \qquad (6)$$

Pictorially, the ideal associative memory with both perfect recall and significant generalization capability is depicted in Fig. 8. Perfect recall is shown by thin lines mapping the values in the input space X to the corresponding correct memories in the output space Y. The generalization capability represents the amount of perturbation or error tolerated in the input key. Thus good generalization implies proper recall when excited by an erroneous (yet similar) key, as shown with the bold line. Physically the erroneous keys may represent an incomplete memory item, or a noisy version of the proper key $\bar{x}_i$.
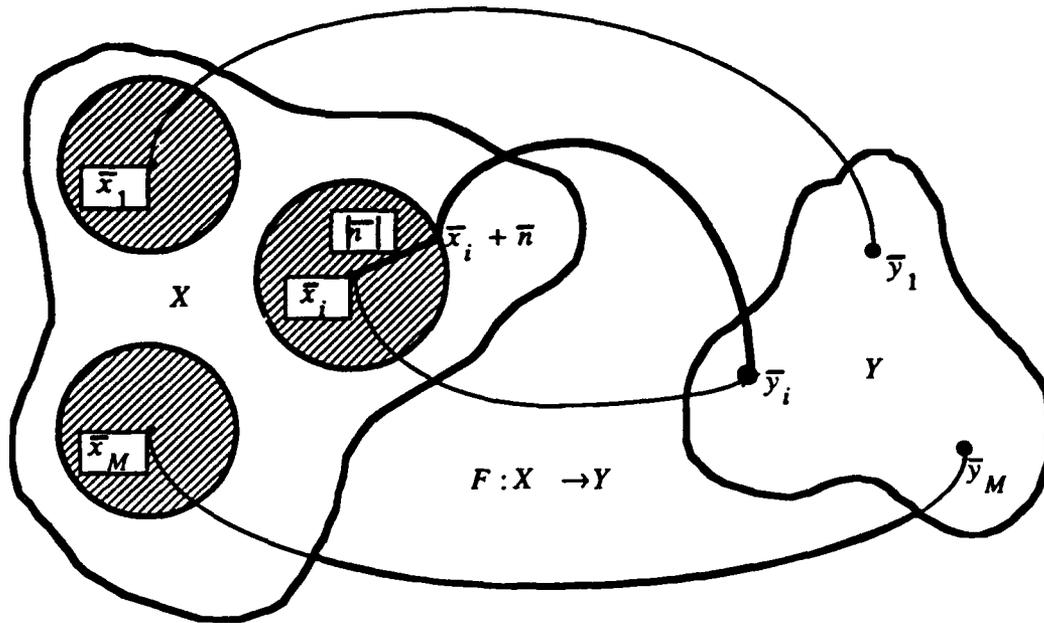
Fig. 8. Associative memory mapping.

Associative memories can be categorized into two classes. Hetero-associative memories involve associations of dissimilar type. That is, the input and output vectors have entirely different meaning, as in the above formulation. An example of hetero-associative memory is the classification problem where objects $\bar{x}_i$ are to be classified into one of L categories. Here $\bar{y}_i = (0, 0,... 0, 1, 0... 0)$, conveying object $\bar{x}_i$ is categorized into class i. Conversely, auto-associative memories have associations of similar type. Specifically $\bar{y}_i = \bar{x}_i$ in the above formulation. Here the actual input key $(\bar{x}_i + \bar{n})$ is just a perturbation of the memory $\bar{x}_i$ (see Fig. 9.).

The appeal of the adaptive filter associative memory is the ability of the filter to adapt (synonymously learn, self-organize) in an effort to improve performance, whereby by the adaption is determined by the data, and hence data driven. Thus the elements of $\bar{T}$ specifying the function mapping the input keys to the memories are determined automatically. In consequence, the function F relating inputs to outputs is learned by the adaptive filter (with an appropriate learning algorithm), and thereby alleviates the laborious tasks often necessary in extracting explicit relationships, and the requirement of a-priori models.

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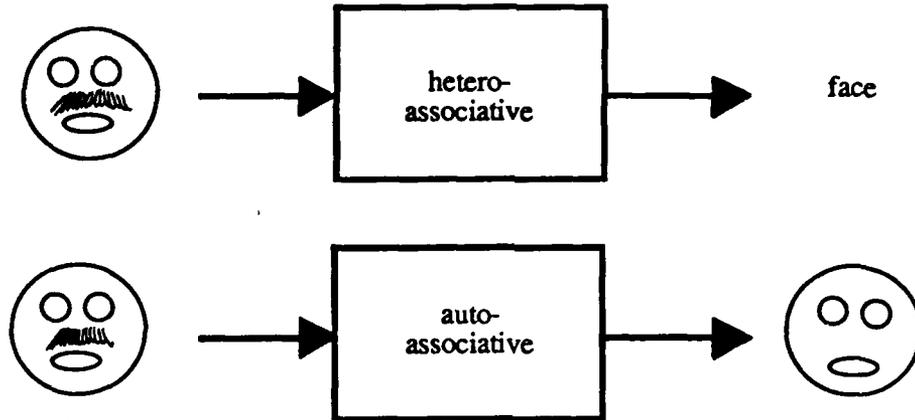
Fig. 9. Example of hetero-associative and auto-associative memories

3.3 Architecture

Further investigation of the adaptive filter function F requires specifying a particular class of functions. In turn, a class of possible functions can be defined in terms of a given architecture. Correspondingly, the architecture which supports the class of adaptive filter functions immediately investigated is shown in Fig. 10. Here the adaptive filter transfer function is dependent upon the processors (shown by circles), the bias values $\{I_i\}$, and the connections with strengths $\{t_{jk}\}$ (t_{jk} = strength (weight) of connection from input x_{ik} to processor j). Thus the adaptive elements are contained in the matrix $\bar{T} = \{t_{jk}\}$, and upon specifying both a rule for the adaption of $\bar{T}$, bias values, and the mathematical form of the processors, the filter is completely specified.

The analogy of the adaptive filter architecture in Fig. 10 with a region of neurons becomes apparent if the weighted connections are seen as the synapses of varying strength, and the processors consists of summations followed by nonlinear threshold activation functions (refer to Fig. 4.). And to construct many regions of neurons to represent a system, simply repeat the above principle architecture.
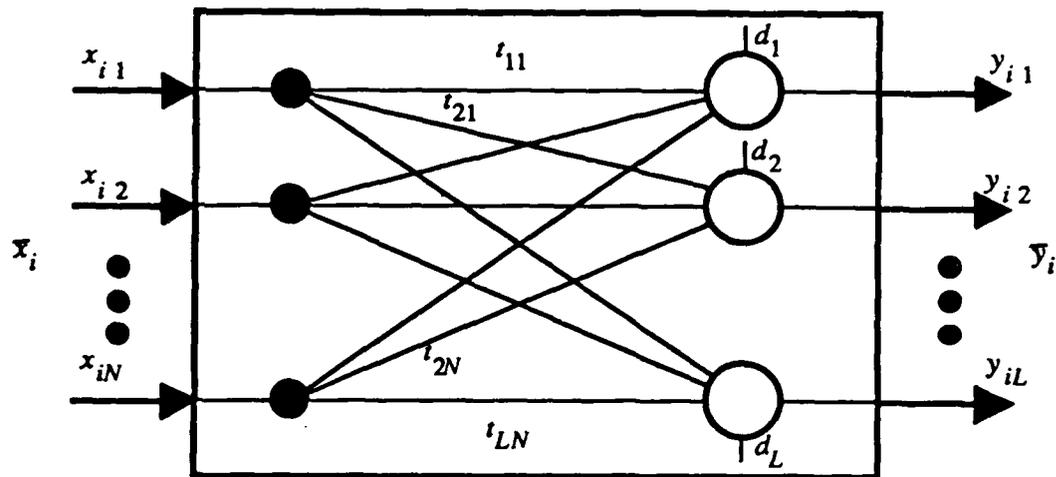
Fig. 10. Adaptive Filter Architecture

3.4 Linear Associative Memory

To provide a sound foundation for further associative memory investigation, the optimal linear associative memory model is first presented. Often fundamental relationships obtained in the linear case provide insight into the nonlinear cases. And as a further justification for examining linear models, they typically perform adequately when operating within the bounds discussed.

The linear architecture is easily obtained by designating the processors in Fig. 10. as mere summations. Hence the output component y_{ij} becomes

$$y_{ij} = \sum_{k=1}^{N} t_{jk} x_{ik} + d_j$$

(7)

or equivalently in vector form

$$\bar{y}_i = F(\bar{x}_i) = \bar{T}\bar{x}_i + \bar{d} \ .$$

(8)

Also, the architecture can be drawn to emphasize the linear matrix formulation, termed the learnmatrix [14,15,16], shown in Fig. 11.

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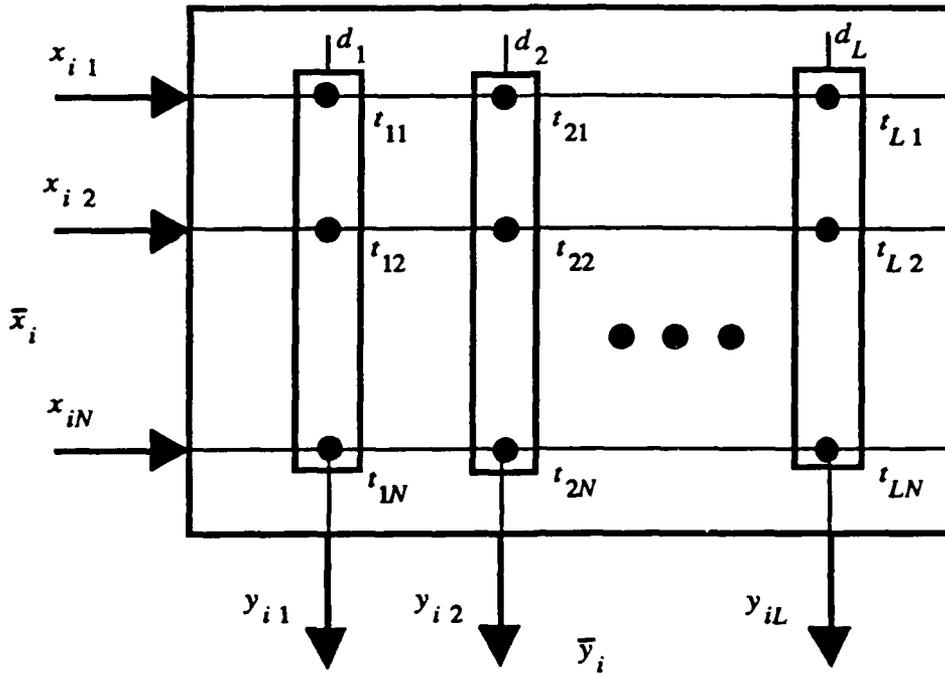
Fig. 11. The learnmatrix.

Next the learning rule (algorithm for adaptive elements $\bar{T}$) is derived to satisfy the first objective, perfect recall (4). Generalization (5) is discussed in Section 3.5. Both general and particular solutions are presented, together with conditions to ensure perfect recall.

Specifically, the problem addressed is to construct a learning rule (matrix $\bar{T}$) such that

$$F(\bar{x}_i) = \bar{T}\bar{x}_i = \bar{y}_i \qquad i = 1, 2... M \qquad (9)$$

given a set of M arbitrary paired associations

$$\{(\bar{x}_1, \bar{y}_1), (\bar{x}_2, \bar{y}_2), ..., (\bar{x}_M, \bar{y}_M)\}. \qquad (10)$$

(Notice the bias vector $\bar{d}$ has been removed for simplicity.) Rewriting (9) in matrix form

$$(\bar{T}\bar{x}_1, \bar{T}\bar{x}_2 ..., \bar{T}\bar{x}_M) = (\bar{y}_1, \bar{y}_2 ..., \bar{y}_M) \qquad (11)$$

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or
$$\bar{T}\bar{X} = \bar{Y}$$

where
$$\bar{X} = (\bar{x}_1, \bar{x}_2, ..., \bar{x}_M) \tag{12}$$

$$\bar{Y} = (\bar{y}_1, \bar{y}_2, ..., \bar{y}_M) \ . \tag{13}$$

In general (where exact solutions may not exist) the solution providing the best recall in the sense of least squares ($\left(\sum_i \|\bar{T}\bar{x}_i - \bar{y}_i\|^2\right)$ minimized) is given by

$$\bar{T} = \bar{Y}\bar{X}^+ \tag{14}$$

where $\bar{X}^+$ is the pseudo-inverse [17].

Exact solutions are obtained in the cases where linear independence occurs. Specifically three cases are detailed below.

A) *Prototype keys* $\{\bar{x}_i\}$ *are linearly independent (* $\Rightarrow M \le N$ *).*

Since the keys are linearly independent, $\bar{X}$ consists of linearly independent columns, and hence $\left(\bar{X}^*\bar{X}\right)^{-1}$ exists yielding

$$\bar{T}\bar{X} = \bar{Y}\left(\bar{X}^*\bar{X}\right)^{-1}\left(\bar{X}^*\bar{X}\right) \cdot \tag{15}$$

$$\left[\bar{Y}\left(\bar{X}^*\bar{X}\right)^{-1}\bar{X}^*\right]\bar{X}$$

therefore
$$\bar{T} = \bar{Y}\left(\bar{X}^*\bar{X}\right)^{-1}\bar{X}^* \tag{16}$$

and perfect recall is assured (* denotes transpose). Notice also that since the $\bar{x}_i \in \mathfrak{R}^N$ are linearly independent at most N memories can be perfectly recalled, or equivalently, the number of memories must be less than or equal to the dimension of the key vector ($M \le N$).

B) *Rows of $\bar{X}$ are linearly independent ($\Rightarrow M > N$).*

Since the rows are linearly independent, $\left(\bar{X}\bar{X}^*\right)^{-1}$ exists yielding

$$\bar{T}\bar{X} = \bar{Y} \tag{17}$$

$$\bar{T}\bar{X}\bar{X}^* = \bar{Y}\bar{X}^*$$

therefore

$$\bar{T} = \bar{Y}\bar{X}^*\left(\bar{X}\bar{X}^*\right)^{-1} .$$

Notice upon expansion

$$\bar{T} = \left(\sum_i \bar{y}_i \bar{x}_i^*\right)\left(\sum_i \bar{x}_i \bar{x}_i^*\right)^{-1} \tag{18}$$

$$= \left(\frac{1}{M} \sum_i \bar{y}_i \bar{x}_i^*\right)\left(\frac{1}{M} \sum_i \bar{x}_i \bar{x}_i^*\right)^{-1}$$

$$= \hat{V}_{yx}\hat{V}_{xx}^{-1}$$

the linear formulation of associative memory with linearly independent rows is seen to be equivalent to linear regression where $\hat{V}_{yx}$ and $\hat{V}_{xx}$ are approximations of the theoretical covariance matrices

$$\bar{V}_{yx} = E\left\{\bar{Y}\bar{X}^*\right\} \tag{19}$$

$$\bar{V}_{xx} = E\left\{\bar{X}\bar{X}^*\right\} \tag{20}$$

based upon the observed realizations $\left\{(\bar{x}_i, \bar{y}_i)\right\}$. Also if the theoretical covariance matrices were known, the best linear unbiased estimator (BLUE) for the memory $\bar{y}$ given the key $\bar{X}$ would result

$$\bar{y} = \bar{V}_{yx}\bar{V}_{xx}^{-1}\bar{x} . \tag{21}$$

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Consequently, when the linear associative memory is overloaded ($M > N$) and the rows of $\bar{X}$ are linearly independent, the memory recalled is best in the sense of least squared error, and is reminiscent of traditional optimal linear regression and estimation (18,21) where the number of data pairs $\{(\bar{x}_i, \bar{y}_i)\}$ exceeds the vector dimensionality.

These linear cases are illustrated in Fig. 12 with $M = 6$ pairs of single dimensional ($N = 1$) associations. For perfect recall, only 1 arbitrary memory can be stored (x_1, y_1). As shown, the compromise for memory overloading is inexact recall, represented by the discrepancy (dashed line) between the true memory y_i and the linear mapping $F(x_i)$.
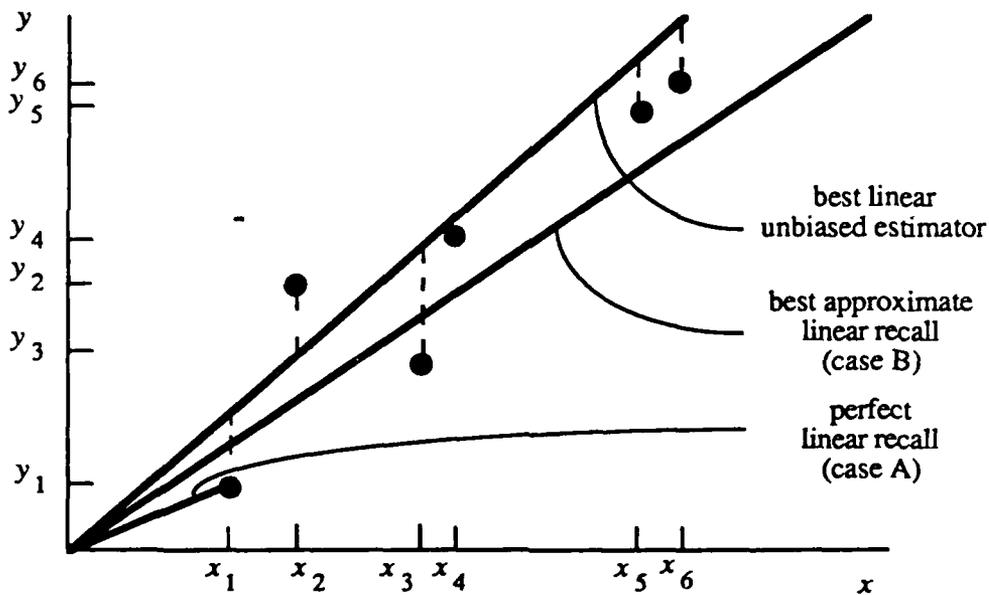

Fig. 12. Comparison of linear regression, estimation, and associative memory.

C) *Prototype keys* $\{\bar{x}_i\}$ *are linearly independent and orthonormal* ($\Rightarrow M \leq N$). Suppose the prototype keys are mutually orthogonal unit vectors. Then by definition

$$\vec{x}_i^* \vec{x}_j = \vec{x}_i \bullet \vec{x}_j \equiv \begin{cases} 1 & i = j \\ 0 & i \neq j \end{cases} \tag{22}$$

together with the linearly independence assumption yields

$$\bar{T} = \bar{Y} \left\{ \begin{bmatrix} \vec{x}_1^* \\ \vec{x}_2^* \\ \vdots \\ \vec{x}_M^* \end{bmatrix} [\, \vec{x}_1 \; \vec{x}_2 \dots \vec{x}_M \,] \right\}^{-1} \bar{X}^* \tag{23}$$

$$= \bar{Y} \bar{I} \bar{X}^* = \bar{Y} \bar{X}^* \ .$$

Now this formulation, termed the correlation matrix or outer product technique, grants insight into how the output memory is retrieved. Suppose the prototype key $\vec{x}_l$ is introduced. The corresponding memory recalled is then

$$\bar{y} = \bar{T} (\vec{x}_l) \tag{24}$$

$$= [\, \bar{y}_1 \; \bar{y}_2 \dots \bar{y}_M \,] \begin{bmatrix} \vec{x}_1^* \\ \vec{x}_2^* \\ \vdots \\ \vec{x}_M^* \end{bmatrix} \vec{x}_l$$

$$= \left(\sum_i \bar{y}_i \vec{x}_i^* \right) \vec{x}_l$$

$$= \bar{y}_l \left(\vec{x}_l^* \vec{x}_l \right) + \sum_{i \neq l} \bar{y}_i \left(\vec{x}_i^* \vec{x}_l \right)$$

$$= \bar{y}_l \left\| \vec{x}_l \right\|^2 + \sum_{i \neq l} \bar{y}_i \left(\vec{x}_i \bullet \vec{x}_l \right)$$
(signal + noise)

$$= \bar{y}_l \quad .$$

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Thus perfect recall is ensured provided the prototype keys are orthogonal. Without orthogonality, crosstalk noise is mixed (24) with the true memory, thereby contributing to erroneous recall. Orthogonality is often achieved by conventional Gram-Schmidt orthogonalization. Consequently, the prototype keys associated with stored memories and the arbitrary input patterns are often preprocessed to enhance orthogonality.

In consequence, the conditions for both perfect recall and best approximate recall have been established for linear associative memory. However to satisfy the ideal objective, both generalization and adaptability must be addressed. Generalization is treated in the next section, while the matrix of elements constructed by (14,16,18, or 23) is generally made adaptive according to the recursion

$$\bar{T}_k = \bar{T}_{k-1} + \bar{g}_k(\bar{y}_k - \bar{T}_{k-1}\bar{x}_k)\bar{x}_k^*$$

(25)

where $\bar{T}_k$ is the new adaptive element matrix formed from the recent matrix utilizing (k-1) data pairs $\{(\bar{x}_i, \bar{y}_i)\}$. Formulas for the gain vector for the cases addressed are contained in [1].

3.5 Generalization Capability of Linear Associative Memory

Generalization in the context of associative memory is the ability to recall the correct memory when excited with an incorrect or perturbed input (key). Typical perturbations may include missing input elements, random noise, or perhaps in vision, variations which often prohibit correct identification. Mathematically, generalization can be viewed as the ability to map all perturbations contained in a neighborhood about a prototype key $\bar{x}_i$ to the correct output memory (see Fig. 13). Here ideal generalization corresponds to maximum input perturbation radius r_I (without overlapping neighborhoods) and minimum output perturbation radius r_o. Now upon specifying a class of perturbations, generalization capability can then be formulated in terms of the parameters which influence the growth of these neighborhoods.
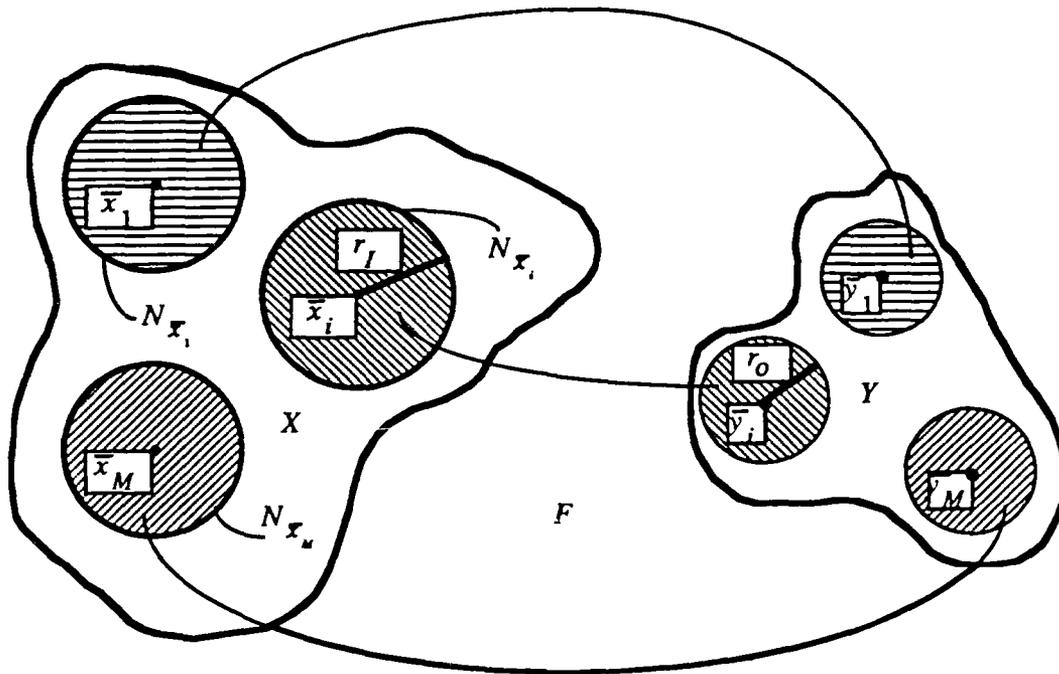
Fig. 13. Function generalization with input neighborhood of perturbation radius r_I being mapped within output neighborhood of radius r_o .

Many perturbations arising in the mapping of a prototype key $\bar{x}_i$ to the correct memory $\bar{y}_i$ can be modeled by

$$F(g(\bar{x}_i)) = \hat{y}_i \tag{26}$$

where g( ) is the perturbation function, and $\hat{y}_i$ is the resulting output given the perturbed input. Ideally, the output $\hat{y}_i$ would be the correct memory $\bar{y}_i$. However depending on the functional form of the perturbation, correct memory recall may be impossible. For an introductory treatment, only random noise perturbations will be examined of the form

$$g(\bar{x}_i) = \bar{x}_i + \bar{n} \quad . \tag{27}$$

Consequently, the objective of this section is to determine quantitatively the relationships which influence the generalization capability of linear associative memories. The treatment begins with conservatively relating the acceptable amount of input noise perturbation (r_I) to the minimum distance between the input prototype keys. Next, the output perturbation

neighborhoods (r_0) are shown to be dependent upon how close to capacity the memory is being operated.

Consider the noise perturbation model (27) where the perturbation $\bar{n}$ is a zero mean random vector of variance σ^2 and normalized (in energy) to the dimension N

$$\bar{n} = \frac{1}{\sqrt{N}} \begin{bmatrix} n_1 \\ n_2 \\ \vdots \\ n_N \end{bmatrix} . \tag{28}$$

The perturbed input is then treated as a prototype key corrupted with additive noise (27). Although the noise elements n_i may be symmetrically distributed (for example multivariate Gaussian), the resultant noise vector $\bar{n}$ tends to lie near the surface of a sphere with radius σ. (Specifically $P\left(\left|\|\bar{n}\|^2 - \sigma^2\right| \geq \Delta\right) \leq \frac{2\sigma^2}{N\Delta^2}$ [18]). Thus for typical associative memories (where $N > 100$), the perturbations encountered tend to be concentrated on a spherical surface centered at the prototype key, with radius equivalent to the noise standard deviation (see Fig. 14..) This apparent concentration of noise, due to large dimensional spaces, is encountered in communication theory and termed sphere hardening [18].
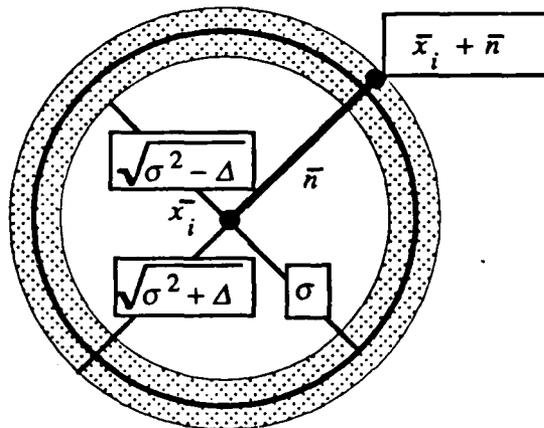

Fig. 14. Sphere hardening at prototype key $\bar{x}_i$.

In a practical setting, the perturbation variance is rarely known. However an upper limit can often be specified. Thus if the variance can be bound by σ^2_{max}, then the

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perturbation is likely to be concentrated on a sphere within radius σ_{max}. Consequently the minimum distance between any two prototype keys must be greater than the maximum perturbation standard deviation to avoid (with high probability) unresolvable recall errors.

$$d_{min}^{x} = \min_{i,j}\ d\left(\bar{x}_i, \bar{x}_j\right) > \sqrt{\sigma_{max}^2 + \Delta} = r_I$$
(29)

Notice an unresolvable recall error occurs when the perturbed input $\bar{x}_i + \bar{n}$ lies on another prototype key $\bar{x}_j$, and hence $\bar{y}_j$ is incorrectly recalled (see Fig. 15.). Clearly the best representation for the prototype keys $\left\{\bar{x}_i\right\}$ would be one which maximizes the separation amongst the keys in the input space, thereby accommodating the largest amount of random perturbation.
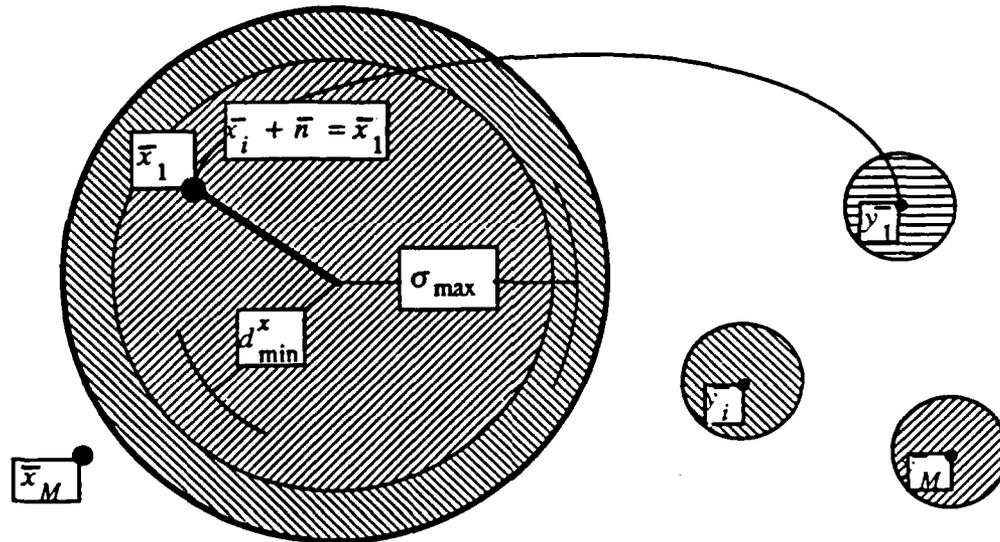
Fig. 15. Unresolvable recall error occurring for $\sigma_{max} > d_{min}^{x}$.

The second relation involves the growth of the output perturbation neighborhood as a function of how close to capacity the memory is being operated. The output perturbation neighborhood about memory $\bar{y}_i$ is that region mapped into the output space arising from inputs within the region about $\bar{x}_i$ of radius r_I . (Mathematically, the neighborhood is written $N_{\bar{y}_i} = \left\{\bar{y} : \bar{y} = F(\bar{x}) ; \bar{x} \in N_{\bar{x}_i}\right\}$). Ideally, the output perturbation

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neighborhoods are desired small as possible, therefore many input keys representing perturbations of the true key would be mapped very near the correct memory.

To obtain the relationship, consider the general linear associative memory with a perturbed input as shown.

$$\bar{x} = \bar{x}_j + \bar{n} \qquad \boxed{\bar{T}} \qquad \bar{y} = T\,(\bar{x})$$
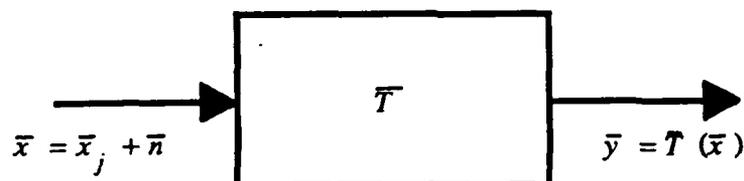
Fig. 16. Perturbation example.

Recall the general solution $\bar{T} = \bar{Y}\bar{X}^+$, hence

$$\bar{y} = \bar{Y}\bar{X}^+\bar{x} \tag{30}$$

$$= \bar{Y}\bar{X}^+\left(\bar{X}\bar{X}^+\bar{x}\right) \quad \text{def. of pseudo inverse}$$

$$= \bar{Y}\bar{X}^+\left(\bar{X}\bar{X}^+\bar{x}_j + \bar{X}\bar{X}^+\bar{n}\right)$$

$$= \bar{Y}\bar{X}\left(\bar{x}_j + \hat{n}\right)$$

where $\hat{n} = \bar{X}\bar{X}^+\bar{n}$ is the projection of the noise vector $\bar{n}$ onto the space spanned by the prototype keys $\{\bar{x}_i\}$. Now the variance of the norm of the effective noise $\hat{n}$ is [1]

$$\delta_n^2 \equiv Var\left(\|\hat{n}\|\right) = \frac{M}{N}\|\bar{n}\|^2 \tag{31}$$

and thus the noise term is attenuated by $\sqrt{M\,/\,N}$ on the average when mixing with the signal that represents perfect recall or the best approximate recall, depending upon the cases previously stated. Therefore, to combat the deleterious effects of input perturbations (potentially causing large deviations in the recalled memory pattern from the true memory) the number of memories stored is to be kept much smaller than the vector dimension ($M << N$) implying operating the memory well under capacity as illustrated in Fig. 17.

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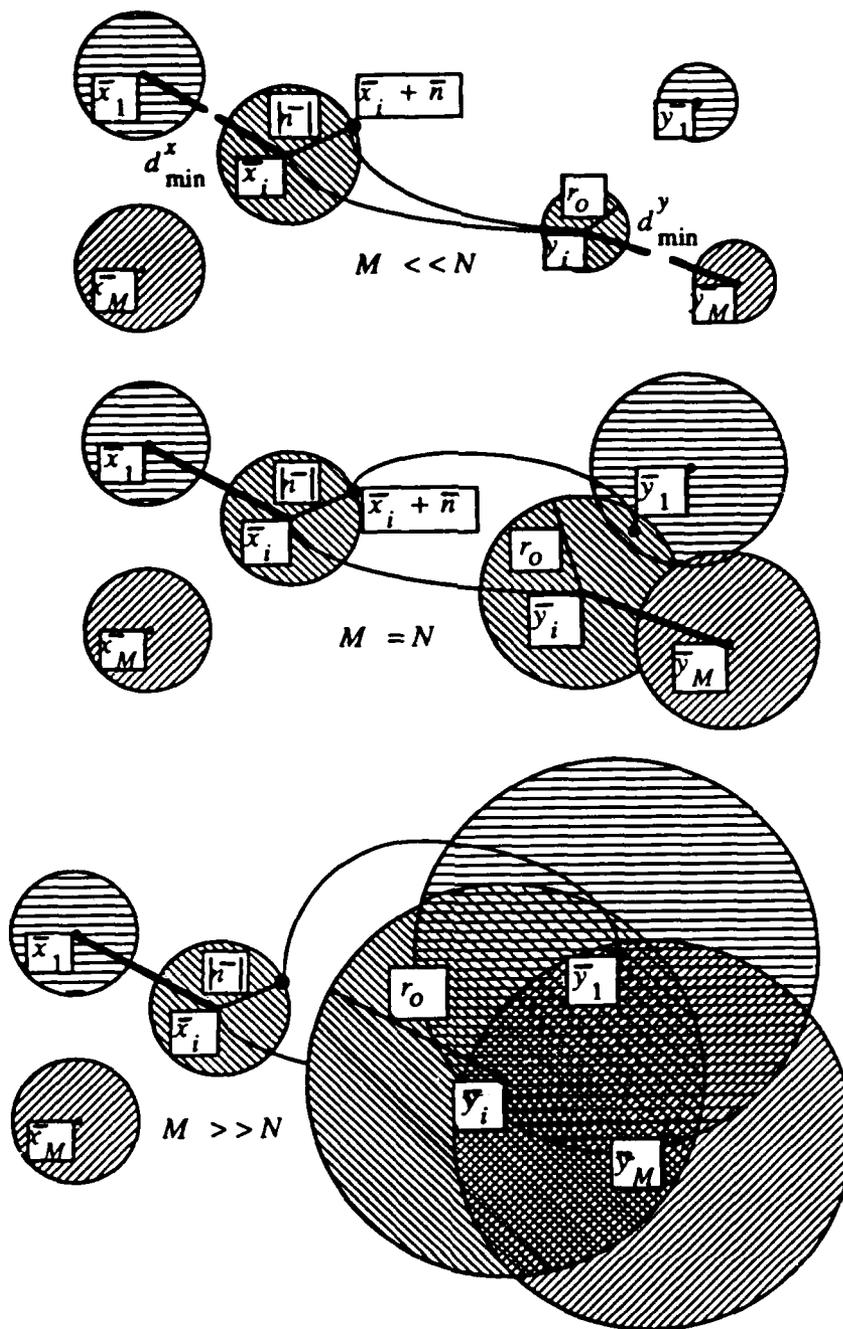
Fig. 17. a) Memories stored well within capacity $(M << N)$, b) Memories stored at capacity $(M = N)$ with spurious recall, c) Memories stored beyond capacity $(M >> N)$ with erroneous recall.

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In summary, generalization is dependent upon the parameters which control the size of the perturbation neighborhoods. Ideally, the input perturbations neighborhoods are desired large, while the output neighborhoods small. For linear associative memory, the maximum input perturbation neighborhood is limited by the distance between the prototype keys. While the output perturbation regions are driven small by operating the memory well below memory capacity, thereby attenuating the perturbation by the square law (31). Several demonstrations of generalization with both random noise and missing fragment perturbations are contained in [1,19].

And for general associative memory, generalization typically follows from selecting a representation where the associated data pairs $\{(\bar{x}_i, \bar{y}_i)\}$ or clusters, are well separated in their respective spaces and the memory is operated well within the memory capacity.

3.6 Nonlinear Associative Memory

Several limitations accompany the linear associative memories described in the previous section. Fundamentally since the mapping is linear, input prototype keys $\{\bar{x}_i\}$ which are close together in the domain X must be mapped close together in the range Y. Thus linear associative memories will not suffice where similar prototype keys need be mapped to dissimilar output memories. Furthermore, the linear memories ignore contextual information which is believed to be of primary importance in biological memory, enabling selective recall amongst seemingly infinite memories. Moreover, often burdensome is the preprocessing requirement (to obtain linearly independent prototype keys) necessary to achieve perfect recall. Together with the low memory capacity (# memories $\leq$ vector dimension) reduced further for good generalization, linear associative memories leave much to be desired in contrast to biological memory.

In an attempt to counter some of the mentioned limitations, nonlinear associative memories have been proposed and several are discussed in detail in the following chapters. For perspective, some of the models are briefly summarized below.

The Hopfield model [20] is an auto-associative memory with feedback, comprised of a linear model (specifically the outer product technique, case C) followed by a nonlinear threshold function. Although the iterative process converges, spurious memories often result [21] and the memory capacity is low [22].

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The Grossberg model [23] creates it's own memories depending upon the degree of similarity desired by the modeler (vigilance parameter) between the keys and respective memories. Since the network is allowed to grow as needed to represent the memories, comparing the memory capacity of such model to the previous models with fixed architectures in inappropriate.

The Poggio associative memory model is optimal amongst memories of matrix polynomial form [24]. Although the memory is nonlinear in the input key vector, the adaptable parameters determined from the least squares criteria are linear, and thus easily calculated.

In the associative net by Willshaw [25], the memory capacity is increased at the expense of restricting the form of the binary input and output vectors. For maximal information storage, the number of ones in the vector keys and memories are to be $\log_2 N$. As a consequence, a sparse connection matrix (approximately half zeros) of binary switches is formed yielding a memory capacity $\left(M = N^2 \frac{\ln^3 2}{\ln^2 N} \right)$ which exceeds linear associative memory.

The perceptron by Rosenblatt [26] is a nonlinear hetero-associative memory which is rather limited in the class of mappings which can be learned [27]. However by cascading several layers of the basic architecture or filter (see Fig. 10.), and incorporating one of several multilayer learning algorithms [28-32], the multilayer perceptron becomes capable of learning much more complex mappings.

Overall, the key to devising a good associative memory lies with the expressivity of the network architecture. That is, the larger the class of functions the network can realize, the more arbitrary the data pairs $(\{\bar{x}_i, \bar{y}_i\})$ can be. For if an associative memory could be constructed capable of mapping arbitrary functions, then any arbitrary set of keys and memories could be associated with perfect recall performance. Although no such universal associative memory has been practically constructed, Kolmogorov has proved existence [33]. And even more striking, the Kolmogorov architecture somewhat resembles a biological neural network per description below.

First realize that a sufficient condition for perfect recall performance amongst arbitrary data pairs is for the associative memory architecture to be capable of realizing arbitrary functions. (This is easily demonstrated in a single dimension example by considering the data pairs plotted in Fig. 18. Perfect recall is ensured $\left(y_i = F(x_i) \; \forall \; i \right)$ provided the architecture can express any function F which intersects all points.)
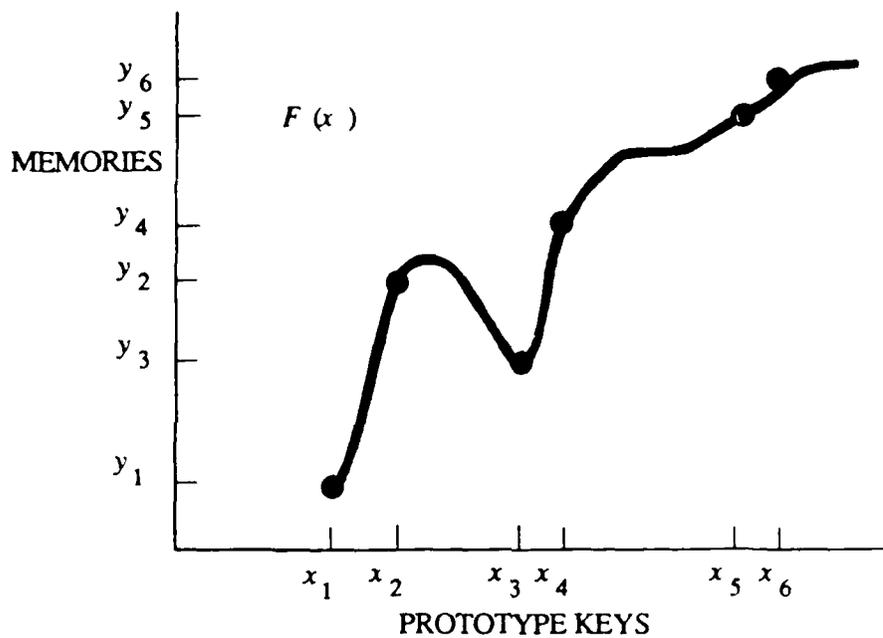

Fig. 18. Perfect recall attained by an associative memory realizing function F.

Now Kolmogorov's theorem states that an arbitrary continuous function of many variables can be realized by a finite superposition of continuous functions, each dependent upon only a single variable, accordingly

$$F_l(\bar{x}) = \sum_{i=1}^{2N+1} G_i \left(\sum_{j=1}^{N} H_{ij}(x_j) \right)$$

(32)

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where H_{ij} are fixed continuous increasing functions and G_i are continuous functions dependent on F_i. Thus in the vector format

$$\bar{y} = F(\bar{X}) = \begin{bmatrix} F_1(\bar{x}) \\ F_2(\bar{x}) \\ \vdots \\ F_L(\bar{x}) \end{bmatrix}$$

(33)

each output component y_i (dependent upon many elements of $\bar{x}$) is expressed according to (32), yielding a vector of Kolmogorov representations. The accompanying network architecture for each output realization y_i is shown in Fig. 19a.). Notice the similarity of the architecture to neural network models, (compare Fig. 4.) whereby the functions H_{ij} represent nonlinear threshold functions amongst neurons comprising the first layer, and G_i being the nonlinear threshold functions for the second layer neurons. However, the architecture is biologically implausible since all synaptic strengths are of equal magnitude.

Later Lorentz [34] and Sprecher [35] extended the results of Kolmogorov to yield the architecture shown in Fig. 19b). Notice the use of N connection weights offset the stringent requirement of $N(2N + 1)$ threshold functions on the first level of neurons. Again the architecture is also biologically unlikely since the same synaptic strengths are repeated to each of the neurons in second layer.

Following the trend of compromising connection weights for nonlinear threshold functions, the question remains as to whether an arbitrary continuous function of many variables can be represented as a finite superposition of single variable functions with the more biologically realistic architecture of Fig. 19c. For if so, this mathematical architecture would prove invaluable towards understanding the vast capabilities of biological associative memory, as well as providing principles for constructing associative memories of far greater capacity.

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$$f(\bar{x}) = \sum_{i=1}^{2N+1} G_i \left(\sum_{j=1}^{N} H_{ij}(x_j) \right)$$

$$f(\bar{x}) = \sum_{i=1}^{2N+1} G \left(\sum_{j=1}^{N} w_j \, H_i(x_j) \right)$$

$$f(\bar{x}) \triangleq L \left(\sum_{i=1}^{2N+1} \alpha_i \, G \left(\sum_{j=1}^{N} w_{ij} \, H(x_j) \right) \right)$$
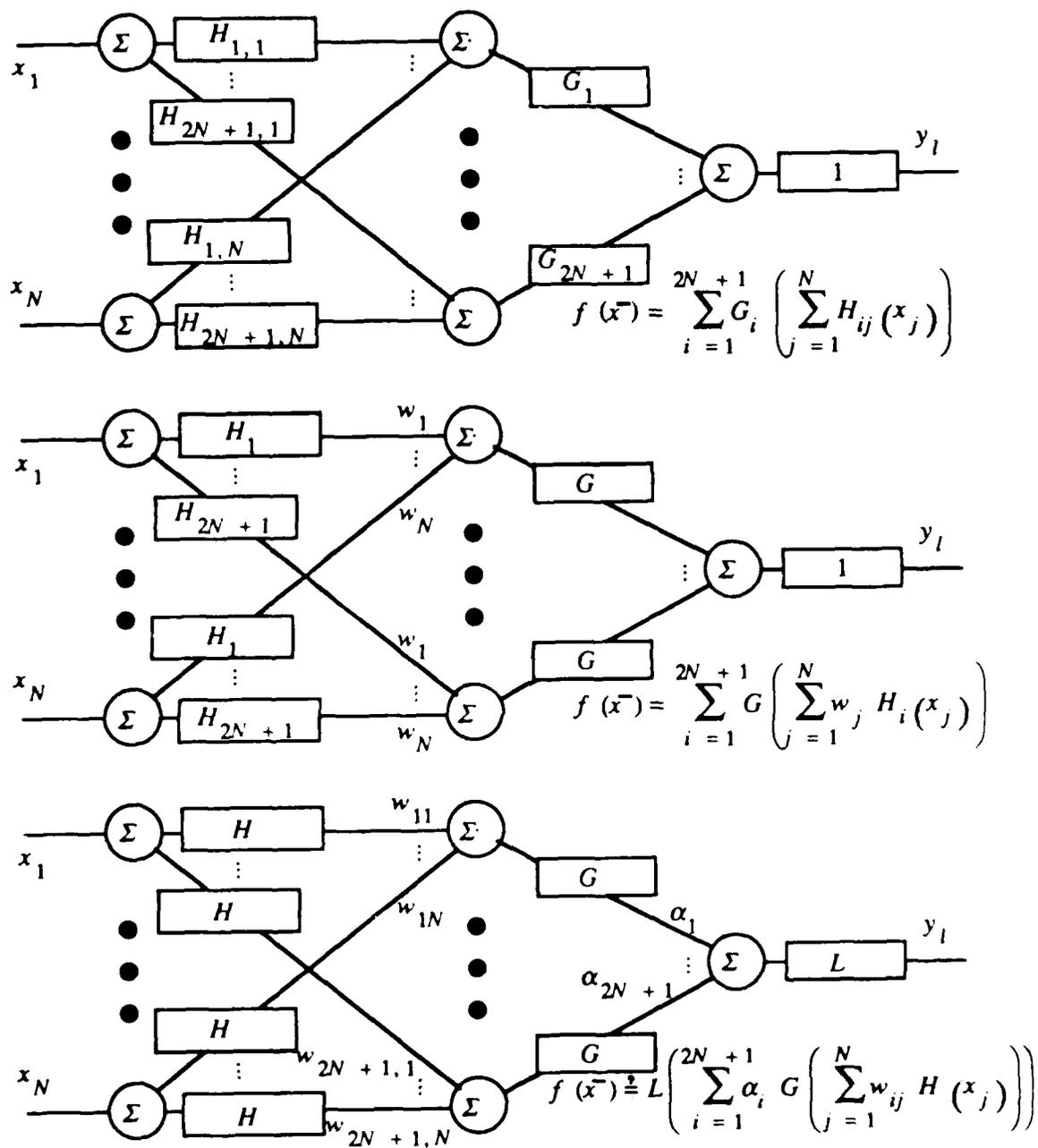
| inputs	functions	weights	functions	weights	outputs
a)N	N(2N+1)	0	2N+1	0	1
b)N	2N+1	N	1	0	1
c)N	1	N(2N+1)	1	2N+1	1

Fig. 19. a)Kolmogorov, b)Lorentz, c)biological (?) representations.

3 1

3.7 Evaluation of Associative Memories

Due to the vast variability in the network architectures employed in associative memories, developing an evaluation protocol can be difficult. This section briefly describes a general set of criteria likely to be instrumental in evaluating various associative memories for application.

The evaluation can be partitioned according to the storage and recall operations. First for memory storage, the memory capacity is of extreme importance. Such capacity is usually expressed as an upper bound on the number of memories which can be reliably recalled. Another storage parameter is the actual efficiency of the memory storage, being expressed as the number of reliable memories stored per architecture size and complexity. Learning efficiency expressed as the amount of computation (number of iterations) required to store a benchmark memory set is also likely to be an important storage evaluation parameter.

Secondly in regard to recall evaluation, most important are speed and accuracy. The accuracy can be evaluated by simply determining the sum squared error resulting from comparing the true memories to the associative memory outputs under key prototype excitation. Recall efficiency or speed entails the amount of time (computation) required to recall a memory given an input key. Finally, the generalization capability can be examined by determining the maximum perturbation neighborhood the associative memory can tolerate under reliable recall.

Both simulation and analytical approaches to determining such evaluation criteria can be employed. Analytical approaches for the linear associative memories as displayed herein are straightforward. However for nonlinear memories, often stochastic approaches are used taking advantage of large sample properties invoked for networks with large numbers of neurons. Monte Carlo simulations also can provide evaluation parameters and often with much less effort. Especially if benchmark memory sets and examples are established, evaluation by simulation may become routine. For illustration, memory capacity bounds obtained analytically [22], and by simulation [20] are shown in Fig. 20. for some associative memories.

3 2
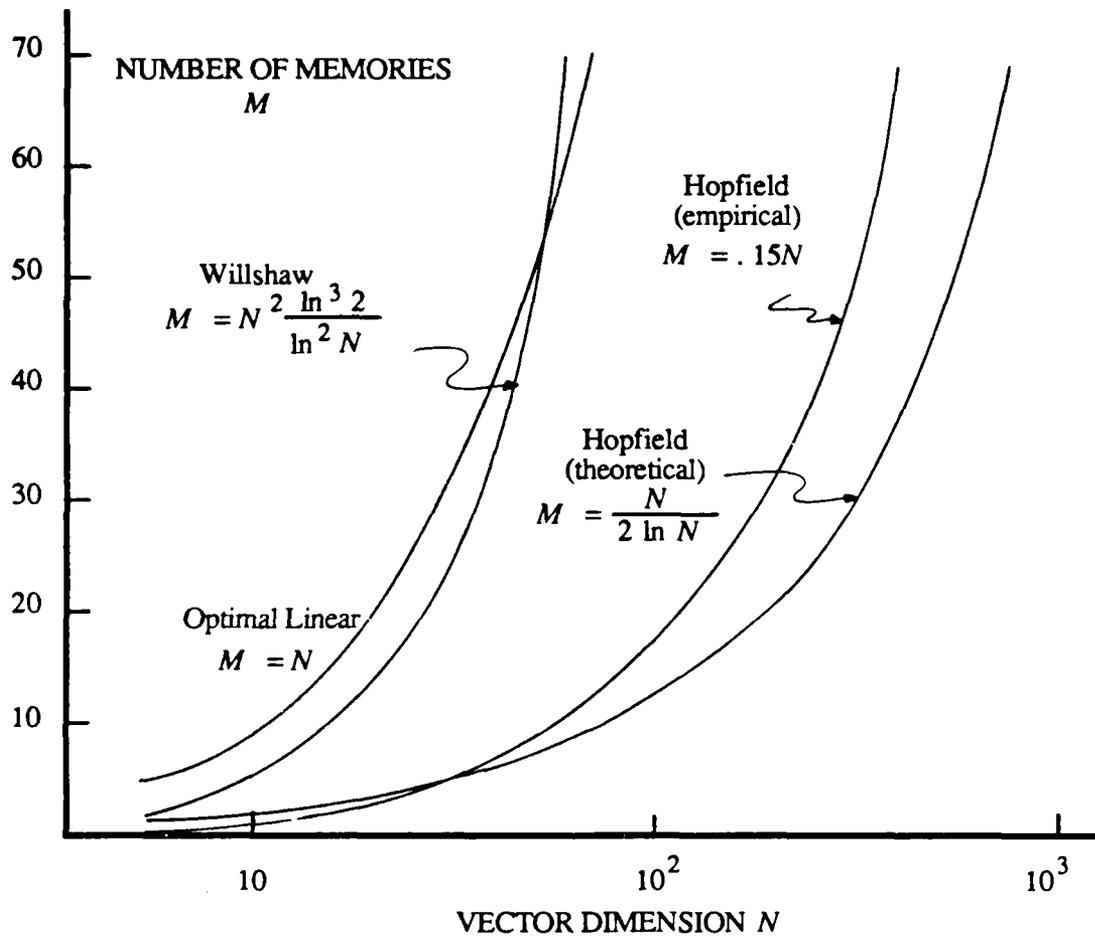
Fig. 20. Memory capacity for some associative memories

Finally like any evaluation, the best associative memory is the candidate with the most favorable evaluation results for those attributes most crucial for the application. Therefore many types of associative memories with distinct favorable attributes are envisioned to be applied.

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4. CONCLUSION

Clearly the mathematical models of associative memory discussed possess certain biological memory characteristics, such as pattern recognition by association, distributed parallel processing, and generalization. Moreover the models, through small scale applications, seem to substantiate the ever prevailing wisdom acknowledging the suitability of neural-like architectures for associative memory pattern recognition and other random problems where algorithmic solutions do not exist [36]. However these architectures developed through decades of research remain distant in performance to their biological counterparts, exhibiting seemingly infinite memory capacity and fast recognition.

Ironically, perhaps the mechanism responsible for the extraordinary capability, namely distributive parallel processing, may well be the barrier which prohibits man from truly understanding the origin of capability. For memory, along with other brain functions, are collective phenomenon, distributed over vast neuronal regions. And in the absence of techniques which enable investigation of brain function on a collective or systems basis, principles underlying such extraordinary capabilities may never be uncovered, nor realized.

In conclusion, realizing the vast differences in pattern processing (speech recognition, image understanding, decision making...) amongst computers and biological systems, future research is likely to be chartered to discovering collective principles underlying biological information processing. And in the process, a sufficient understanding may be gained offering insight towards the development of specialized neuronal architectures, borrowing from both biological and physical sciences, for assisting man in learning and problem solving.

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A tutorial is presented encompassing both biological and mathematical aspects of associative memory for pattern processing. A systems viewpoint is adopted whereby biological associative memory is viewed as a system of adaptive filters, with the free parameters of the filter corresponding to the strengths of the biological neural connections. Certainly such viewpoint is not intended to accurately depict the true mechanisms underlying the extraordinary capabilities of biological associative memory - fast pattern recognition and apparently infinite memory capacity. For such mechanisms will unlikely be discovered in the absence of tools allowing the observance of collective behavior over systems of neurons. However, the viewpoint does serve to integrate both mathematics and biology on a general level.

Of most significance is perhaps the systematic treatment of mathematical associative memory. In the adaptive filter framework, associative memory is described and compared to traditional statistical techniques. Also, new insight into the generalization capability of associative memory is expressed. Conditions are presented to ensure both correct memory recall and significant generalization.

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