

# Scalable Evolutionary Design of Pattern Classifier with Feature Selection Capabilities based on Cellular Automata

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Indian Institute of Technology, Kharagpur  
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# Outline

- 1 **Objective**
- 2 **Introduction**
  - Classification Problem
  - MACA Characteristics
- 3 **MACA based Classifier**
  - Basic Idea
  - MACA Classifier
  - Making the classifier Scalable
- 4 **Experiments**
  - Small Applications of Classifier
- 5 **Feature Selection**
  - Experiment of Molecular Classification of Cancer
- 6 **Assimilation**

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# Aim of Project

## Objective

Design a Scalable Pattern Classifier based on Cellular Automata (CA) and Study its Characteristics

## Objective 1

Design and implement a Scalable Pattern Classifier based on CA

## Objective 2

Evaluate the Classifier on datasets of different topologies and experiment to test for Scalability

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Experiment on real world datasets and Study the characteristics of the Classifier (Feature Selection)

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# Classification Problem and Cellular Automata

## Classification Problem

Classification Problem can be viewed as partitioning the feature space into partitions labeled by classes

## Machine Learning

ML methods provide technique to determine the boundaries of the partitions in the features space and hence help in learning the classes

## MACA Property

MACA, a special class of Cellular Automata partitions the feature space into basins

# Classification Problem and Cellular Automata

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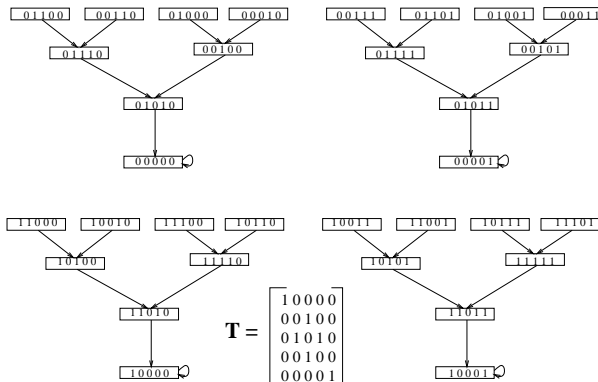
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MACA, a special class of Cellular Automata partitions the feature space into basins

# MACA



- Given MACA of size  $n=5$ , the feature space is of the size  $2^n$  ( $2^5=32$ ).
- An MACA is characterized by  $T$  Matrix, which captures the basin distribution.

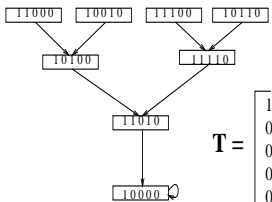
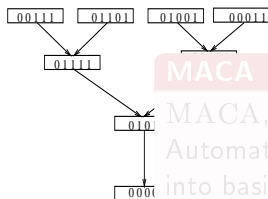
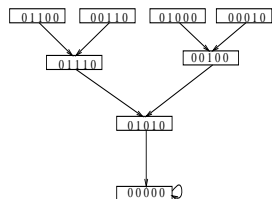
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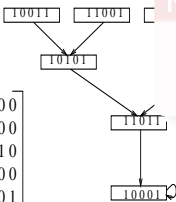
## Next State

$$s_{t+1} = T \cdot s_t \text{ i.e., } s_{t+p} = T^p \cdot s_t$$



$T =$

1	0	0	0	0
0	0	1	0	0
0	1	0	1	0
0	0	1	0	0
0	0	0	0	1



# MACA Property

## MACA

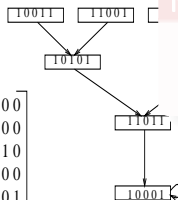
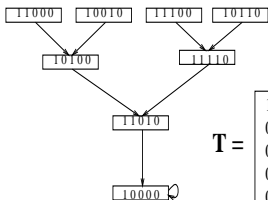
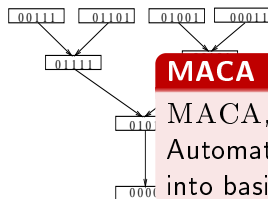
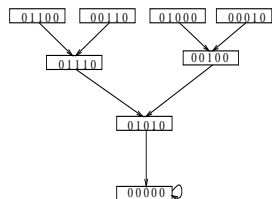
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# MACA Property

## MACA

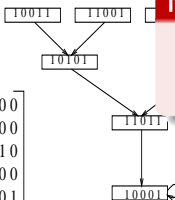
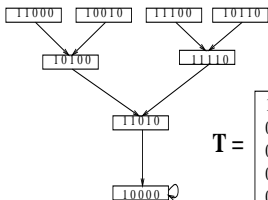
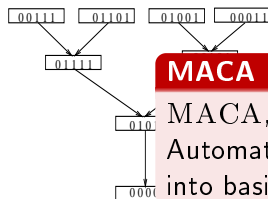
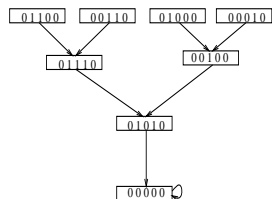
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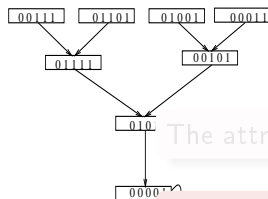
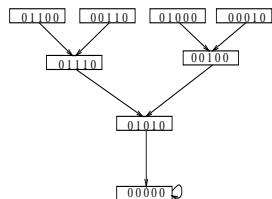
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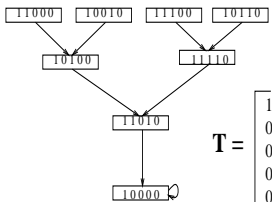
# Attractors



The attractors represent the Class

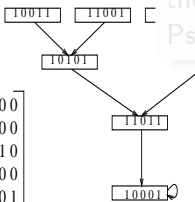
## PEF Bits

the attractors are characterized by Pseudo-Exhaustive Field (*PEF*)bits



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1	0	0	0	0
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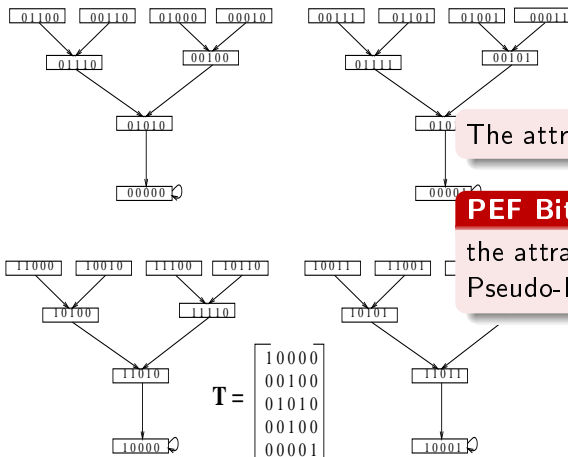
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$T =$

10000
00100
01010
00100
00001

# Attractors



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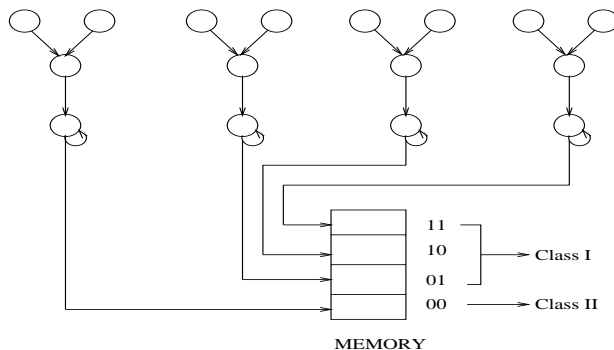
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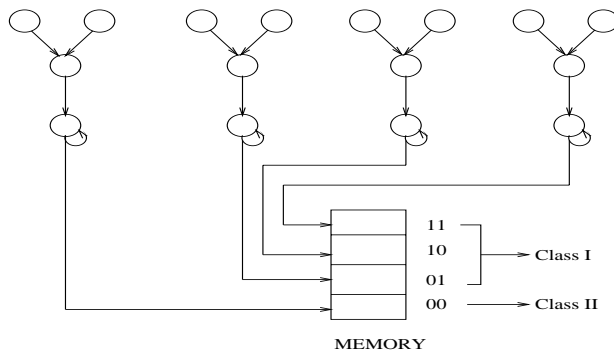
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## Basic Idea



The features space is divided into basins by the MACA and the basins will be assigned to the classes.

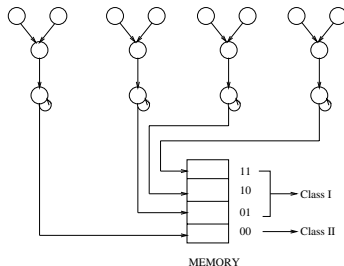
We just need to remember which attractors belong to which class



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# How it Works



Find an /maca/ that classifies your data and find the attractors corresponding to the classes

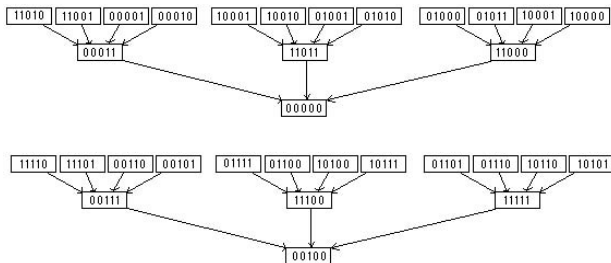
When an incoming pattern comes, Multiply it by the  $T$  matrix repeatedly until you reach an attractor

Look up the attractor's class

# Learning an MACA

- 1 We want an MACA that partitions the feature space correctly for us
- 2 Correctly in the sense that all the patterns belonging to different classes are in different basins
- 3 We use a GA formulation to search for our appropriate MACA
- 4 The T Matrix is encoded in a Pseudo-Chromosome and GA is run over it
- 5 The cost function for GA is calculated over the Training samples based on item 1

# Pseudo-chromosome



Pseudo Chromosome

[2 0 -1 2 0]

PEF bit

$$\begin{bmatrix} 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 & 1 \end{bmatrix}$$

The basin distribution obtained when T Matrix synthesized using Method() only

[2 0 -1 2 0]

$X^2$   $(I+X)$   $X^2$



## Lot of Matrix Multiplication

In determining which basin a pattern belongs to, you have to repeatedly multiply the pattern with the T Matrix to get the attractor (which characterizes the basin which the pattern belongs to)

We would like to have a scheme in which, by just looking at the pattern we can determine the basin/attractor of the class

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# Isomorphism in T Matrix

Modifying the algorithm that generates the T Matrix from pseudo-chromosome, we found that a pseudo-chromosome represents an equivalent class of T Matrix which have same Basin Distribution

The new scheme enabled us to find out the basin of the pattern by just knowing the PEF bits PEF

In the new scheme we do away with the T matrix altogether, thus saving space

Only the pseudo-chromosome (which contains the position of the PEF bits) is required

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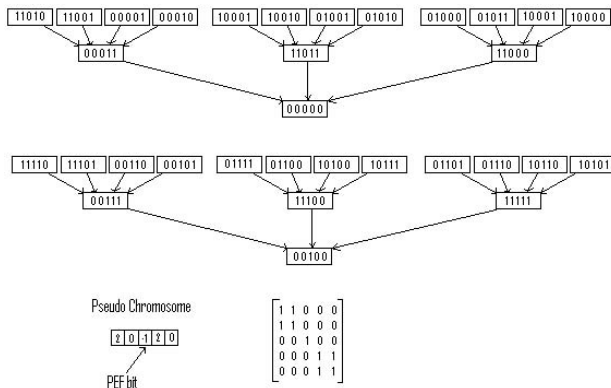
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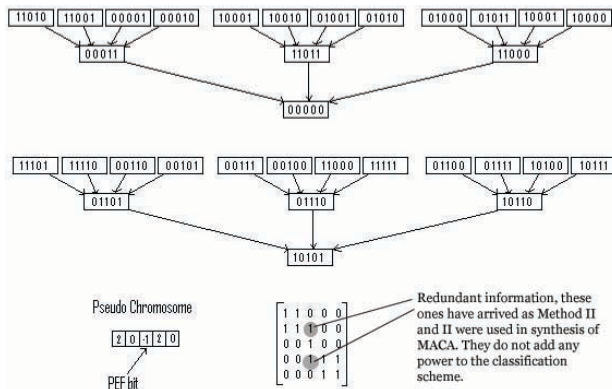
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# Isomorphism



The basin distribution obtained when T Matrix synthesized using Method() only

# Isomorphism



The Basin distribution obtained when T Matrix is synthesized using Method II and III



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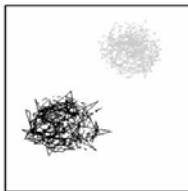
We have a Scalable classifier and we want to see it classify some standard datasets

We artificially create four different topologies of binary classification

- 1 Linearly Separable Dataset
- 2 Concave Datasets
- 3 Spiral Datasets
- 4 Annular Datasets

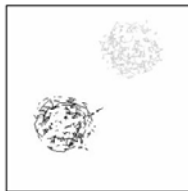
We also compare the performance of the classifier against a Linear Kernel SVM (implementation by Tim Joachims)

# Datasets used

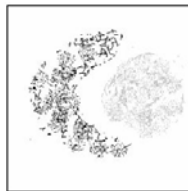


training

(a) Linear classification problem

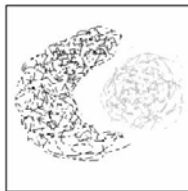


test

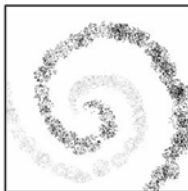


training

(b) Concave Classification Problem

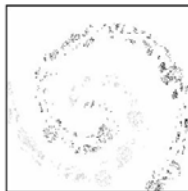


test

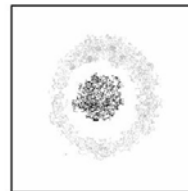


training

(a) Spiral classification problem

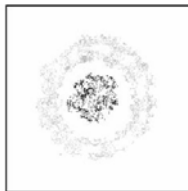


test



training

(b) Annular Classification Problem



test

# Results on the Datasets

Dataset	Scalable <i>MACA</i> classifier accuracy on		<i>SVMLight</i> Accuracy
	Training Data	Test Data	results
<b>Linear</b>	99.24%	99.61%	99.71%
<b>Concave</b>	92.77%	91.99%	95.44%
<b>Spiral</b>	83.88%	77.45%	82.46%
<b>Annular</b>	73.8%	75.94%	75.95%

**Table:** Accuracy test results across different Classification problems

# Scalability Test

The datasets used previously were small in dimension of feature and small in number of Training Examples

We scaled up both to obtain satisfactory results

# Scalability Test

The datasets used previously were small in dimension of feature and small in number of Training Examples

We scaled up both to obtain satisfactory results

# Scalability Results

Dataset	Training Data		Test Data		Time taken in seconds
	Accuracy	Examples	Accuracy	Examples	
<b>16</b>	99.24%	4311	99.61%	2313	2
<b>32</b>	98.42%	12000	97.66%	2000	3.0
<b>64</b>	96.22%	50000	96.33%	8000	28
<b>100</b>	100.00%	60000	98.54%	10000	32
<b>100</b>	100.00%	4000	99.69%	2000	3

**Table:** Scalability Test results

# IRS Dataset

Given

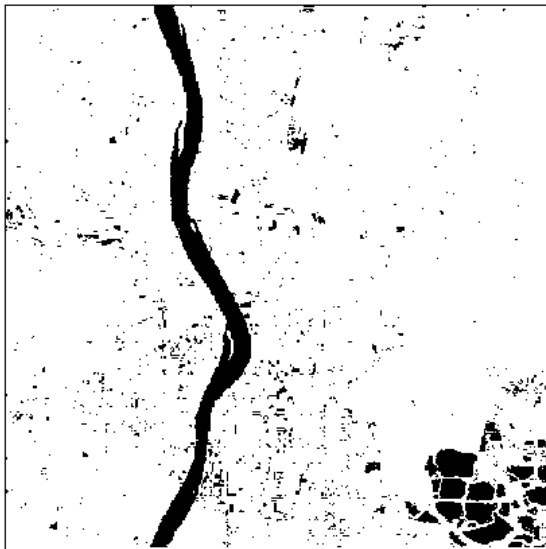
- a 4 band image taken by IRS satellite of Kolkata
- Two classes- (Water body or Man-made construction) or Otherwise
- Take a Set of tagged pixels and learn the classifier and then regenerate the whole image

Training Data		Test Data	
accuracy	samples	accuracy	samples
97.76%	120000	97.26%	20000

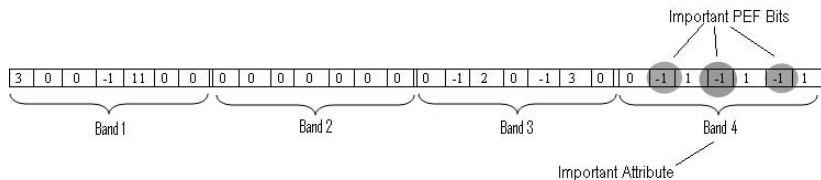
**Table:** Accuracy results on IRS Dataset



# Reconstructed image



# Observation made on the Classifier



Hints at Feature Selection capabilities

# Outline

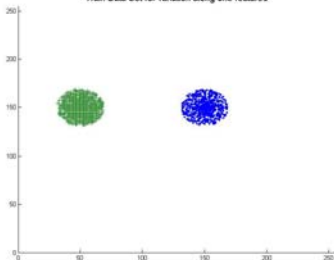
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To ascertain that there is some sort of feature selection, we perform two more experiments on artificial Datasets. The Dataset had two classes-

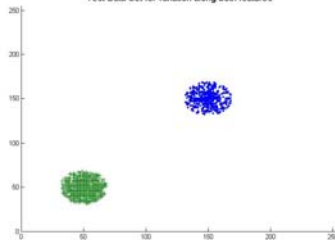
- 1 Variation along only one feature
- 2 Variation along both features

# Datasets

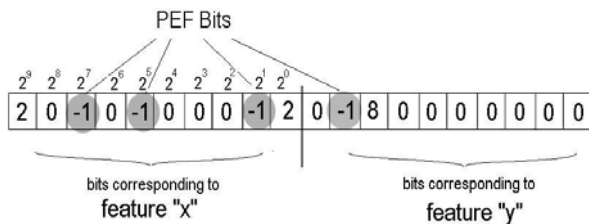
Train Data Set for variation along one features



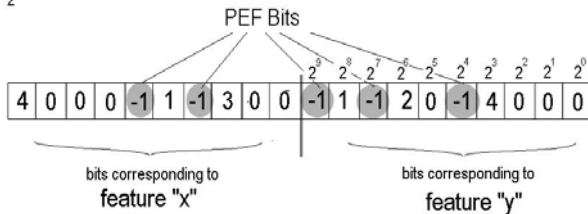
Test Data Set for variation along both features



# Classifiers Learnt Corresponding to the Datasets



2



Feature Selection Observed again

Something more than Feature Selection observed too!!

Feature Selection Observed again

Something more than Feature Selection observed too!!



# Gene expression Dataset

A generic approach to cancer classification based on gene expression monitoring by DNA microarrays is described and applied to human acute leukemias as a test case in work done by T. Golub.

- 38 Train samples and 34 Test Samples
- Two classes- ALL and AML
- Each Sample has 7129 features each of whose range can be captured with 19 bits
- Need to classify the Test cases and identify the important genes which the Cancer (Leukemia) Type (ALL or AML ) depends.

Golub had medically identified the genes and reported them

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# Results

32 out of 34 test cases correctly identified -same accuracy as reported in Golub's work

Features selected were from the important genes reported by Golub!!

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Designed a Scalable Pattern Classifier using cellular Automata.

Extensive experiments done with the proposed classifier

Feature Selection Property observed

Hints at possibility of Rule Generation from the training dataset

# Future Work

Dynamics of the classifier to be understood.

Multi-class Classifier based on Decision Tree approach

Investigate Rule generation and inference mechanism based on the classifier as this is of prime interest in data mining

*Thank You!!!*