

**ICOR 2014:  
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**GENETIC ALGORITHMS  
WITH DIVERSITY  
MEASURES FOR  
MULTIPLE CLASSIFIER  
SYSTEMS**

Authors:  
Leidys Cabrera Hernández  
Alejandro Morales Hernández  
Gladys M. Casas Cardoso  
Yailen Martínez Jiménez

Universidad Central «Marta Abreu» de Las Villas  
Santa Clara, Villa Clara, Cuba

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## Introduction

- The combination of classifiers is an active research area of the machine learning communities.
- Diversity measures are used to decide what base classifiers combine.
- Genetic algorithm are emerging as tools for solving complex search and optimization problems.

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## The Objective

- To combine
  - diversity measures results
  - accuracy classifiers results
- using Genetic Algorithms to obtain a good multiclassifier.

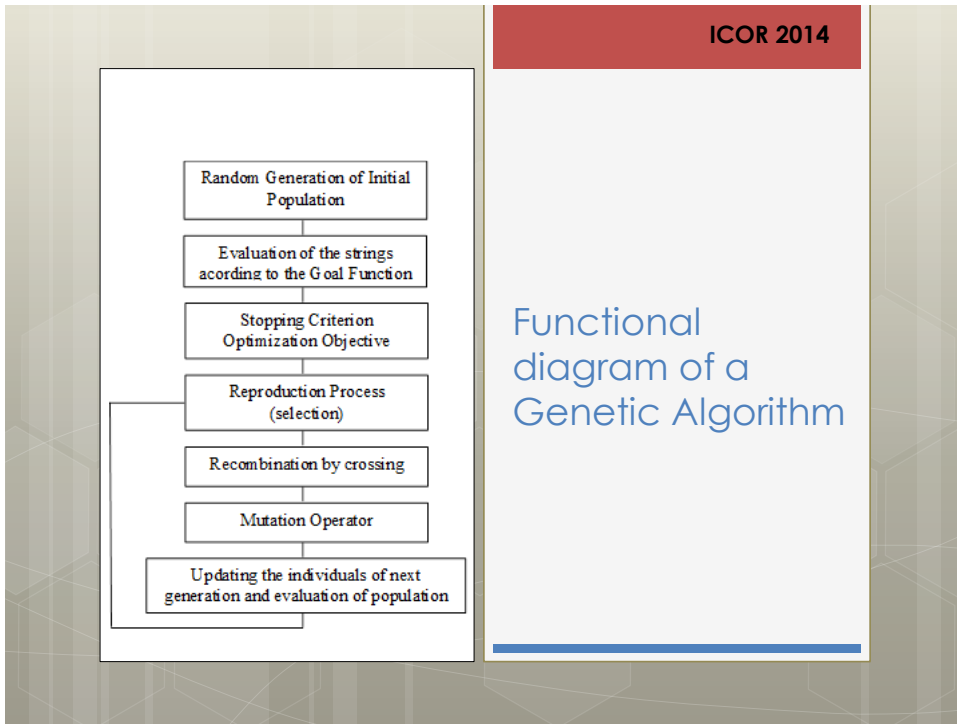
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## Diversity in Classifiers Ensembles

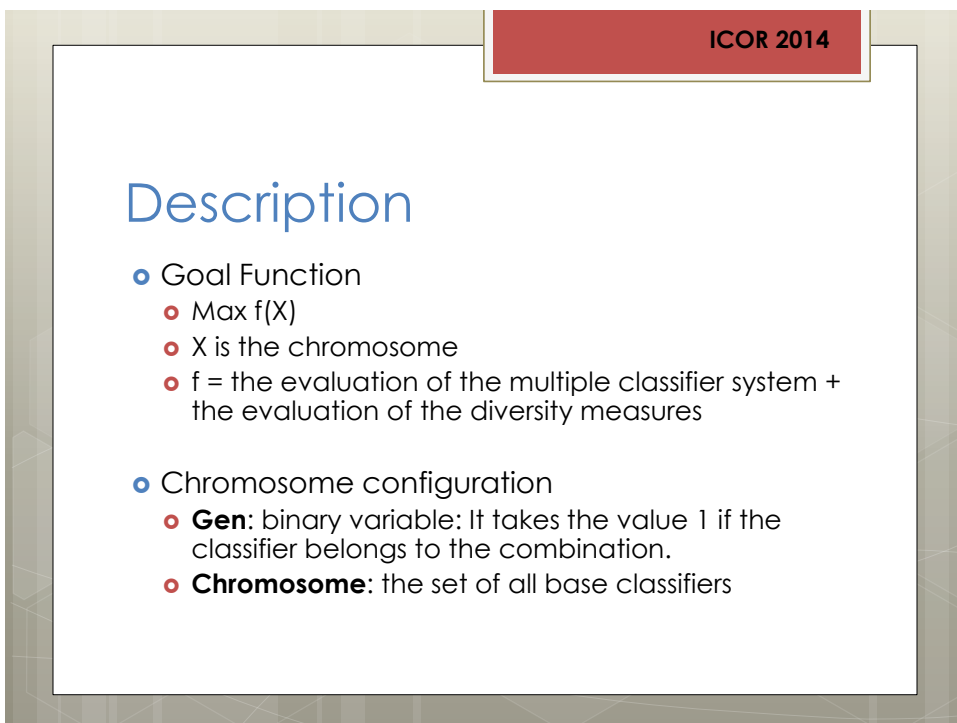
- **The Disagreement Measures (D)<sup>1</sup>**
  - Diversity within the three or more base classifiers are calculated by averaging all pair of classifiers.
- **The Correlation Coefficient Measure ( $\rho$ )<sup>1</sup>**
  - The diversity of two predictors is inversely proportional to the correlation between them.
- **The Double Fault Measure (DF)<sup>1</sup>**
  - The diversity decreases when the value of the double fault measure increases.
- **The Q Statistic<sup>1</sup>**
  - Classifiers that tend to recognize the same objects correctly will have positive values of Q. It can be proved that  $|\rho| \leq |Q|$

<sup>1</sup> Kuncheva, L. "Combining Pattern Classifiers: Methods and Algorithms", 2004

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## Description

- Configuration of the population
  - The population size can be calculated as  $2^{\frac{Sc}{2}}$ , where Sc denotes the size of the chromosome
- Probability of mutation: 0.2
- Probability of crossover: 0.75

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## Description

- Selection operator
  - The roulette method was implemented.
- Input parameters
  - Generations: 100
  - Diversity Measures:
    - D (The Disagreement Measures (D))
    - DF (The Double Fault Measure)

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## Real Application: Hepatitis <sup>1</sup>

Classifier	Accuracy
Naivesbayes	0.83
Multilayer Perceptron	0.81
Lazy.IBK	0.79
Trees.J48	0.79
Functions.Logistic	0.84
Random Tree	0.83
Trees.LMT	0.84
Functions.SMO	0.88
Lazy.KStar	0.90
Functions.SGD	0.88

<sup>1</sup> UCI Repository of Machine Learning Databases

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## Real Application: Hepatitis <sup>1</sup>

Hepatitis	Measure Value	Goal Function	Chromosome	Multiple Classifier System
D	0.17	1.11	0100010101	0.94
DF	0.94	1.88	0100010101	0.94
D + DF	0.56	1.50	0100010101	0.94

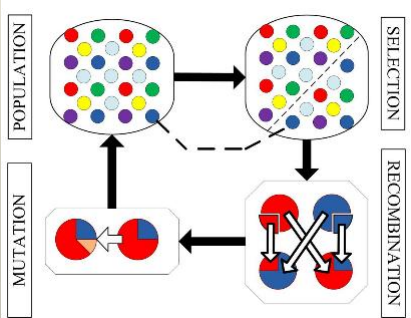
<sup>1</sup> UCI Repository of Machine Learning Databases

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## Conclusions

- This paper shows a novel technique using genetic algorithms to find a good subset of diverse classifiers.
- A case of study of Hepatitis data was used to exemplify the contribution.
  - Ten base classifiers were applied and their individual accuracies were not higher than 90%.
  - By using the proposed genetic algorithm with diversity measures we obtain a multiclassifier with a better accuracy: 94%.

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The diagram illustrates the genetic algorithm process. It starts with a 'POPULATION' of diverse classifiers (represented by colored dots). This leads to 'SELECTION', where a subset is chosen. 'RECOMBINATION' follows, where the selected classifiers are combined. Finally, 'MUTATION' is applied to the resulting population, and the cycle repeats.

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