Evolutionary Algorithms

Inteligencia Artificial en los Sistemas de Control Autónomo Máster en Ciencia y Tecnología desde el Espacio

Departamento de Automática





Objectives

• Describe the most relevant EAs

Bibliography

 $\bullet~$ Eiben, A.E. and Smith, J.E. Introduction to Evolutionary Computing. Springer 2003.

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Introduction (I)

Introduced by Holland in the 70's

- John H. Holland "Adaptation in Natural and Artificial Systems", MIT Press
- GA is the most popular EA
- Usually EAs confused with GA

Canonical GA (which is not canonical)

- Fixed length strings
- Binary codification
- Holland's Theorem

Representation	Bit strings
Recombination	1-point
Mutation	Bit flip
Parent select	Fitness prop
Survivor select	Generational



Introduction (II)

GAs are a family of algorithms, with common features

- Representation in strings, named chromosomes
- Mutation and recombination
- Usually fixed length

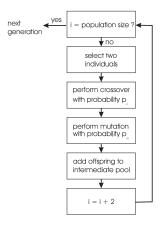
GAs are like a toolbox with customizable components

- Representations, genetic operators, selections mechanism, ...
- These components are interdependent

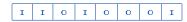
Rule of thumb: Small genotype changes \Rightarrow Small phenotype changes



Introduction (III)



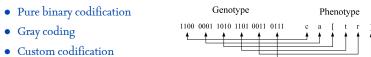
Representation: Binary



One of the oldest and widely used codifications

- Consequence of Holland's Theorem
- Strong historical influence

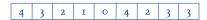
Often used to codify non-binary information (not recommended)



Hint: Use binary codification to represent binary information



Representation: Integer



Chomosome as a sequence of integers

- More natural codification for many problems
- Optimization of integer values
- Integer representation ($\{1, 2, 3, 4\} = \{\text{North, East, South, West}\}$)



Representation: Floating-point

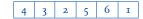


Chomosome as a sequence of floating-point values

- Common in optimization problems
- Solutions with continous nature



Representation: Permutation



Some problems involve order

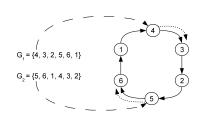
- Sequence of integers
- No repeated numbers
- Range of valid numbers
- Special genetic operators

Information can be contained in

• The locus (position) $[3, 1, 2, 4] \Rightarrow [C, A, B, D]$

• The allele (value)

$$[3, 1, 2, 4] \Rightarrow [B, C, A, D]$$



Integer codification to solve TSP

Mutation

Mutation: Genetic operator that uses one parent

- Introduces randomness into the genotype
- Depends on representation

Main objectives

- Avoid local minima (premature convergence)
- Enhances exploration

Often dependent on the mutation rate

- Significant influence in the algorithm behaviour
- Higher mutation rate, higher exploration



Mutation for binary representations

Flip bit with probability p_m



Optimal p_m depends on the problem and goals

- Need of high fitness population
- Need of high fitness individual
- Need of genetic diversity
- Modality of the problem
- Algorithm dynamics

Rule of thumb: $p_m = \frac{1}{lenoth}$



Mutation for integer representations

Two main mutations applied to each gene

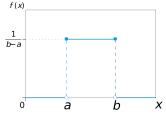
- Random resetting: Choose new random value with p_m
- Creep mutation: Add small (positive or genative) random value with p_m

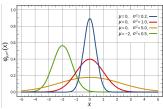


Mutation for floating-point representations

Set new value with value drawn from a distribution

- Uniform mutation Choose new random value from [L, U] with p_m
- Non-uniform mutation Usually adding a value drawn from a zero-mean gaussian distribution







Mutation for permutation representations

Genes are no longer independent

• No gene mutation, p_m affects the whole chromosome

Swap mutation	Insert mutation	
123456789	123456789	
Scramble mutation	Inversion mutation	
123456789	1 2 3 4 5 6 7 8 9	

Recombination

Recombination creates one individual from two or more parents

- Also known as crossover (specially for two parents)
- Basic feature in GA
- Parents selection mechanism needed

Usually applied to all new individuals

- Not used when elitism is applied
- Sometimes applied with $\mathfrak{p}_{\mathfrak{c}} \in [0,5,1]$

Objectives of recombination

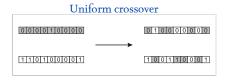
- Combine parents' behavior ⇒ No new genetic material
- Constructive role
- Enhances explotation



Recombination: Binary and integer representations

Three crossover mechanisms for binary and integer encodings

Two-points crossover



Recombination: Floating point representations (I)

Discrete recombination

- Analogous to binary recombination
- No new genetic material

Arithmetic recombination

- Combines the parents' genes
- Weighted sums of genes: $z_i = \alpha x_i + (1 \alpha) y_i$
- Usually, $\alpha = 0.5$ (average values)
- Different arithmetic recombinations



Recombination: Floating point representations (II)

Whole arithmetic recombination (All genes are included)



Simple arithmetic recombination

(Similar to one-point crossover)



Single arithmetic recombination (Similar to uniform crossover)

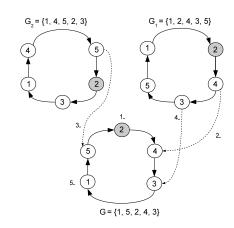
0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.5 0.9 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.5 0.3



Recombination: Permutation representations

Specialized recombinations

- Partially Mapped Crossover
- Edge Crossover
- Order Crossover
- Cycle Crossover



Selection

Two purposes for selection

- Parent selection: Individuals to generate offspring
- Survivor selection: Individuals to remplace

Usually same methods applied to both

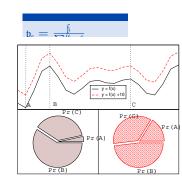


Selection: Fitness Proportional Selection

Selection probability proportional to fitness

- Premature convergence
- Lack of selective pressure for close fitness values
- Selective pressure not customizable
- Susceptibility to function transposition

Historically relevant





Selection: Ranking Selection

Selection probability proportional to rank

- Individuals are sorted by fitness
- Arbitrary rank to probability mapping
- Avoid problems with super individuals
- Selective pressure independent of fitness
- Selective pressure not customizable

Linear mapping

$$P_{lin_rank}(i) = \frac{(2-s)}{\mu} + \frac{2i(s-1)}{\mu(\mu-1)}$$

Exponential mapping

$$P_{exp_r\alpha nk}(\mathfrak{i})=\frac{1-e^{-\mathfrak{i}}}{c}$$

c = normalization factor



Selection: Tournament Selection

Algorithm of tournament size k

- I. Select randomly k chromosomes
- 2. Compute their fitness
- 3. Select the fittest one
- 4. Go to 1

Customizable selective pressure

• Depends on k and μ

De facto standard

- Good for parallel computation
- Efficient implementation

Usually k = 2 in GA, in GP k = 7



Selection: Survival selection

Two strategies

- Generational (all the population is remplaced)
- Steady-stade (partial remplacement)

Survival selection algorithms

- Fitness-Based Replacement (inverse of the previous ones)
- Age-Based Replacement
- Elitism



Introduction (I)

GP is a family of algorithms

- Evolve programs
- Self-programming computers
- GP, Linear GP, Cartesian GP, EDA, ...

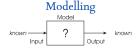
GP introduced by Koza in the 90's

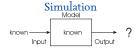
Koza, J.R. "Genetic Programming: On the Programming of Computers by Means of Natural Selection", MIT Press. 1992

GA and ES focused on optimization

• GP focused on Machine Learning







Introduction (II)

Example: Credit scoring problem within a bank. Develop a model describing good customers

Id	Children	Salary	Status	Credit
Id-1	2	45.000	Married	О
Id-2	0	30.000	Single	I
Id-3	I	40.000	Married	I
Id-4	2	60.000	Divorced	I
Id-X	2	50.000	Married	I

Possible model:

IF (children=2) AND (Salary>80.000) THEN good ELSE bad

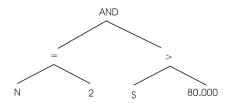


Introduction (III)

General form

IF (Formula)
THEN good
ELSE bad

In EC terms
Phenotype: Formula
Fitness: Classification accuracy



(children=2) AND (Salary>80.000)

Representation (I)

GP representation differs in two aspects

- Nonlinear structure
- Variable size

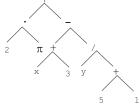
New representation and genetic operators

• Same selection (done in phenotipic space)



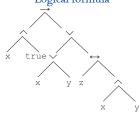
Representation (II)



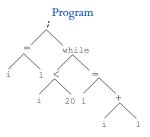


$$\left(2\pi + \left((x+3) - \frac{\gamma}{5+1}\right)\right)$$

Logical formula



$$\begin{array}{l} (x \wedge \mathsf{true}) \to \\ ((x \vee \gamma) \vee (z \leftrightarrow (x \vee \gamma))) \end{array}$$



Representation (III)

Two types of nodes

- Function set Internal nodes. It has an ssociated number of attributes
- Terminal set Leaves of the tree

Danger: Inviable trees

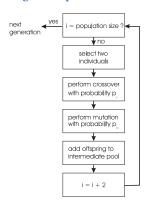
- Grammar-aware GP variants
- Strongly Typed Genetic Programming (STGP), Grammatical Evolution (GE), ...

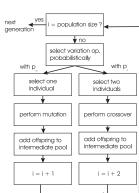
(Complex representation example)



Mutation (I)

Application of genetic operators in GP contrast to GA

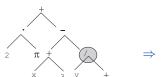




Mutation (II)

Subtree mutation

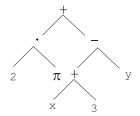
- 1. Select a random node
- 2. Delete subtree
- 3. Add new random subtree



Parameters

 Probability of choosing a terminal node

Highly correlated with code bloat



Mutation (III)

Alternative mutation operators

- Size-fair subtree mutation.
- Node replacement mutation (point mutation)
- Hoist mutation
- Shrink mutation



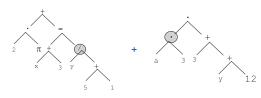
Recombination (I)

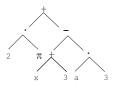
Subtree crossover

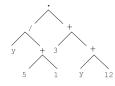
- Take a random node from both parents
- 2. Swap subtrees

Parameters

• Probability of choosing a terminal node







Recombination (II)

Alternative recombination operators

- Homologous crossover
- Uniform crossover
- Size-fair crossover
- Node replacement mutation (point mutation)
- Hoist mutation
- Shrink mutation



Initialization

Three initialization methods

- Full. Introduces non-terminals nodes until max depth
- Grow. Introduces terminal or non-terminal with equal probability
- Ramped half-n-half. Applies full or grow with equal probability

Genetic Programming

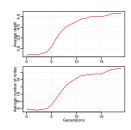
Bloat in Genetic Programming

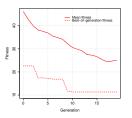
Code bloat: Uncontrolled grow of tree sizes

- Intrinsic to variable-length representations
- Undesirable effects
- Perhaps, the worse problem in GP

Countermeasures

- Depth limitation in genetic operators
- Parsimony pressure
- Tree plunning
- Multiobjective techniques







Genetic Programming

Example of reporting

Cuadro 1: Main parameters used to obtain the approximations for secrets ID in the Genetic Tango attack against David-Prasad authentication protocol.

Parameter	ID
Population	500
Generations	10
Terminal Set	A, B, D, E, F, P_{ID1} , P_{ID2}
Function set	And, or, xor
Fitness	Hamming distance to secret
Fitness tags	5
Fitness sessions	100
Min. depth	I
Max. depth	3
Selection	Lexicographic tournament
Tournament size	4
Crossover	0.9
Reproduction	O.I
Elitism size	I
Terminals	0.1
Non terminals	0.9
Initialization	Rampled H-H

Introduction (I)

Introduced by Rechenberg and Schwefel in the 60's

- Motivated by wing shape optimization
- Real-function optimization

ES properties

- Emphasis on mutation
- Mutation is gaussian noise
- Self-adaptation

Representation	Real-valued vectors
Recombination	Discrete
Mutation	Gaussian perturbation
Parent selection	Uniform
Survivor selection	(μ,λ) or $(\mu+\lambda)$
Speciality	Self-adaptation



Evolution Strategies

Introduction (II)

Example of basic ES

- Representation: Vector of real values
- Recombination: Not used
- Mutation: Gaussian noise with step-size σ

Adaptative σ (1/5 rule)

- Theoretical foundations
- Based on the ratio of success mutations (ps)
- After k iterations a new σ is computed

$$\sigma = \begin{cases} \sigma/c & \text{if } \mathfrak{p}_s > 1/5, \\ \sigma \cdot c & \text{if } \mathfrak{p}_s < 1/5, \\ \sigma & \text{if } \mathfrak{p}_s = 1/5 \end{cases}$$

where $0.817 \le c \le 1$ is a parameter



Representation

Nowdays ES is usually self-adapted

- Step size (σ) is included in the genotype
- Evolution includes variables and parameters

One or more σ values

- One σ : $\langle \underbrace{x_1, x_2, ..., x_n}_{\bar{x}}, \sigma \rangle$
- $\bullet \ \, \text{Several:} \, \sigma: \big\langle \underbrace{x_1, x_2, ..., x_n}_{\bar{x}}, \underbrace{\sigma_1, \sigma_2, ..., \sigma_{n_\sigma}}_{\bar{\sigma}} \big\rangle$

Mutation

Genetic operators to modify σ

Mutation with one step size:

$$\begin{aligned} x_i' = & x_i + N_i(0, \sigma') \\ \sigma' = & \sigma \cdot e^{\cdot N(0, \tau)}, \tau \propto 1/\sqrt{n} \end{aligned}$$

au is analogous to learning rate in ANN

Mutation with n step sizes:

$$\mathbf{x}_{i}' = \mathbf{x}_{i} + \mathbf{N}_{i}(0, \sigma_{i})$$

$$\sigma' = \sigma \cdot e^{\cdot \mathbf{N}(0, \tau') + \mathbf{N}_{i}(0, \tau)}$$

with
$$au' \propto 1/\sqrt{2\mathfrak{n}}$$
 and $au \propto 1/\sqrt{2\sqrt{\mathfrak{n}}}$



Recombination

Secondary operator in ES

- Discrete recombination. Like uniform crossover in GA
- Intermediate recombination. Like arithmetic crossover in GA

ES tends to use global recombination

• More than two parents



Parent and survivor selection

The whole population is seen as parent

- Select individual with uniform probability
- No selective pressure in parent selection

After creating the offspring, the λ fittests individuals are selected

Deterministic procedure

Two selection mechanisms depending on who can be selected

- (μ, λ) selection. Only the offpring.
- $(\mu + \lambda)$ selection. Parents and offpring

 (μ, λ) selection is more popular



Search phases

Initial phase: Random distribution, high genetic diversity Advanced phase: Begins to converge **Convergence**: Around one or few points, low genetic diversity

Premature convergence if population not located in global maxima



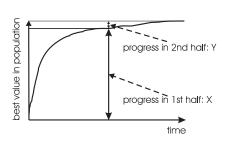


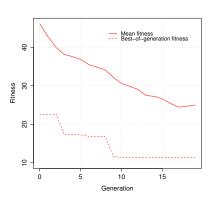


(Animation)



Fitness dynamics

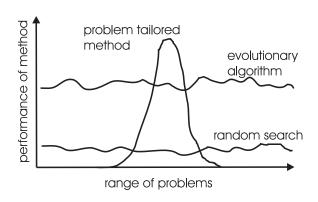




Few long runs or many short runs?



When EAs are useful





Advanced EAs

- Multiobjective Evolutionary Algorithms (MOEAs)
- Optimization with constrains
- Coevolution
- Dinamic optimization
- Islands models
- Memetic algorithms
- Hyperheuristics

