

## GENETIC ALGORITHMS - HISTORY

10



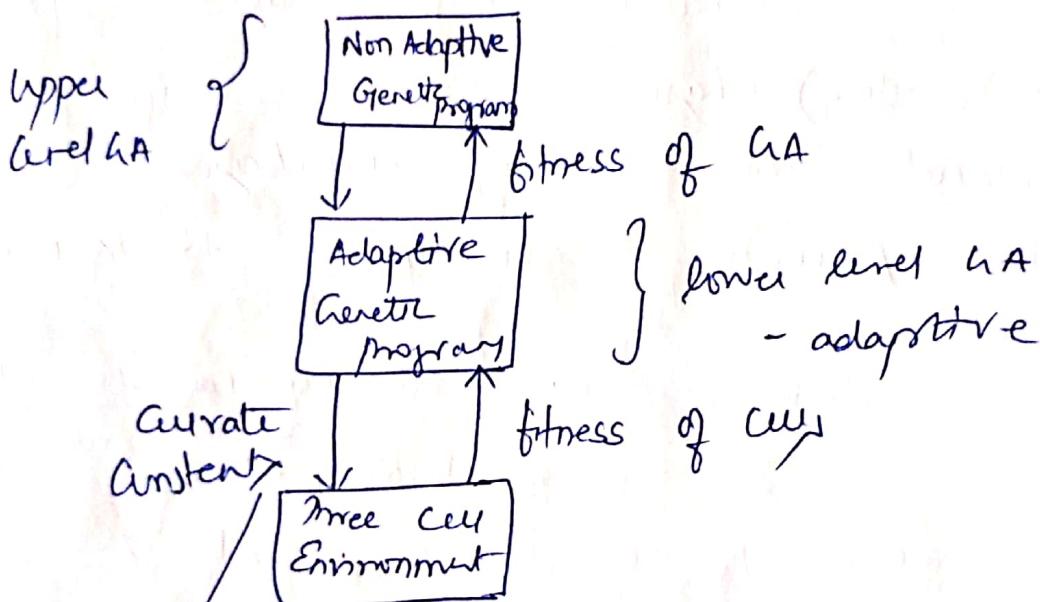
*bonnitus*

- \* Rosenberg (67) cell simulation:
  - ↳ Biological work  $\rightarrow$  population of single organisms with permeable membrane
  - ↳ Diploid representation (finite length string with a pair of chromosomes)
  - ↳ string length limited to size '20' genes  
 @ 16 alleles per gene.
  - ↳ Chemical concentration  $x_j$ ; desired  $c \in \overline{x_j}$  (ccc)
  - ↳ Antifitness fn (for  $i^{\text{th}}$  property) =  $\sum (x_j - \bar{x}_j)^2 \rightarrow f_i$   
 $\downarrow \rightarrow$  all chemicals
  - ↳ Selection Based on Antifitness measure.  
 " searching for cells that minimize antifitness
    - $\Leftrightarrow$  Nonlinear Equations Solving (finding roots)
  - ↳ defined the offspring generation function (OGF) for Competitive Selection.  
 $S = \frac{bi + bj}{\bar{J}}$ ;  $i, j \rightarrow$  parents.  
 $\bar{J} \rightarrow$  average of population.
  - ↳ Adaptive crossover — Each gene has "linkage factors"  $\rightarrow x_i$  along with allele values.
    - ↳ Range of  $0 \rightarrow 7$
    - : cross site determined by prob. over linkage factors.
 
$$P_i = n_i / \sum x_j$$

- (2)
- \* CanicNo - Pattern Recognition:
    - ↳ Application of GAN to pattern recognition and selection problem.
    - ↳ Image digitized  $25 \times 25$  grid (625 pixels) (only 2 shades - black/light, dark)
    - ↳ set of feature detectors
      - ↳ subset of pixels
    - ↳ Training phase - known feature detector stored with associated image class name
    - ↳ Recognition (Testing) phase - unknown image is sure matched with training database.
    - ↳ 110 detectors / device on average; 2 to 8 pixels per detector  
 for eg. a chromosome
 
$$l = 110 \cdot \log_2 \left( \frac{625}{4} \right) = \boxed{3581}$$

$$\begin{array}{ccccccc} +5 & +372 & +9 & +\cancel{0} & -518 & -213 & -35 \\ \underbrace{\qquad\qquad\qquad}_{\text{first detector pixels}} & \underbrace{\qquad\qquad\qquad}_{\text{2nd...}} & & & & & \end{array}$$
    - ↳ with an average of 110 detectors and 4 pixels per detector; Binary string length  $\rightarrow$
    - ↳ crossover and reproduction op with SGA.
    - ↳ Mutation  $\rightarrow$  change a single pixel within a detector
      - $\rightarrow$  " all " "
      - $\rightarrow$  change pixel association b/w adj. detectors
    - ↳ Preselection - good offspring replaced partly
      - population diversity
    - ↳ population size  $n$  (12-20)

- ↳ Many of centralized control based Genetic Search rather than simulating with parameters fixed.
- \* Weinberg (1970) - cell simulation and Metalevel GAs:
  - ↳ Multilayered GA to select set of 15 constants
  - ↳ constants  $\rightarrow 10^{-6}$  to  $10^6$ .
  - ↳ crossover and Inversion @ parametric boundaries (directed mutation)



generate test populations of size 40.

- \* Hollstein and function optimization (1971)
  - ↳ optimize function of 2 variables  $y = f(x_1, x_2)$
  - ↳ using dominance, crossover, mutation
  - ↳ proposed 5 selection methods
    - (a) Progeny testing  $\rightarrow$  fitness of offspring controls subsequent breeding of its parents.
    - (b) Individual selection  $\rightarrow$  fitness of individual - future parents.
    - (c) Family selection  $\rightarrow$  fitness of family controls life of family members or parents.

(4) Within family selection — fitness of individual  
within family controls selection of parents for breeding within family.

(5) Combined selection — hybrid of earlier methods.

↳ 8 schemes of mating preference:

(1) Random → All males are equally likely to mate with one another.

(2) Inbreeding → "Related parents" — mated

(3) Line Breeding → A unique + valuable individual bred with base population → Offsprings act as "parents"

(4) Out Breeding → Individuals with genetically & (distinctly) different phenotype values breed — act as parents

(5) Self-fertilization — An individual breeds with itself

(6) Clonal propagation — Replica of Individual.

(7) Positive assortive mating — like individuals are bred with others like individuals.

(8) Negative assortive mating — unlike individuals are bred.

↳ Binary coded representation / Gray code representation

- \* DeJong's function Optimization
  - ↳ Next major contribution after Holland
  - ↳ Test Environment of 5 problems in function minimization with foll. char:-.
  - (a) Continuous / Discontinuous
  - (b) Convex / Nonconvex
  - (c) Unimodal / Multimodal
  - (d) Quadratic / Non quad.
  - (e) Low Dim / High Dim.
  - (f) Det. v/s stochastic
- ↳ Two parameters to measure "Convergence" and "Ongoing Performance" (op.)

- ↳ offline (convergence) and online (op.)
  - ↳ fn. evaluations can be simulated / saved and used after some terminating criteria
  - ↳ online - fn. evaluations thru real experiments
  - ↳ focus : "Premium on Acceptable Performance"

Online performance  $n_e(s)$  of strategy  $s$  on environment

$$\rightarrow n_e(s) = \frac{1}{T} \sum_{t=1}^T f_e(t)$$

↓ obj. fn. value for env.  $e$   
on trial  $t$ .

⇒ Online performance → "average of all function evaluations upto and including current trial"

Offline Performance

$$n_e^*(s) = \frac{1}{T} \sum_{t=1}^T b_e^*(t)$$

$\hookrightarrow = \text{best } \{f_e(1), f_e(2), \dots, f_e(T)\}$

Offline performance - running average of best performance values to a particular time

↳ Test bed of '5 functions' and '2 Criteria of goodness'; studied various plans.

### ① RI (Reproductive plan)

↳ 3 operators - Roulette wheel selection, Simple crossover (with random mating), Simple mutation

Population - Primary strings → mapped, concatenated Unsigned Binary integer.

Four parameters in RI

$n \rightarrow$  Population size;  $P_c \rightarrow$  crossover prob;  $P_m$  and  $G \rightarrow$  Generation gap

↳ to permit overlapping populations

from overlapping population  $\rightarrow "n \cdot G"$  individuals  $\rightarrow$  selected for further genetic action.

↳ ~~④~~ Larger population — ~~④~~ better offline performance  
( $\because$  large / diverse pool of schemata).

↳ ~~④~~ Smaller populations — ~~④~~ can change more rapidly  
 $\rightarrow$  Better Initial Online Performance

↳ Diversity — Increased mutation rates

Low mutation — decreases lost alleles — degrades offline + offline performance.

$P_m = 0.5 \rightarrow$  random search — indep. of  $n, P_c$  values.

↳  $P_c = 0.6 \rightarrow$  Balance for good on/offline performance.

↳ Non overlapping population ideal for most optimization.

↳ Smaller 'G' does not affect (degrade) online perf.

Five Variants of RI done by DeJong

(2) R2 - Eutist Model

↳ Preserve Best Structure

4 Let  $a^*(t)$  — Best Individual upto time  $t$ ;

If after  $A(t+1)$  normally;  $a^*(t)$  not in  $A(t+1)$

→  $a^*(t)$  included in  $A(t+1)$  as  $(N+1)^{th}$  Member

EUTISM

↳ Eutism improves on/off line perf. on unimodal surface; but degrades on multimodal.

↳ Eutism favours "local search over global".

(3) R3 - Expected Value Model

↳ Reduce stochastic Error of R-10 selection.

✓ (+) average fitness of schemata calculation not a real possibility — sequential finite sampling.

✓ (+) selection process prone to variance (@ times large)

↳ expected and actual no. of copies

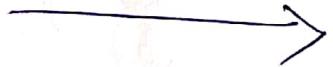
R3 reduces ↓ this err.

R/W Selection — Actual schemata average fitness calculation done by sequential finite sampling  
— one source of Err.

↳ Variance b/w expected and actual number of copies.

↳ Ex. No. of offspring calculated ( $b/f$ ) later when string was selected for mating and crossover ; offspring count decreased by 0.5.

i (2) 1  
1 )  
1 )



↳ Copy of individual strings selected for reproduction w/o mating, crossover - Count is decreased by 1.

↳ No. of offsprings  $\leftarrow \boxed{(f/\bar{f} + 1)}$  and observation of  $\leftarrow \boxed{\bar{f}/f + 0.5}$

- ↳ R<sub>3</sub> superior to R<sub>1</sub> on on/off line performance
- ↳ R<sub>2</sub> better than R<sub>3</sub> in low dim / unimodal fns,
- R<sub>3</sub> Outperforms R<sub>2</sub>, R<sub>1</sub> in on/offline performance over the entire fns test bed.

#### (4) R<sub>4</sub> - Eutist Expected Value Model

↳ Combination of R<sub>2</sub>, R<sub>3</sub> plans

↳ Better in unimodal fns. test bed

↳ degradation compared to R<sub>2</sub> in other fns.

#### (5) R<sub>5</sub> - Crowding factor Model

↳ Enforce principles of crowding encountered in real life

↳ Increased Comp. for limited resources decreases life expectancy / birth rates of individuals

↳ less crowded individuals collecting - closer to near potential birthrates / expectancy

↳ Simulate crowding pressure in GA.

↳ Generation Gap = 0.1 ; crowding factor parameter

Q5  $\rightarrow$  "Crowding Model" - "As an individual is created, one is selected to die"  
↳ one that has most bit-bit similarity with the current offspring.

- ↳ Almost Gancchion's notion of Preselection.
- ↳  $CF = 2$  — global performance on some functions.

### (b) Generalized Crossover Model - R6.

↳ No. of Crossover points parameter ( $cp$ )

$cp=1 \rightarrow$  Simple Crossover

↳ even  $cp$  values — treat chromosome as ring with no beginning (or) end;  $cp$  points selected around the circle

(Refer notes on Types of Xover)

with  $cp = 2 \rightarrow (1C_2)$  diff. ways of picking two cross points

In gen  $\boxed{(1C_{cp})}$  for multiple crossover with  $cp$ .

## Selection Schemes

↳ objective of evolving selection methods that reduce stochastic errors of Roulette wheel selection.

↳ few in literature

- (a) Deterministic Sampling
- (b) Remainder Stochastic Sampling w/o replacement
- (c) Stochastic Sampling w/o replacement
- (d) (b) with replacement
- (e) (c) with replacement
- (f) Stochastic tournament (Ranking scheme)

c  $\Leftrightarrow$  Roulette wheel method

c  $\Leftrightarrow$  Expected value model (R<sub>3</sub> plan)

(a)  $\rightarrow$  prob. of selection =  $f_i / \sum f_i$

Ex. No. of Individuals for a string;  $e_i$

$$e_i = p_{\text{select}} \cdot n$$

↳ Each string is allocated copies = integer part of  $e_i$

↳ Population sorted on "fractional part"

↳ Remainders of strings to make population → top of the sorted list.

(b) and (c) start similarly to Deterministic Sampling

↳ (Integer part) No. of copies

In (d) - fractional parts of  $e_i$  - determine weights for roulette wheel to fill up the rest of the population.

In (b) - fractional parts - probabilities

Thus if  $e_i = 0.5$

I sue copy and another with prob 0.5.

(6) stochastic Tournament - Tournament selection

↳ one of two competing (drawn @ random or  $\oplus$ ) is declared winner and inserted in new population

↳ successive pairs of individuals are drawn using r/w selection.

↳ gen. observation of good performance. (b) in most applications



\* Dominance, Diploidy, Abeyance

↳ Diploidy - pair of chromosomes

.. dominance - genotype to phenotype mapping.

↳ Previous representations - haploid (or) single stranded chromosome

Diploid - Genotype carries 'one (or) more pairs' of

chromosomes (Homologous chromosomes), each containing information for the same function

↳ Issue of Redundancy / Duplications. Pairs of genes that decode to same fn. (values)?

↳ Consider following diploid structure:-

$\begin{cases} ABCDE \\ abcde \end{cases}$        $A, a \}$  → different characteristics

↳ Could be "Eye color" -  $A \rightarrow$  Blue;  $a \rightarrow$  Brown, etc.

But both are not present @ any time.

↳ Conflict resolved by operator - Dominance.

↳ An allele is dominant if expressed in phenotype assuming 'Copy' are all dominant

dominant  $\leftarrow (A)bCDe \rightarrow ABCDE$

allele  $\leftarrow (a)Bcd e$

recessive

Dominance/ Rules

Recurring

$\begin{cases} Aa \rightarrow A \\ AA \rightarrow A \\ aa \rightarrow a \end{cases}$       heterozygous  
                        homo "

Dominance is a genotype  $\rightarrow$  phenotype map. fn.

Diploidy  $\rightarrow$  Way for remembering gene/ combination useful.

Penninshy

Dominance  $\rightarrow$  Protect  
Shield



such alleles from harmful selection.

$\hookrightarrow$  Diploidy allows multiple solns (to same problem) to be carried along, however only one soln is expressed.

Hollstein's study :- Diploidy + Evolving Dominance

Each binary gene  $\rightarrow$  controlled by two genes

(values)  $\rightarrow$  modifiers and functional gene.

Functional Gene  $\rightarrow$  0/1 values  $\rightarrow$  decoded to a normal parameter.

Modifier Gene  $\rightarrow$  N/m "

Dominance  $\rightarrow$  of 0 if atleast one 'N' allele is present.

1  $\rightarrow$  Two locus scheme evolved to a simpler 1 locus - Third allele @ each loci

Value values from  $\{0, 1, 2\}$  set.

	OM	Om	1M	1m
OM	0	0	0	0
Om	0	0	0	1
1M	0	0	1	1
1m	0	1	1	1

Two locus Dominance Maps

2  $\rightarrow$  dominant 1

1  $\rightarrow$  Recessive 1

Rules: 2 and 1  $\rightarrow$  1

2 dom 0		
0 dom 1		

		R1	D1	
		0	1	2
		0	0	0
		1	0	1
		2	1	1
			1	1

b. Holland modified Holsteini scheme with a clearer symbol of  $\{0, 1_0, 1\} \Leftrightarrow \{0, 1, 2\}$ .

### ⑦ Brindley Dominance Schemes :-

(1) Random fixed global dominance - dominant map

fixed @ start of run;

\* dominant allele "if heterozygous / homozygous  
reculsive " " homozygous

(2) Variable Global Dominance :-

dom of 0/1 @ a locus based on prop. of  
0/1 and 1/1 in current generation; allele expression  
by Bernoulli trial

(3) Deterministic (Variable global dominance)

as in (2) + allele expression by " allele with  
greatest proportion " is the winner (dominant allele)

(4) Dominance by choice of random chromosome  
↳ an alleles of chosen chromosome r dominant

(5) Dominance of Better chromosome - fitness based  
selection of one of the two (best)

(6) Haplloid controls Diploid adaptive dominance

(similar to a Monk) - a third chromosome  
carrying a dominance maps to determine the  
expression of the diploid pair

$c_1$  }  
 $c_2$  }  $\rightarrow$  Haplloid

$c_3 \rightarrow$  Diploid  
 $R_i \rightarrow (c_1/c_2)_i$

Demerits :- (1) Dominance step is separated from (of Pseudo's scheme) (Modifying genes) the functional genes (Normal Chromosome)

(2) This violates the biological viewpoint of tightly linking both

(3) Schemes require global information - not encouraged in GA viewpoint  
? Global data come from.

(4) GA's approach of "Global Performance by local operators" has to be encouraged.  
+

Analysis of Dominance and Diploidy in GA search :-

$$m(H_1t+1) \geq m(H_1t) \frac{f(H)}{f} \left[ 1 - p_c \frac{\delta(H)}{t-1} - o(H)p_m \right]$$

→ ①    ↓  
    / Schema Diversity

① has to be analyzed incorporating "Dominance and Diploidy" and its effect on Schema Average fitness ( $f(H)$ )

↳ Separate physical schema ( $H$ ) from Expressed schema ( $H_e$ ) - : [a physical  $H$  may/may not be expressed depending on dominance and its homologous partner]

$$① \rightarrow m(H_1t) \frac{f(H_e)}{f} \rightarrow \text{as before} \rightarrow ②$$