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Computational Intelligence

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Note: Slides of Thomas Jansen used with permission!

Important Parameters of EAs (1)

- dimension n of search space
  - no parameter of EA, but given by the problem
  - measures the size of the search space: $\{0,1\}^n$, $\mathbb{R}^n$, S_n
  - plays the same role as input length in classical runtime analysis
  - other parameters are often chosen dependent on n (e. g. mutation probability $p_m = 1/n$)
- population size μ
  - obviously $\mu = n^{O(1)}$
  - often $\mu = \Theta(n)$ or $\mu = \Theta(\sqrt{n})$
  - $\mu = O(1)$ or even $\mu = 1$ are not unusual
- number of offspring λ
  - obviously $\lambda = n^{O(1)}$
  - often $\lambda = 1$
  - $\lambda = \mu$ or $\lambda \gg \mu$ not unusual
  - selection method influences reasonable choice of λ

Important Parameters of EAs (2)

- crossover probability p_c
  - in general $p_c \in [0;1]$ arbitrary
  - often $p_c \in [1/2;4/5]$ constant
- probability of applying mutation
  - don't confuse with mutation probability!
  - we will always use 1
  - Remark
    $p_m = 1/n \Rightarrow \text{Prob}\left(\text{no mutation}\right) = \left(1 - 1/n\right)^n \approx 1/e$

Methods for parameter control

- static parameter control

  parameter values constant during the whole run

  - often used
  - + simple
  - − maybe it's better to vary the parameter value during the run?!
- dynamic parameter control

  parameter values change during the run according to some time-dependent scheme

  - + more flexible than static approach
  - − cannot deal with non-time-dependent changes
  - unusual for EAs
- adaptive parameter control

  parameter values can change dependently on every individual and any random experiment

  - + very flexible
  - − hard to analyze
  - − computationally expensive
  - often used for EAs

Self-adaptation

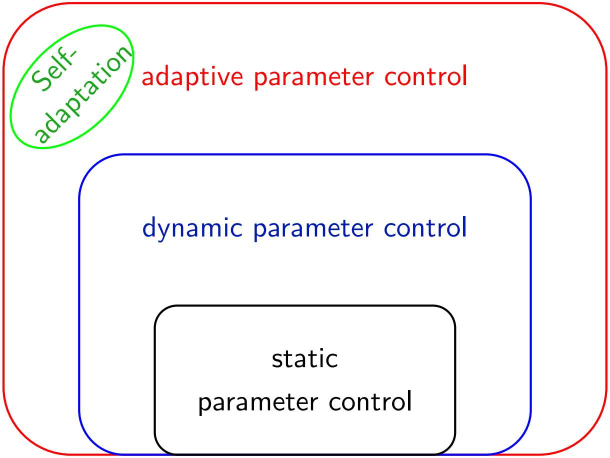
Idea good parameter values evolve together with good individuals

implementation	code parameter values together with individual
formally	$S \times Q$ instead of S
	unchanged $f\colon S \to R$

e. g. for mutation probability

- every individual has its own mutation probability
- first vary the mutation probability
- then mutate with varied mutation probability
- afterwards normal selection
- important don't swap steps

Hierarchy of parameter control methods



Evolutionary Algorithms: Historical Notes

Idea emerged independently several times: about late 1950s / early 1960s.

Three branches / “schools“ still active today.

- **Evolutionary Programming (EP)**:
  Pioneers: Lawrence Fogel, Alvin Owen, Michael Walsh (New York, USA).

  Original goal: Generate intelligent behavior through simulated evolution.
  Approach: Evolution of finite state machines predicting symbols.
  Later (~1990s) specialized to optimization in $\mathbb{R}^n$ by David B. Fogel.

- **Genetic Algorithms (GA)**:
  Pioneer: John Holland (Ann Arbor, MI, USA).

  Original goal: Analysis of adaptive behavior.
  Approach: Viewing evolution as adaptation. Simulated evolution of bit strings.
  Applied to optimization tasks by PhD students (Kenneth de Jong, 1975; et al.).

- **Evolution Strategies (ES)**:
  Pioneers: Ingo Rechenberg, Hans-Paul Schwefel, Peter Bienert (Berlin, Germany).

  Original goal: Optimization of complex systems.
  Approach: Viewing variation/selection as improvement strategy. First in $\mathbb{Z}^n$, then $\mathbb{R}^n$.

Evolutionary Algorithms: Historical Notes

“Offspring“ from GA branch:

- **Genetic Programming (GP)**:
  Pioneers: Nichael Lynn Cramer 1985, then: John Koza (Stanford, USA).

  Original goal: Evolve programs (parse trees) that must accomplish certain task.
  Approach: GA mechanism transfered to parse trees.
  Later: Programs as successive statements → Linear GP (e.g. Wolfgang Banzhaf)

Already beginning early 1990s:

Borders between EP, GA, ES, GP begin to blurr ...

⇒ common term **Evolutionary Algorithm** embracing all kind of approaches

⇒ broadly accepted name for the field: **Evolutionary Computation**

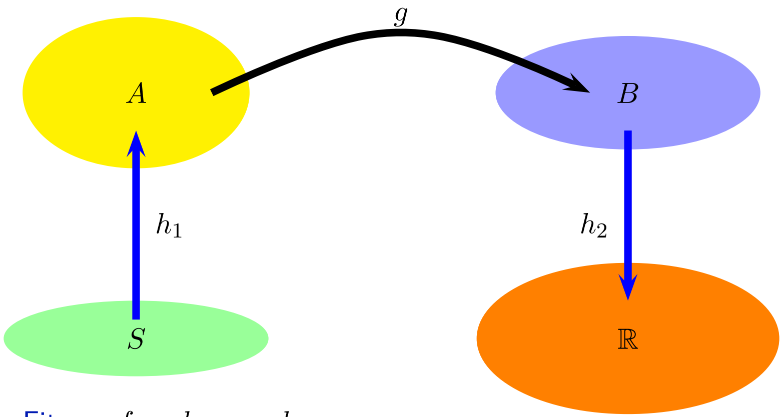
scientific journals: *Evolutionary Computation* (MIT Press) since 1993,
IEEE Transactions on Evolutionary Computation since 1997,
several more specialized journals started since then.

Design of EAs

Idea	Methodology to apply standard EAs
Goal	standard EAs do not have to be changed

Requirement	problem is given as $g\colon A \to B$
	g has to be maximized (or minimized)
	A arbitrary set, B partially ordered
EA	operates on search space S
	'maximizes' fitness $f : S \to \mathbb{R}$

Definition of mappings



$$\begin{tikzcd}
A \arrow[r, bend left, "g"] & B \arrow[d, "h_2"] \\
S \arrow[u, "h_1"] & \mathbb{R}
\end{tikzcd}$$

Fitness $f := h_2 \circ g \circ h_1$

h_1 is genotype-phenotype-mapping.

Genotype-Phenotype-Mapping $\mathbb{B}^n \to [L, R] \subset \mathbb{R}$

- Standard encoding for b $\in \mathbb{B}^n$

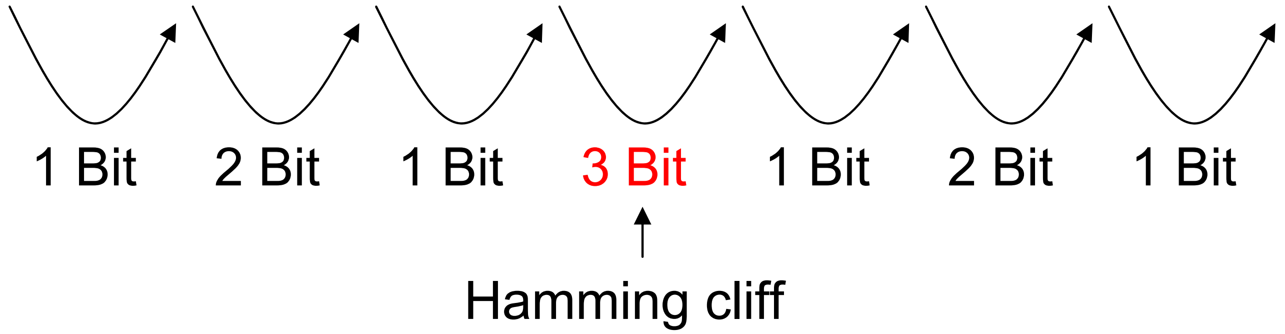
$$x = L + \frac{R-L}{2^n - 1} \sum_{i=0}^{n-1} b_{n-i}\, 2^i$$

→ Problem: *hamming cliffs*

000	**001**	**010**	**011**	**100**	**101**	**110**	**111**
0	1	2	3	4	5	6	7

L = 0, R = 7

n = 3



Genotype-Phenotype-Mapping $\mathbb{B}^n \rightarrow [L, R] \subset \mathbb{R}$

- Gray encoding for $b \in \mathbb{B}^n$

  Let $a \in \mathbb{B}^n$ standard encoded. Then $b_i = \begin{cases} a_i, & \text{if } i = 1 \\ a_{i-1} \oplus a_i, & \text{if } i > 1 \end{cases}$

  $\oplus$ = XOR

000	001	011	010	110	111	101	100	← genotype
0	1	2	3	4	5	6	7	← phenotype

OK, no hamming cliffs any longer …

$\Rightarrow$ small changes in phenotype „lead to“ small changes in genotype

since we consider evolution in terms of Darwin (not Lamarck):

$\Rightarrow$ small changes in genotype lead to small changes in phenotype!

but: 1-Bit-change: **000** $\rightarrow$ **100** $\Rightarrow$ ☹

Genotype-Phenotype-Mapping $\mathbb{B}^n \to \mathbb{P}^n$ (example only)

- e.g. standard encoding for $b \in \mathbb{B}^n$

individual:

010	**101**	**111**	**000**	**110**	**001**	**101**	**100**	← genotype
0	1	2	3	4	5	6	7	← index

consider index and associated genotype entry as unit / record / struct;

sort units with respect to genotype value, old indices yield permutation:

000	**001**	**010**	**100**	**101**	**101**	**110**	**111**	← genotype
3	5	0	7	1	6	4	2	← old index

= permutation

Requirements on h_1 and h_2

obvious requirements

- h_1 and h_2 can be computed efficiently
- h_2 suits g, i. e. good points in B are mapped to good points in $\mathbb{R}$
- h_1 maps on many (all) important points of A
- Optima of f correspond to optima of g

Caution requirements can be hard to achieve in practice

for non-obvious requirements a metric is important

Definition

Mapping $d\colon M \times M \to \mathbb{R}_0^+$ is a metric on the set M $:\Leftrightarrow$

1. $\forall x, y \in M\colon x \neq y \Leftrightarrow d(x,y) > 0$ (positivity)
2. $\forall x, y \in M\colon d(x,y) = d(y,x)$ (symmetry)
3. $\forall x, y, z \in M\colon d(x,y) + d(y,z) \geq d(x,z)$ (triangle inequality)

Metric-based EAs

Assumption Metric d_A on A known
(d_A reflects application knowledge)

Requirement metric d_S is known

if h_1 injective, $d_S(x,x') := d_A(h_1(x),h_1(x'))$ is metric

Requirement monotonicity

$$\begin{aligned} \forall x,x',x'' \in S\colon \quad & d_S(x,x') \le d_S(x,x'') \\ \Rightarrow \quad & d_A(h_1(x),h_1(x')) \le d_A(h_1(x),h_1(x'')) \end{aligned}$$

Variation as randomized mapping

now Design-rules for variation operators

hence Formalize variation operators as randomized mappings

$r\colon X \to Y$ randomized mapping
$\Leftrightarrow r(x) \in Y$ depends on $x \in X$ and random experiment

formally probability space (Ω, p)

$$r\colon X \times \Omega \to Y$$

$$\text{Prob}\left(r(x) = y\right) = \sum_{\omega \in \Omega\colon\, r(x,\omega)=y} p(\omega)$$

Example 1-bit mutation
$\Omega := \{1, 2, \ldots, n\}$, $\forall i \in \Omega\colon p(i) = 1/n$

1-bit mutation is randomized mapping $m\colon \{0,1\}^n \to \{0,1\}^n$
where $m(x,i) := x \oplus 0^{i-1}10^{n-i}$

Design-rules for mutation

favor small changes

$$\forall x, x', x'' \in S: \quad d_S(x,x') < d_S(x,x'') \Rightarrow \text{Prob}\left(m(x) = x'\right) > \text{Prob}\left(m(x) = x''\right)$$

no bias

$$\forall x, x', x'' \in S: \quad d_S(x,x') = d_S(x,x'') \Rightarrow \text{Prob}\left(m(x) = x'\right) = \text{Prob}\left(m(x) = x''\right)$$

Design-rules for crossover

offspring similar to parents

$$\begin{aligned} \forall x, x', x'' \in S\colon \qquad & \text{Prob}\left(c(x,x') = x''\right) > 0 \\ \Rightarrow \quad & \max\left\{d_S(x,x''), d_S(x',x'')\right\} \leq d_S(x,x') \end{aligned}$$

no bias

$$\begin{aligned} & \forall x, x' \in S\colon \forall \alpha \in \mathbb{R}_0^+\colon \\ & \qquad \text{Prob}\left(d_S(x, c(x,x')) = \alpha\right) = \text{Prob}\left(d_S(x', c(x,x')) = \alpha\right) \end{aligned}$$

Any EA that fulfills these four design-rules is called a metric-based EA (MBEA).

Three tasks:

1. Choice of an appropriate problem representation.
2. Choice / design of variation operators acting in problem representation.
3. Choice of strategy parameters (includes initialization).

ad 1) different “schools“:

(a) operate on binary representation and define genotype/phenotype mapping
+ can use standard algorithm
– mapping may induce unintentional bias in search

(b) no doctrine: use “most natural” representation
– must design variation operators for specific representation
+ if design done properly then no bias in search

ad 2) **design guidelines for variation operators**

a) reachability

every $x \in X$ should be reachable from arbitrary $x_0 \in X$
after finite number of repeated variations with positive probability bounded from 0

b) unbiasedness

unless having gathered knowledge about problem
variation operator should not favor particular subsets of solutions
$\Rightarrow$ formally: maximum entropy principle

c) control

variation operator should have parameters affecting shape of distributions;
known from theory: weaken variation strength when approaching optimum

ad 2) design guidelines for variation operators in practice

binary search space X = $\mathbb{B}^n$

variation by k-point or uniform crossover and subsequent mutation

a) ***reachability***:

regardless of the output of crossover
we can move from x ∈ $\mathbb{B}^n$ to y ∈ $\mathbb{B}^n$ in 1 step with probability

$$p(x,y) = p_m^{H(x,y)}\,(1 - p_m)^{n-H(x,y)} > 0$$

where H(x,y) is Hamming distance between x and y.

Since min{ p(x,y): x,y ∈ $\mathbb{B}^n$ } = δ > 0 we are done.

b) ***unbiasedness***

Definition:

Let X be discrete random variable (r.v.) with $p_k = P\{ X = x_k \}$ for some index set K. The quantity

$$H(X) = -\sum_{k \in K} p_k \log p_k$$

is called the ***entropy of the distribution*** of X. If X is a continuous r.v. with p.d.f. $f_X(\cdot)$ then the entropy is given by

$$H(X) = \int_{-\infty}^{\infty} f_X(x) \log f_X(x) dx$$

The distribution of a random variable X for which H(X) is maximal is termed a ***maximum entropy distribution***. ■