



Introduction to Genetic Algorithms

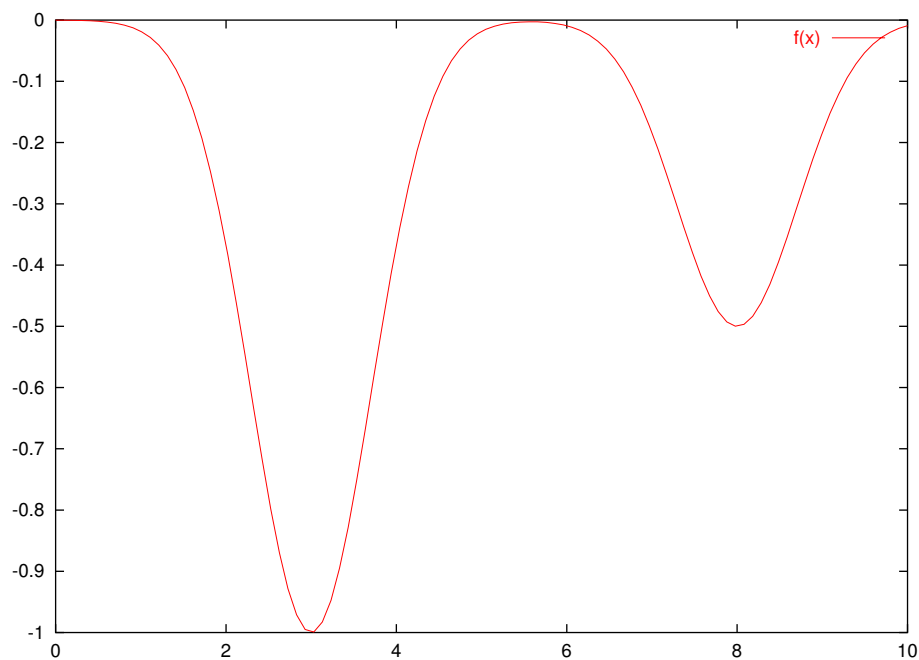
Dr. Paul A. Bromiley
Imaging Science and Biomedical Engineering

Overview

- Optimisation methods and robustness
- Simple three-operator GAs:
 - reproduction
 - crossover
 - mutation
- Why GAs work: schemata and building blocks
- Problems:
 - premature convergence
 - genetic drift
 - diversity preservation
- Multi-objective GAs

Optimisation Methods

- One aim: robustness
 - efficient + effective over many problems
- Two types of optima: local and global



- Three types of algorithm
 - calculus-based
 - enumerative
 - random

Calculus-Based Methods

- First derivative discrete: set equal to zero

$$f(x) = x^2$$

$$\frac{df(x)}{dx} = 2x = 0 \Rightarrow x = 0$$

- First derivative available at any point: hill-climb (many methods)
 - assumes meaningful derivatives (smoothness)
 - local
- Not robust (effectiveness)

Enumerative Methods

- Discretise the search space and test every point
 - not efficient
- Not robust (efficiency)

Random Methods

- True random methods e.g. random search
 - no better than enumerative methods
- Randomised methods e.g. simulated annealing
 - Boltzmann equation

$$P = \exp\left(-\frac{E}{kT}\right)$$

- start with random state: energy = cost
- random change with probability

$$p = \exp\left(-\frac{(E_2 - E_1)}{kT}\right)$$

- decrease temperature: annealing schedule
 - solves TSP but AS problem dependent
- Randomised methods \neq random search
 - Not robust (effectiveness)

Genetic Algorithms

- None of the previous methods are robust:
 - assume smoothness / local
 - inefficient
 - problem specific
- Nature optimises by evolution: cost function
 - discontinuous
 - multi-modal
 - high-dimensional
 - dynamic
- Copy evolution: Genetic Algorithms
 - investigate natural evolution
 - produce robust optimisation method

Genetic Algorithms: Outline

- Code parameters as a binary string
 - bit = gene
 - value (0,1) = allele
 - string = chromosome
- Create random population (typically ~ 100)
- Apply three operators:
 - reproduction
 - crossover
 - mutation

Genetic Algorithms: Example

- Example: optimise x^2 over $x=0$ to 31
- Code parameters as five bit unsigned integer
 - $x=0$ at 00000, $x=31$ at 11111
- Population=4

String	x	Fitness $f(x)$
01101	13	169
11000	24	576
01000	8	64
10011	19	361

- Average fitness = 293 : Max fitness = 576

Genetic Algorithms: Example 2

- Reproduction
 - copy strings with prob. f_1/\bar{f}
- Roulette wheel selection
 - choose strings to copy at random, weighted by their proportional fitness:

String	x	f(x)	$\frac{f_i}{\bar{f}}$	Expected count	Actual count
01101	13	169	0.14	0.58	1
11000	24	576	0.49	1.97	2
01000	8	64	0.06	0.22	0
10011	19	361	0.31	1.23	1

- Note that RWS is noisy

Genetic Algorithms: Example 3

- Crossover
 - randomly pair the strings
 - randomly select a position and swap ends

MP	Mate	Crossover site	New pop	x	f(x)
0110—1	2	4	01100	12	144
1100—0	1	4	11001	25	625
11—000	4	2	11011	27	729
10—011	3	2	10000	16	256

Average fitness = 439: Max fitness = 729

- Mutation: flip bits at random
 - very low probability

Schemata

- Why does this work?

Initial pop	Final pop
01101	01100
11000	11001
01000	11011
10011	10000

- sub-string 11^{***} confers high fitness
- Template = *schema* (pl. *schemata*)
 - 3^l possible schemata for string length l
 - single string contains 2^l schemata
 - population of size n contains from 2^l to $n2^l$ schemata, depending on diversity.
- Schemata have two important properties:
 - order $o(H)$
 - defining length $\delta(H)$
- e.g. $H=1^{**}0^*$: $o(H)=2$, $\delta(H) = 3$

Schemata 2: Reproduction

- m examples of schema H at time t
- $f(H)$ = average fitness of strings containing H

$$m(H, t+1) = m(H, t) \cdot n \cdot \frac{f(H)}{\sum f_j} = m(H, t) \frac{f(H)}{\bar{f}}$$

- If H retains fitness $c\bar{f}$

$$m(H, t+1) = m(H, t) \frac{\bar{f} + c\bar{f}}{\bar{f}} = (1 + c)m(H, t)$$

$$m(H, t) = m(H, 0)(1 + c)^t$$

- Above (below) average schemata grow (decline) exponentially in proportion to the ratio of their fitness to the population average

Schemata 3: Crossover and Mutation

- Crossover may disrupt a schema if the crossover site falls within the schema
 - there are $\delta(h)$ such sites
 - there are $(l - 1)$ possible sites
 - apply crossover with probability p_c
 - probability of survival is:

$$p_s \geq 1 - p_c \frac{\delta(H)}{(l - 1)}$$

- Mutation may disrupt a schema if a defined bit is flipped
 - there are $o(H)$ defined bits
 - each is flipped with probability p_m .
 - probability of survival is:

$$(1 - p_m)^{o(H)} \approx (1 - o(H))p_m \text{ for } p_m \ll 1$$

Schemata 4: The Fundamental Theorem of Genetic Algorithms

- Collecting terms gives

$$m(H, t+1) \geq m(H, t) \frac{f(H)}{\bar{f}} \left[1 - p_c \frac{d(H)}{l-1} - o(H) p_m \right]$$

Fundamental Theorem of Genetic Algorithms

- Above average fitness, low-order, short defining length schemata grow exponentially
- Call these schemata *building blocks*
- Is this a good thing? k-armed bandit problem (Holland, 1975)

How Many Schemata are Usefully Processed?

- How many survive crossover with probability p_s i.e. error rate $\epsilon < (1 - p_s)$?

$$p_s = 1 - \frac{\delta(H)}{l - 1}$$

$$l_s < \epsilon(l - 1) + 1$$

where $\delta(H) = l_s - 1$.

- Number of schemata of length l_s or less:

$$2^{(l_s-1)}(l - l_s + 1)$$

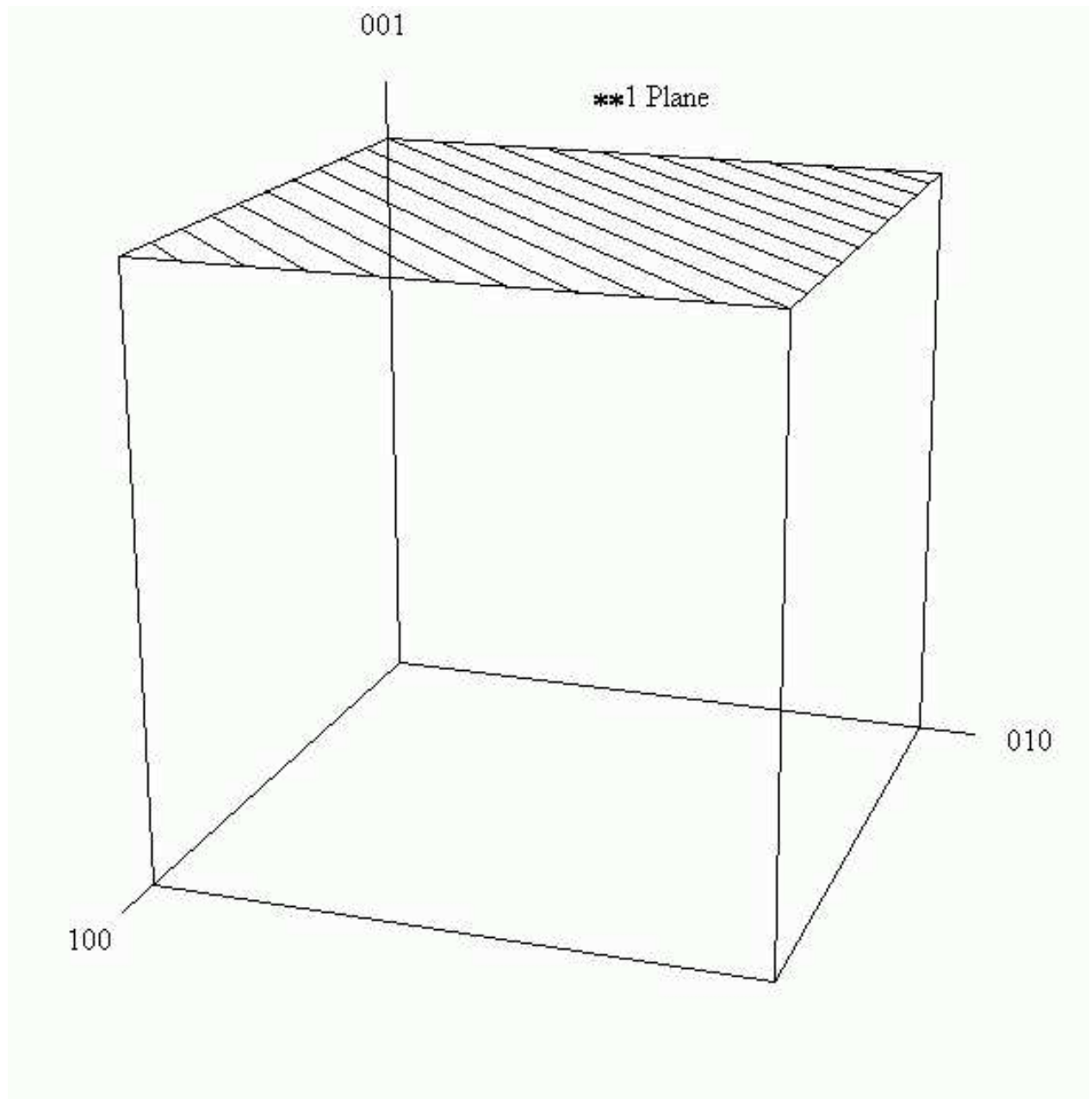
- pick population size of $n = 2^{l_s/2}$: ≤ 1 of each schema of length $l_s/2$ or more.
- half shorter, half longer: pick longer half

$$n_s \geq \frac{n(l - l_s + 1)2^{l_s}}{4} = \frac{(l - l_s + 1)n^3}{4}$$

- $O(n^3)$: many more schemata than strings are processed: *implicit parallelism*

Schemata as Hyperplanes

- A schema represents a hyperplane in the search space:



Codings

- Most important factor
- Coding should generate as many building blocks as possible
 - minimum cardinality alphabet \Rightarrow binary
- Coding should allow effective manipulation of building blocks
 - building blocks should be relevant to problem and relatively independent

Gray Codes

- Notable coding: Gray codes

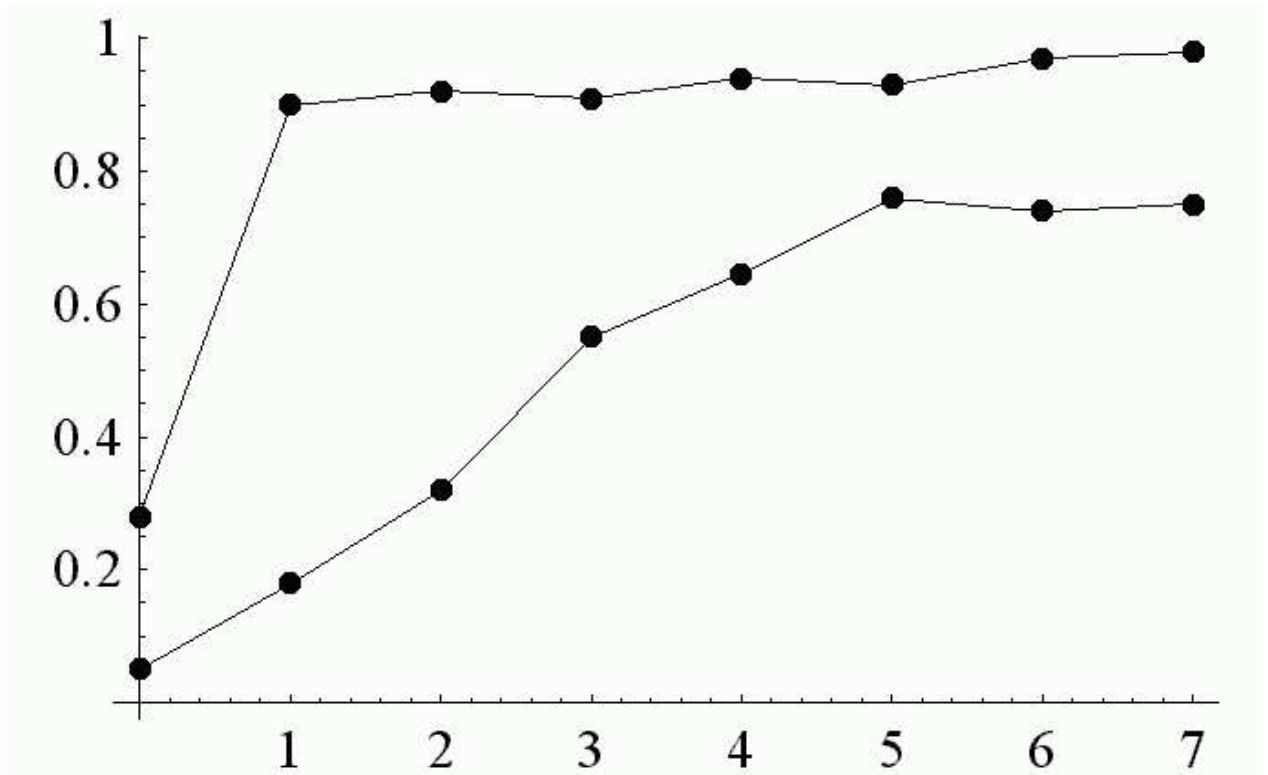
Integer	Binary	Gray Code
0	0000	0000
1	0001	0001
2	0010	0011
3	0011	0010
4	0100	0110
5	0101	0111
6	0110	0101
7	0111	0100
8	1000	1100
9	1001	1101
10	1010	1111
11	1011	1110
12	1100	1010
13	1101	1011
14	1110	1001
15	1111	1000

– Adjacent integers differ by a single bit

- Holstien, 1971: Gray Codes
- Janikow and Michalewicz, 1991; Wright, 1991: real-valued
- Optimal coding problem dependent

Premature Convergence

- Simple example: $f(x) = (x/c)^{10}$
 - range $x = 0$ to 1 : 30-bit binary encoding
 - $p_m = 0.03$, $p_c = 0.6$, $n = 30$ (De Jong, 1975)



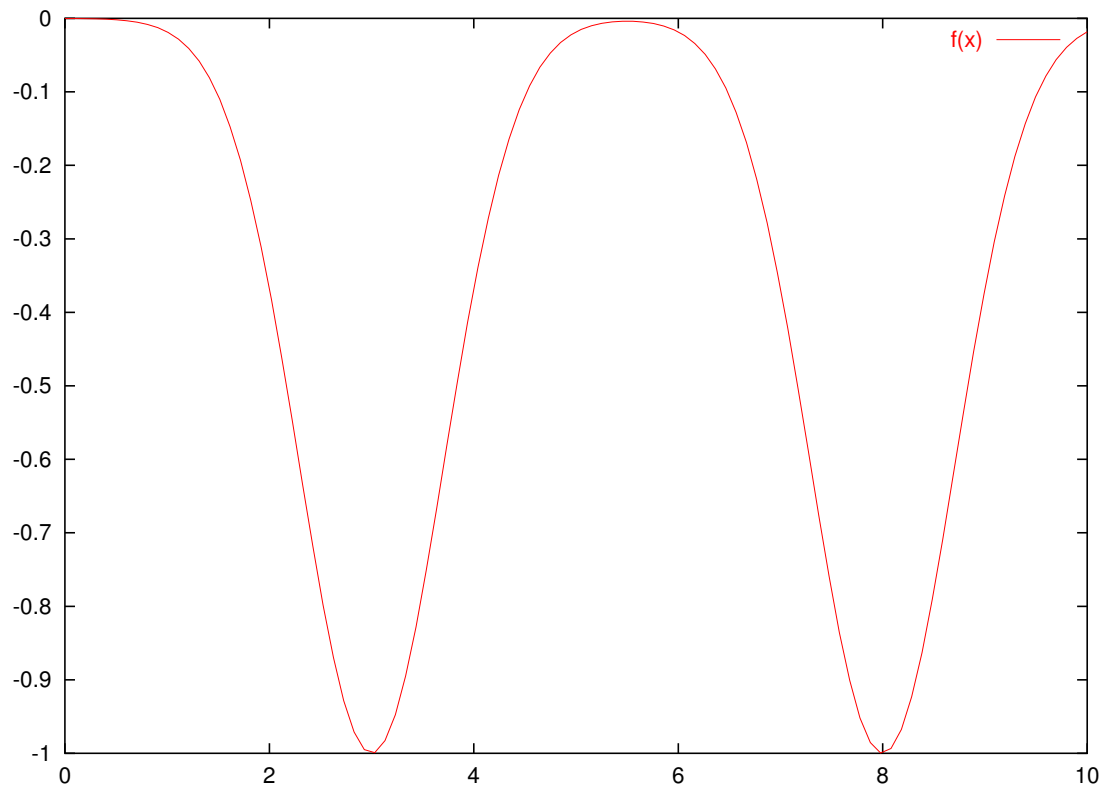
Fitness vs. Generation

- Approaches optimum, but does not reach it
 - population is degenerate by generation 7
 - diversity loss
 - premature convergence

Sources of Diversity Loss

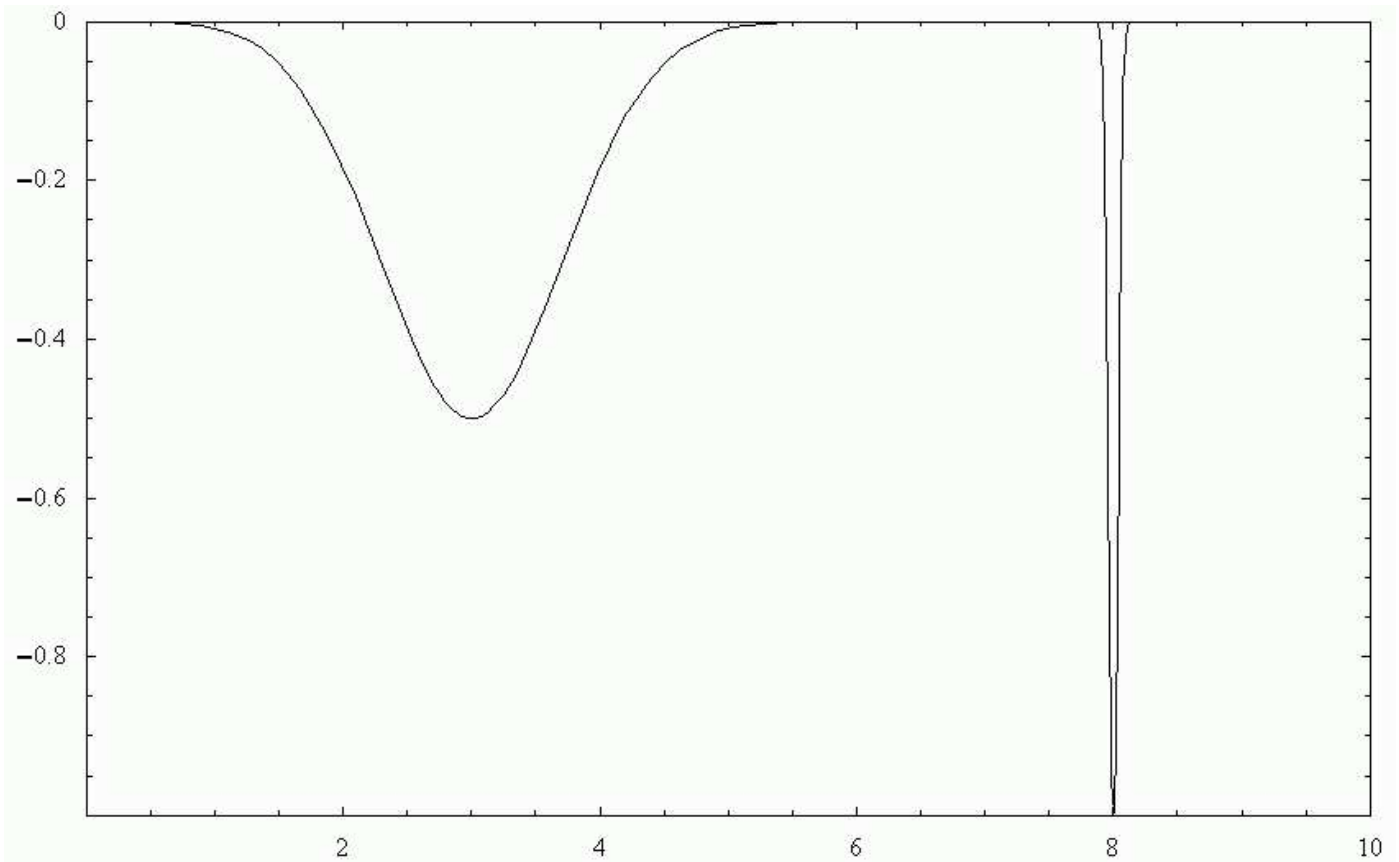
- Selection noise
 - De Jong (1975): schemata fitness from finite sample, stochastic errors in roulette wheel
- Selection pressure
 - lower fitness schemata eliminated
- Operator disruption
 - crossover and mutation destroy schemata

Sources of Diversity Loss: Selection Noise



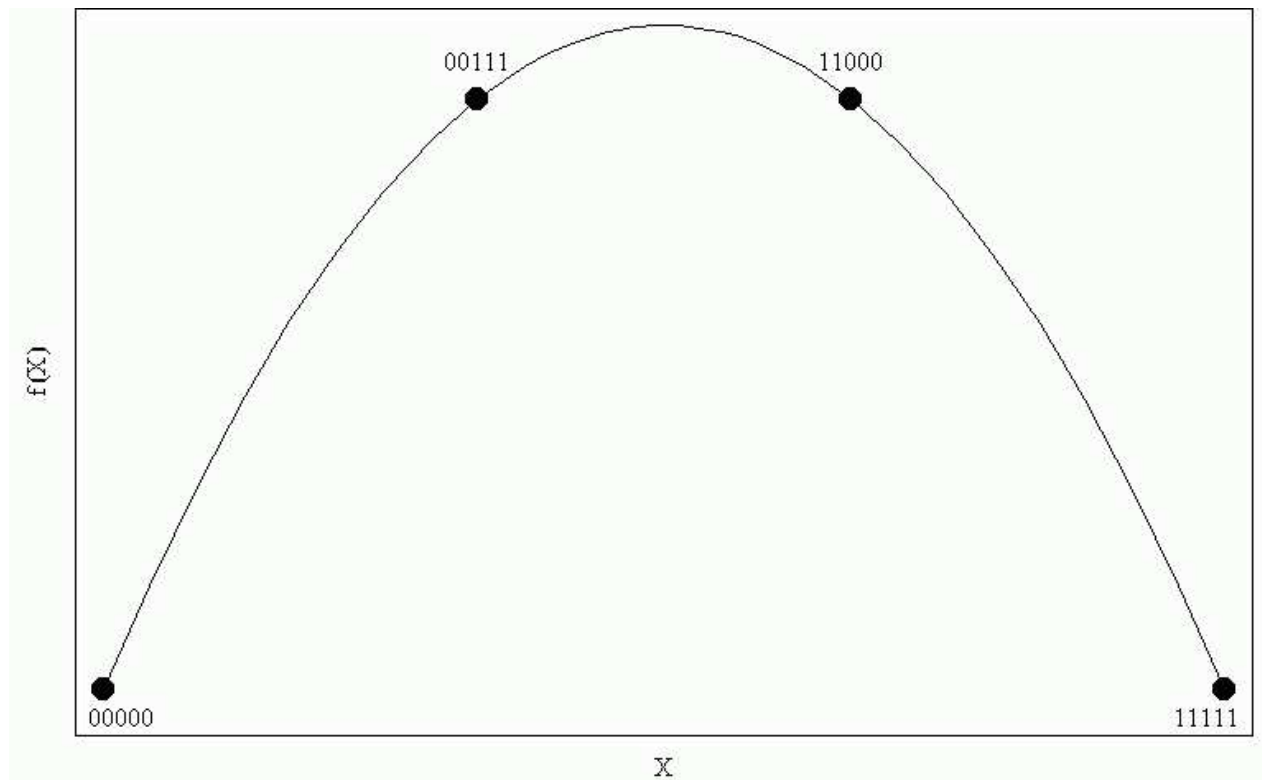
- Multi-modal functions
 - gambler's ruin
 - selection noise *will* eliminate one peak

Sources of Diversity Loss: Selection Pressure



- Broad local peak, narrow global peak
 - schemata near global peak get eliminated
 - global peak never found (deceptive function)
- Less-fit schemata eliminated, even if they provide partial solutions for global optima
 - *super-fit* individuals

Sources of Diversity Loss: Operator Disruption



- Crossover between individuals optimising different local optima is unhelpful.

Diversity Preservation

- Most GA research focuses on diversity preservation
- Many schemes:
 - alternative selection schemes
 - fitness scaling
 - crowding and preselection
 - niching and speciation
 - mating restriction

Alternative Selection Schemes

- From the simple example:

String	Expected count	Actual count
01101	0.58	1
11000	1.97	2
01000	0.22	0
10011	1.23	1

- De Jong (1975): variance of roulette wheel is main source of allele loss
- Expected value model:
 - calculate offspring count as usual $\frac{f_i}{f}$
 - reduce by 0.5 every time string is selected
 - if offspring count ≤ 0 , string is never selected
 - total offspring $\leq \frac{f_i}{f} + 1$
 - influence of super-fit individuals reduced

Fitness scaling

- Start: few super-fit individuals dominate
- End: all individuals roughly same fitness: random search
- Fitness scaling: control this competition
- E.g. linear: scale fitness so that
 - $f'_{avg} = f_{avg}$
 - $f'_{max} = C_m f_{avg}$
 - $C_m = 1.2$ to 2 for $n = 50$ to 100
- Level of competition fixed
- Other scaling functions:
 - sigma
 - power law
 - review: Forrest (1985)

Crowding and preselection

Generational GA:

- replace whole population at each iteration

Steady-state GA:

- replace only a portion of the population
- Preselection:
 - Cavicchio, 1970
 - fit offspring replace their own parents
- Crowding:
 - De Jong, 1975
 - crowding: offspring replace similar individuals from subset of population
 - similarity: bitwise distance in Hamming space
- compare to speciation in natural evolution
- Mahfoud (1992): stochastic errors still lead to diversity loss

Niching and Speciation

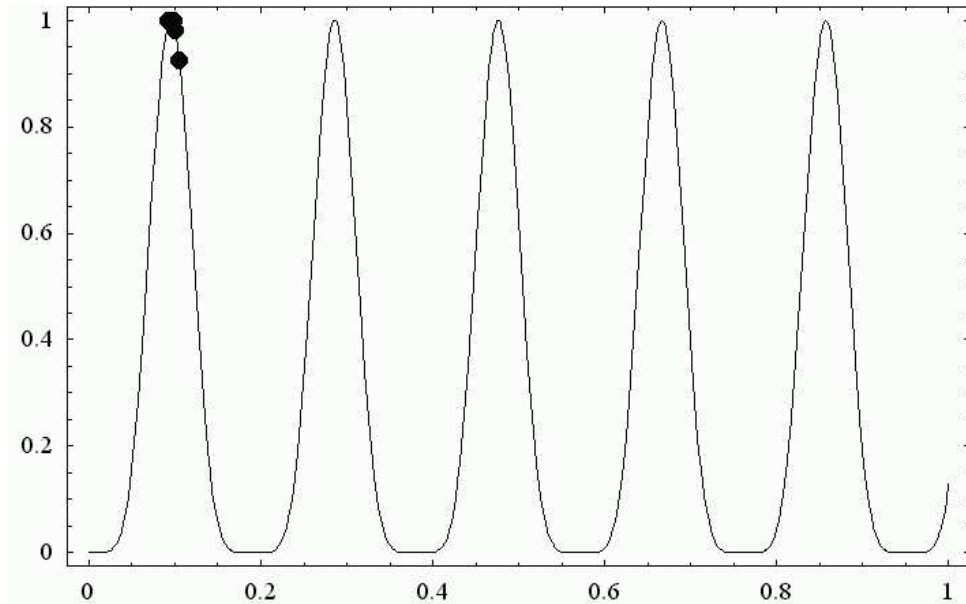
- Crowding and preselection examples of niching:
 - impose competition between like individuals
 - generate species on each local optimum
- Fitness sharing
 - Goldberg and Richardson (1987)
 - impose competition directly
 - fitness scaled by

$$f_s(x_i) = \frac{f(x_i)}{\sum_{j=1}^n s(d(x_i, x_j))}$$

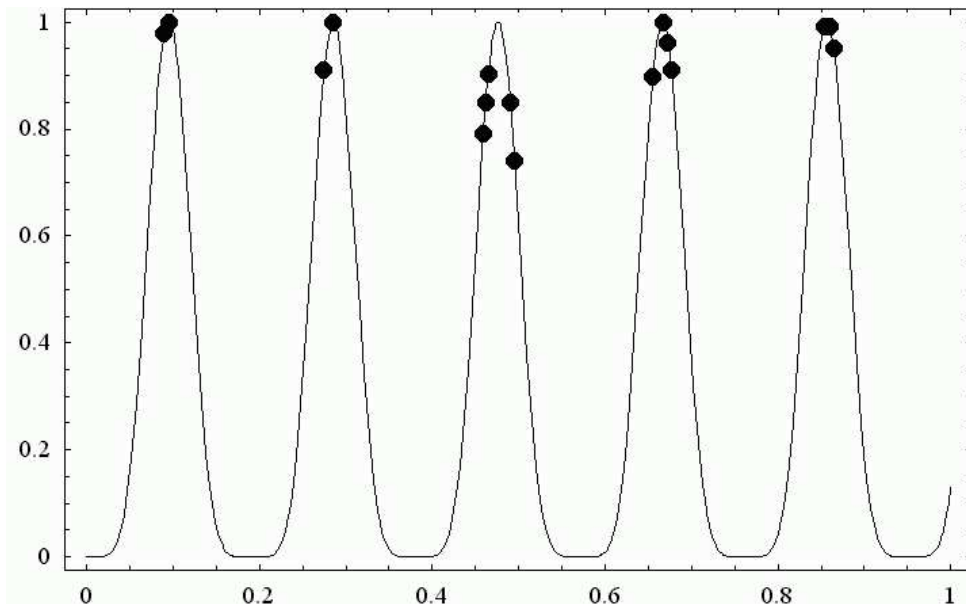
- d = distance, s = sharing function
- Example: triangular sharing function

Niching and Speciation 2

- Results from Goldberg and Richardson



Generation 100: no mutation, no sharing

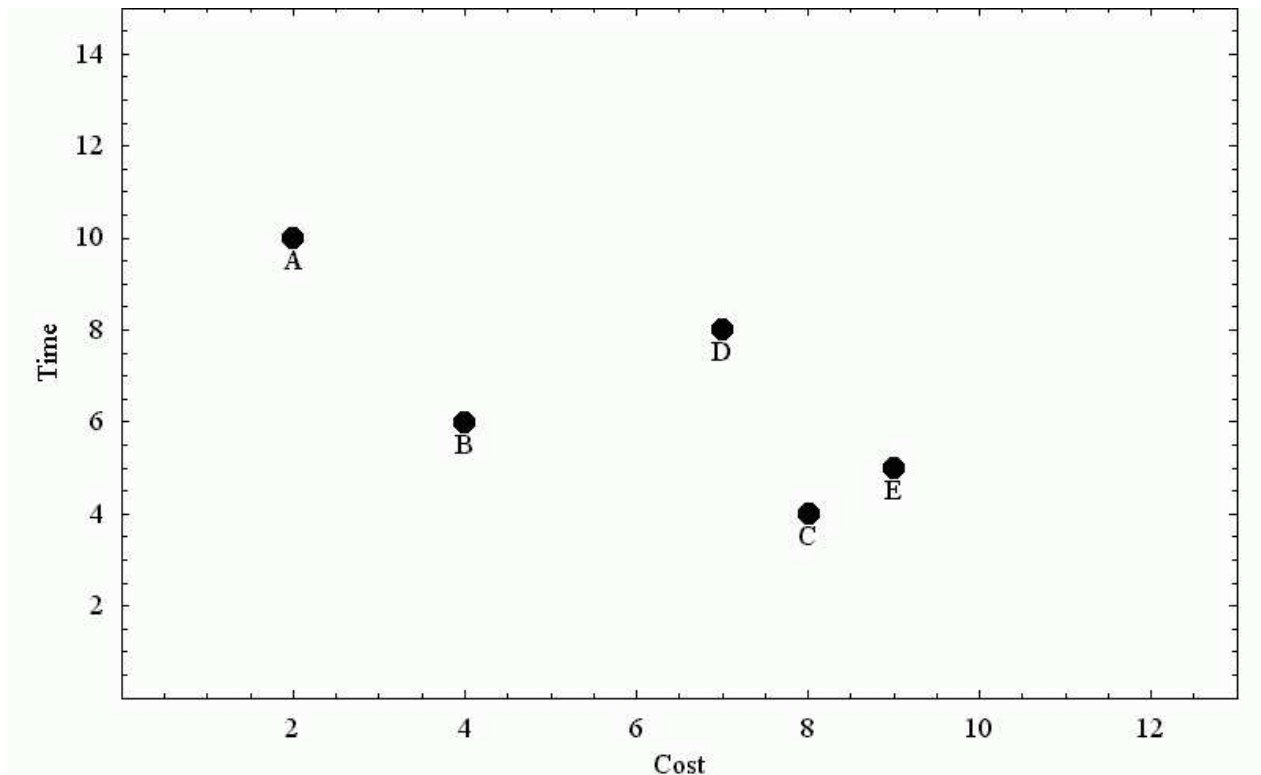


Generation 100: no mutation, sharing

Mating Restriction

- Impose niching by restricting mating
- Hollstien (1971)
 - traditional farming practises
- Line-breeding: champion individual repeatedly bred with others
 - good for unimodal cost functions
- Inbreeding with intermittent cross-breeding
 - close individuals mate if fitness goes up
 - if not, mate outside family
 - improvement for multi-modal functions

Multi-objective Optimisation



- D, E: *dominated* solutions
- A, B, C: *non-dominated* solutions
- Non-dominated solutions form the *Pareto Front*
- GAs ideal:
 - multiple individuals in population
 - entire Pareto Front in a single run
 - diversity must be preserved

Conclusions

- GAs implementation
 - code parameters as binary string
 - initialise multiple random strings
 - reproduction, crossover and mutation
- GA theory
 - schemata
 - Fundamental Theorem of Genetic Algorithms
 - implicit parallelism
- GA problems
 - selection noise, selection pressure, operator disruption
 - loss of diversity
 - hence diversity preservation methods
- GA advantages
 - robust
 - multi-objective optimisation
 - suitable for parallel architectures