Genetic Algorithms

Patricia J Riddle
Computer Science 760

Motivation

- Analogy to biological evolution
- GAs generate successor hypotheses by repeatedly mutating and recombining parts of the best currently known hypotheses
- The collection of hypotheses, ***population***, is updated by replacing some fraction of the population by offspring of the fittest current hypotheses
- Generate-and-test beam-search of hypotheses in which variants of the fittest current hypotheses are most likely to be considered next

Popularity

- Evolution is known to be a successful, robust method of adaptation within biological systems
- GAs can search spaces of hypotheses containing complex interacting parts, where the impact of each part on overall hypothesis fitness may be difficult to model.
- Genetic algorithms are easily parallelized and can take advantage of the decreasing costs of powerful computer hardware.

Fitness

- The ***best*** hypothesis is defined as the one that optimizes a predefined numerical measure called ***fitness function***
- Fitness could be
  - accuracy of the hypothesis over the training data or
  - number of games won by the individual when playing against other individuals in the current population
- The algorithms iteratively update the pool of hypotheses (i.e., ***population***)

General Method

- On each iteration:
  1. All members of the population are evaluated according to the fitness function.
  2. A new population is generated by probabilistically selecting the most fit individuals from the current population.
  3. Some of these individuals are carried forward into the next generation population intact.
  4. Others are used for creating new offspring individuals by applying genetic operations such as crossover and mutation.

Genetic Algorithm

```
GA($Fitness$, $Fitness\_threshold$, $p$, $r$, $m$)
    Fitness: A function that assigns an evaluation score, given a hypothesis.
    Fitness_threshold: A threshold specifying the termination criterion.
    p: The number of hypotheses to be included in the population.
    r: The fraction of the population to be replaced by Crossover at each step.
    m: The mutation rate.
• Initialize population: $P \leftarrow$ Generate $p$ hypotheses at random
• Evaluate: For each $h$ in $P$, compute $Fitness(h)$
• While $[\max_h Fitness(h)] < Fitness\_threshold$ do
    Create a new generation, $P_S$:
    1. Select: Probabilistically select $(1-r)p$ members of $P$ to add to $P_S$. The probability $\Pr(h_i)$ of
           selecting hypothesis $h_i$ from $P$ is given by
               $\Pr(h_i) = \frac{Fitness(h_i)}{\sum_{j=1}^{p} Fitness(h_j)}$
    2. Crossover: Probabilistically select $\frac{r \cdot p}{2}$ pairs of hypotheses from $P$, according to $\Pr(h_i)$ given
           above. For each pair, $\langle h_1, h_2 \rangle$, produce two offspring by applying the Crossover operator.
           Add all offspring to $P_s$.
    3. Mutate: Choose $m$ percent of the members of $P_s$ with uniform probability. For each, invert
           one randomly selected bit in its representation.
    4. Update: $P \leftarrow P_s$.
    5. Evaluate: for each $h$ in $P$, compute $Fitness(h)$
• Return the hypothesis from $P$ that has the highest fitness.
```

Algorithm Properties

- Inputs:
  - The fitness function,
  - The size of the population
  - Threshold defining an acceptable level of fitness for terminating the algorithm
  - Parameters that determine how successor populations are generated
    - the fraction of the population to be replaced each generation, and
    - the mutation rate

Probability of Inclusion

- Probability of inclusion of hypothesis, h_i , in the next generation,

$$\Pr(h_i) = \frac{Fitness(h_i)}{\sum_{j=1}^{p} Fitness(h_j)}$$

- The probability that a hypothesis will be selected is proportional to its own fitness and inversely proportional to the fitness of the other competing hypotheses in the current population
- Hypothesis is chosen with replacement!!

Additional Algorithm Properties - Crossover

- Additional members are generated using crossover
- Crossover takes two parent hypothesis from the current population and creates two offspring hypothesis by recombining portions of both parents.
- The parents are chosen probabilistically using the same formula mentioned above.
- Now the new generation contains the desired number of members.

Additional Algorithm Properties - Mutation

- Now a certain fraction ***m*** of these members are chosen at random and random mutations are performed.

What is the hypothesis space?

- Randomized, parallel beam search for hypothesis that perform well according to the fitness function

Representing Hypotheses

- Hypothesis in GAs are often represented by bit strings, which are easily manipulated by crossover and mutation.

- These can be quite complex
  - a set of if-then rules

Representation Example

- Attribute: ***Outlook***
  - Values: ***Sunny***, ***Rainy***, ***Overcast***
- Use a bit string of length 3, where each position corresponds to one of the values. Placing a 1 in some position indicates that the attribute is allowed to take on the corresponding value.
- So 010 represents ***Outlook = Overcast*** and 011 represents ***Outlook = Overcast or Rainy***

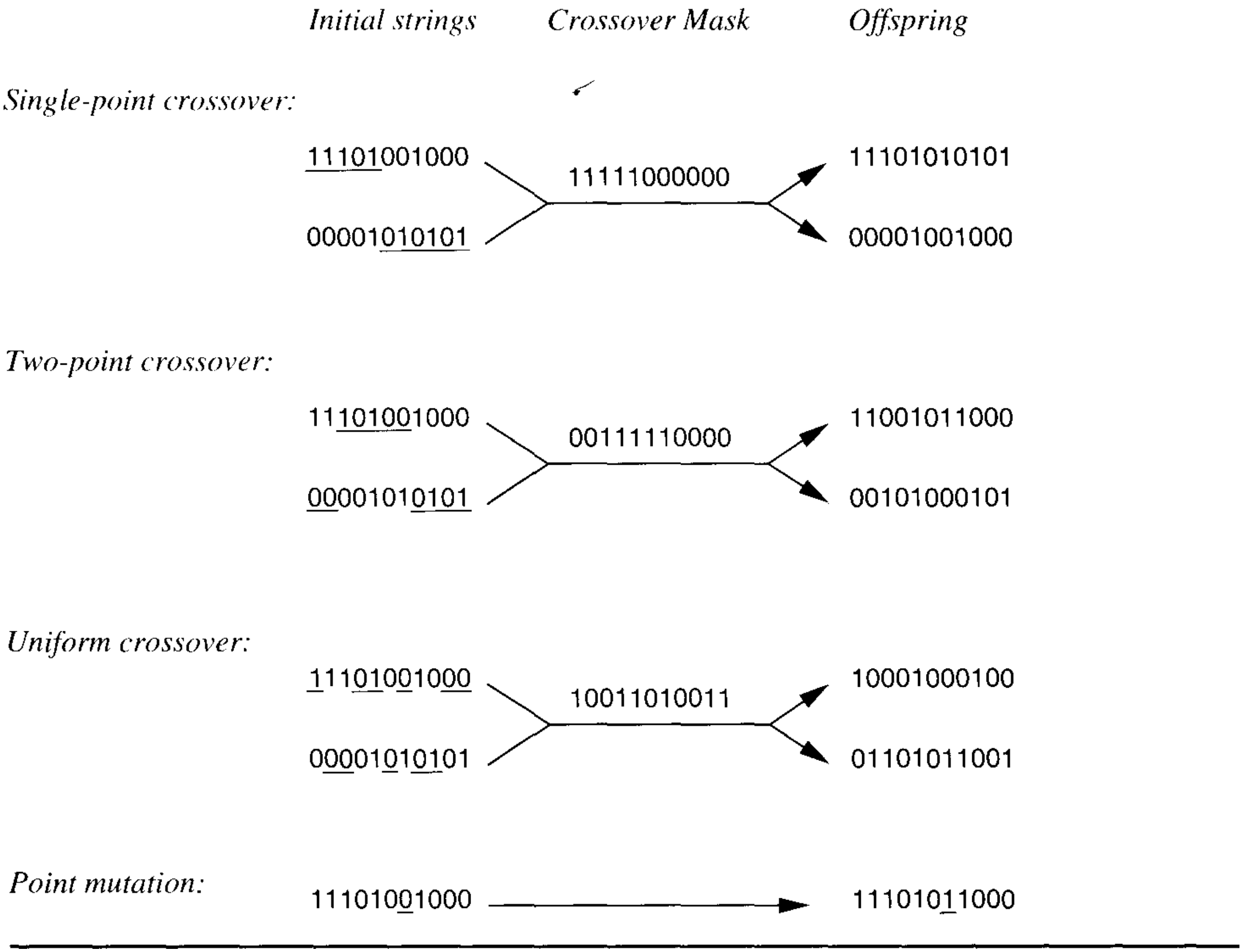
More Representations

- Conjunctions of constraints can be represented by concatenation. So ***011 10*** represents ***Outlook = Overcast or Rainy and Wind = Strong***
- Postconditions can be represented in the same way ***111 10 10*** represents ***If Wind = Strong then PlayTennis = Yes***. Notice that ***111*** represents the "don't care" condition on Outlook
- Fixed length bit strings of rules
- Sets of rules can be represented by concatenating single rules, but now are not fixed length!

Representations III

- It is best if every syntactically legal bit string represents a well-defined hypothesis
- So 111 10 11 represents a rule whose postcondition does not constrain the target PlayTennis. To avoid this
  - allocated just one bit to PlayTennis to indicate Yes or No, or
  - alter the genetic operators so they explicitly avoid constructing such bit strings, or
  - assign them a very low fitness (only works if there are only a few).
- Some GAs represent hypothesis as symbolic descriptions rather than bit strings (more later).

Genetic Operators



	Initial strings	Crossover Mask	Offspring
Single-point crossover:	11101001000 00001010101	11111000000	11101010101 00001001000
Two-point crossover:	11101001000 00001010101	00111110000	11001011000 00101000101
Uniform crossover:	11101001000 00001010101	10011010011	10001000100 01101011001
Point mutation:	11101001000		11101011000

Crossover & Mutation

- Single-point crossover: n chosen randomly each time the crossover operator is applied
- Two-point crossover: n_0 & n_1 chosen randomly each time applied
- Uniform crossover: each bit chosen at random and independent of the others
- Mutation: Flip one random bit (sometimes two mutation parameters)
- Some systems add new operators that do specialization or generalization

Fitness Function Selection

- **Fitness proportionate** selection: ratio of fitness to the fitness of other members of the current population (**Roulette wheel**)
- **Tournament Selection**: two hypothesis chosen at random, with some predefined probability, p, the more fit is selected and with probability (1-p) the less fit is selected, More diverse population.
- **Rank Selection**: Sorted by fitness. The probability that a hypothesis will be selected is then proportional to its rank.

GABIL System

- GABIL uses a GA to learn boolean concepts represented by a disjunctive set of propositional rules.
- Comparable in generalization accuracy to C4.5
- GABIL used the algorithm given earlier
- ***r***, fraction replaced by crossover, was 0.6
- ***m***, mutation rate, was 0.001
- ***p***, population size varied from 100 to 1000, depending on the task

GABIL Representation

- Each hypothesis is a disjunctive set of propositional rules
- Conjunction of constraints on fixed set of attributes - bit string representations of individual rules
- So the hypothesis consisting of the two rules follows:

IF a_1= T ∧ a_2 = F then c = T ∨ IF a_2=T then c=F

10 01 1 11 10 0

- The length of the bit string grows with the number of rules. This causes a modification to the crossover operator.

GABIL Genetic Operators

- Same mutation operator
- Crossover occurs only between like sections of the bit strings
- Standard extension to two-point crossover
- Two crossover points are chosen at random in the first parent string
- Calculate d_1 (d_2), the distance from the leftmost (rightmost) of the crossover points to the rule boundary immediately to its left
- Crossover points are randomly chosen in the second parent with the constraint that they must have the same d_1 and d_2 values

Genetic Operators Example

- H_1: 10 01 1 11 10 0
- H_2: 01 11 0 10 01 0
- If the crossover points for the 1st parent are <1,8> then the allowable crossover points for the second parent are <1,3>, <1,8> and <6,8>
- If happen to choose <1,3> then the two offspring would be:
  - H_3: 11 10 0 and
  - H_4: 00 01 1 11 11 0 10 01 0
- All bit strings generated in this fashion represent well-defined rule sets

GABIL Fitness Function

- Fitness(h) = (correct(h))^2,

- Where ***correct(h)*** is the percent of all training examples correctly classified by hypothesis ***h***

GABIL Extensions

- Two new genetic operators
- AddAlternative - generalises constraints by changing a 0 to a 1
- In an attribute substring 10010 becomes 10110
- This operator was applied with probability .01

DropCondition

- DropCondition - performs more drastic generalisation step by replacing all bits for a particular attribute by a 1
- In an attribute substring 10010 becomes 11111
- This operator was applied with probability .60
- The addition of these operators increased accuracy from 92.1% to 95.2% on a range of datasets

Evolving Search Methods

- Even tried new attributes AA and DC specifying whether these operators can apply to these hypothesis
- Worked better on some datasets and worse on others
- In this way GAs can be used to evolve their own hypothesis search methods

Hypothesis Space Search

- Randomized beam search method to seek maximally fit hypothesis
- GAs vs, Backpropagation (GD)
  - GD moves smoothly from one hypothesis to a new one which is very similar
  - GAs move much more abruptly - replacing a parent with an offspring that maybe radically different
- GA is therefore less likely to fall into the same kind of local minima that plague GD
- GAs have their own problems - crowding

Crowding

- Some individual is more fit and so copies of this individual and very similar individuals quickly take over

- This lowers the diversity of the population and slows further progress by the GA - in worse case down to mutation

Crowding Solutions

- Use tournament or rank selection
- Fitness sharing: the fitness of an individual is reduced by the presence of other similar individuals
- Restrict the kinds of individuals allowed to recombine - multiple subspecies - related approach is to spatially distribute individuals and allow only nearby individuals to recombine

Bloat - The Other Problem

- Problem with variable length representations
- Longer individuals usually have a better chance of a higher fitness
- What happens when there is no selection pressure?

Cameron Skinner's Thesis

- Discovery & Retention
  - Crossover & Mutation???
- Tournament Selection
- Two-point crossover
- Bloat & Absorbing Boundaries
- Reseeding instead of Mutation
- When to use GAs

Creature Demo

Population Evolution

- Can we mathematically characterise the evolution over time of the population within a GA
- Schema theorem of Holland
- Schema is a string composed of 1s 0s and *s
  - * is “don’t care”
- Schema 0*10 represents the set of bit strings 0010, 0110
- The bit string 0010 represents 2^4 different schemas

Schemas

- Population of bit strings can be viewed by the set of schemas it represents and the number of individuals associated with each schema
- ***m(s,t)*** is the number of instances of schema s at a time t

Schema Theorem

- Determine the expected value of schema

$$E[m(s,t+1)] \geq \frac{\hat{u}(s,t)}{\bar{f}(t)} m(s,t)(1 - p_c \frac{d(s)}{l-1})(1 - p_m)^{o(s)}$$

- Average fitness of individuals of schema s

$$\hat{u}(s,t) = \frac{\sum_{h \in s \cap p_t} f(h)}{m(s,t)}$$

Terms

- $\bar{f}(t)$ Average fitness of all individuals in the population at time ***t***

- $\boldsymbol{h \in s \cap p_t}$ indicates an individual h is both a representative of schema s and in the population at time ***t***

- $\boldsymbol{P_c}$, probability that the single-point crossover will be applied

Terms 2

- P_m, probability that the mutation operator will be applied
- ***O(s)*** is the number of defined bits
- ***d(s)*** is the distance between the leftmost and rightmost defined bits
- ***l*** is the length of the bitstrings

Schema Theorem Intuition

- Whether an individual representing schema s at time t will be selected for time t+1, or still represent s after crossover, or still represent s after mutation
- Effects of crossover increase with the number of defined bits
- Effects of mutation increase with the distance between defined bits
- More fit schemas will grow in influence, especially schemas with a small number of defined bits and especially when these defined bits are near each other in the bit string

Problems with Schema Theorem

- Incomplete because it fails to take into account the positive effects of crossover and mutation (i.e., only gives lower bound) - numerous more recent theoretical analyses

Genetic Programming

- Form of evolutionary computation where the individuals are computer programs instead of bit strings
- Typically represented by trees corresponding to parse trees of the program
- User must define primitive functions
- Fitness is determined by executing the program on the training data
- Crossover replaces a randomly chosen subtree from one parent with one from the other

Program Tree

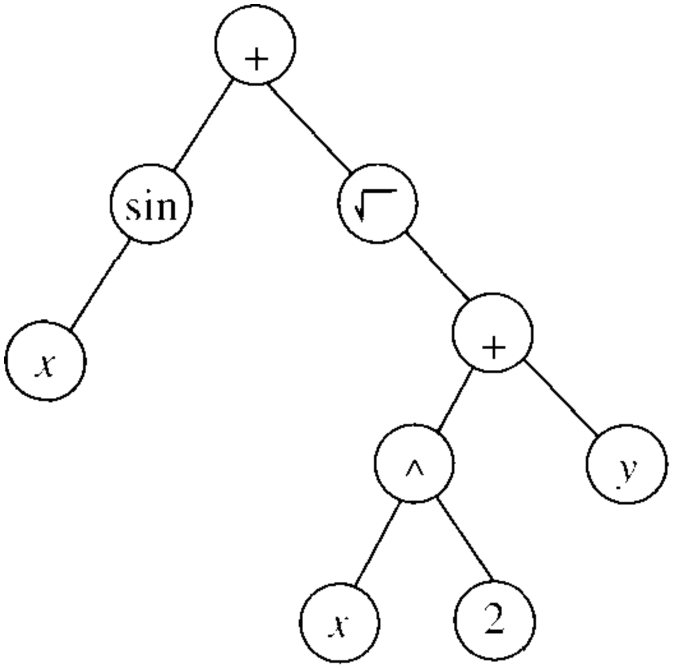


FIGURE 9.1
Program tree representation in genetic programming. Arbitrary programs are represented by their parse trees.

Crossover of Program Trees

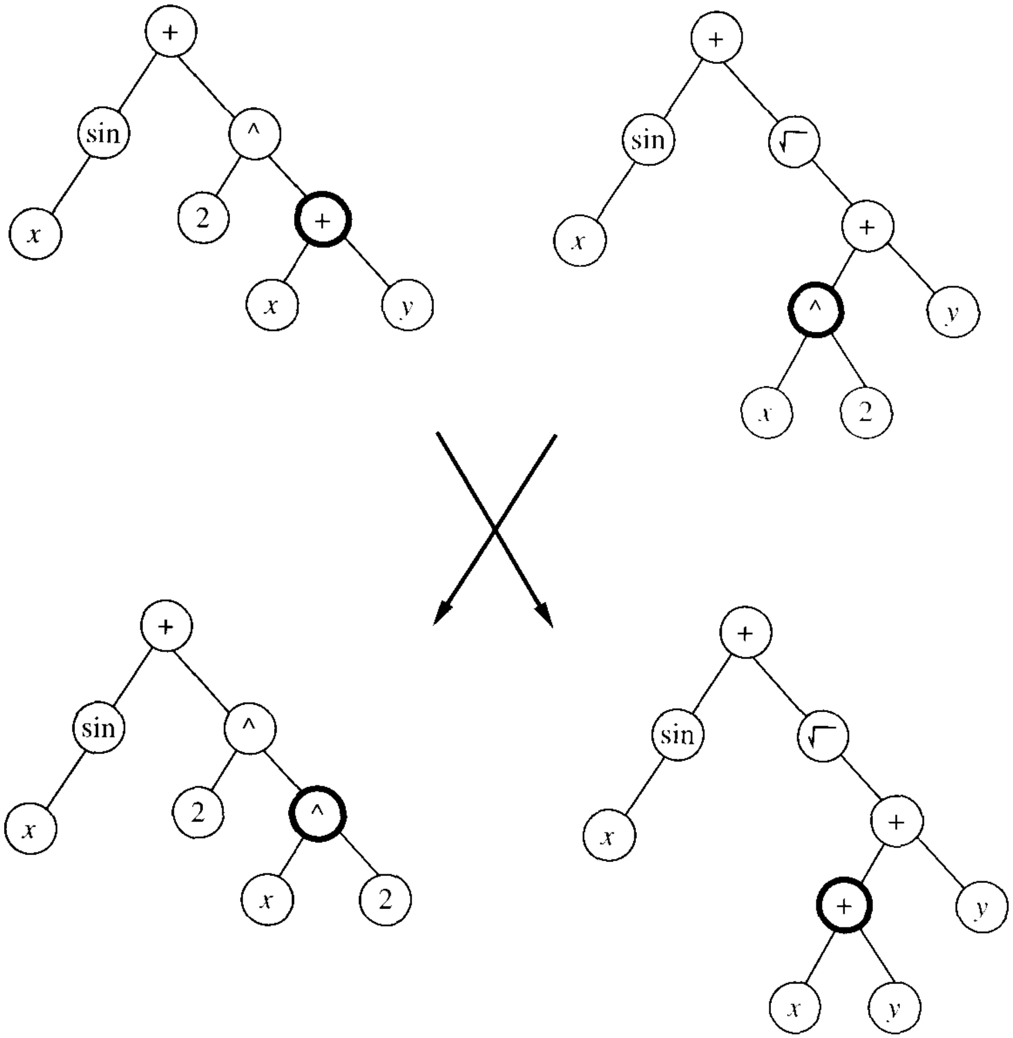


FIGURE 9.2

Crossover operation applied to two parent program trees (top).

Genetic Programming Example

- Develop an algorithm for stacking blocks in a single stack that spells the word “universal” independent of the initial configuration of the blocks
- In GP applications, problem representation has a significant impact on the ease of solving the problem, 3 terminal arguments:
  - CS returns the name of the top block on the stack or F if there is no current stack
  - TB returns the top block on the stack that is in the correct order
  - NN returns the name of the next block needed or F if no blocks are needed
- Imagine the difficulty if the terminal arguments returned x,y coordinates of the blocks

Primitive Functions!!!

- (MS x) moves x to the top of the stack and returns T otherwise does nothing and returns F,
- (MT x) if block x is in the stack it moves the top block off the stack and puts it on the table and returns T otherwise it does nothing and returns F
- (EQ x y) returns T if x=y and returns F otherwise
- (Not x) returns T if x=F and F if x=T
- (Du x y) executes the expression x repeatedly until y returns the value T

Experiment Results

- 106 training examples representing a broad variety of initial block configurations and degrees of difficulty - must contain all boundary conditions!

- Fitness of a program was the number of these examples solved, population was initialized to 300 random programs

Experiment Results II

- After 10 generations -
  - (EQ (DU (MT CS)(Not CS))(DU (MS NN)(Not NN)))
  - solves all 166 problems
  - unstack loop followed by a stack loop
  - EQ used for sequencing only
- was 10 runs an average or just a lucky try?
- what was the variance?

Experiment Results III

- GAs have been used to design electronic filter circuits and classify segments of protein molecules
  - But circuit example used a population of 640,000!!!

Models of Evolution

- Lamarkian Evolution - evolution over many generations was directly influenced by the experiences of individual organisms - if an individual learned during its lifetime to avoid some toxic food it could pass the trait on genetically to its offspring.
- Repudiated in biological systems but this can be used to improve the effectiveness of GAs

Baldwin Effect

- Evolutionary pressure to favor individuals who can learn
- An individual can perform a small local search during its lifetime to maximize its fitness
- It can support a more diverse gene pool and therefore more rapid evolutionary adaptation

Baldwin Effect Example

- Evolving population of neural networks
  - genes determined which weights could change
  - weights changed during lifetime
  - over generations more weights became fixed as the population optimized
  - what would happen if the fitness function kept moving??

Parallelizing Genetic Algorithms

- Coarse grain - subdivide population into demes, each deme is assigned a computational node, GA search performed at each node, communication and cross-fertilization across demes occurs less frequently by migration, also reduces crowding
- Fine grain - assign one processor per individual - recombination occurs among neighbors - neighborhood could be planar or torus

Summary

- GAs randomized parallel hill-climbing search for hypothesis that optimize a predefined fitness function
- Based on analogy to biological evolution
- Diverse population of competing hypotheses, at each iteration most fit members of the population are selected, combined by crossover and subjected to random mutation

Summary II

- GAs show how learning can be seen as a special case of optimization
  - learning task is finding optimal hypothesis

- this suggests other optimization techniques - like simulated annealing - can be applied to machine learning

Summary III

- GAs most commonly been applied to optimization problems outside machine learning
  - especially suited to learning tasks where hypotheses are complex and the objective to be optimized may be an indirect function of the hypothesis (e.g., the acquired rules successfully controls a robot).
- Genetic Programming is a variant of GAs where the hypotheses are programs. Demonstrated to learn programs to simulate robot control and recognize objects in visual scenes.