Artificial Life Lecture 12

This will look at 3 aspects of Evolutionary Algorithms:

1) Genetic Programming – GP
2) Classifier Systems
3) Species Adaptation Genetic Algorithms -- SAGA

Genetic Programming

GP (a play on General Purpose) is a development of GAs where the genotypes are pretty explicitly pieces of computer code.

This has been widely promoted by John Koza, in a series of books and videos, eg:

Genetic Programming, John Koza,
MIT Press 1992
Followed by volumes II and III

GP

At first sight there are a number of problems with evolving program code, including

(1) How can you avoid genetic operators such as recombination and mutation completely screwing up any half-decent programs that might have evolved?

(2) How can you evaluate a possible program, give it a fitness score?

GP solution to problem 1

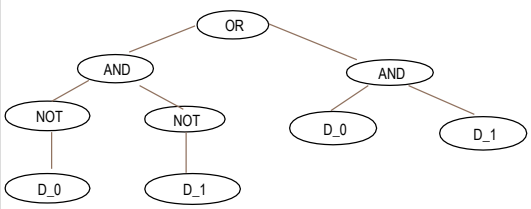
Both these 2 problems were basically cracked in work that predated Koza:

N. Cramer *A representation for the adaptive generation of simple sequential programs* In J Grefenstette (ed) *Proc of Int Conf on Genetic Algorithms*, Lawrence Erlbaum, 1985.

(1) Use LISP-like programs, which can be easily pictured as rooted point-labelled trees with ordered branches.

Picturing a Lisp program

(OR (AND (NOT D_0) (NOT D_1)) (AND D_0 D_1)



Recombining 2 Lisp programs

Picture each of 2 parent Lisp programs in tree form.

Then **recombination** between 2 parents involves taking their 2 trees, choosing random points to chop off sub-trees, and swapping the sub-trees.

This maintains the general form of a program, whilst swapping around the component parts of programs.

Mutating a Lisp program

Mutation in GP is rarely used:

"Nonetheless, it is important to recognize that the mutation operator is a relatively unimportant secondary operation in the conventional GA", says Koza
(op. cit. p. 105), citing Holland 1975 and Goldberg 1989.

When it is used, it operates by randomly choosing a subtree, and replacing it with a randomly generated new subtree.

GP solution to problem 2

How do you measure the fitness of a program? (this was the 2nd problem mentioned earlier)

Usually, fitness is measured by considering a fixed number of test-cases where the correct performance of the program is known.

Put a number on the error produced for each test-case, sum up the (absolute) value of these errors => fitness.

Normalising fitness

Often there is some adjustment or normalisation, eg so that normalised fitness nf ranges within bounds $0 < nf < 1$, increases for better individuals, and $sum(nf)=1$.

Normalised fitness => fitness-proportionate selection

A typical GP run

- has a large population, size 500 up to 640,000
- runs for 51 generations (random initial + 50 more)
- has 90% crossover -- ie from a population of 500, 450 individuals (225 pairs) are selected (weighted towards fitter) to be parents
- and 10% selected for straight reproduction (copying)
- no mutation
- maximum limit on depths of new trees created
- selection is fitness-proportionate

Different problems tackled by GP

Koza's GP books detail applications of GP to an enormous variety of problems.

- Eg finding formulas to fit data
- control problems (eg PacMan)
- evolution of subsumption architectures
- evolution of building blocks (ADF automatic definition of (sub-)functions)
- etc etc etc

Choice of primitives

In each case the primitives, the basic symbols available to go into the programs, must be carefully chosen to be appropriate to the problem.

Eg for PacMan:
Advance-to-Pill
Retreat-from-Pill
Distance-to-Pill
... ...
IFB(C D) If monsters blue, do C, otherwise D
IFLTE(A B C D) If A<=B, do C, otherwise do D

Criticism of GP

GP has been used with some success in a wide range of domains. There are some criticisms:

Much of the work is in choice of primitives

Successes have not been in General Purpose ('GP') programming -- very limited success with partial recursive programs (eg those with a DO_UNTIL command)

Lack of success with partial recursion

The most complex partial recursive program done with GP faster than with random search (as far as I know) is Highest Common Divisor, by Lorenz Huelsbergen.

This is a trivial program

```
MOD(r0,r1);
MUL(r2,r5);
SUB(r1,r0);
LSR(r3,r1);
DEC(r10);
JNZ(r0,-7);
CLEAR(r11);
OR(r2,r5);
MUL(r10,r6);
XOR(r5,r1);
JNZ(r3,+15);
JG(r0,+6);
MUL(r4,r8);
OR(r2,r5);
J(+11);
INC(r2);
```


ADATE

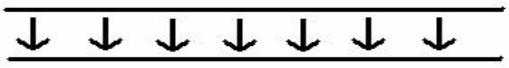
- Exception to this scepticism about evolving programs
- ADATE: **Automatic Design of Algorithms Through Evolution**
- Roland Olsson
- http://www-ia.hiof.no/~rolando/adate_intro.html

- Impressive – can e.g. do strstr()
- Significantly different from GP, and currently is probably the best such system around

Wide and short, not long and thin

GP practitioners such as Koza typically use very large populations such as 640,000 for only 51 generations.

This is closer to random search than to evolution.
Very WIDE and SHORT



Classifier Systems

Just a brief mention here of an alternative GA approach to evolving things-a-bit-like-programs.

A classifier is an if-then rule such as

001##0:101010

is interpreted as 'wild card' or 'dont-care' character

So for example 001000 or 001110 both match the classifying condition 001##0 on the left.

More Classifier Systems

There is a 'blackboard' with a starting set of strings such as 001000, and a set of classifiers can be applied to the strings on the blackboard. Any that match are replaced by the RHS of the classifiers -- then one starts again looking for new matches.

This can be seen as a kind of program, which could (eg) be used for robot or agent control.

For further details see Goldberg (1989), or follow up useful citations on the comp.ai.genetics FAQ
http://www.cs.cmu.edu/Groups/AI/html/faqs/ai/genetic/top.html

SAGA

SAGA, for Species Adaptation Genetic Algorithms, is in many respects the very opposite of GP. Papers on my web page
http://www.informatics.susx.ac.uk/users/inmanh/

Best reference is:
I. Harvey (2001): *Artificial Evolution: A Continuing SAGA*

It is intended for *very long term evolution*, for design problems which inevitably take many many generations, quite possibly through incremental stepping-stones.

Long and thin, not wide and short

So in contrast to GP, there is typically a relatively small population (30-100) for many generations (eg 1000s or 10,000s).

'*Long and narrow*' not 'wide and shallow'

The population is very largely 'genetically converged' -- ie all members genetically very similar, like a plant or animal ***SPECIES.***

Mutation vs. Recombination

Mutation is the main genetic operator, adding diversity and change to the population.

Recombination is only secondary (though useful).

This is completely contrary to the usual emphasis in GP

Convergence (1)

The term 'convergence' is often used in a confused way in the GA/GP literature. People fail to realise that it can be applied with at least two different meanings.

(1) Genetic convergence -- when the genetic 'spread' of the population has settled down to its 'normal' value, which is some balance between:

- selection of the fittest -> reduces spread, and
- mutation -> increases spread.

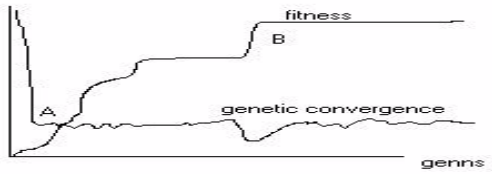
Convergence (2)

(2) convergence of the fitness of the population onto its final value, or (very similarly) convergence of the 'search' of the popn onto its final resting-place.

In sense (2) people talk of 'premature convergence', particularly when they are worried about the population converging onto a local optimum in the fitness landscape, one that is very different from the global optimum.

A common, completely false, myth is that convergence in sense (1) implies convergence in sense (2).

Monitoring Genetic Convergence



B is the point of convergence (defn 2), often after 'punctuated equilibria'

A is the point of genetic convergence (defn 1), which may well be (surprisingly?) within the first 10 or so generations !

Long term incremental evolution

SAGA was originally developed with a view to long term incremental evolution, where one would start with (relatively) short genotypes encoding (eg) relatively simple robot control systems ...

... then over time evolution would move to longer genotypes for more complex control systems.

In this long term evolution it is clear that the population will be genetically converged for all bar the very start

… also long term non-incremental evolution

BUT though SAGA was originally developed with the view of long term incremental evolution (where genotype lengths probably increased from short, originally, to long and then even longer…)

It soon became apparent that the lessons of evolution-with-a-genetically-converged species were **ALSO** applicable to *any* long term evolution, even if genotype lengths remain the same!

Consequences of convergence (1)

It soon became apparent that even with fixed-length genotypes, one still has genetic convergence of the population from virtually the start -- even though this is not widely recognised.

Consequences: recombination does not 'mix-and-match' building blocks quite as expected -- because typically the bits swapped from mum are very similar to the equivalent from dad.

Consequences of convergence (2)

Evolution does not stop with a genetically-converged population (GCP) -- eg the human species, and our ancestors, have evolved as a GCP (… or *species)* for 4 billion years, with incredible changes.

Mutation is the main engine of evolutionary change, and should be set at an appropriate rate – which to a first approximation (depending on selection) is:

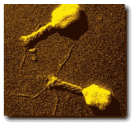
… …

Optimal mutation rate for Binary Genotypes

Binary alphabet or small alphabet eg DNA:-

1 mutation in the expressed (non-junk) part of the genotype

CF phages with 4500 'characters' in genotype have something of the order of 1 mutation per genotype



And so do humans with 3,000,000,000 'characters'

NB: with REAL-valued genotypes it is different

All the above advice is for **Binary** (or similar) genotypes

A mutation at one locus is then a big change at that locus, 0 -> 1 or 1-> 0

So you don't have/need many mutations

But with real-valued genotypes, mutation at each locus will be a small **creep-mutation**, eg. 0.510 -> 0.514, or -> 0.504

So you need **lots** of such small mutations simultaneously, **Cheap Method**: add a 'creep' amount from suitable range eg [+0.1, -0.1] to ***every*** value

More principled method – mutating real values

Construct a vector in some **random** direction in n-space (where n is number of dimensions on genotype) and mutate by moving a small distance in this direction. **HOW?**

ADD n component vectors, one along each axis, lengths drawn from a Gaussian distrn

THEN normalise length of resultant vector to exactly 1.0;

THEN multiply vector length by factor drawn from Gaussian distribution mean 0.0 std.dev. 0.1 (or suitable value);

THIS is your mutation vector – move by this much

Why should there be an optimal mut-rate?

Mutation rate too low, in limit zero, would mean no further change, evolution ceases -> no good

Mutation rate too high, eg every bit flipped at random, implies random search -> no good.

What decides the ideal rate?

Some ideal rate (or range of rates) inbetween -- but where ?

Very rough version of argument: to a first approximation (tho not a 2nd !) at any stage in evolution some N bits of the genotype are crucial -- any mutations there are probably fatal -- while the rest is junk.

The *error threshold* shows that maximum mutation rate survivable under these circumstances is of the order of 1 mutation in the N bits

So what is SAGA?

SAGA is not a specific GA, it is just a set of guidelines for setting the parameters of your GA when used on any long term evolutionary problem -- with or without change in genotype length

1) Expect the population to genetically converge within the very first few generations
2) Mutation is the important genetic operator

… SAGA ctd

3) Set the mutation rate to [***if binary*** genotypes] something of the order of 1 mutation per non-junk element of the genotype. If abnormal selection pressures, for 1 substitute log(S) where S is the expected no. of offspring of the fittest member [***real genotypes: different!***]
5) Often there is quite a safe range of mutation rates around this value -- ie although it is important to be in the right ballpark, exact value not too critical
7) Recombination generally assists evolution a bit
8) Expect fitness to carry on increasing for many many generations

Any other implications ?

Yes, Neutral Networks may well be crucial -- as covered in a previous lecture – and these SAGA ideas on mutation rates are completely consistent with such NNs.

Time for Questions?