Using Gas to Evolve Strategies for Prisoner's Dilemma

<table>
<thead>
<tr>
<th>Pay-off</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>D</td>
<td>5</td>
<td>0</td>
</tr>
</tbody>
</table>

How to encode strategies as strings

- If CC then C
- "CD" = D
- "DC" = C
- "DD" = D

Memory: 1 previous move

Encode Tit for Tat as CD CD

Axelrod used 3 previous moves

<table>
<thead>
<tr>
<th>CC</th>
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<tr>
<td>CC</td>
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<td>CD</td>
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Strategy: string in \( \{C, D\}^6 \)

+ 6 letters that encode 3 hypothetical previous games

Used to decide in initial 3 games

String in \( \{C, D\}^7 \)
Axelrod had organized two tournaments between humans

62 strategies
picked 8 representative strategies
(but not tit for tat)

Fitness:

Each individual in population
played iterated games with
each of the 8 strategies
Fitness = average score

Population size: 20
40 runs 50 generations each

Most strategies that evolved
were tit for tat like

Per run: 20 x 50 individuals
= 1000

Out of 2^70 possible

Sometimes GA found strategies
that scored higher than tit
for tat
2ND SET OF EXPERIMENTS:
AT EVERY GENERATION EACH INDIVIDUAL
PLAYED AGAINST OTHERS

-INITIALLY UNCOOPERATIVE STRATS
-AFTER ABOUT 10-12 GENERATIONS
RECPIRCIAL COOPERATION (I.E. VARIANTS
OF TIT FOR TAT)

GA'S TO EVOLVE SORTING NETWORKS

\[ n = 16 \]

Figure 1.4 The “Batcher sort” \( n = 16 \) sorting network (adapted from Knuth 1973). Each
horizontal line represents an element in the list, and each vertical arrow represents a compar-
ison to be made between two elements. If the elements being compared are out of order,
they are swapped. Comparisons in the same column can be made in parallel.

1962 BOSE, NELSON 65
1964 BATCHER & FLOYD, KNUTH 64
1965 SHAPIRO 62
1969 GREEN 60
REPRESENT NETWORK AS SEQUENCE OF PAIRS:
\[(2, 5), (4, 2), (7, 14), \ldots\]

\[60-120\text{ PAIRS}\]

PHENOTYPE

```
codons:  1011  0101  0111  1001  1110  0100  1010  1001
   ↑       ↑       ↑       ↑       ↑       ↑       ↑       ↑
integers:  11  5  7  9  14  4  10  9
comparisons to insert in phenotype:
      (11, 5)  (7, 9)  (14, 4)  (10, 9)
```

```
chrom. A:
1011  0101
1011  0101
(11, 5)  (7, 9, 2, 7)
```

```
chrom. B:
0111  1001
0010  0111
1110  0100
1010  1001
0101  1100
1010  1001
(14, 4, 2, 12)  (10, 9)
```

HOMOZYGOS: ONE PAIR CONTRIBUTED TO GENOTYPE
HETEROZYGOS: TWO PAIRS

INITIAL POPULATION:
FIRST 32 COMPARISONS THE SAME
REST RANDOM
FITNESS:
PERCENTAGE OF RANDOM LISTS SORTED CORRECTLY

INDIVIDUALS PLACED ON 2-DIM GRID
HOPE: DIFFERENT NETWORKS ARISE IN DIFFERENT SPATIAL LOCATIONS

HALF ARE ALLOWED TO SURVIVE
MATE WITH SURVIVING NEIGHBOR

---

\[\text{Parent 1 (diploid):}\]
\[\begin{array}{c}
A: 10110101 \\
B: 00001011 \\
\end{array}\]
\[\text{Parent 2 (diploid):}\]
\[\begin{array}{c}
C: 00001111101011011101 \\
D: 11111110101101101010 \\
\end{array}\]

\[\text{Gametes:}\]
\[\begin{array}{c}
10110110110011111010101010 \\
00001111100011110101111010 \\
\end{array}\]

\[\text{Offspring (diploid):}\]
\[\begin{array}{c}
1011011101011011001111101010101010 \\
0000111110001111110101111110101110 \\
\end{array}\]

**Figure 3.6** An illustration of diploid recombination as performed in Hillis’s experiment. Here an individual’s genotype consisted of 15 pairs of chromosomes (for the sake of clarity, only one pair for each parent is shown). A crossover point was chosen at random for each pair, and a gamete was formed by taking the codons before the crossover point in the first chromosome and the codons after the crossover point in the second chromosome. The 15 gametes from one parent were paired with the 15 gametes from the other parent to make a new individual. (Again for the sake of clarity, only one gamete pairing is shown.)
IMPORTANT COMPARISONS BECOME HOMOZYGOUS

5.12 TO 10^6 INDIVIDUALS
5000 GENERATIONS

65 COMPARISON NETWORK FOUND!

NOT SATISFIED!

HAD THE TESTCASES EVOLVE AS WELL
(they got HARDER AND HARDER
i.e. co-evolution)
IMPROVED TO 61!
BIOLICAL EVOLUTION

- WHAT ARE IDIOSYNCRASIES?
- WHAT ARE GOOD FEATURES?

TRANSLATION TO A. ACID

TRIPLET PROTEIN
ATG METHIONINE
CAA GLUTAMINE
CAG "

64 CODONS
20 AMINO ACIDS

SEVERAL CODONS PRODUCE SAME A. ACID
EFFICIENCY MAY VARY FROM CODON TO CODON

\[ \text{MUTATION} \]

\[ \text{CAA} \quad \rightarrow \quad \text{CAG} \]

CHANGES RATE OF PRODUCTION OF PROTEIN
IN WHICH GLUTAMINE IS NEEDED

PROTEIN NOT CHANGED

MUTATION CAUSES SUBTLE CHANGES

EVEN WHEN EFFICIENCY OF CODON AS THE
SAME THEN STRUCTURE OF RNA/DNA
MIGHT CHANGED.
Genes are locations on the DNA that decide on a trait.

Variations of same trait called alleles.

Above view simplistic.

One gene one protein.

Now:
One gene one polypeptide sequence.

Intron  |  Exon  |  Intron  |  Exon

Cut out

Code for something useful?

Most eukaryotic DNA consists of junk DNA.

Is the equivalent of junk DNA useful for GP?
Genotype: DNA sequence

One copy from each parent

Offspring

Mutations and crossover act upon genome

Phenotype: Observable properties of organism (body, behavior)

Natural selection acts upon phenotype not genotype

Ontogeny: Development of organism from fertilization to maturity

Environment

G → Ontogeny → P
ONTogeny IS One-WAY STREET
CHANCE IN DNA CAN CHANGE ORGANISM
BUT NOT VICA VERSA

Genome IS bottleneCK
A genome Gets thru bottleneCK
If phenome Does facilitate repro-
duction

- Evolution Possible WITHOUT Physical
  Difference BETWEEN Genotype AND
  Phenotype

- Evolution Possible WITHOUT Ontogeny

- Is Genotype/Phenotype Distinction
  Usefull For GA?
STABILITY AND VARIABILITY OF GENETIC TRANSMISSION

- Stable and variable

If not stable then coupling between parent and offspring lost

Stability

- Redundancy of codons
  Mutations just change amount of protein

- Repair

- Homologous sexual recombination
  - Exchange can only occur between identical or almost identical DNA segments

- DNA strands align themselves where base pairs are identical or almost identical before cross over

- Horse can only mate with horse
Individual 1 DNA Before Homologous Exchange

| Pr A (variant 1) | Pr B (variant 1) | Pr C |

Individual 1 DNA After Homologous Exchange

| Pr A (variant 1) | Pr B (variant 2) | Pr C |

| Pr A (variant 2) | Pr B (variant 1) | Pr C |

Individual 2 DNA Before Homologous Exchange

Species 1 DNA Before Non-Homologous Exchange

| Pr A | Pr B | Pr C |

| PP D | PP E | rRNA F |

Species 2 DNA Before Non-Homologous Exchange

Species 1 DNA After Non-Homologous Exchange

| Pr A | Pr B | Pr C |

| PP D | PP E | rRNA F |

Species 2 DNA After Non-Homologous Exchange

Non-Homologous Exchange is like large scale mutation.

How can we setup GP so that we have homologous cross over?

Aligned before swap

Integrity preserved

Crucial pieces missing
SPECIES:
SET OF INDIVIDUALS FOR WHICH ANY TWO CAN PRODUCE Viable OFF-SPRING.

IN CASE OF ASEXUAL REPRODUCTION DEF. OF SPECIES MORE VAGUE
(E. COli BACTERIA, SCION WOOD)

POPULATION CONSISTS OF CLONES OF SUCCESSFUL VARIANTS

MULLER'S RACHET FOR ASEXUAL POPULATIONS:
BAD MUTATIONS TEND TO ACCUMULATE

SEXUAL RECOMBINATION

- COMBINE LOTS OF GOOD MUTATIONS QUICKLY INTO ONE INDIVIDUAL

- AMELIORATE EFFECT OF MULLER'S RACHET
SUMMARY:

SMALL CHANGES IN PROGRAM
→ SMALL CHANGES IN FITNESS

HOW TO ORGANISE GP SO THAT
WE HAVE HOMOLOGOUS RECOMBINATION

DANGER:

GP DEGENERATES INTO
BLIND MULTIMEMBERED
SEARCH