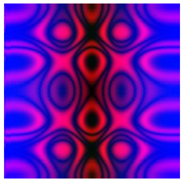
The Genetic and Evolutionary Computation Conference

GECCO 2011 Tutorial:
Cartesian Genetic Programming



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GECCO'11, July 12–16, 2011, Dublin, Ireland.
ACM 978-1-4503-0690-4/11/07.

Abstract

Cartesian Genetic Programming (CGP) is an increasingly popular and efficient form of Genetic Programming that was developed by Julian Miller in 1999 and 2000.

In its classic form, it uses a very simple integer based genetic representation of a program in the form of a directed graph. Graphs are very useful program representations and can be applied to many domains (e.g. electronic circuits, neural networks). In a number of studies, CGP has been shown to be comparatively efficient to other GP techniques. It is also very simple to program.

Since then, the classical form of CGP has been developed made more efficient in various ways. Notably by including automatically defined functions (modular CGP) and self-modification operators (self-modifying CGP). SMCGP was developed by Julian Miller, Simon Harding and Wolfgang Banzhaf. It uses functions that cause the evolved programs to change themselves as a function of time. Using this technique it is possible to find general solutions to classes of problems and mathematical algorithms (e.g. arbitrary parity, n-bit binary addition, sequences that provably compute pi and e to arbitrary precision, and so on).

The tutorial will cover the basic technique, advanced developments and applications to a variety of problem domains.

Contents

- Classic CGP
- Modular CGP
- Self-modifying CGP
- Developmental CGP
- Cyclic CGP
- Applications
- Resources
- Bibliography

Genetic Programming

- The automatic evolution of computer programs
  - Tree-based, Koza 1992
  - Stack-based, Perkis 1994, Spector 1996 onwards (push-pop GP)
  - Linear GP, Nordin and Banzhaf 1996
  - **Cartesian GP,** Miller 1997
  - Parallel Distributed GP, Poli 1996
  - Grammatical Evolution, Ryan 1998
  - Lots of others…

Origins of Cartesian Genetic Programming (CGP)

- Grew out of work in the evolution of digital circuits, Miller and Thomson 1997. First actual mention of the term *Cartesian Genetic Programming* appeared at GECCO in 1999.
- Originally, represents programs or circuits as a two dimensional grid of program primitives.
- This is loosely inspired by the architecture of digital circuits called FPGAs (field programmable gate arrays)

What defines CGP?

- The genotype is a list of integers (and possibly parameters) that represent the program primitives and how they are connected together
  - CGP represents programs as *graphs* in which there are *non-coding genes*
- The genes are
  - Addresses in data (connection genes)
  - Addresses in a look up table of functions
  - Additional parameters
- This representation is very simple, flexible and convenient for many problems

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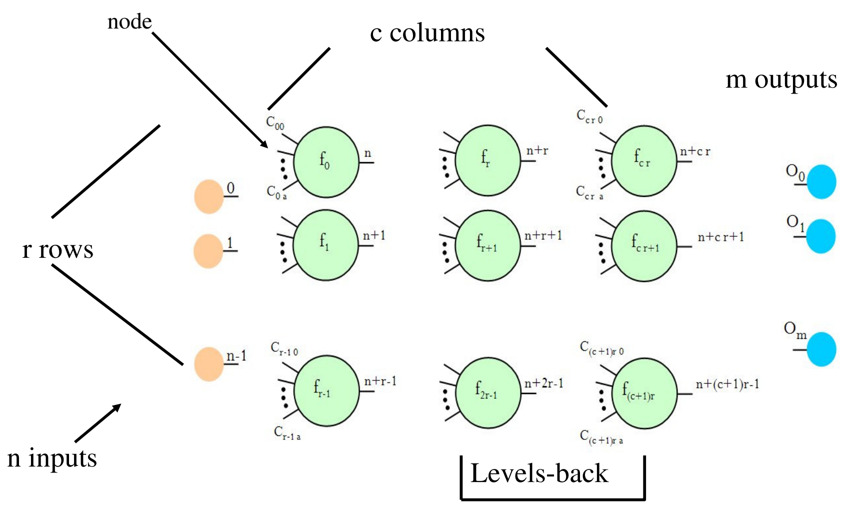
CGP General form



Note: Nodes in the same column are not allowed to be connected to each other

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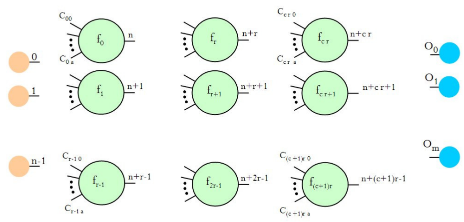
Allelic constraints for directed acyclic graphs



All function genes f_i must takes allowed function alleles

$$0 \le f_i \le n_f$$

Nodes connections C_{ij} of a node in column j, and levels-back *l*, must obey (to retain directed acyclicity)

$j \ge l$ $\quad n + (j-l)r \le C_{ij} \le n + jr$

$j < l$ $\quad 0 \le C_{ij} \le n + jr$

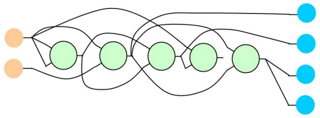
Output genes (can connect to any previous node or input)

$$0 \le 0_i \le n + cr - 1$$

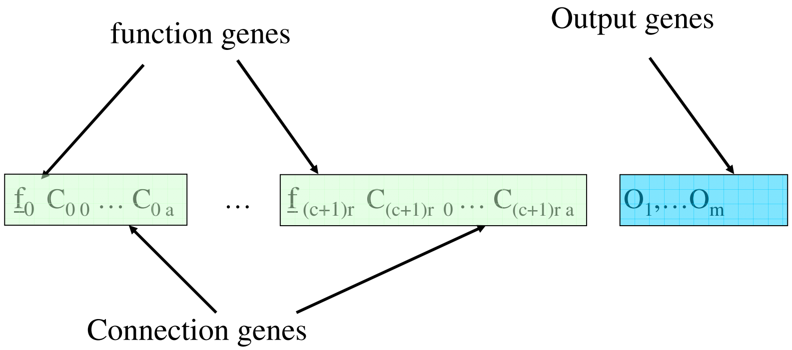
Types of graphs easily controlled

- Depending on *rows*, *columns* and *levels-back* a wide range of graphs can be generated

- When *rows* =1 and *levels-back* = *columns* *arbitrary* directed graphs can be created with a maximum depth
  - In general choosing these parameters imposes the least constraints. So without specialist knowledge this is the best and most general choice



CGP genotype



function genes

Output genes

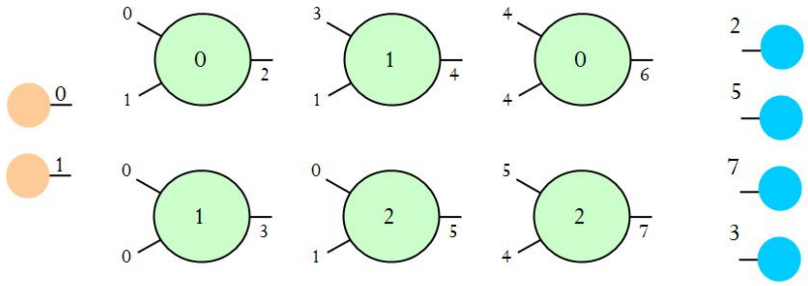
f_0 $C_{0\,0} \ldots C_{0\,a}$ … $f_{(c+1)r}$ $C_{(c+1)r\ 0} \cdots C_{(c+1)r\ a}$ $O_1,\ldots O_m$

Connection genes

Usually, all functions have as many inputs as the *maximum* function arity

Unused connections are ignored

Example



Encoding of graph as a list of integers (i.e. the genotype)

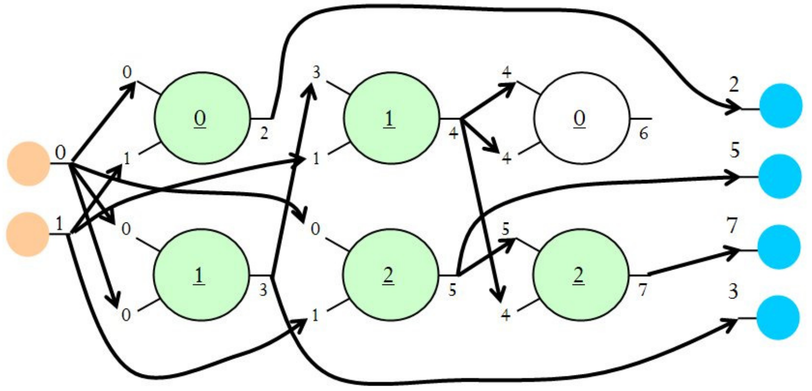
<u>0</u> 0 1 <u>1</u> 0 0 <u>1</u> 3 1 <u>2</u> 0 1 <u>0</u> 4 4 <u>2</u> 5 4 2 5 7 3

Example: Function look up table

The function genes are the *addresses* in a user-defined lookup table of functions

<u>0</u>	+ Add the data presented to inputs
<u>1</u>	- Subtract the data presented to inputs
<u>2</u>	* Multiply data presented to inputs
<u>3</u>	/ Divide data presented to inputs (protected)

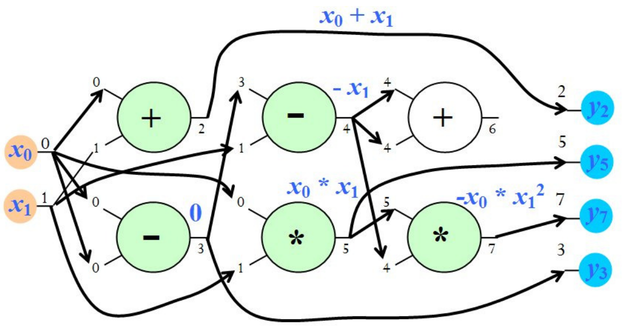
Obtaining the graph



Encoding of graph as a list of integers (i.e. the genotype)

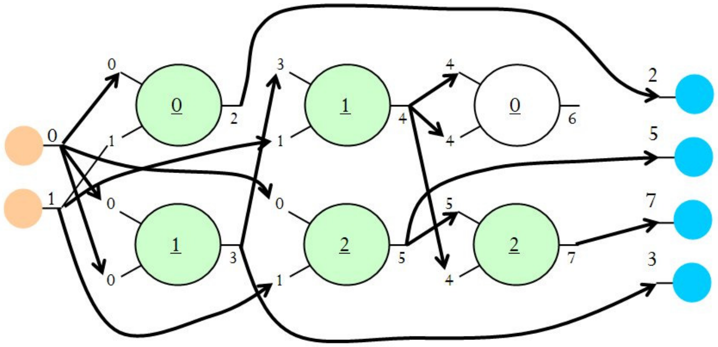
0 0 1   1 0 0   1 3 1   2 0 1   0 4 4   2 5 4   2 5 7 3

So what does the graph represent?



$$y_2 = x_0+x_1$$
$$y_5 = x_0*x_1$$
$$y_7 = -x_0*x_1^2$$
$$y_3 = 0$$

What happened to the node whose output label is 6?



The node was not used so the genes are *silent* or *non-coding*

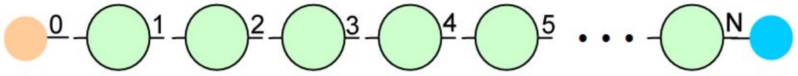
0 0 1   1 0 0   1 3 1   2 0 1   0 4 4   2 5 4   2 5 7 3

The CGP genotype-phenotype map

- When you decode a CGP genotype many nodes and their genes can be ignored because they are not referenced in the path from inputs to outputs
- These genes can be altered and make no difference to the *phenotype*, they are non-coding
- Clearly there is a many-to-one genotype to phenotype map
- How redundant is the mapping?

A mathematical aside: CGP and Stirling numbers

- Assume that a CGP graph has the following parameters
- Number of rows_= 1
- Levels-back = num_cols = *n*
- Arity of functions = 1
- There is one input
- Assume that the output is taken from the last node



The number of genotypes, *G*, that have a phenotype of size *k*(nodes) can be shown to obey a recurrence relation obeyed by *unsigned Stirling numbers of the first kind.*

$$G(n+1, k) = nG(n,k) + G(n, k-1)$$

How many genotypes of length n map to a phenotypes of length k?

n	*k*								
	1	2	3	4	5	6	7	8	9
1	1								
2	1	1							
3	2	3	1						
4	6	11	6	1					
5	24	50	35	10	1				
6	120	274	225	85	15	1			
7	720	1764	1624	735	175	21	1		
8	5040	13068	13132	6759	1960	322	28	1	
9	40320	109584	118124	67284	22449	4536	546	36	1

Average number of active nodes in a genotype of length 9 is 2.83

Clearly, with say a genotype of 100 nodes, the number of genotypes that map to a phenotype with say about 10 nodes is an astronomical number

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Decoding CGP chromosomes is easy

①
```
// L  = MaxGraph.Length
// I  = Number of program inputs
// N = Number of program outputs
bool          ToEvaluate[L]
double        NodeOutput[L+I]
```

②
```
// identify initial nodes that need to be evaluated
p = 0
do
   ToEvaluate[OutputGene[p]] = true
   p = p + 1
while (p < N)

// work out which nodes are used
p = L-1
do
   if (ToEvaluate[p])
      x = Node[p].Connection1
      y = Node[p].Connection2
     ToEvaluate[x] = true
     ToEvaluate[y] = true
   endif
   p = p - 1
while ( p >= 0)
```

③
```
// load input data values
p = 0
do
   NodeOutput[p] = InputData[p]
   p = p + 1
while (p < I)
```

④
```
//Execute graph
p = 0
do
   if (ToEvaluate[p])
      x = Node[p].Connection1
      y = Node[p].Connection2
      z = NodeFunction[p].Function
      NodeOutput[p+I] = ComputeNode(NodeOutput[x], NodeOutput[y],z)
  endif
  p = p + 1
while (p < L)
```

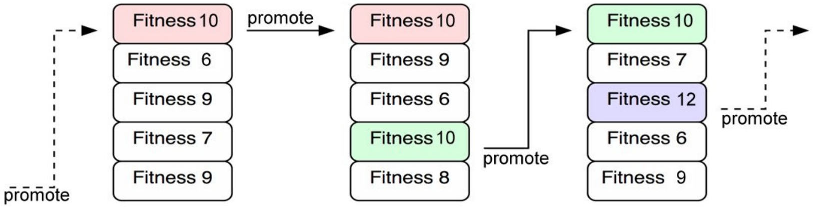
Point mutation

- Most CGP implementations only use mutation.
- Carrying out mutation is very simple. It consists of the following steps.

The genes must be chosen to be valid alleles

```
//Decide how many genes to change:num_mutations
while (mutation_counter < num_mutations)
{
            get gene to change
            if (gene is a function gene)
              change gene to randomly chosen new valid function
            else if (gene is a connection gene)
              change gene to a randomly chosen new valid connection
            else
              change gene to a new valid output connection
}
```

Evolutionary Strategy



- CGP often uses a variant of a simple algorithm called (1 + 4) Evolutionary Strategy
  - However, an offspring is always chosen if it *is equally as fit* or has better fitness than the parent

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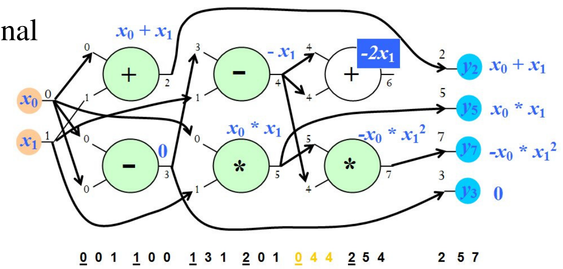
Crossover or not?

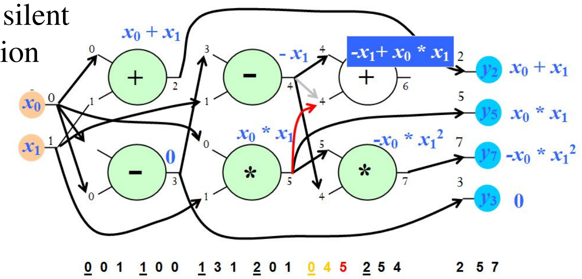
- Recombination doesn't seem to add anything *(Miller 1999, "An empirical study…")*
- However if there are multiple chromosomes with independent fitness assessment then it helps a LOT (*Walker, Miller, Cavill 2006, Walker, Völk, Smith, Miller, 2009)*
- Some work using a floating point representation of CGP has suggested that crossover might be useful (*Clegg, Walker, Miller 2007)*

Silent mutations and their effects

Original



After silent mutation



No change in phenotype but it changes the programs *accessible* through *subsequent* mutational change

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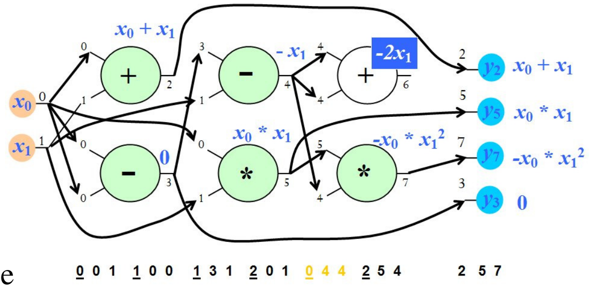
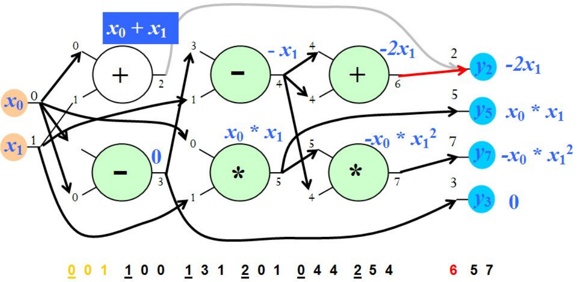
Non-silent mutations and their effects

Original



After active mutation

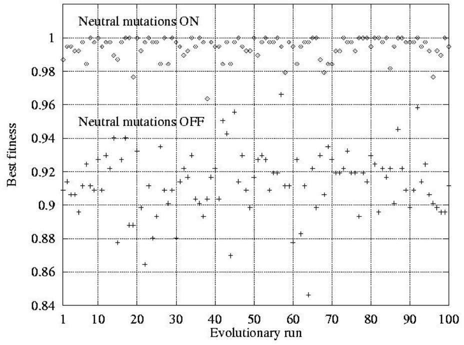


Massive change in phenotype is possible through simple mutation

Neutral search is fundamental to success of CGP

- A number of studies have been carried out to indicate the importance to neutral search
  - *Miller and Thomson 2000, Vassilev and Miller 2000, Yu and Miller 2001, Miller and Smith 2006*)

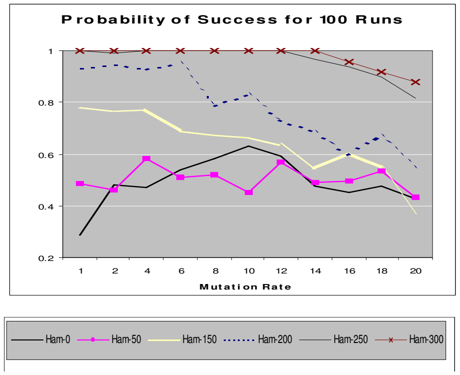
Neutral search and the three bit multiplier problem (Vassilev and Miller 2000)



Importance of neutral search can be demonstrated by looking at the success rate in evolving a correct three-bit digital parallel multiplier circuit.

Graph shows final fitness obtained in each of 100 runs of 10 million generations with neutral mutations enabled compared with disabling neutral mutations.

Effectiveness of Neutral Search as a function of mutation rate and Hamming bound (Yu and Miller 2001)

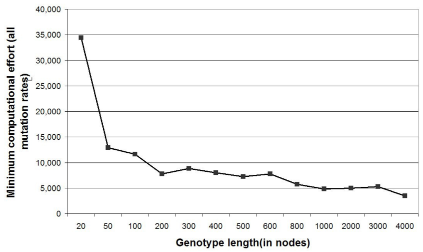


- Hamming Distance H(g,h)
  g1=213 012 130 432 159
  g2=202 033 132 502 652
  hamming distance H(g1,g2)=9.
- If genotypes are selected so that $H(g_{new},g_{old}) = 0$. No neutral drift is permitted.
- If genotypes are selected so that $H(g_{new},g_{old}) = \text{length}(g)$. Any amount of neutral drift is permitted.

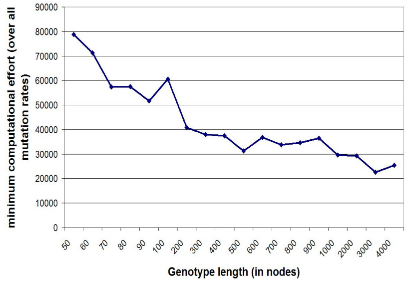
In CGP, large genotypes and small mutation evolve solutions to problems more quickly [Miller and Smith 2006]

Even 3 parity with gate set

{AND, OR, NAND, NOR}.

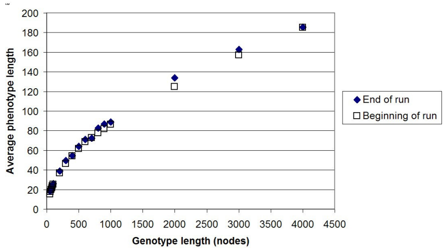


Two-bit multiplier with gate set



•However big genotypes does NOT mean big phenotypes (programs)….

Phenotype length versus genotype length (two-bit multiplier)

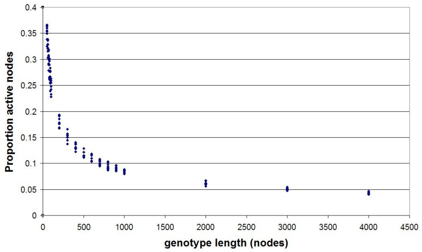


Average phenotype length for the initial population contrasted with the average phenotype length at conclusion of evolutionary run versus genotype length with 1% mutation

NO BLOAT

Average proportion of active nodes in genotype at the conclusion of evolutionary run for all mutation rates versus genotype length

SEARCH MOST EFFECTIVE WHEN 95% OF ALL GENES ARE INACTIVE!!

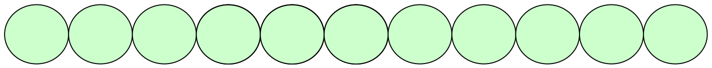


Modular/Embedded CGP (Walker, Miller 2004)

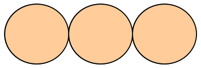
- So far have described a form of CGP (classic) that does not have an equivalent of Automatically Defined Functions (ADFs)
- Modular CGP allows the use of modules (ADFs)
  - Modules are dynamically created and destroyed
  - Modules can be evolved
  - Modules can be re-used

MCGP Example

Genotype

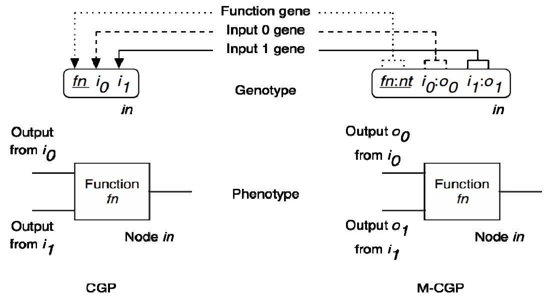


Module List



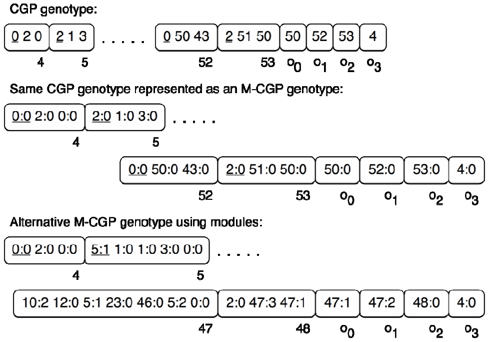
Module Creation

Representation Modification 1



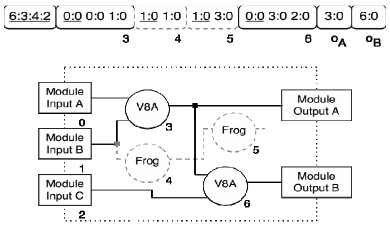
- Each gene encoded by *two* integers in M-CGP
  - Function/module number and node type
  - Node index and node output
    - nodes can have multiple outputs

Representation Modification 2



- M-CGP has a bounded variable length genotype
  - Compression and expansion of modules
    - Increases/decreases the number of nodes
  - Varying number of module inputs
    - Increases/decreases the number of genes in a node

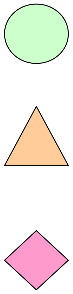
Modules



- Same characteristics as M-CGP
  - Bounded variable length genotype
  - Bounded variable length phenotype
- Modules also contain inactive genes as in CGP
- Modules can not contain other modules!

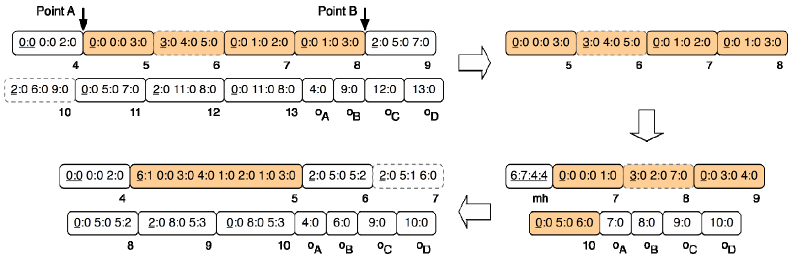
Node Types

- Three node types:
  - Type 0
    - Primitive function
  - Type I
    - Module created by compress operator
  - Type II
    - Module replicated by genotype point-mutation



- Control excessive code growth
  - Genotype can return to original length at any time

Creating and Destroying a Module



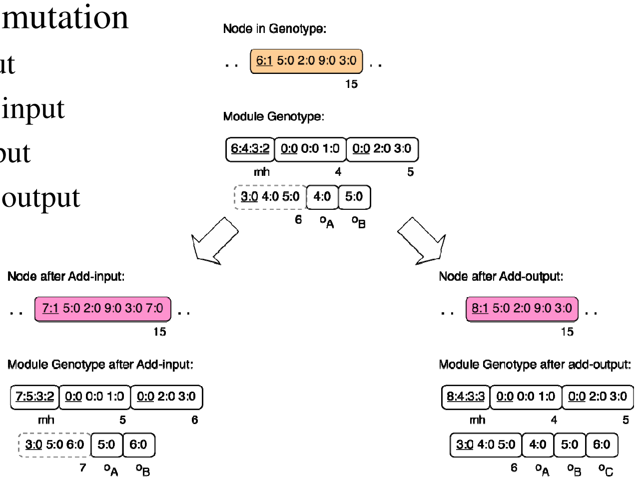
- Created by the compress operator
  - Randomly acquires sections of the genotype into a module
    - Sections must ONLY contain type 0 nodes
- Destroyed by the expand operator
  - Converts a random type I module back into a section of the genotype

Module Survival

- Twice the probability of a module being destroyed than created
- Modules have to replicate to improve their chance of survival
  - Lower probability of being removed
- Modules must also be associated with a high fitness genotype in order to survive
  - Offspring inherit the modules of the fittest parent

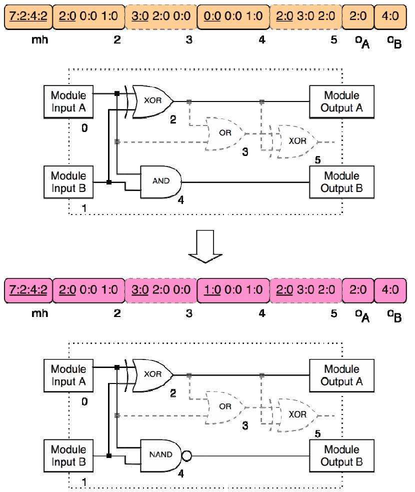
Evolving a Module I

- Structural mutation
  - Add input
  - Remove input
  - Add output
  - Remove output



Evolving a Module II

- Module point-mutation operator
  - Restricted version of genotype point-mutation operator
  - Only uses primitive functions



Re-using a Module

- Genotype point-mutation operator
  - Modified CGP point-mutation operator
- Allows modules to replicate in the genotype
  - Primitive (type 0) → module (type II)
  - Module (type II) → module (type II)
  - Module (type II) → primitive (type 0)
- Does NOT allow type I modules to be mutated into primitives (type 0) or other modules (type II)
  - Type I modules can only be destroyed by Expand

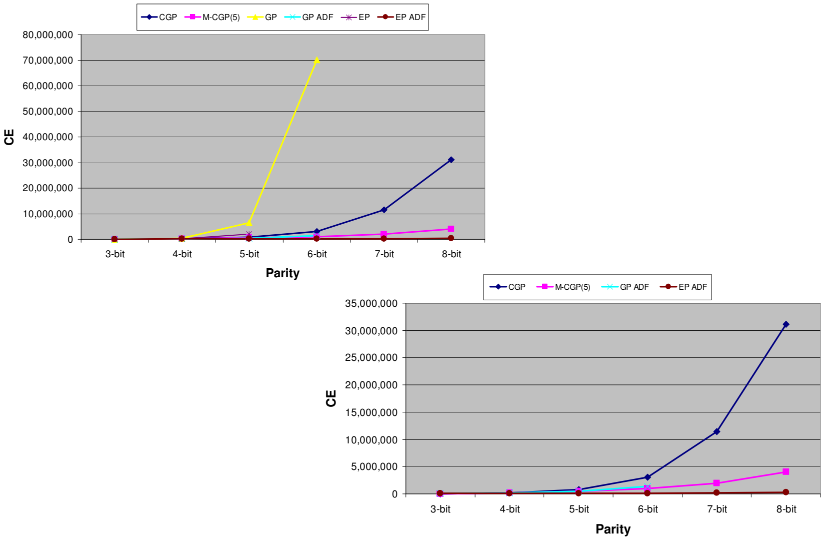
Experimental parameters

Parameter	Value
Population size	5
Initial genotype size	100 nodes (300 genes)
Genotype point mutation rate	3% (9 genes)
Genotype point mutation probability	1
Compress/Expand probability ◊	0.1/0.2
Module point mutation probability ◊	0.04
Add/Remove input probability ◊	0.01/0.02
Add/Remove output probability ◊	0.01/0.02
Module list initial contents ◊	Empty
Number of independent runs	50

NOTES: ◊ these parameters only apply to Modular (Embedded) CGP

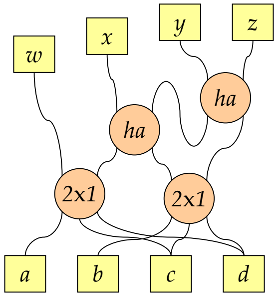
The results are heavily dependent on the maximum number of nodes allowed. Much better results are obtained when larger genotype lengths are used.

Even Parity Results

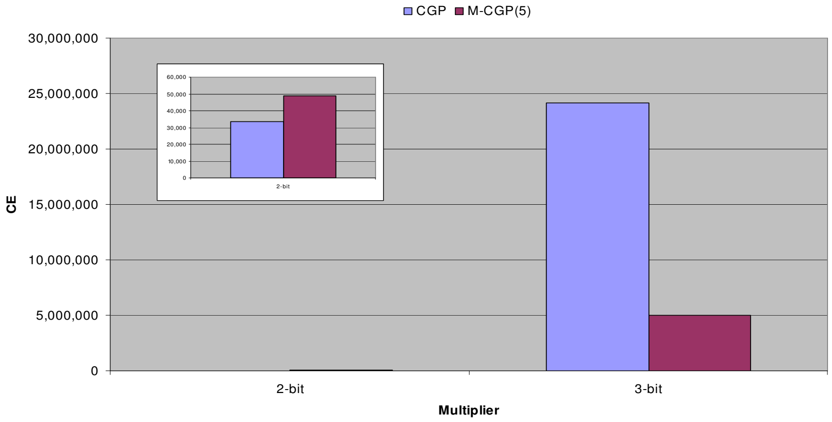


Digital Multiplier

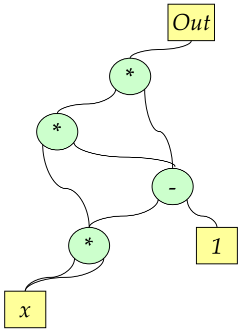
- Two digital multiplier problems:
  - 2-bit and 3-bit
- Function set:
  - AND, AND (one input inverted), XOR, OR
- Fitness Function:
  - Number of phenotype output bits that differ from the perfect *n*-bit digital multiplier solution
  - Perfect solution has a fitness of zero
- Results are averaged over fifty independent runs



Multiplier Results

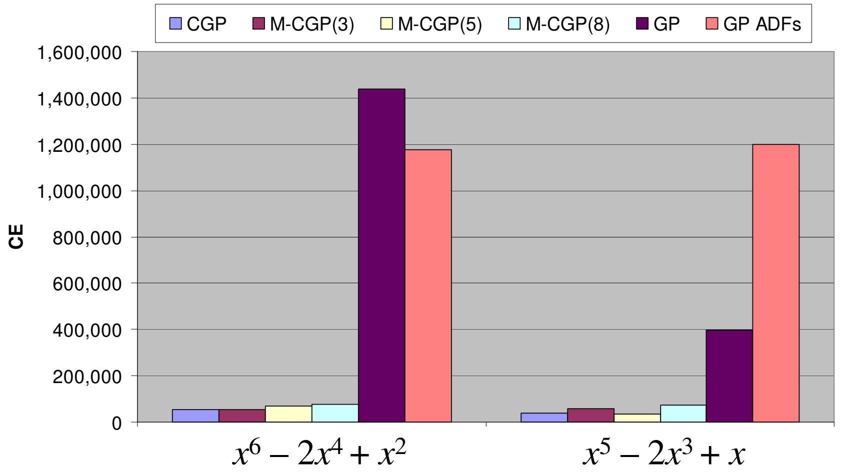


Symbolic Regression



- Two problems:
  - $x^6 - 2x^4 + x^2$
  - $x^5 - 2x^3 + x$
- Function set:
  - +, -, *, / (protected)
- Fitness Function:
  - Absolute error over all fifty points in the input set
  - Solution found when absolute error is within 0.01 of each point
- Results averaged over fifty independent runs

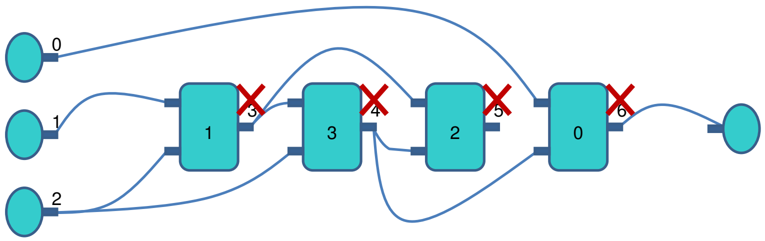
Symbolic Regression Results



Self-modifying Cartesian Genetic programming

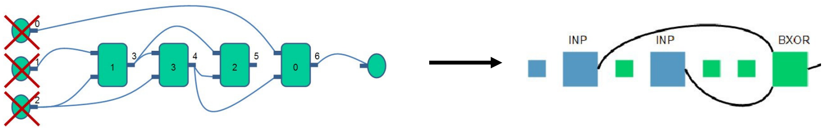
- A developmental form of Cartesian Genetic Programming (CGP)
  - Includes self modification functions.
  - ‘General purpose’ GP system
  - Phenotype can vary over time (with iteration)
  - Can switch off its own self-modification

Changes to CGP: relative addressing



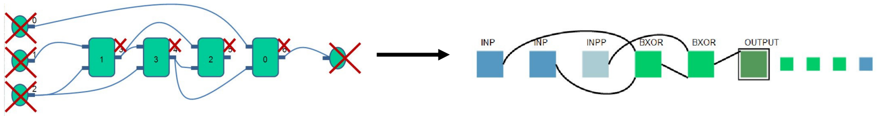
- Replaced direct node addressing with relative addressing
  - Always use 1 row (not rectangular)
  - Connection genes say how many nodes back

Changes to CGP: Inputs



- ❖Replace input calls with a function.
  - We call these functions INP, INPP, SKIPINP
- ❖Pointer keeps track of 'current input'.
  - Call to INP returns the current input, and moves the pointer to the next input.
- ❖Connections beyond graph are assigned value 0.

Changes to CGP: Outputs



- ❖Removed output nodes.
- ❖Genotype specifies which nodes are outputs.
- ❖If no OUTPUT function then last active node is used
  - Other defaults are used in situations where the number of outputs does not match the number required

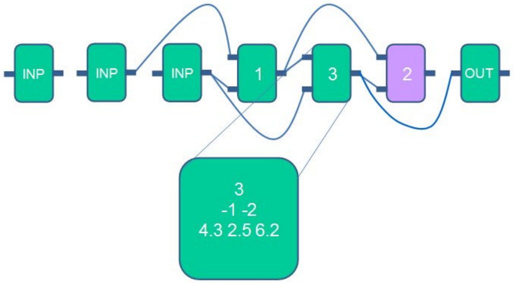
---

Changes to CGP: Arguments

- ❖Nodes also contain a number of 'arguments'.
  - 3 floating point numbers
  - Used in various self-modification instructions
  - Cast to integers when required

SMCGP Nodes: summary

- ❖Each node contains:
  - Function type
  - Connections as relative addresses
  - 3 floating point numbers



SMCGP: Functions

- Two types of functions:
  - Computational
    - Usual GP computational functions
  - Self-modifying
    - Passive computational role (see later)

Some Self-Modification Functions

Operator	Parameters: use node address and the three node arguments	Function
MOVE	Start, End, Insert	Moves each of the nodes between Start and End into the position specified by Insert
DUP	Start, End, Insert	Inserts copies of the nodes between Start and End into the position specified by Insert
DELETE	Start, End	Deletes the nodes between Start and End indexes
CHF	Node, New Function	Changes the function of a specified node to the specified function
CHC	Node, Connection1, Connection2	Changes the connections in the specified node

---

SMCGP Execution

- Important first step:
  - Genotype is duplicated to phenotype.
  - Phenotypes are executed:
    - Self modifications are only made to the phenotype.

Self Modification Process: The To Do list

- Programs are iterated.
- If triggered, self modification instruction is added to a To Do list.
- At the end of each iteration, the instructions on this list are processed.
- The maximum size of the To Do list can be predetermined

Computation of a SM node

- ❖Functions are appended to the To Do list if:
  - The first input > the second input.
- ❖And:
  - The To Do list isn't too big.

Publications using SMCGP

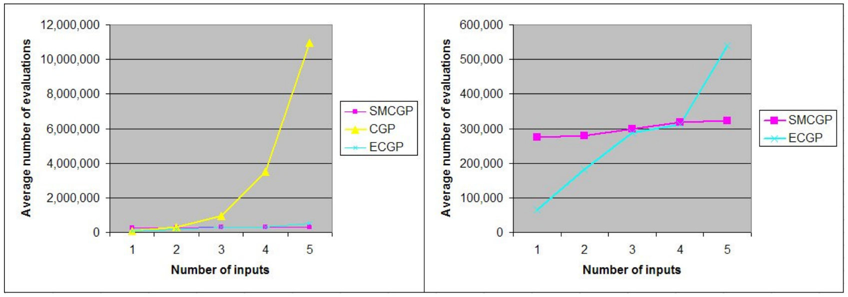
- ❖General Parity Problem (CEC 2009)
- ❖Mathematical Problems (EuroGP 2009, GECCO 2007)
- ❖Learning to Learn (GECCO 2009)
- ❖Generating Arbitrary Sequences (GECCO 2007)
- ❖Computing the mathematical constants pi and e (GECCO 2010 in GDS track)
- ❖General adder and many other problems (GPEM Tenth Anniversary Special Issue, 2010)

Authors: Harding, Miller, Banzhaf

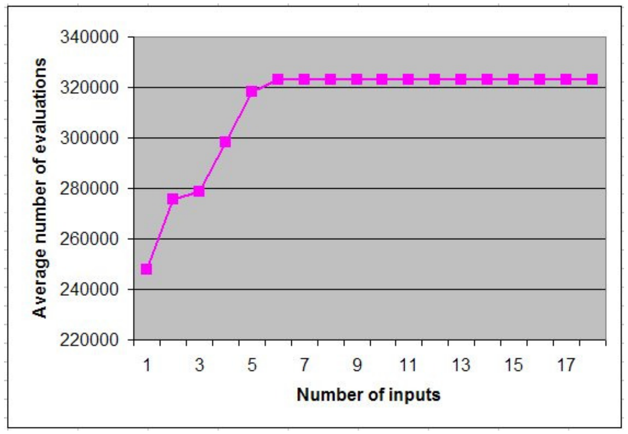
Evolving Parity

- ❖Each iteration of program should produce the next parity circuit.
  - On the first iteration the program has to solve 2 bit parity. On the next iteration, 3 bit ... up to 22 parity
  - Fitness is the cumulative sum of incorrect bits
- ❖Aim to find general solution
- ❖CGP or GP cannot solve this problem as they have a finite set of inputs (terminals)

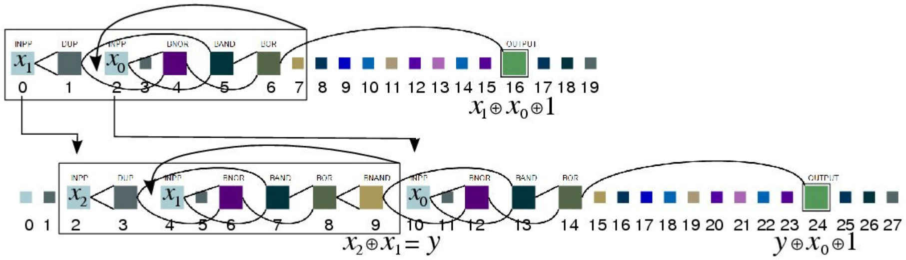
Parity results: SMCGP versus CGP and ECGP



Scaling behaviour of SMCGP



A evolved general solution to parity



Evolving pi

- Iterate a maximum of 10 times
- If program output does not get closer to pi at the next iteration, the program is stopped and large fitness penalty applied
- Fitness at iteration, *i*, is absolute difference of output at iteration *i* and pi
- One input: the numeric constant 1.

Evolving pi: an evolved solution

- An evolved solution

$$f(i) = \begin{cases} cos(sin(cos(sin(0)))) & i = 0 \\ f(i-1) + sin(f(i-1)) & i > 0 \end{cases}$$

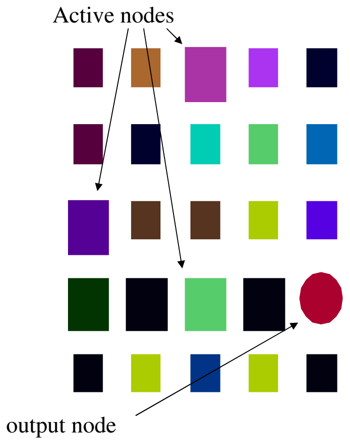
- f(10) is correct to the first 2048 digits of pi
- It can be proved that *f*(*i*) rapidly converges to pi in the limit as *i* tends to infinity

Further results

- Mathematically provable results found so far:
  - Evolved a program that can carry out the bitwise addition of an arbitrary number of inputs
  - Evolved a sequence that converges to e
- Other results
  - Evolved a sequence function that generates the first 10 Fibonacci numbers
  - Evolved a power function x^n
  - Bioinformatics classification problem (finite inputs)
    - – SMCGP performed no worse than CGP

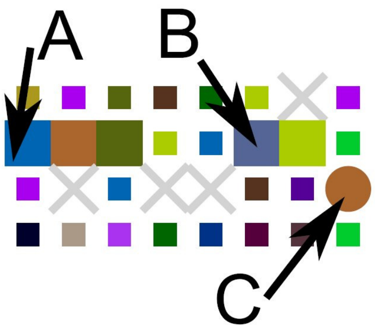
Two dimensional SMCGP (SMCGP2)

- Recently a two-dimensional version of SMCGP has been devised (see GDS and poster tracks at this conference)
- SMCGP2: genes
  - Function
  - Connections
  - Numeric Constant
- Arguments are now 2 D vectors
  - SM size (SMS)
  - SM location (SML)



SMCGP2: Vector relative addressing and Empty nodes

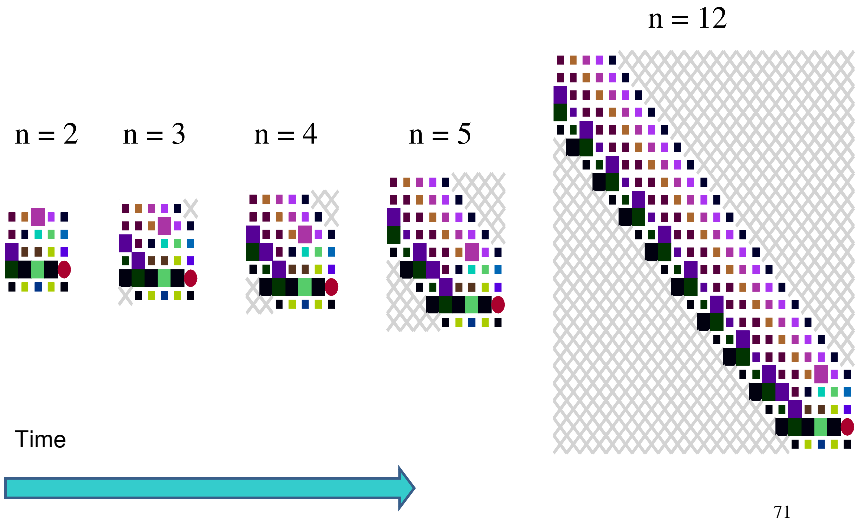
- There are **empty nodes** are represented by X (see later)
- The relative address from C to B is (2, 1)
  - meaning 2 nodes to the left, and one node up.
- The relative address of C to A is (4,1).
- Note how the empty nodes are not counted when computing how many nodes back to connect.



SMCGP2: Self Modifying Functions

- Simplified SM function set
  - Duplicate section, insert elsewhere.
  - Duplicate section, overwrite elsewhere.
  - Crop to a section.
  - Delete a section.
  - Add a row or column.
  - Delete a row or column.
  - NULL
- E.g. overwrite function (‘OVR’), the nodes that are copied and overwritten are found by adding the location address of the calling node (NL) to the SM Location (SML). The size argument (SMS) determines the dimensions of the area to be copied and overwritten.
- Nodes (SML+NL) to (SML+NL+SMS) are overwritten at (SML+NL)

SMCGP2: Solving even-n parity



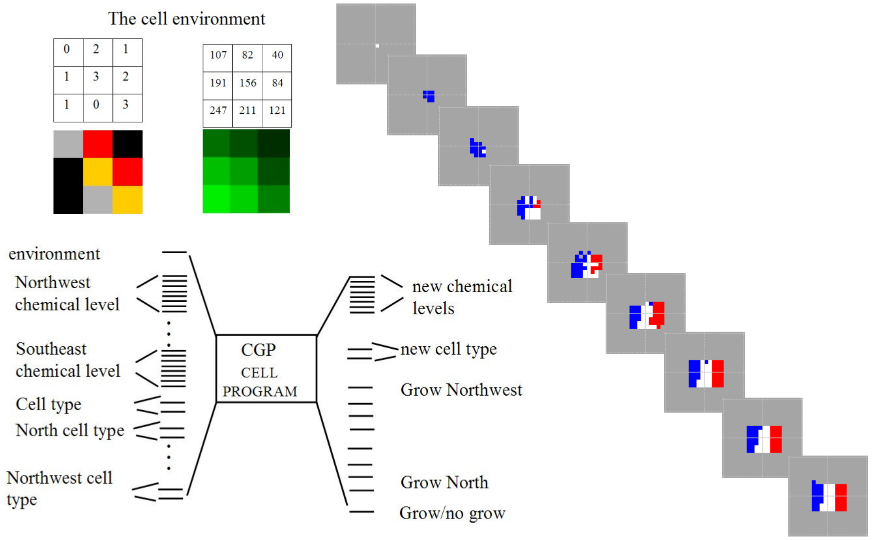
SMCGP:Some observations

- In SMCGP there are implicit
  - Loops
  - Recursion
  - Modules/functions
  - Halting (telomeres)
- Also have “partial” loops/recursion

Other Developmental CGP

- Various types of CGP inspired by biological development, graph re-writing and neuro-development have been devised
  - Cellular developmental (*Miller 2003, 2004*)
  - Graph re-writing (*Miller 2003*)
  - Neuro-developmental (*Khan, Miller and Halliday 2007, Khan and Miller 2008, Khan and Miller 2009, Khan and Miller 2010*)

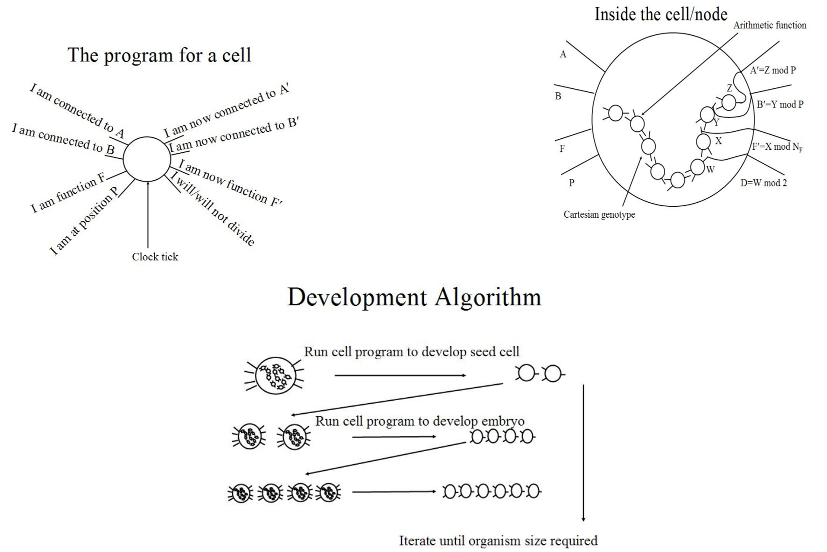
Bio-inspired developmental CGP


The cell environment

0	2	1
1	3	2
1	0	3

107	82	40
191	156	84
247	211	121

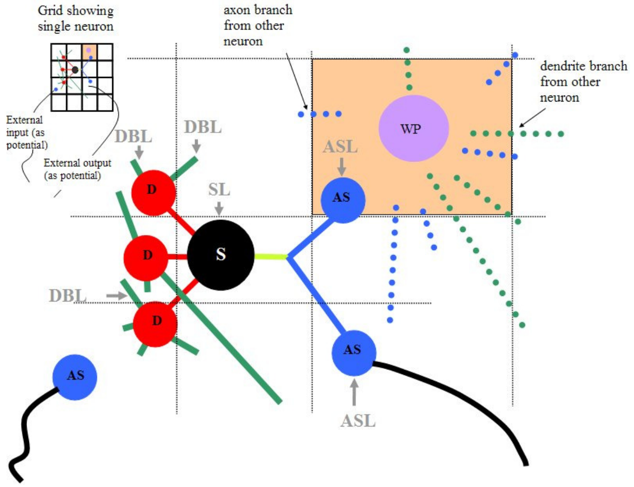
Graph re-writing CGP



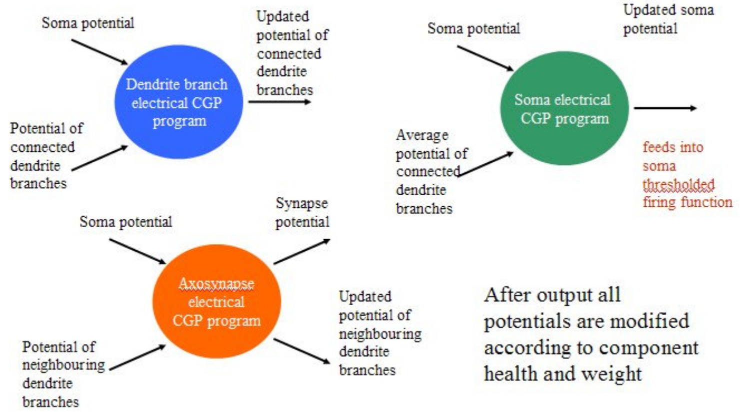
Neuro-inspired developmental CGP

- Real neurons are immensely complex
- Like other cells, they replicate and change
- They also have complex electrical behaviour and communicate with each other
- Most learning occurs through morphological changes (new neurons, dendritic, axonal growth and new synapses)
- In neuro-inspired developmental CGP a neuron has been represented by seven CGP chromosomes
    - Applied to wumpus world, checkers, maze solving

Neuro-inspired developmental CGP



Three 'electrical' CGP chromosomes


Soma potential

Potential of connected dendrite branches

Dendrite branch electrical CGP program

Updated potential of connected dendrite branches

Soma potential

Average potential of connected dendrite branches

Soma electrical CGP program

Updated soma potential

feeds into soma thresholded firing function

Soma potential

Potential of neighbouring dendrite branches

Axosynapse electrical CGP program

Synapse potential

Updated potential of neighbouring dendrite branches

After output all potentials are modified according to component health and weight

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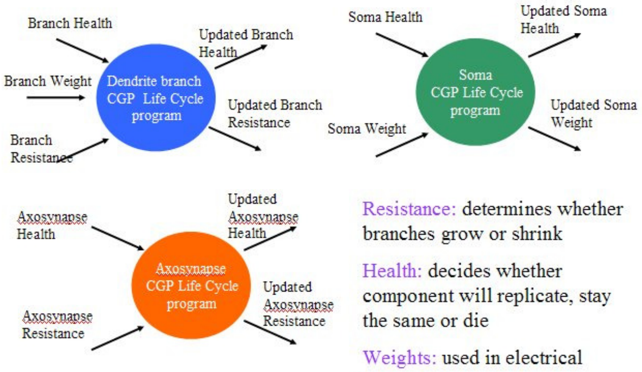
Three developmental CGP chromosomes



Resistance: determines whether branches grow or shrink

Health: decides whether component will replicate, stay the same or die

Weights: used in electrical programs

One weight adjustment chromosome

CGP encoded Artificial Neural Networks (CGPANN)

- CGP has been used to encode both feed-forward ANNs and recursive ANNs. The nodes genes consist of:
- Connection genes (as usual)
- Function genes (two)
  - Sigmoid, hyperbolic tangent
- Weights
  - Each connection gene carries a real-numbered weight
- Switch genes
  - Binary genes that switch off or on the connection
- Applied to markovian and non-markovian single and double pole –balancing problems
  - Shown to outperform all previously published topology and weights altering evolutionary ANNS (TWEANNs) (*Khan, Khan and Miller 2010*)

Cyclic CGP

- When outputs are allowed to connect to inputs through a clocked delay (flip-flop) it is possible to allow CGP to include feedback.
- By feeding back outputs generated by CGP to an input, it is possible to get CGP to generate sequences
  - In this way iteration is possible
- There are a couple of recent publications using recursion or iteration in CGP (*Khan, Khan and Miller 2010, Walker, Liu, Tempesti,Tyrrell*)

Applications of CGP

- Digital Circuit Design
  - ALU, parallel multipliers, digital filters, analogue circuits
- Mathematical functions
  - Prime generating polynomials
- Control systems
  - Maintaining control with faulty sensors, helicopter control, general control, simulated robot controller
- Image processing
  - Image filters
  - Mammary Tumour classification
- Bio-informatics
  - Molecular Post-docking filters
- Artificial Neural Networks
- Developmental Neural Architectures
  - Wumpus world, checkers, maze solving
- Evolutionary Art
- Artificial Life
  - Regenerating ‘organisms’
- Optimization problems
  - Applying CGP to solve GA problems

CGP Resources

- Home site:

  http://www.cartesiangp.co.uk
- Julian Miller: C implementations of CGP and SMCGP available at

  https://sites.google.com/site/julianfrancismiller/professional
- Simon Harding

  http://www.cs.mun.ca/~simonh/
- David Oranchak has implemented CGP in Java. Documentation is available at

  http://oranchak.com/cgp/doc/
- Book is available now, published by Springer

Conclusions

- Cartesian Genetic Programming is a graph based GP method
- Genetic encoding is compact, simple and easy to implement and can handle multiple outputs easily.
- The unique form of genetic redundancy in CGP makes mutational search highly effective
- The effectiveness of CGP has been compared with many other GP methods and it is very competitive

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