

THE UNIVERSITY *of York*



Cartesian Genetic Programming encoded Artificial Neural Networks: A Comparison using Three Benchmarks

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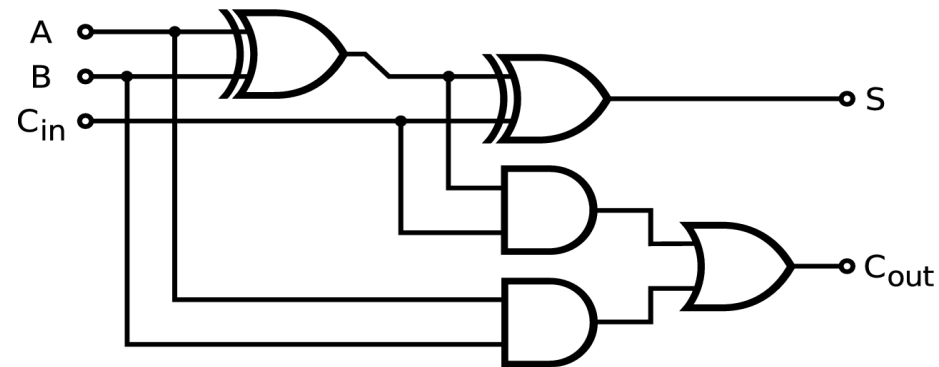


First Implemented by J. F. Miller & P. Thomson, 2000

Web page: <http://www.cartesiangp.co.uk/>

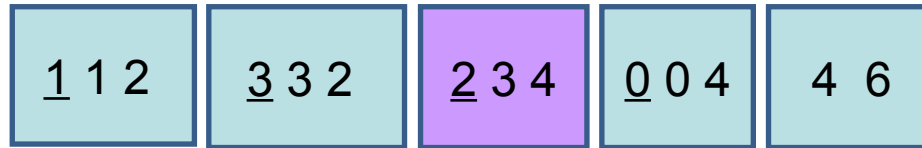
Key Points

- Form of Genetic Programming
- Cyclic and acyclic graphs
- Any data type e.g. ints, floats, images, videos ...
- Any function e.g. XOR, sigmoidal, sin ...
- Inbuilt neutrality and genetic drift (Miller et al, 2006)
- Natural resilience to bloat (Miller, 2001)
- Typically uses a (1+4)-ES
- Mutation only (no crossover)
- Not just for circuits



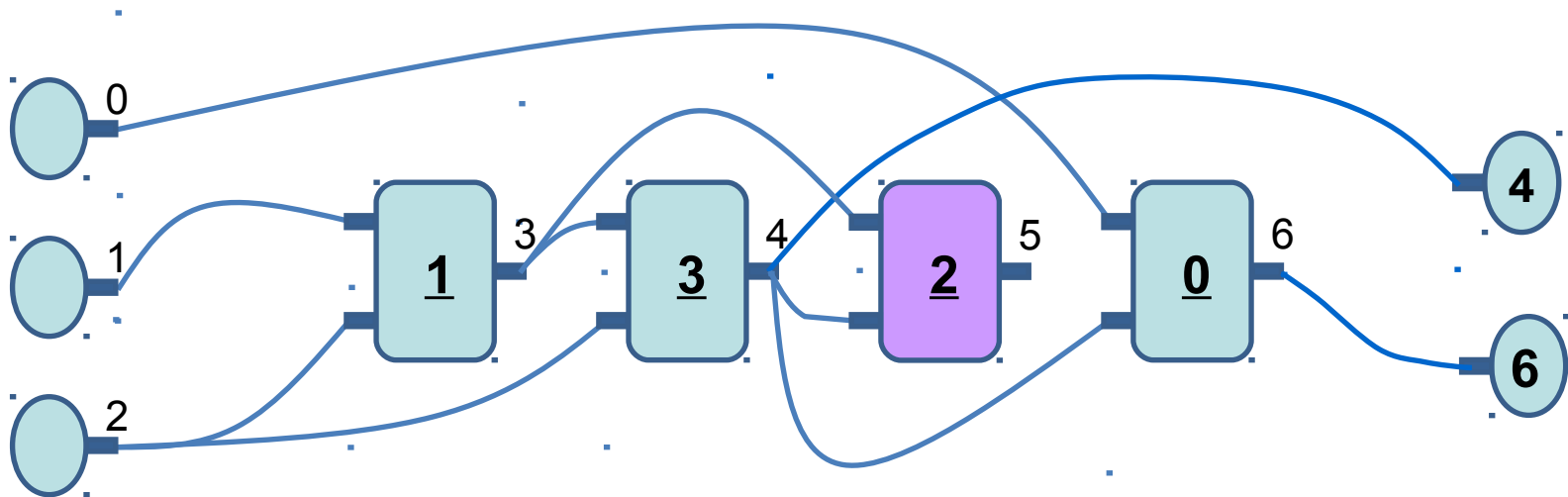


Genotype



One row, four columns

Phenotype





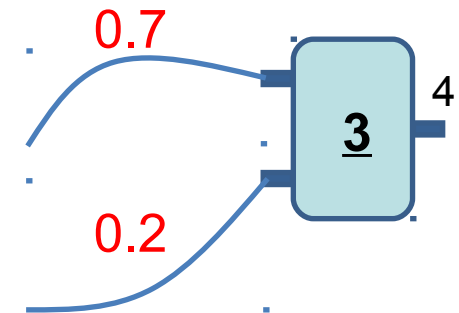
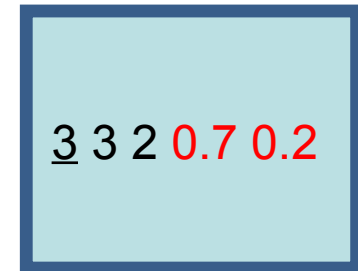
First published by Maryam. M. Khan et al, 2010

Minor changes to CGP to encode Neural Networks

- F Function i.e. sigmoid, radial basis...
- C Unchanged
- W Connection Weight
- Inputs Unchanged
- Outputs Unchanged

CGPANN Features

- Evolves Weights
- Evolves Number of Neuron
- Evolves Topology
- Evolves Arity of Neurons (indirectly)
- Evolves Functions
- All of the advantages of CGP





Weight Evolution

- Does not require differentiable neuron functions
- Does not require a precise fitness function
- Does not struggle to train deep topologies
- Searches weight space

Topology Evolution

- Does not require a suitable topology to be known in advance
- Produces topologies which would not usually be considered
- Searches topology space

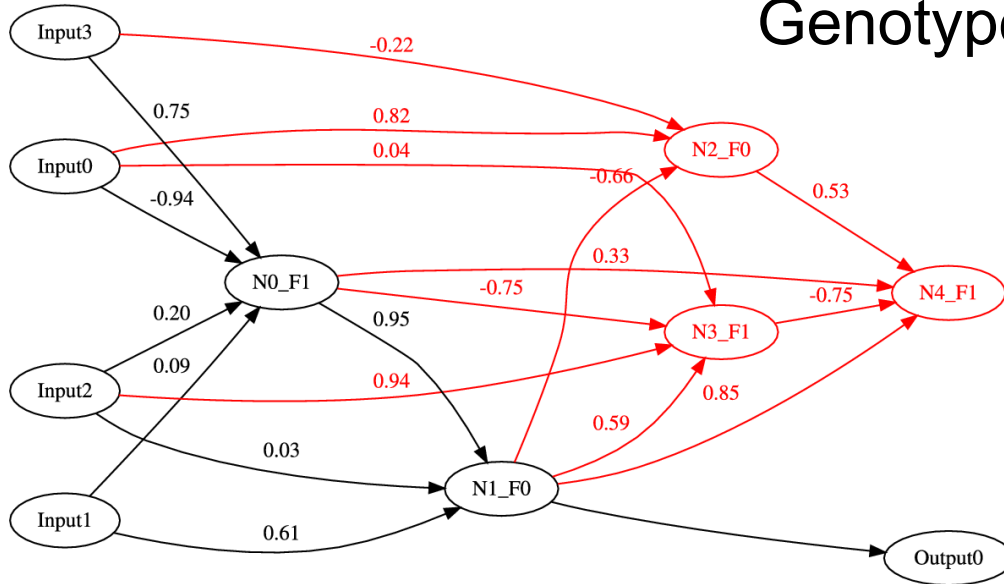
Node Transfer Evolution

- Does not require suitable node functions to be known in advance
- Can easily use a mix of node functions
- Searches function space

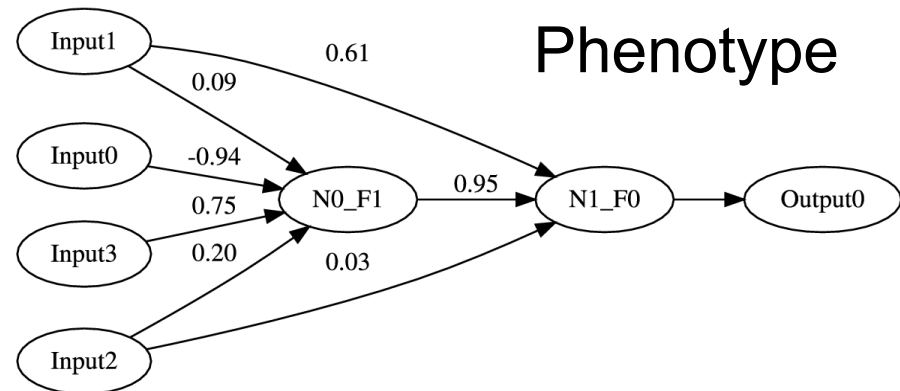


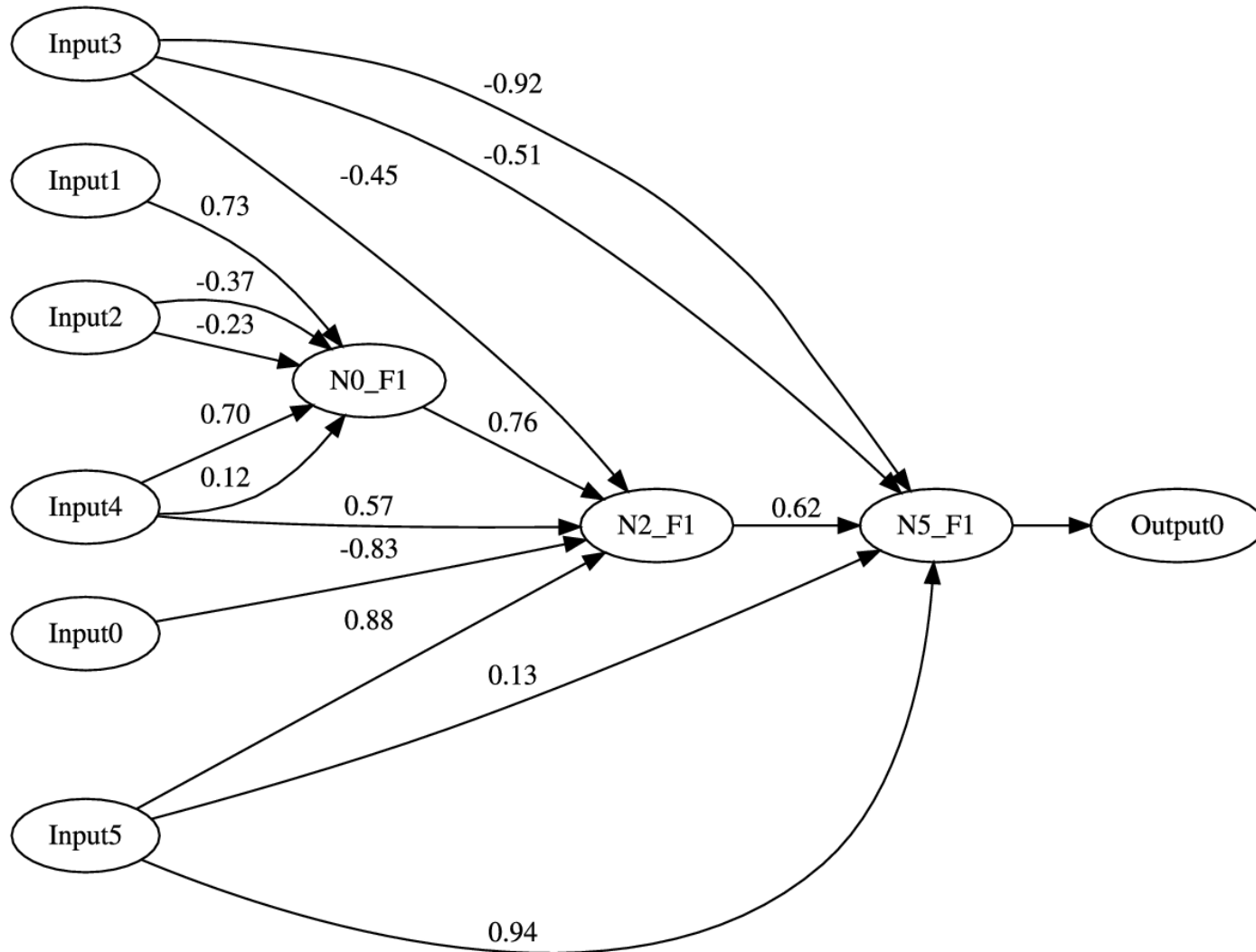
- Inactive Nodes
- Active Nodes

Genotype



Phenotype

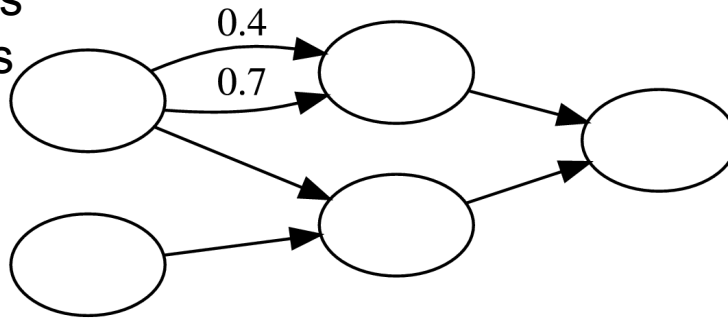




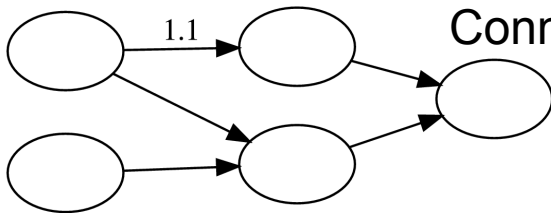


Multiple Connections

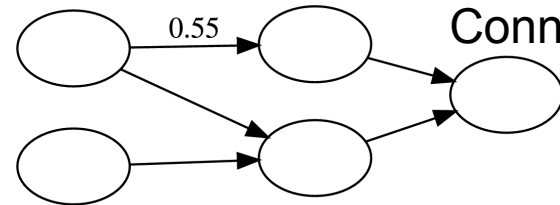
Multiple Connections
between two nodes



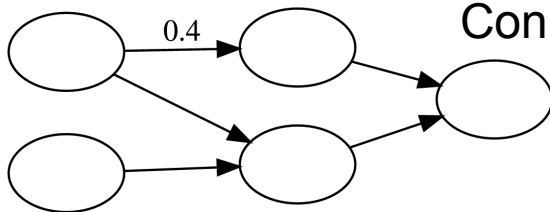
Allow Multiple
Connections



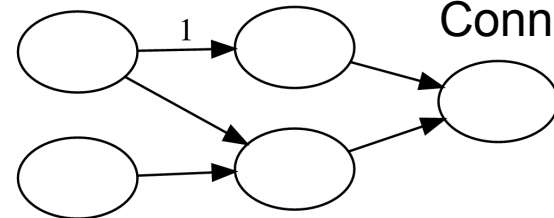
Average
Connections



Only use first
Connection



Cap
Connection





Benchmarks

- Double Pole Balancing
- Ball Throwing
- Proben1: Cancer1

Parameters

- (1+4)-ES
- Uniform Mutation
- No Crossover
- Only Bipolar or Unipolar Sigmoid
- Allowed multiple connections between nodes

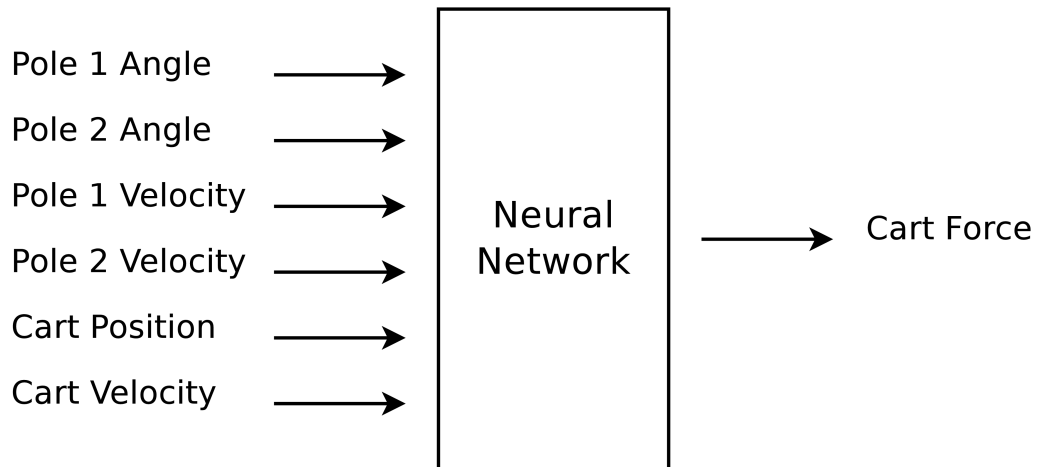
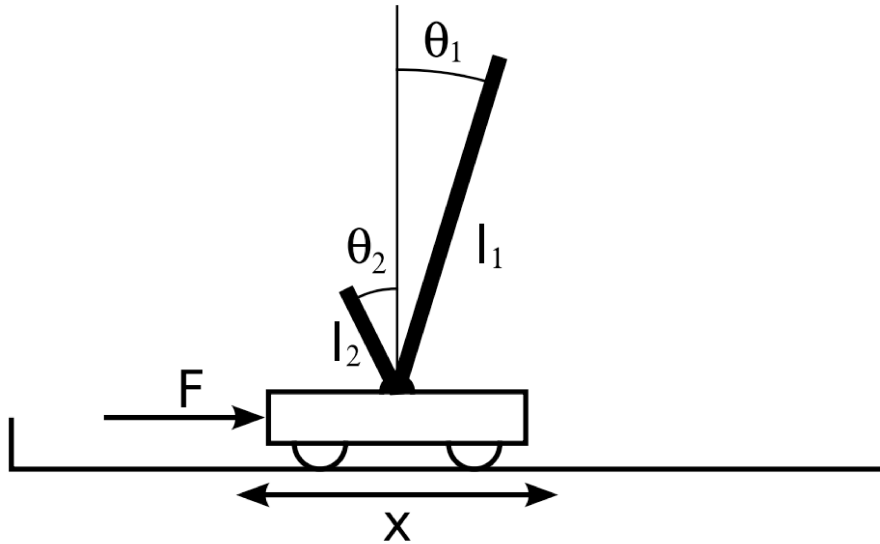
Comparison

- Can only use averages
- Data not available for statical significance tests

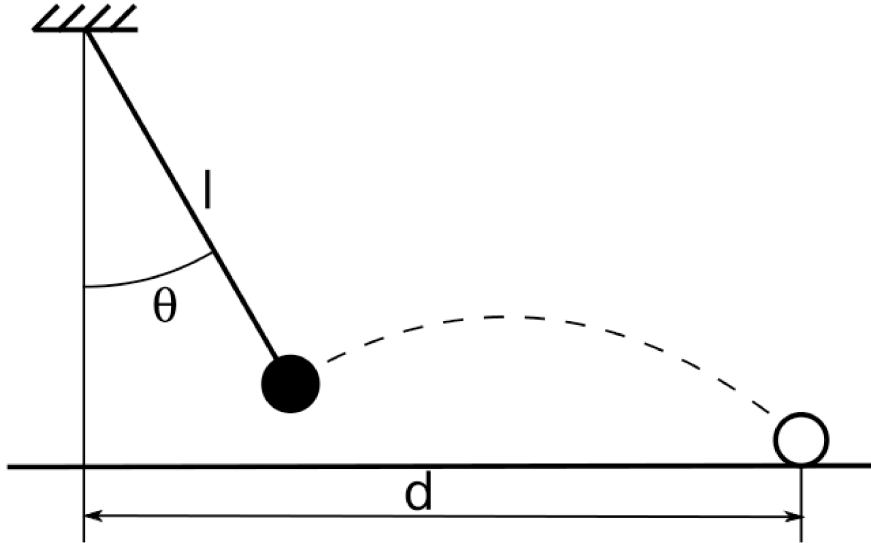




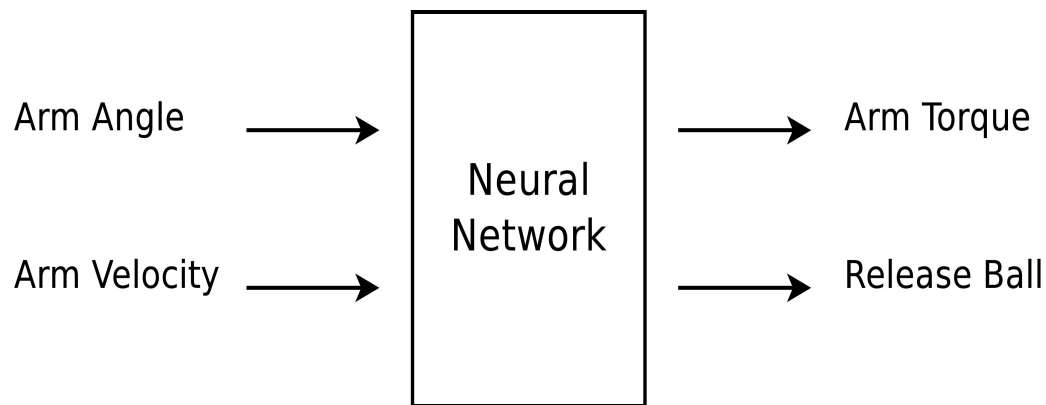
Double Pole Balancing

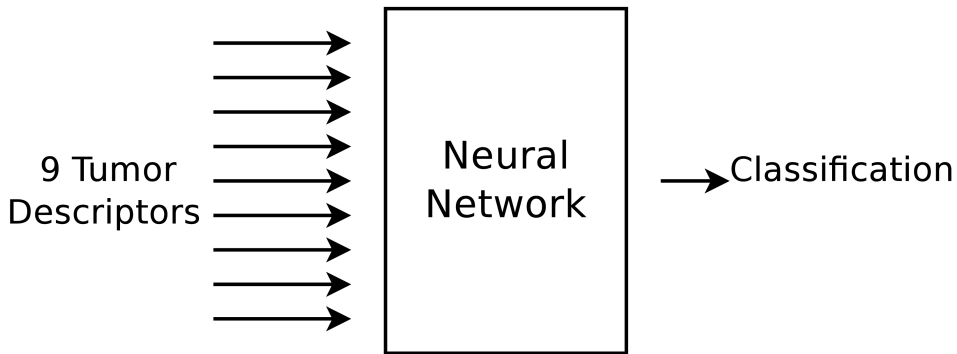


Method	Evaluations
DirE	410
CMA-ES	859
CoSyNE	954
CGPANN	1111
NEvA	2177
NEAT	3578
ESP	3800
Q-MPL	10583
SAIN	12600
EuSAIN	~19000
CNE	22100
CE	34000
EP	307200



Method	Evaluations
CGPANN	6069
Compressed CoSyNE	8220
CoSyNE	10224





Data from University of Wisconsin Hospital
(O. Mangasarian et al, 1990)

Following the Proben1 Document
(L. Prechelt, 1994)

Method	Train Err %	Test Err %
MFN	-	1.38
M-RAN	-	1.72
CGPANN	2.68	1.89
GA-MOO-ANN	-	1.9
MFNNCA	24.86	2
ACS	-	2.184
BP	-	3.506
CMAC ANN	0.59	3.94

**Overall:**

CGPANN is a highly competitive NeuroEvolutionary strategy which assumes very little about the structure of the neural network to be evolved.

Take Home Message:

CGPANN directly evolves the weights, number of nodes, topology, and nodes function of artificial neural networks. CGPANN also indirectly evolves the arity of each node. Additionally CGPANN has all of the benefits of CGP; natural resilience to bloat and neutrality in the genotype aiding evolution through genetic drift.



Questions

