

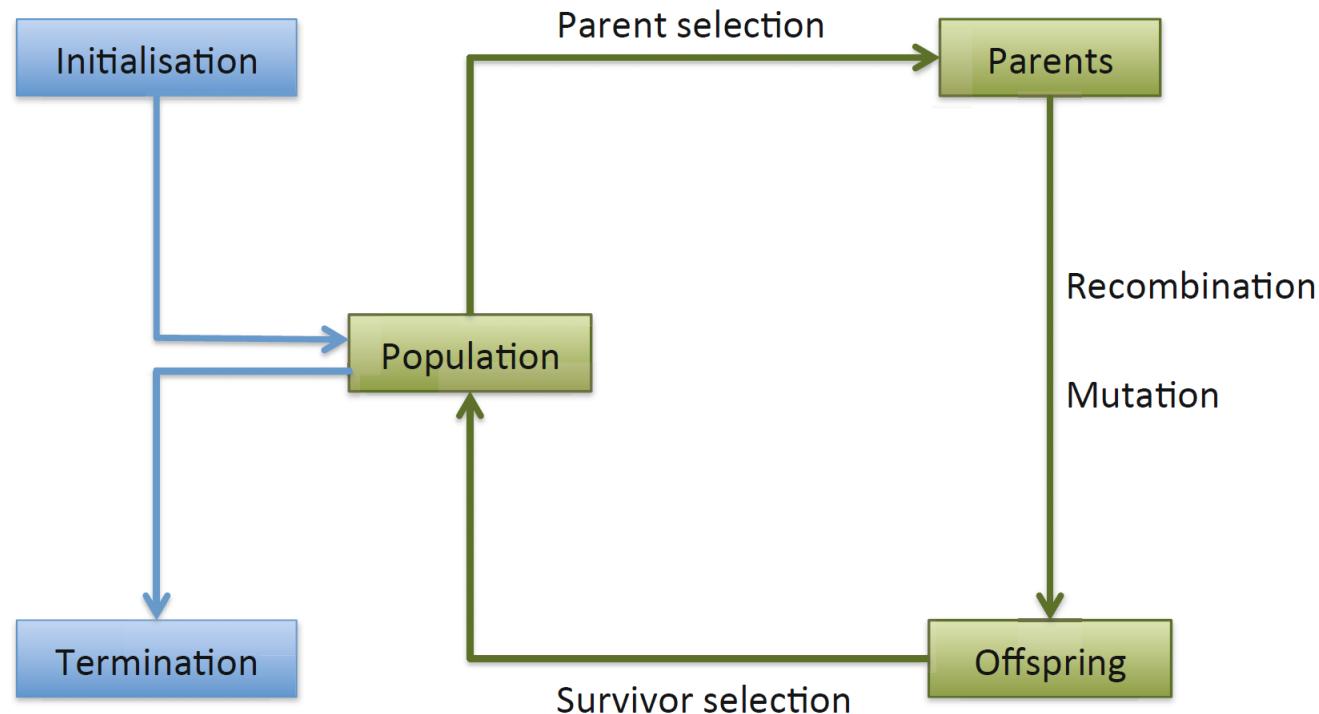
# NEAT

## Neuroevolution of augmenting topologies

# Contents

- ▶ Evolutionary computation
  - basic idea, parts of EA
- ▶ Neural Network
  - Perceptron, Connections, Activation functions
- ▶ NEAT
  - Introduction, Encoding, Species, Mutation, Crossover, Performance, Verification
- ▶ Examples of NEAT
  - Sharp-NEAT
    - Xor Black box
    - Pendulum

# Evolutionary Computation



# Evolutionary Computation

- ▶ Initialization
  - Random creation of candidates solution
- ▶ Candidate
  - Genotype vs. Fenotype
  - Encoding
  - Population
  - Generation
  - Offspring

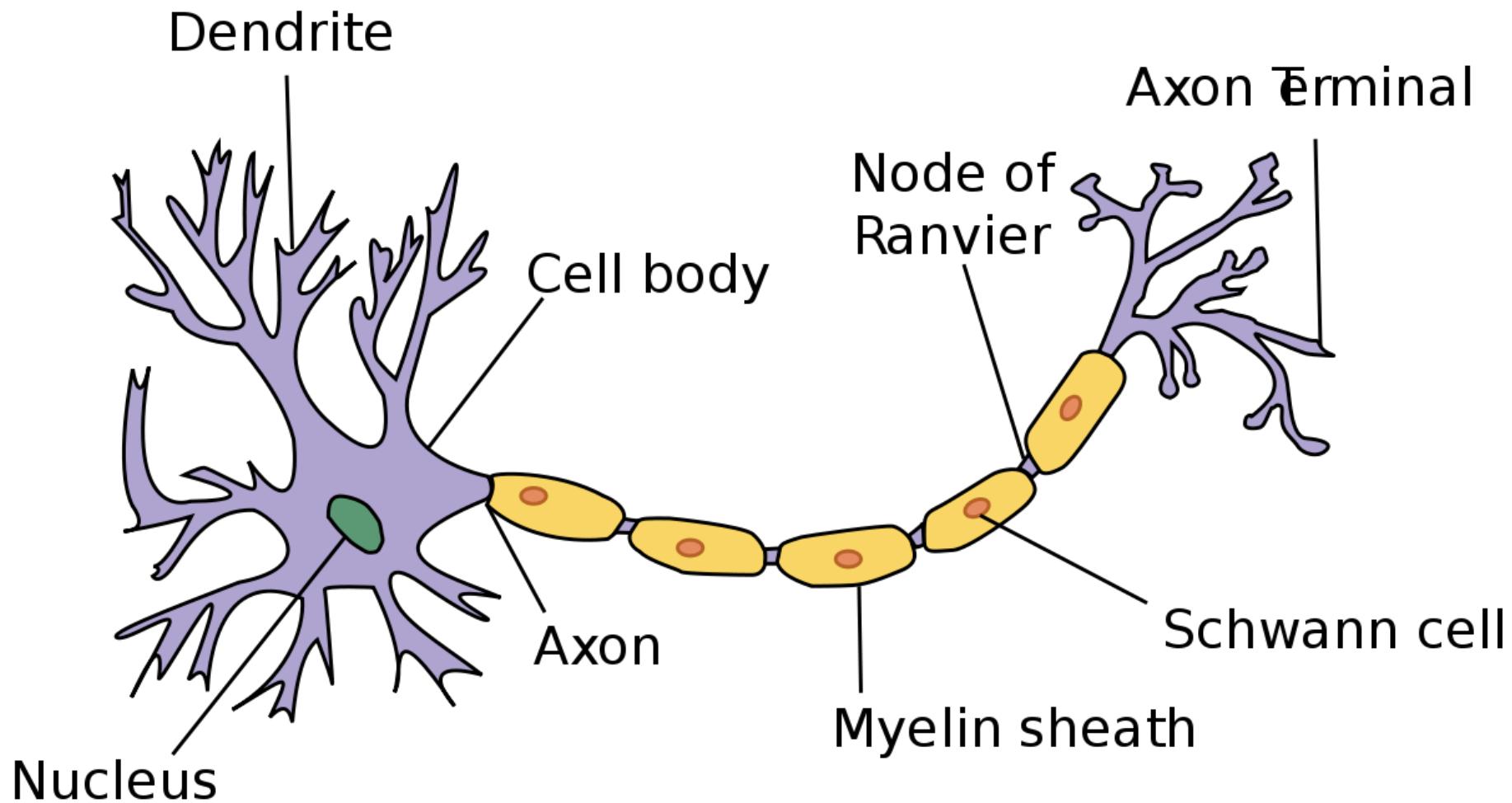
# Evolutionary Computation

- ▶ Evolution of the solution
  - Termination condition
  - Fitness value
  - Problem, Environment
  
- ▶ Selections
  - Parental Selection
  - Environment(Survivor) Selection

# Evolutionary Computation

- ▶ Variation operators
  - Rekombination(Crossover) operator
  - Mutation operator
- ▶ History
  - Genetic algorithm (c: bit string)
  - Evolution strategies (c: vector of real numbers)
  - Evolutionary programming (c: finite automata)

# Neural Network



# Neural Network

- ▶ Neuron
  - Perceptron, Dendrites, Axon
- ▶ Neural Network
  - Deep networks, input, hidden, output layer
- ▶ Activation functions
  - Step func, Linear,  $\tanh(x)$  etc.

# NEAT - Introduction

- ▶ Presented in Evolving Neural Networks through Augmenting Topologies
  - Introduced by:
    - Kenneth O. Stanley (Austin)
    - Risto Miikkulainen (Austin)
- ▶ NEAT = NeuroEvolution of augmenting topologies
- ▶ Evolving topologies along weights

# Authors



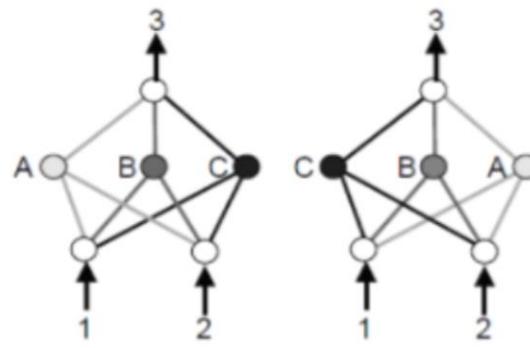
# NEAT – Why?

- ▶ NE of fully connected topologies
  - NEAT is faster
- ▶ NE of fixed topologies
  - Neat do not require decission before NE
  - Neat can not so easily stucked
- ▶ NEAT topologies attempt to stay small

# NEAT - TWEANN

- ▶ Topology and Weight Evolving Artificial Neural Networks
- ▶ ENCODING:
  - Direct:
    - Binary(connection matrix, linear string of bits to represent graph)
    - Graph(dual representation) [for subgraph crossover]
  - Indirect:
    - Cellular encoding(graph encoding language)
- ▶ NONMATING in TWEANN

# TWEANN – Encoding Problems



$$\begin{array}{c} [A,B,C] \\ \times [C,B,A] \end{array}$$

Crossovers:  $[A,B,A]$     $[C,B,C]$   
(both are missing information)

Figure 1: The competing conventions problem. The two networks compute the same exact function even though their hidden units appear in a different order and are represented by different chromosomes, making them incompatible for crossover. The figure shows that the two single-point recombinations are both missing one of the 3 main components of each solution. The depicted networks are only 2 of the 6 possible permutations of hidden unit orderings.

# TWEANN - Encoding Problems

- ▶ Permutation of nodes & same topologies
  - damaged offspring
- ▶ Different topologies & similar solution
  - Memory requirements, unnecessary complex solutions
- ▶ Homology
  - E Coli motivation
  - NEAT : historical origin of node

# TWEANN- Protecting Innovation

- ▶ New structure

- By mutation
  - Not optimal from creation

- ▶ Species

- „Nitching“ (koutek, místečko)
  - Not compete with population at large
  - How to select species
    - NEAT – fitness sharing

# NEAT – Init Population & Topological innovation

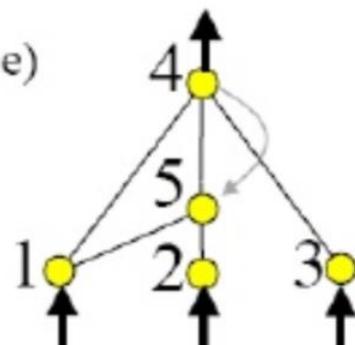
- ▶ TWEANN –
  - random topologies from beginning
    - incorrect topologies
    - Non minimal solutions
  - Fitness penalization
- ▶ NEAT
  - From minimally solution
  - Specing

# NEAT - encoding

Genome (Genotype)							
Node	Node 1	Node 2	Node 3	Node 4	Node 5		
Genes	Sensor	Sensor	Sensor	Output	Hidden		
Connect.	In 1	In 2	In 3	In 2	In 5	In 1	In 4
Genes	Out 4	Out 4	Out 4	Out 5	Out 4	Out 5	Out 5
Weight	0.7	-0.5	0.5	0.2	0.4	0.6	0.6
Enabled	DISABLED		Enabled	Enabled	Enabled	Enabled	Enabled
Innov	Innov 1	Innov 2	Innov 3	Innov 4	Innov 5	Innov 6	Innov 11



Network (Phenotype)



# NEAT - Encoding

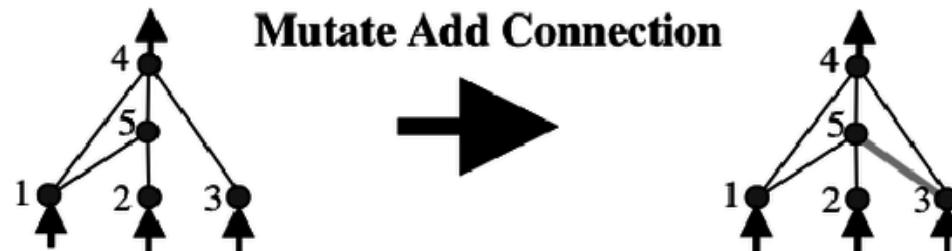
- ▶ **Genome**
  - List of network connectivity
  - List of network nodes (input, output, hidden)
- ▶ **Node**
  - Number of node
  - Input(Sensor), Hidden, Output
- ▶ **Connection**
  - In-node, out-node
  - weight
  - enable-bit
  - Innovation number

# NEAT - Mutation

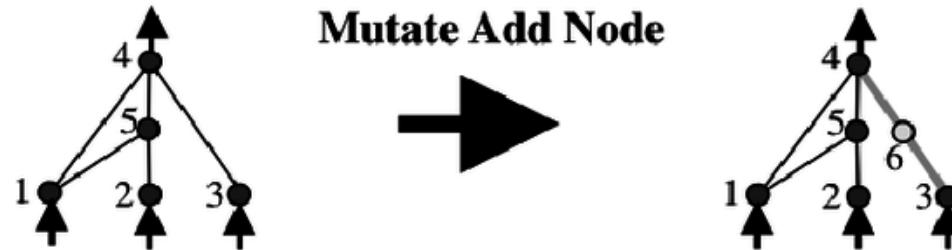
- ▶ Can change weights, network structures
- ▶ Same for weights (even if perturbed, not in all)
- ▶ Changes in structure
  - Add connection
  - Add node

# NEAT - mutation structure

1 1->4	2 2->4	3 3->4	4 2->5	5 5->4	6 1->5
DIS				DIS	



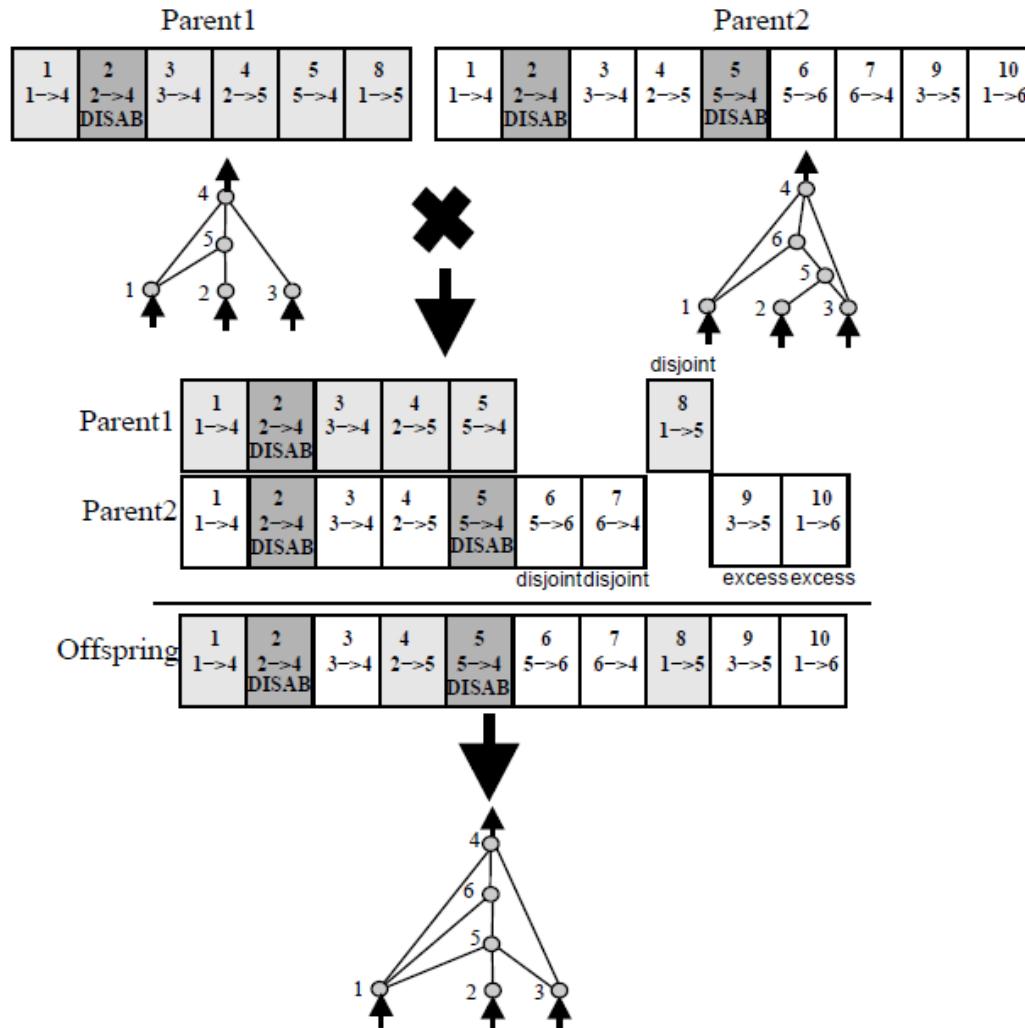
1 1->4	2 2->4	3 3->4	4 2->5	5 5->4	6 1->5
DIS				DIS	



# NEAT - tracking genes

- ▶ Historical markings
  - Global innovation number
  - No changes after crossover
  - Easy genes matching
- ▶ Not matching genes
  - Excess, disjoint – from more fit parent

# NEAT - Crossover



# Protecting Innovation

- ▶ Speciating – niche competition
- ▶ Niche = topology matching
  - By historical markings
  - Compatibility distance
    - number of excess & disjoints
  - Representing by one random genome from previous generation

$$\delta = \frac{c_1 E}{N} \frac{c_2 D}{N} + c_3 \overline{W}.$$

# NEAT – Fitness sharing

- ▶ Same species share fitness
- ▶ Explicit fitness sharing
- ▶ Threshold:
  - Distance between  $i, j$
  - sh function:

$$f'_i = \frac{f_i}{\sum_{j=1}^n sh(\delta(i, j))}$$
$$\delta(i, j) = 0$$

$$\delta(i, j) > \delta_t \implies sh(\delta(i, j)) = 0$$

$$\delta(i, j) < \delta_t \implies sh(\delta(i, j)) = 1$$

# NEAT - Incremental Grow

- ▶ From minimal candidate
- ▶ All inputs connected directly to the outputs
- ▶ Survival only of the useful through fitness evaluation

# NEAT - Validation

- XOR Network
  - Does NEAT evolve something?
- POLE balancing test
  - Does NEAT work efficiently than other NE?
- Sharp-NEAT
  - <http://sharpneat.sourceforge.net/>
  - <https://github.com/colgreen/sharpneat>

# Videos:

## MARIO

- ▶ <https://www.youtube.com/watch?v=qv6UVQ0F44>

## Flappy Birds

- ▶ <https://www.youtube.com/watch?v=L6bbFgjkqK0>

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