

Artificial Neural Networks

NeuroEvolution = ANN + EA



Jan Drchal
drchajan@fel.cvut.cz

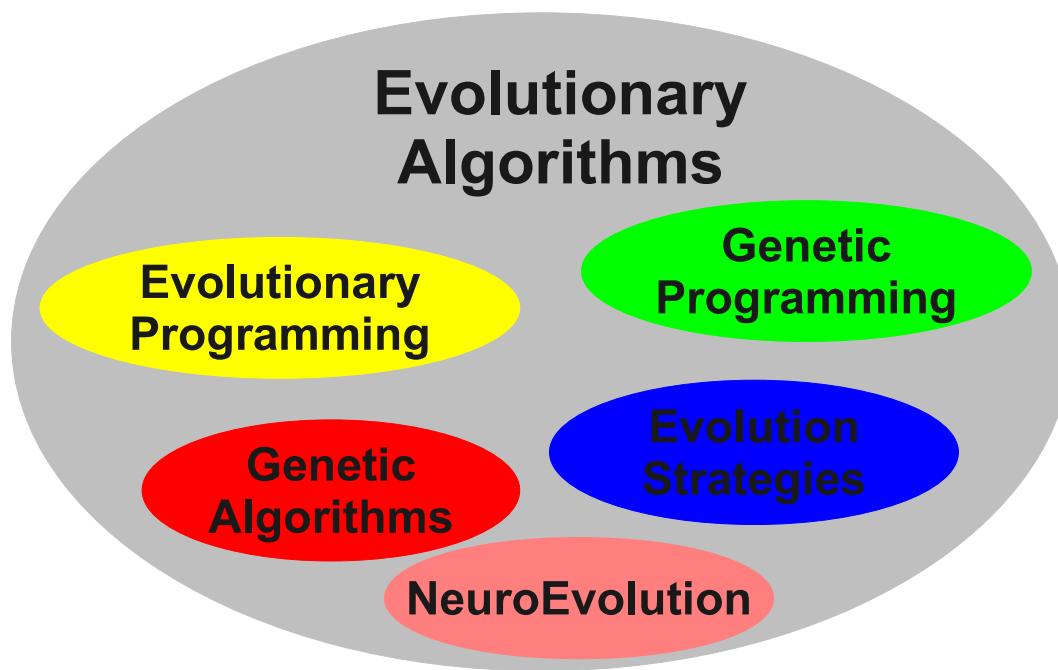
*Computational Intelligence Group
Department of Computer Science and Engineering
Faculty of Electrical Engineering
Czech Technical University in Prague*



Motivation

- Learning ANNs = optimization of weights (or potentially structure).
- Problem of local extremes → unable to learn hard task/large networks.
- Use of **Evolutionary Algorithms** → slower, but more robust than classic gradient methods like Back-Propagation.

Evolutionary Algorithms (EAs)



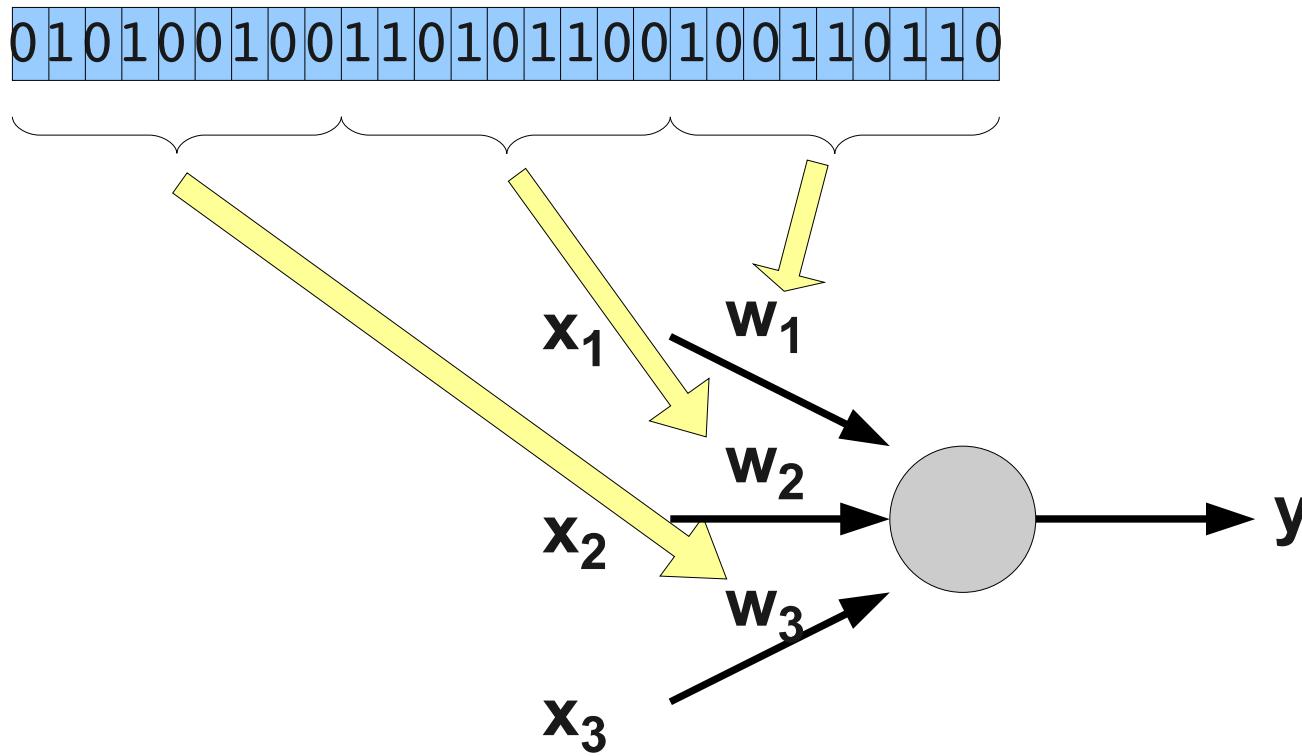
- **Genetic Algorithms:** binary strings
- **Evolutionary Strategies:** real vectors, only mutation.
- **Genetic Programming:** evolution of program trees.
- **Evolutionary Programming:** evolving FSMs
- **NeuroEvolution**

What is Neuro Evolution?

- **Neuro-evolutionary algorithm is just another special kind of EA** → the task is to evolve (learned) neural networks.
- Both parameters (weights) and topology can be optimized by evolution.
- **But how to encode a network into a genome?** → A network with fixed topology is described by a vector of all its weights (real numbers)...

Direct Encoding of Neural Network

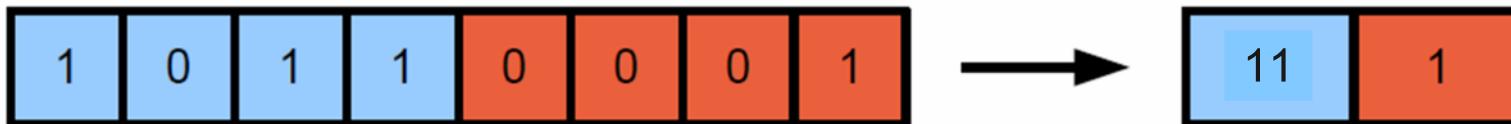
- Directly encode the weights as a bit string:



- Can we do it better? Yes.

Floating-Point Encoding

- Motivation: simplicity, precision



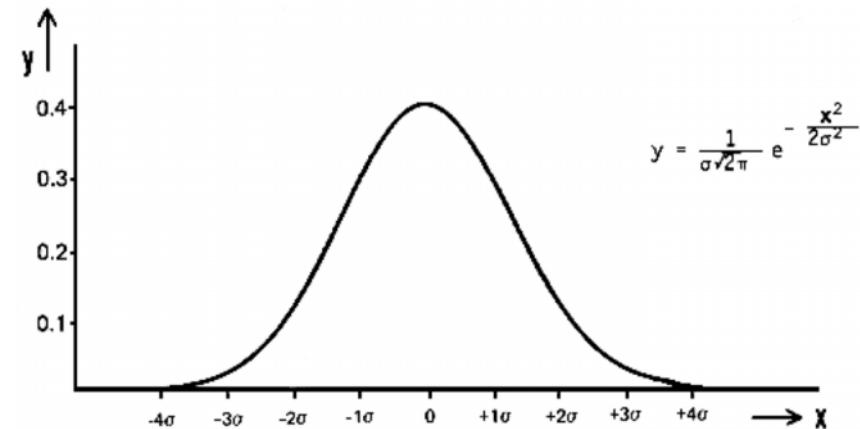
Binary string encodes vector of 2 numbers .

The same encoded using floating-point encoding.

What about mutation? -> Gaussian noise.

Idea:

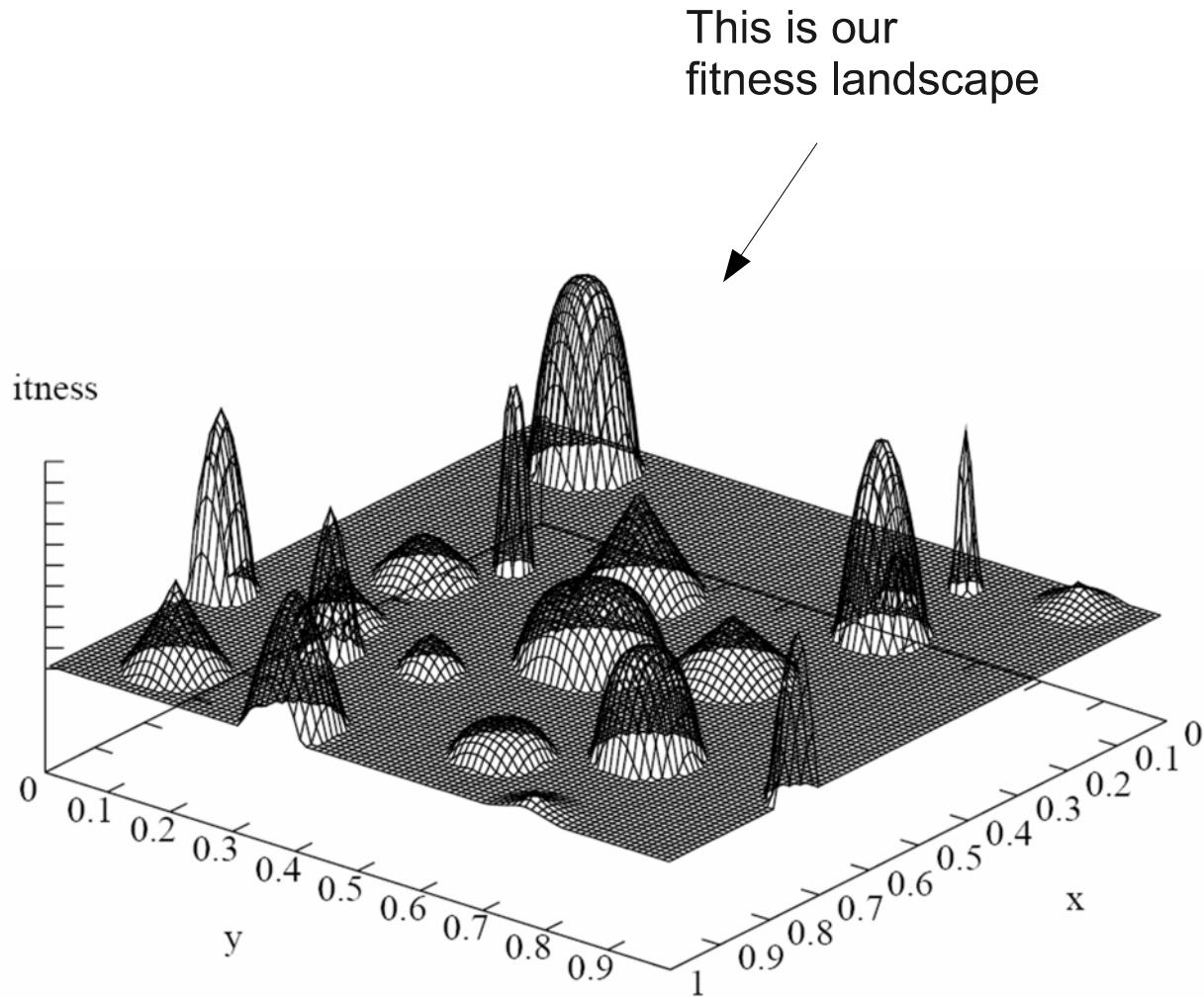
*small changes with higher probability,
large changes with lower.*



- Useful for integers and floats ...

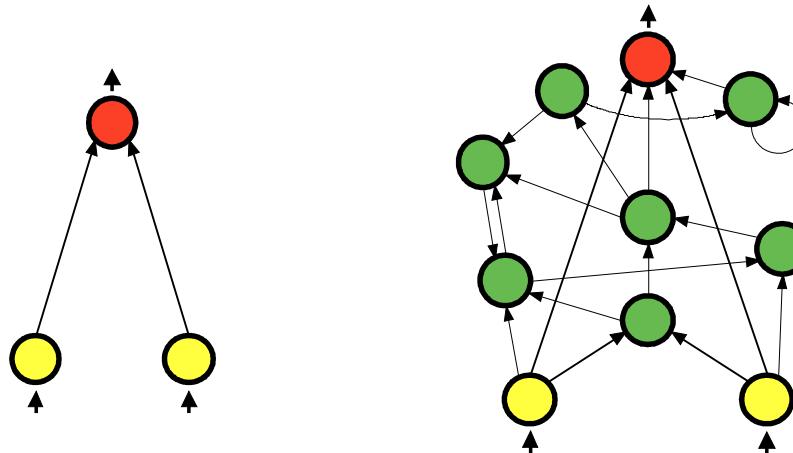
Multimodal Domains

- Multimodal functions:
 - multiple optima,
 - many local.
- Too many attractors → hard optimization :(
- ANN fitness/error landscapes look like this.



NEAT

- NeuroEvolution of Augmenting Topologies:
Kenneth O. Stanley, 2001, The University Of Texas at Austin
- Complexification – start from small topologies:
evolution add neurons/links as needed by task.



Kenneth O. Stanley and Risto Miikkulainen: **Evolving Neural Networks Through Augmenting Topologies**

NEAT 2

- Topology is augmented by adding neurons and links between.
→ Variable genome length.
- Mutations:
 - parametric – Gaussian noise,
 - structural – adding neurons & links (no pruning), switch on/off links.
- Mating – special crossover two parents → single child.

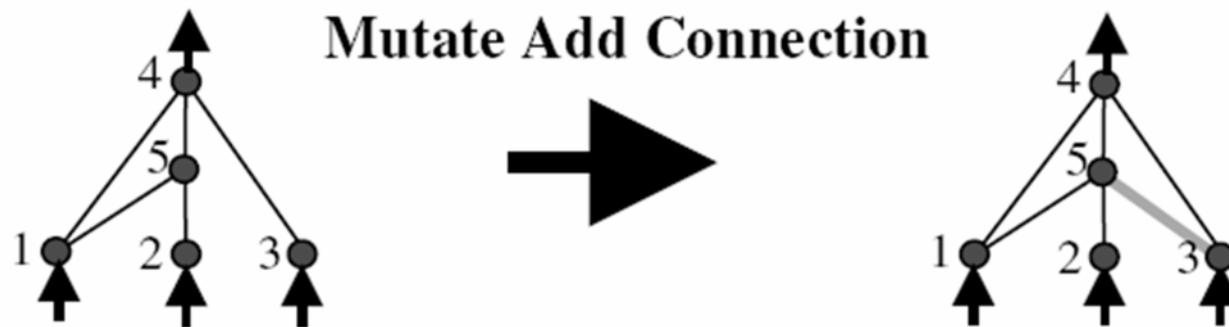
Note, some newer implementations use pruning However, it is not essential.



Add Link Mutation

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

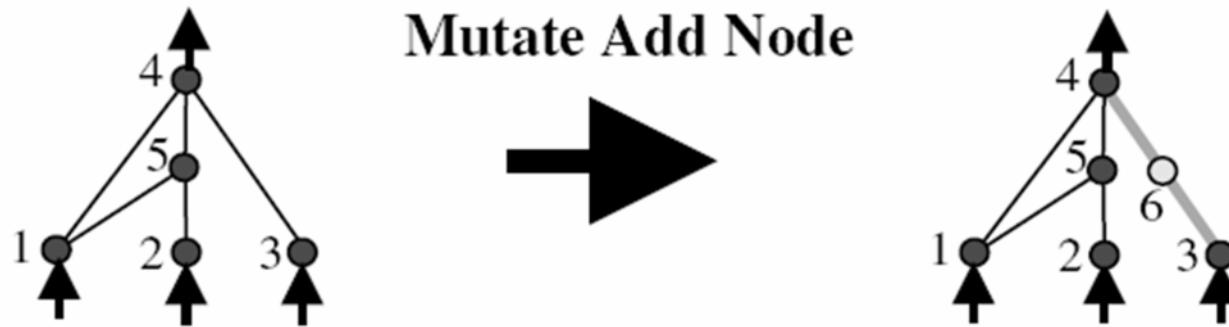
1 1->4	2 2->4 DIS	3 3->4	4 2->5	5 5->4	6 1->5	7 3->5
-----------	------------------	-----------	-----------	-----------	-----------	-----------



Add Neuron Mutation

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

1 1->4	2 2->4 DIS	3 3->4 DIS	4 2->5	5 5->4	6 1->5	8 3->6	9 6->4
-----------	------------------	------------------	-----------	-----------	-----------	-----------	-----------



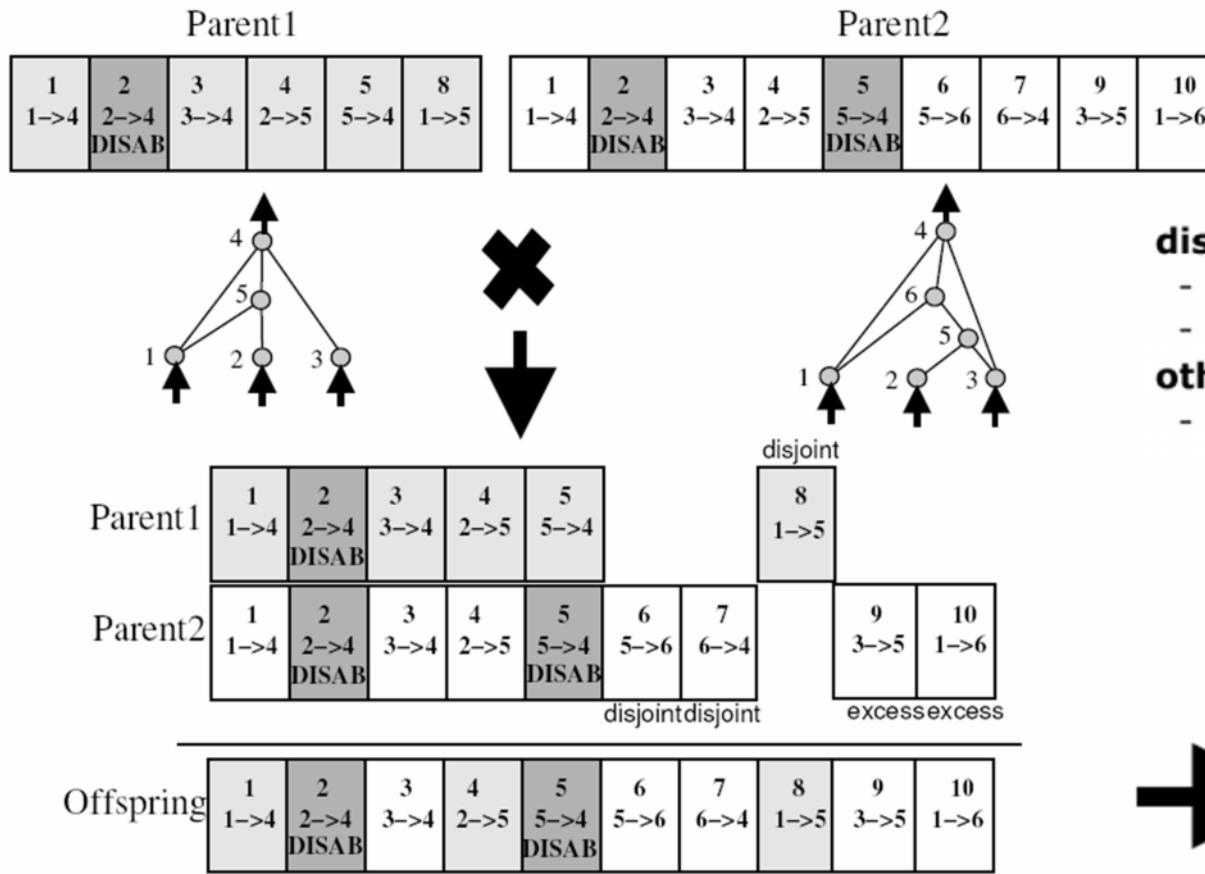
The weights of new neuron's incoming/outgoing links are set in a way which minimizes the difference between original and mutated networks.

Historical Markings

- **Q:** How to *align* two genomes of different size representing two different networks?
- **A:** let's use “the creation date” of a particular gene (caused by a structural mutation) – **historical marking (innovation number)**.
- Aligning two genomes:
 - when two genes with matching HMs are found, it is likely they have similar function in the network.
- HM is a counter, the same value is assigned for the same innovation within a single generation (i.e. adding a link between neurons #3 and #4).

Mating

Let's use historical marking.

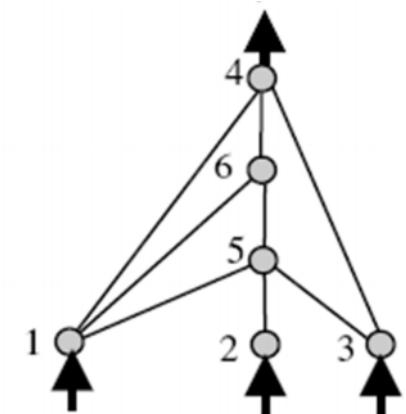


disjoint or excess

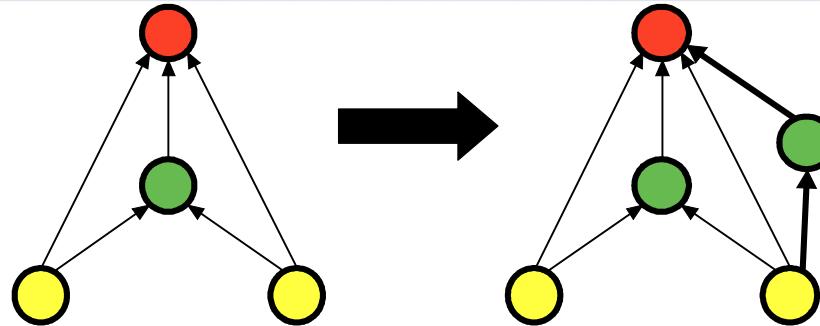
- inherit more fit
- if equal fitness inherit randomly

other

- inherit randomly



Niching



- There are networks of different sizes in the population.
- Adding a new structure:
 - likely lowers the fitness,
 - larger networks → longer genome → more time needed to optimize parameters.
- **New topologies must be protected** → niching.
- Here we use Explicit Fitness Sharing:
Separate the population into species → selection and reproduction only among similar individuals → HMs again used to compute similarity of two genomes.

The Three Most Important Ideas Behind NEAT

- **Complexification** – start with small networks, gradually add neurons/links (reminds GMDH or GAME approaches).
- Concept of **historical markings** - cross/match only corresponding genes → **deals with competing conventions.**
- Use of **niching** - allows the survival of larger, recently structurally innovated networks → gives them time to optimize their weights and “show” that the structural innovation was beneficial.