NEAT: NEUROEVOLUTION OF AUGMENTING TOPOLOGIES

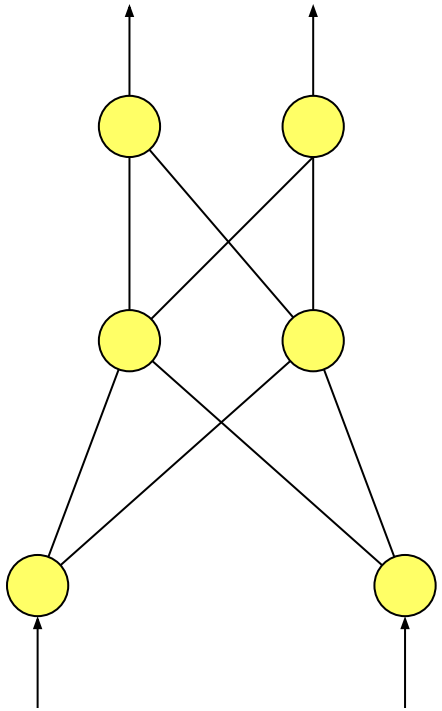
Michael Prestia

COT 4810

April 8, 2008

RECAP: ARTIFICIAL NEURAL NETWORKS

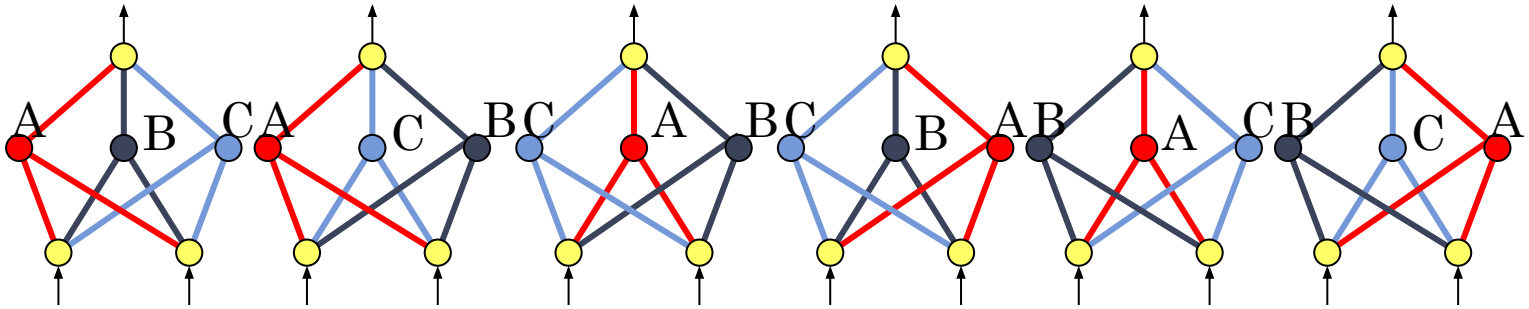
- Composed of neurons and weights
- Sum products of weights and inputs to activate



RECAP: NEUROEVOLUTION

- Evolves weights of a neural network
- Genome is direct encoding of weights
- Weights optimized for the given task

COMPETING CONVENTIONS PROBLEM



3! = 6 different representations of the same network

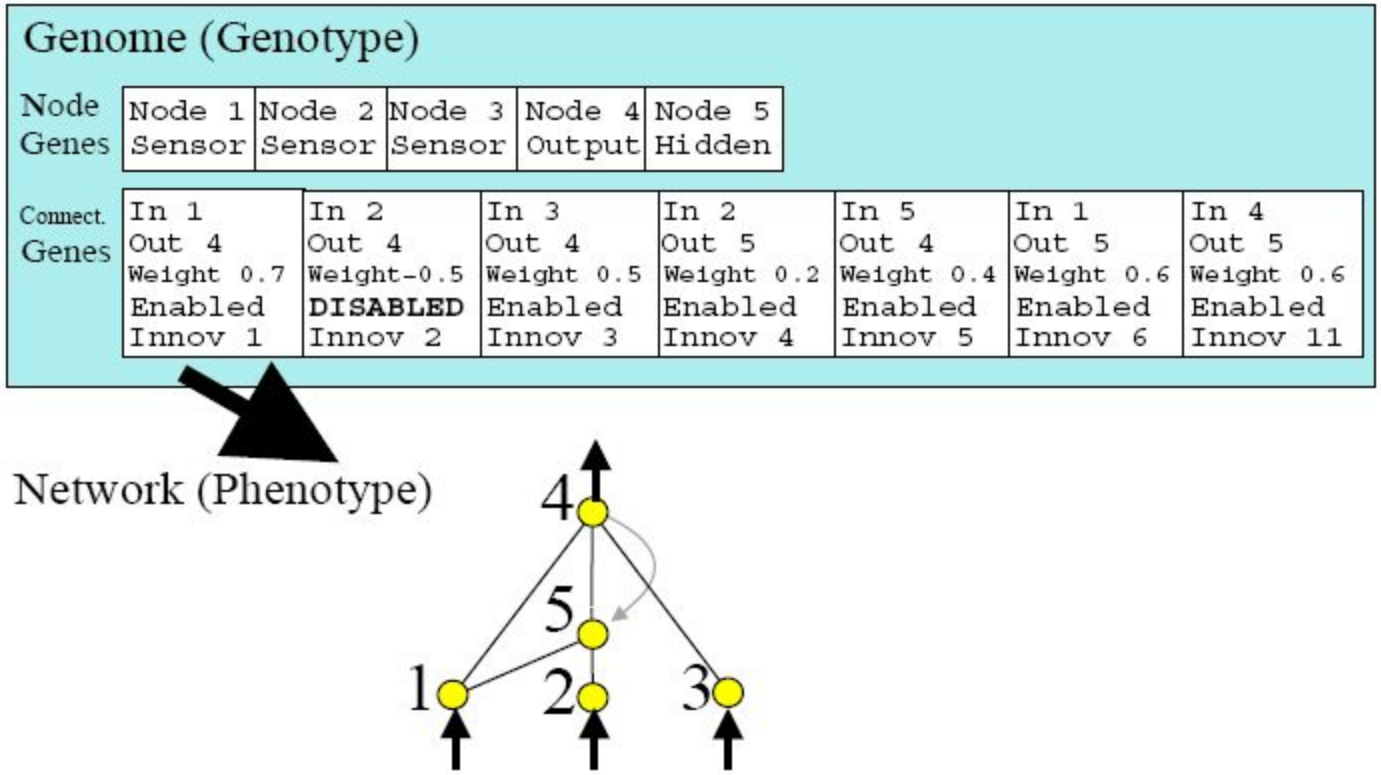
NEUROEVOLUTION OF AUGMENTING TOPOLOGIES

- Uses node-based encoding
- Keeps an historical record of innovations
- Keeps size of networks to a minimum
  - Start with minimal topologies and random weights
- Biological motivation

NEAT GENOME

- List of neuron genes
  - ID number
  - Node type
- List of link genes
  - Start node
  - End node
  - Weight
  - Enabled flag
  - Innovation number

GENETIC ENCODING IN NEAT



MUTATION IN NEAT

- Four types of mutations
  - Perturb weights
  - Alter activation response
  - Add a link gene
  - Add a neuron gene
- Adding of a link gene or neuron gene is an innovation

WEIGHT PERTURBATION

- Works similarly to previously discussed method
- Each weight modified depending on mutation weight
- Weights can be completely replaced
  - Controlled by user-defined parameter

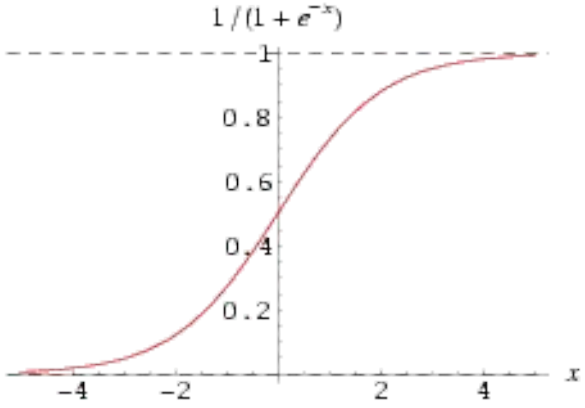
ACTIVATION RESPONSE MUTATION

- Activation response determines curvature of activation function

Neuron j activation:

$$H_j = \sigma\left(\sum_{i=1}^{n} x_i w_{ij}\right)$$

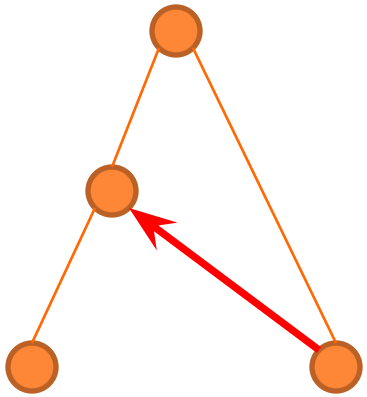
$$\sigma(x) = \frac{1}{1+e^{-a/p}}$$



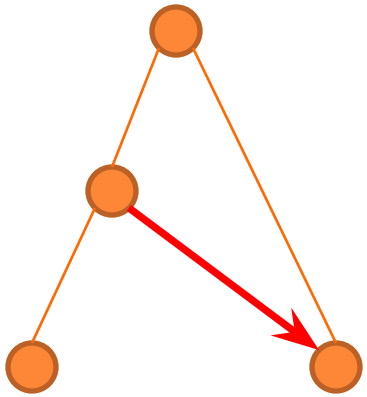
ADDING A LINK GENE

- Adds a connection between any nodes in the network

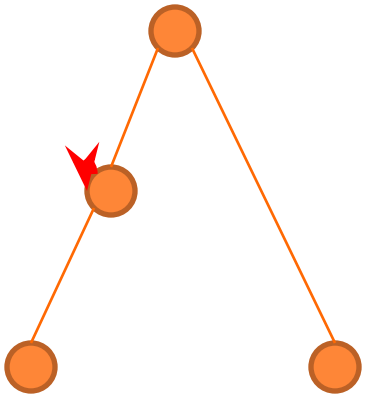
- Three types of links



forward



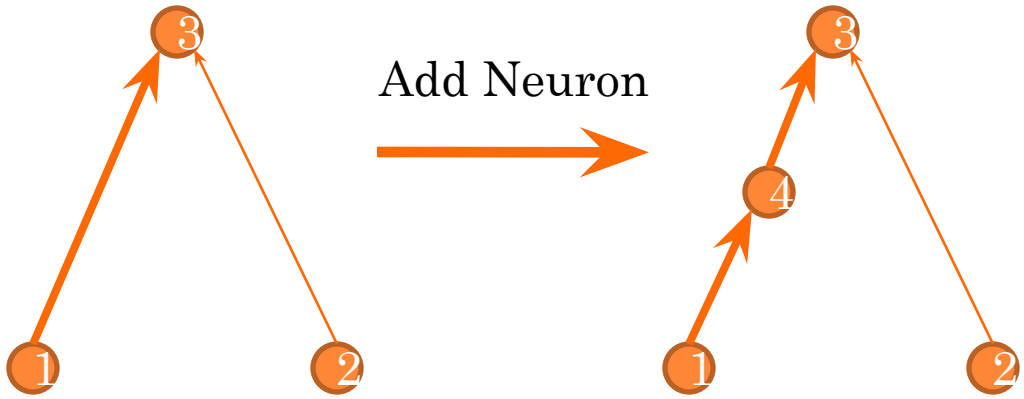
backward



recurrent

ADDING A NEURON GENE

- Link chosen and disabled
- Two new links created to join new neuron
  - One link has weight of disabled link
  - Other link has weight of 1
- Problem: chaining effect

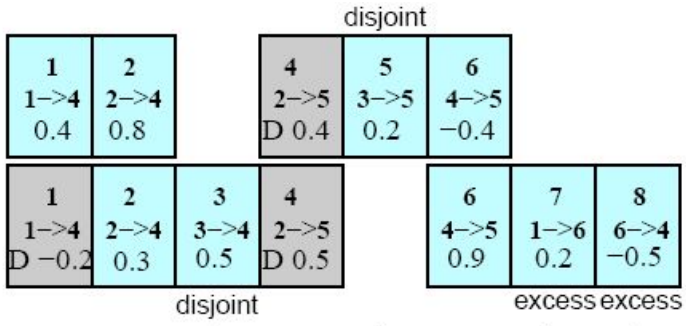


INNOVATIONS

- Global database of innovations
- Each innovation has unique ID number
- Each added neuron or link is compared to database
- If not in database
  - new innovation ID given to gene
  - innovation added to database

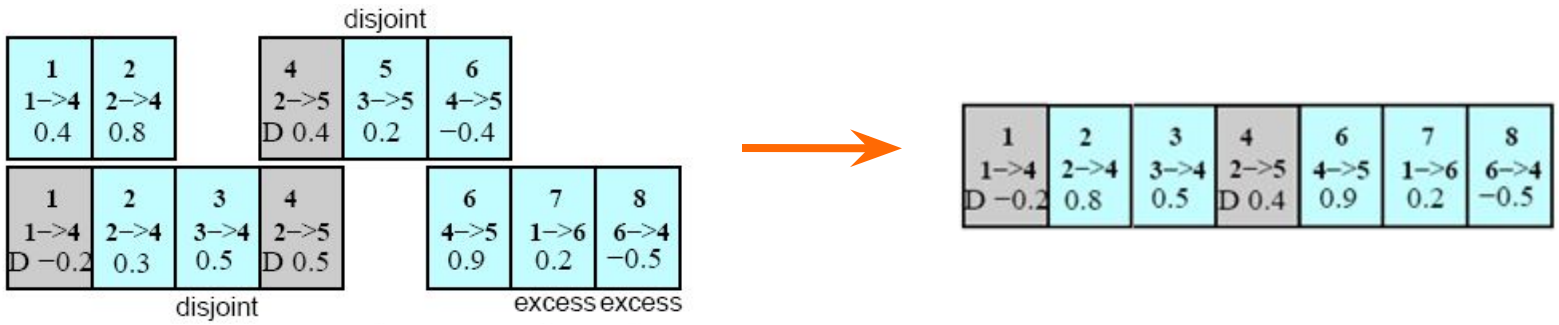
CROSSOVER

- Arrange genes by innovation number
- Non-matching genes are called disjoint genes
- Extra genes at end of genome are called excess genes



CROSSOVER

- Matching genes inherited randomly
- Disjoint and excess genes inherited from fittest parent



SPECIATION

- New topologies typically poor performer at first
  - High probability individual will die out
- Separate population into species
- Similar individuals only compete among themselves
- Helps prevents premature extinction

COMPATIBILITY DISTANCE

- Species determined by compatibility distance
- Calculated by measuring diversity genomes of two individuals
- $$C.Dist = \frac{c_1 E}{N} + \frac{c_2 D}{N} + c_3 W$$
- Greater distance, greater diversity

EXPLICIT FITNESS SHARING

- Further helps prevent premature extinction
- Shares fitness scores among a species
- individual fitness divided by size of species
- Species killed off if no improvement over set number of generations
  - Exception if species contains fittest

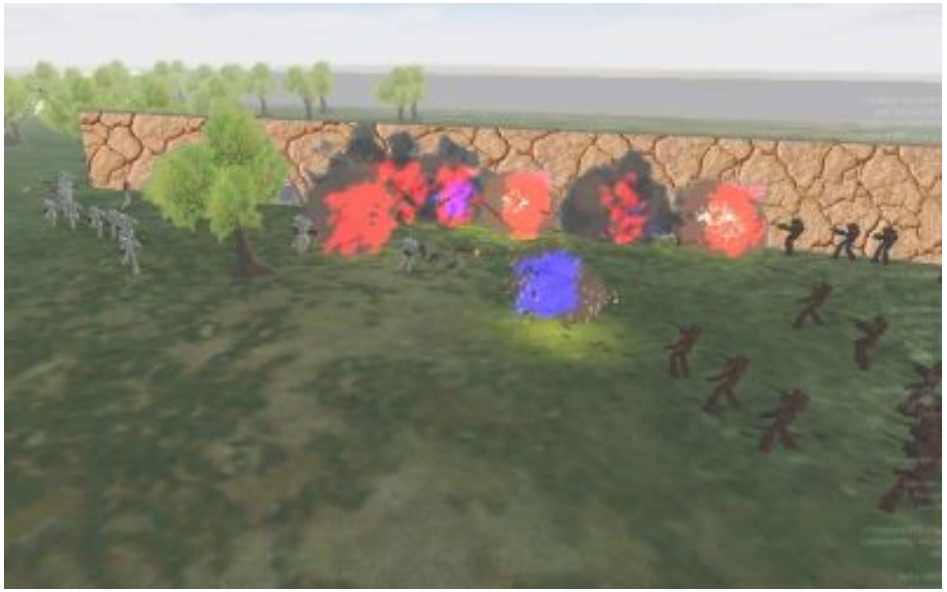
ACTIVATION

- No predefined layers as in other neural networks
  - Needs to activate differently

- Two activation modes
  - Active – uses activations from previous time step
  - Snapshot – iterates through all neurons with each update

APPLICATION OF NEAT

- NERO – Neuro Evolving Robotic Operatives
- www.nerogame.org



http://nerogame.org/

REFERENCES

- Buckland, Mat. AI Techniques for Game Programming. Cincinnati: Premier Press, 2002.
- AI for Game Programming: Kenneth Stanley
- Images copied with permission from http://www.cs.ucf.edu/~kstanley/cap4932spring08dir/CAP4932_lecture13.ppt

HOMEWORK QUESTIONS

- How does NEAT avoid the competing conventions problem?
- What is one way NEAT protect innovation?