Comparison of genotype encodings for 3D agents

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Details of this research are available in [KR01].

Goals

- co-evolve bodies and brains
- design various methods of description of body and brain
- study and compare the effectiveness of evolution using these methods
- in a single system.

Why co-evolve brains and bodies?

- because it yields better results than with body separated from brain
- because it is natural

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- embodiment: physical interactions (between body parts, signal processing) perform computations, a part of overall behavior
- brain and body strongly connected
  - evolution of body changes the cognitive space of the brain (e.g., an eye placed on a limb, or new senses)
  - evolution of brain changes usage of the body
- co-evolution: can cause change even in the absence of environmental change

What is the trouble?

- the ‘matching’ problem
  - parts of brain (neurons, nodes) must be connected to parts of body (sensors, actuators)
  - if matching is explicit, it can be disrupted by the change of either side, which can be catastrophic
- both are variable size
- crossover on complex representations

Goals
Experiments
Conclusions
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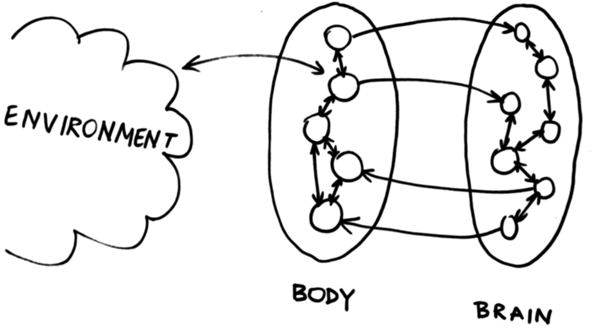

General problems in optimization of realistic autonomous agents

- infinite search space
- discrete-continuous space
- hard to define neighborhood
- solutions contain varying amount of information
- hard to choose representation
- very strong dependencies and connections between parts of a solution
- evaluation function with many local optima
- many non-feasible solutions and diverse constraints
- non-determinism and complexity of evaluation
- multi-criteria evaluation, complex definition of criteria, evaluation delayed to action
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. . . the big problem is the size and nature of the search space.

Genetics is important...

...because each representation and its operators:

- establish different structure and order in the search space
- define important information and 'building blocks' in another way
- are scalable to a different degree
- introduce different bias which leads to finding qualitatively different solutions
- impose diverse local optima and display various levels of robustness against being trapped into them
- can limit the space of valid solutions in a particular way
- have a specific degree of coherency, redundancy, easiness of interpretation, etc.

Current artificial genomes – very diverse

Simple (direct)

Complex (biologically inspired)

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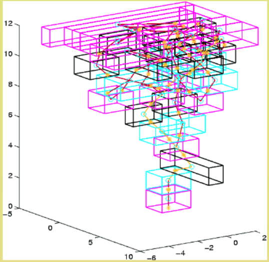

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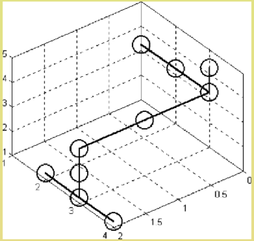

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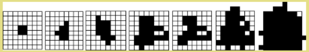

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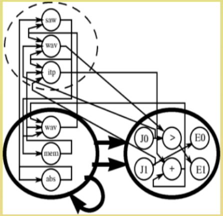

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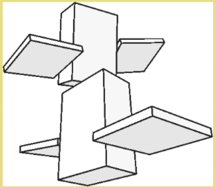

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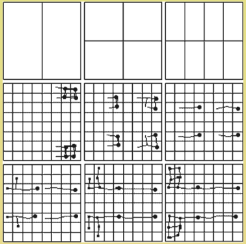

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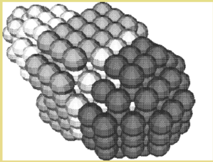

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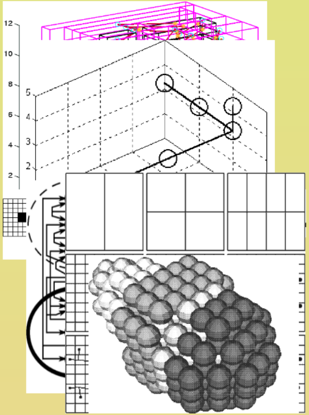

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- explicit/implicit
- different systems
- etc. . .

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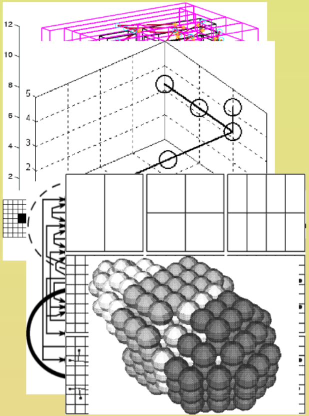

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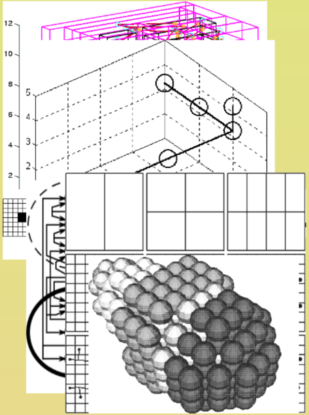

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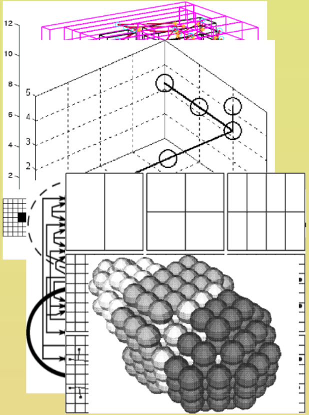

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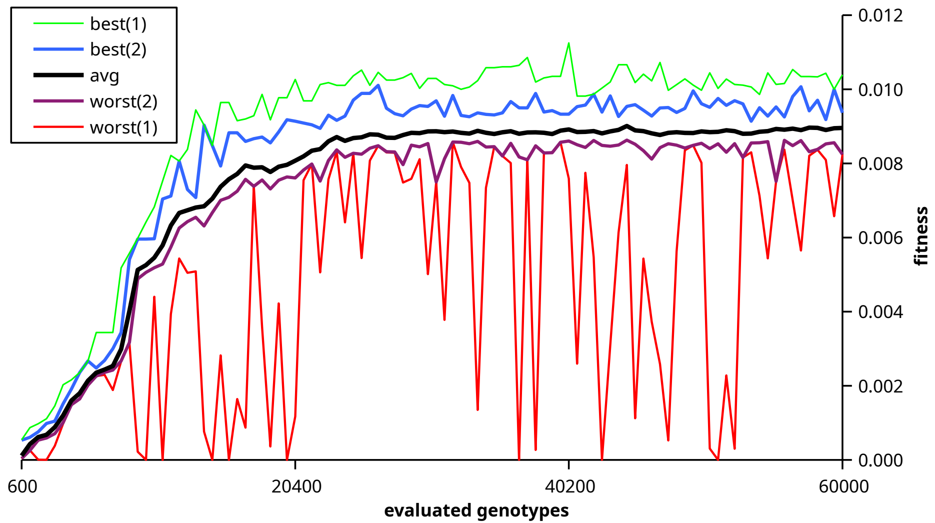
What is the best representation?

- fitness values
- nature of solutions
- simplicity
- understandability

Experiments

- 3 one-criterion tasks
  - average height of agent center (maximize; NN turned off)
  - average height of agent center (maximize; NN turned on)
  - average velocity (maximize)
- 3 genetic representations: simul (**f0**), recur (**f1**), devel (**f4**)
- 10 runs for each task and each genetic representation
- $3 \times 3 \times 10 = 90$ runs in total
- system main parameters
  - steady-state
  - population size: 200
  - cloning probability: 20%
  - mutation probability: 64%
  - crossing over probability: 16%
  - stabilization period

Non-deterministic evaluation



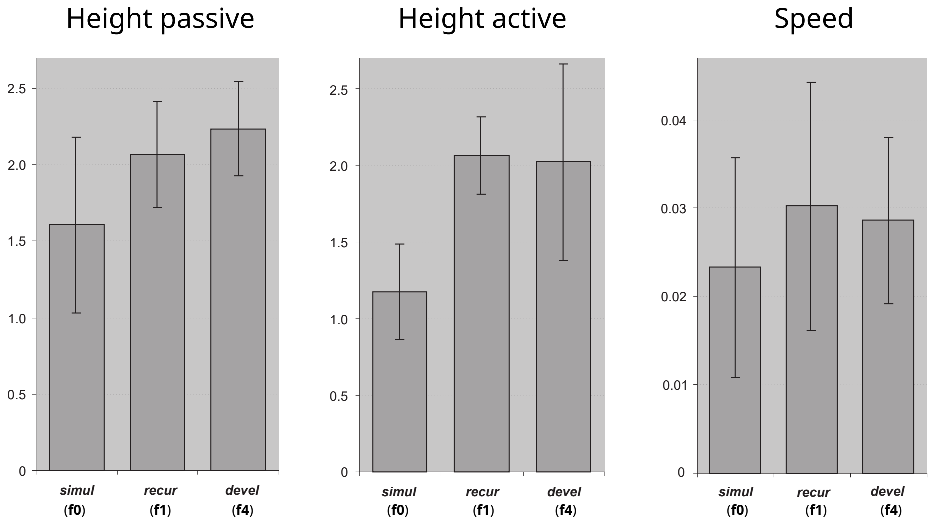
Results

Note:

The following results are from 2001. While the grammar of **f0**, **f1**, and **f4** encodings in Framsticks changed only slightly since then, the mutation operators were significantly improved and probabilities of individual mutation subtypes were changed – so the results would be likely different if such an experiment was performed today.

A more modern version of this experiment with more (eight) genetic representations compared, but only two fitness criteria (vertical position of the center of mass and vertical position of the top vertex) was performed in 2012 [Kom12]. For that version, the reservations about the differences from the modern implementation of genetics still apply.

Results (quantitative)



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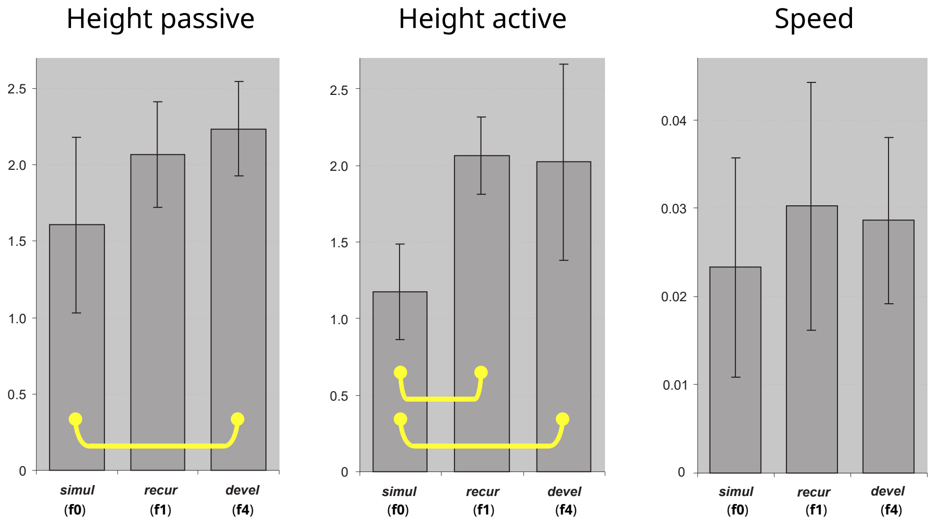

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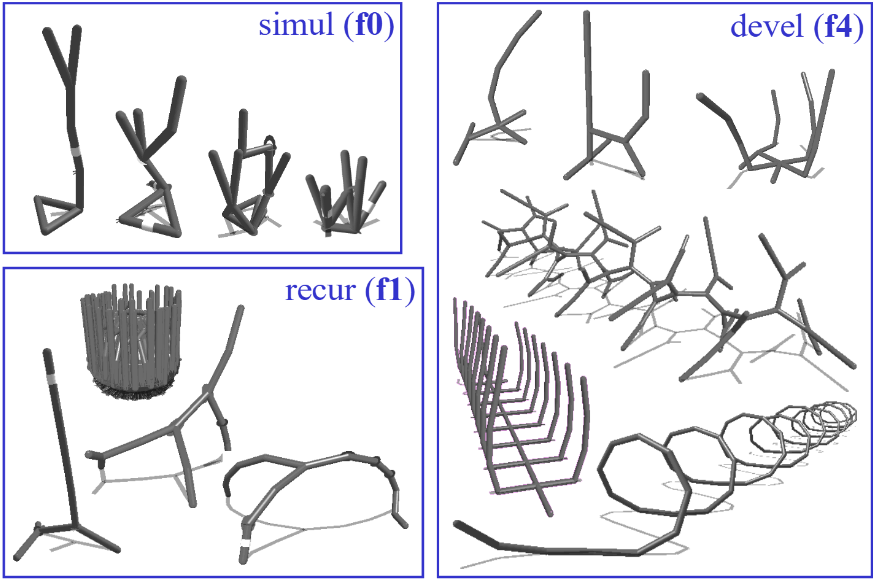

Conclusions

- simul (**f0**) representation with full abilities of expressing agents was the worst one
- the limitation of the search space by higher level representations has not deteriorate results, but has improved them
- the most advanced devel (**f4**) encoding was not significantly better than recur (**f1**)
- each higher-level representation introduces a specific bias and new quality (characteristics) into solutions
- for all representations, the best individuals were successful in terms of fitness value. It was difficult or impossible to construct better agents by hand, mainly because of high time costs
- it may be sometimes worthwhile to introduce advanced mechanisms into a representation in order to obtain a different nature of solutions, even when they are not improved in terms of fitness

Conclusions, cont.

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- convergence
- exploitation of simulator imperfections
- redundancy, randomness
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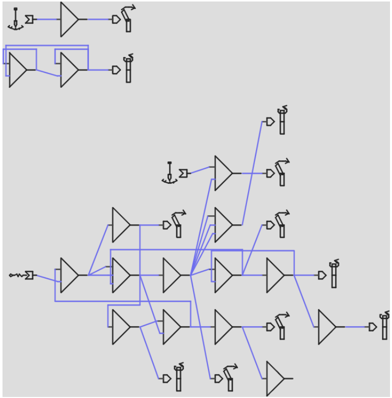

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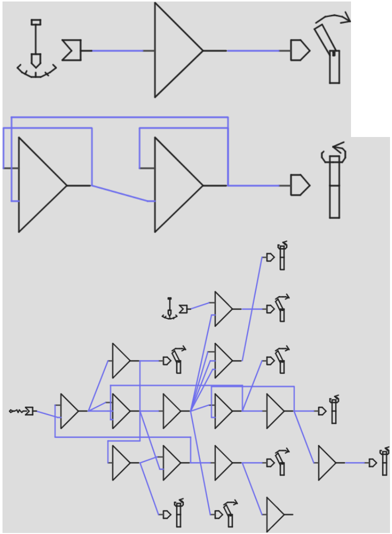

References I

[Kom12] Maciej Komosinski. *Evolutionary design of tall structures*. Research report RA–06/12. Poznan University of Technology, Institute of Computing Science, 2012. URL: http://www.framsticks.com/files/common/EvolutionaryDesignOfTallStructures.pdf.

[KR01] Maciej Komosinski and Adam Rotaru-Varga. "Comparison of different genotype encodings for simulated 3D agents". In: *Artificial Life Journal* 7.4 (Fall 2001), pp. 395–418. DOI: 10.1162/106454601317297022. URL: http://www.framsticks.com/files/common/ComparisonGeneticEncodings3DAgents.pdf.