Computational learning and discovery

CSI 873 / MATH 689

Instructor: I. Griva

Wednesdays 7:20 – 10:00 pm

Evolutionary Computation

1. Computational procedures patterned after biological evolution
2. Search procedure that probabilistically applies search operators to set of points in the search space

Motivation

- **Evolution is a successful, robust method of adaptation for biological systems**
- **Can models complex interacting parts of hypotheses and so can build a rich hypothesis space**
- **Can be easily parallelized**

Ideas taken from biological evolution

Lamarck and others:

- Species "transmute" over time

Darwin and Wallace:

- Consistent, heritable variation among individuals in population
- Natural selection of the fittest

Mendel and genetics:

- A mechanism for inheriting traits
- genotype $\rightarrow$ phenotype mapping

Hypotheses Representation

Represent

$$(Outlook = Overcast \vee Rain) \wedge (Wind = Strong)$$

by

$$\begin{array}{cc} Outlook & Wind \\ 011 & 10 \end{array}$$

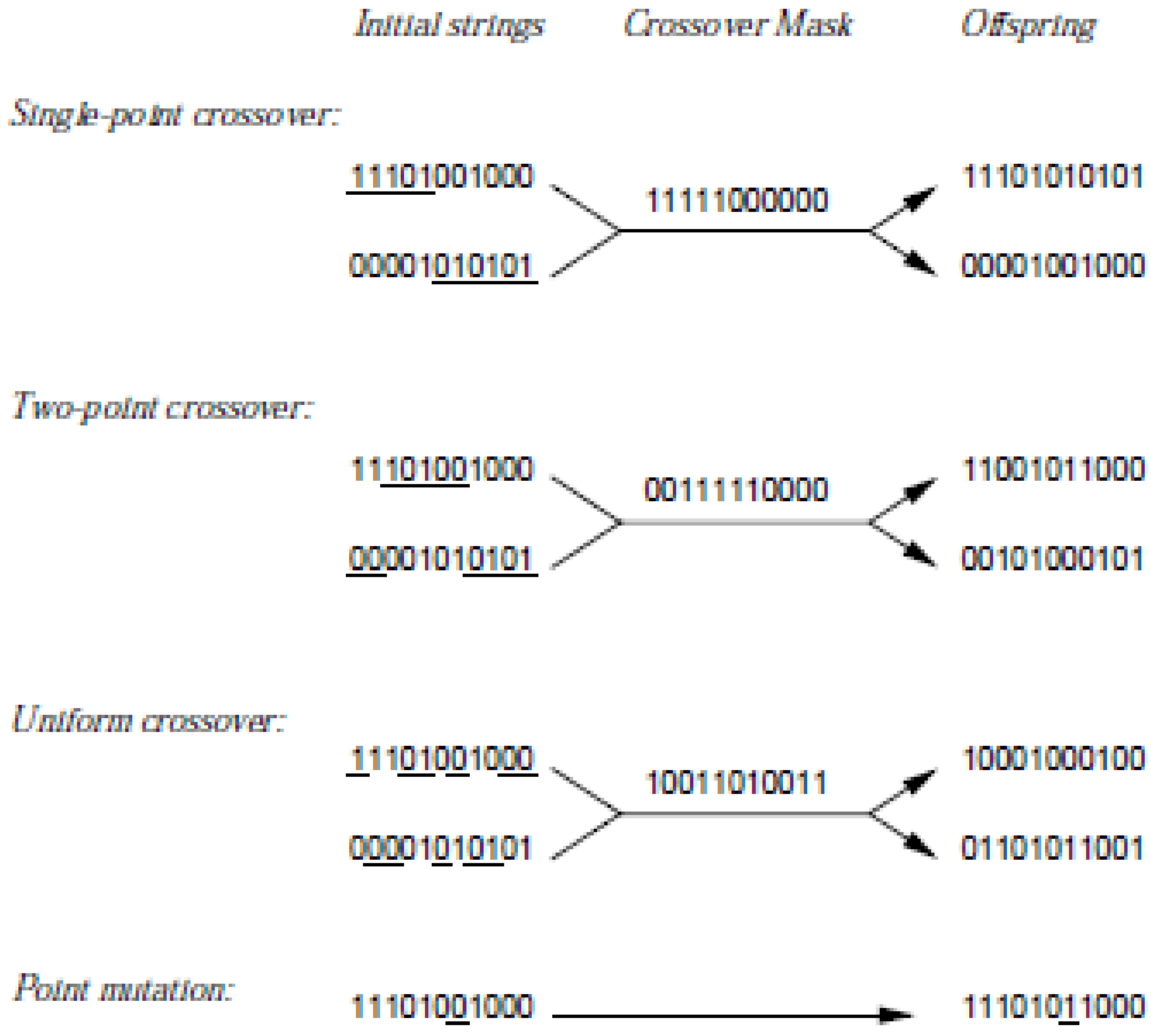
Represent

IF $Wind = Strong$ THEN $PlayTennis = yes$

by

$$\begin{array}{ccc} Outlook & Wind & PlayTennis \\ 111 & 10 & 10 \end{array}$$

Operators



Initial strings
Crossover Mask
Offspring
Single-point crossover:
11101001000
00001010101
11111000000
11101010101
00001001000
Two-point crossover:
11101001000
00001010101
00111110000
11001011000
00101000101
Uniform crossover:
11101001000
00001010101
10011010011
10001000100
01101011001
Point mutation:
11101001000
11101011000

Hypothesis selection

Fitness proportionate selection:

$$\Pr(h_i) = \frac{Fitness(h_i)}{\sum_{j=1}^{p} Fitness(h_j)}$$

... can lead to *crowding*

Tournament selection:

- Pick h_1, h_2 at random with uniform prob.
- With probability p, select the more fit.

Rank selection:

- Sort all hypotheses by fitness
- Prob of selection is proportional to rank

Genetic Algorithm

GA($Fitness, Fitness\_threshold, p, r, m$)

- *Initialize:* $P \leftarrow p$ random hypotheses
- *Evaluate:* for each h in P, compute $Fitness(h)$
- While $[\max_h Fitness(h)] < Fitness\_threshold$

  1. *Select:* Probabilistically select $(1-r)p$ members of P to add to P_S.
  $$\Pr(h_i) = \frac{Fitness(h_i)}{\sum_{j=1}^{p} Fitness(h_j)}$$
  2. *Crossover:* Probabilistically select $\frac{r \cdot p}{2}$ pairs of hypotheses from P. For each pair, $\langle h_1, h_2 \rangle$, produce two offspring by applying the Crossover operator. Add all offspring to P_s.
  3. *Mutate:* Invert a randomly selected bit in $m \cdot p$ random members of P_s
  4. *Update:* $P \leftarrow P_s$
  5. *Evaluate:* for each h in P, compute $Fitness(h)$

- Return the hypothesis from P that has the highest fitness.

GABIL, DeJong et al, 1993

Learn disjunctive set of propositional rules, competitive with C4.5

Fitness:

$$Fitness(h) = (correct(h))^2$$

Representation:

IF $a_1 = T \wedge a_2 = F$ THEN $c = T$; IF $a_2 = T$ THEN $c = F$

represented by

a_1	a_2	c	a_1	a_2	c
10	01	1	11	10	0

Genetic operators: ???

- want variable length rule sets
- want only well-formed bitstring hypotheses

Crossover, variable length bitstrings

Start with

$$\begin{array}{lcccccc} & a_1 & a_2 & c & a_1 & a_2 & c \\ h_1: & 10 & 01 & 1 & 11 & 10 & 0 \\ h_2: & 01 & 11 & 0 & 10 & 01 & 0 \end{array}$$

1. choose crossover points for h_1, e.g., after bits 1, 8
2. now restrict points in h_2 to those that produce bitstrings with well-defined semantics, e.g., $\langle 1,3 \rangle$, $\langle 1,8 \rangle$, $\langle 6,8 \rangle$.

Crossover, variable length bitstrings

Start with

$$
\begin{array}{rcccccc}
 & a_1 & a_2 & c & a_1 & a_2 & c \\
h_1: & 10 & 01 & 1 & 11 & 10 & 0 \\
 & & & & & & \\
h_2: & 01 & 11 & 0 & 10 & 01 & 0
\end{array}
$$

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1. choose crossover points for h_1, e.g., after bits 1, 8
2. now restrict points in h_2 to those that produce bitstrings with well-defined semantics, e.g., $\langle 1, 3 \rangle$, $\langle 1, 8 \rangle$, $\langle 6, 8 \rangle$.

if we choose $\langle 1, 3 \rangle$, result is

$$\begin{array}{lccc} & a_1 & a_2 & c \\ h_3: & 11 & 10 & 0 \end{array}$$

$$\begin{array}{lccccccccc} & a_1 & a_2 & c & a_1 & a_2 & c & a_1 & a_2 & c \\ h_4: & 00 & 01 & 1 & 11 & 11 & 0 & 10 & 01 & 0 \end{array}$$

Extensions

Add new genetic operators, also applied probabilistically:

1. *AddAlternative*: generalize constraint on a_i by changing a 0 to 1
2. *DropCondition*: generalize constraint on a_i by changing every 0 to 1

And, add new field to bitstring to determine whether to allow these

a_1	a_2	c	a_1	a_2	c	AA	DC
01	11	0	10	01	0	1	0

So now the learning strategy also evolves!

Results

Performance of GABIL comparable to symbolic rule/tree learning methods C4.5, ID5R, AQ14

Average performance on a set of 12 synthetic problems:

- GABIL without AA and DC operators: 92.1% accuracy
- GABIL with AA and DC operators: 95.2% accuracy
- symbolic learning methods ranged from 91.2 to 96.6

Schemas

How to characterize evolution of population in GA?

Schema = string containing 0, 1, * ("don't care")

- Typical schema: 10**0*
- Instances of above schema: 101101, 100000, ...

Characterize population by number of instances representing each possible schema

- $m(s, t)$ = number of instances of schema s in pop at time t

Schemas

- $\bar{f}(t)$ = average fitness of pop. at time t
- $m(s,t)$ = instances of schema s in pop at time t
- $\hat{u}(s,t)$ = ave. fitness of instances of s at time t

Probability of selecting h in one selection step

$$\begin{aligned}\Pr(h) &= \frac{f(h)}{\sum_{i=1}^{n} f(h_i)} \\ &= \frac{f(h)}{n\bar{f}(t)}\end{aligned}$$

Probabilty of selecting an instance of s in one step

$$\begin{aligned}\Pr(h \in s) &= \sum_{h \in s \cap p_t} \frac{f(h)}{n\bar{f}(t)} \\ &= \frac{\hat{u}(s,t)}{n\bar{f}(t)} m(s,t)\end{aligned}$$

Expected number of instances of s after n selections

$$E[m(s,t+1)] = \frac{\hat{u}(s,t)}{\bar{f}(t)} m(s,t)$$

Schema Theorem

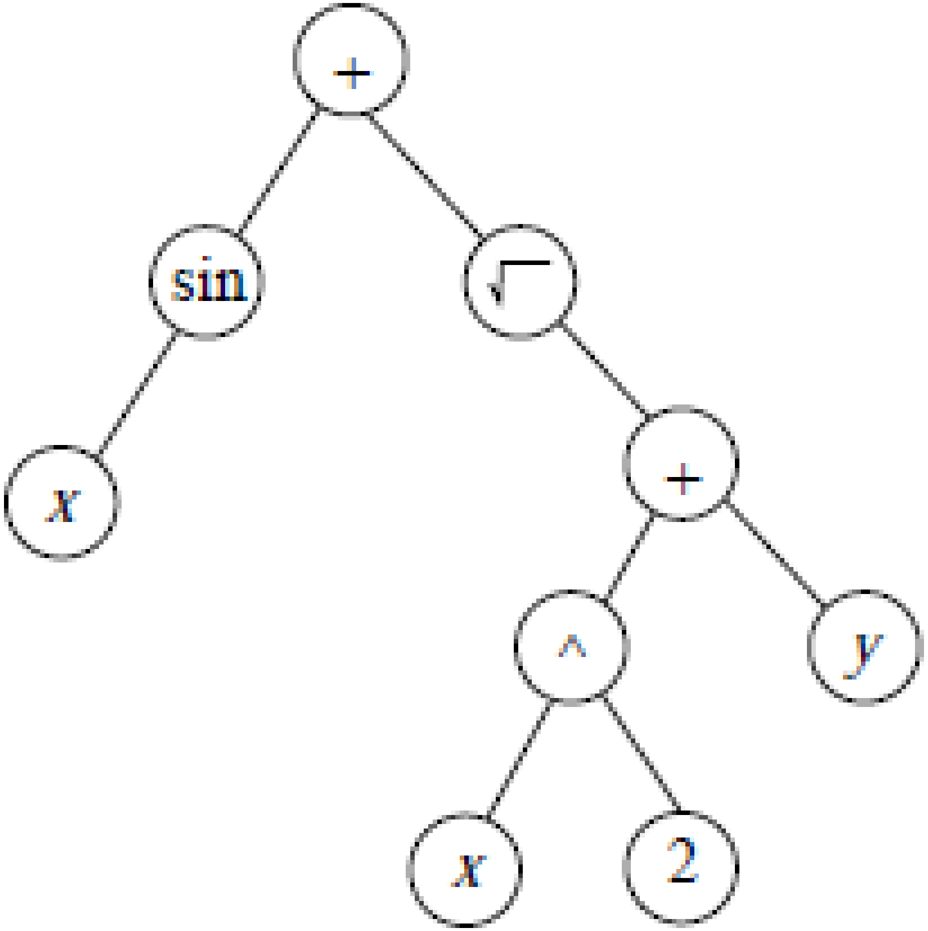
$$E[m(s,t+1)] \geq \frac{\hat{u}(s,t)}{\bar{f}(t)} m(s,t) \left(1 - p_c \frac{d(s)}{l-1}\right) (1-p_m)^{o(s)}$$

- $m(s,t)$ = instances of schema s in pop at time t
- $\bar{f}(t)$ = average fitness of pop. at time t
- $\hat{u}(s,t)$ = ave. fitness of instances of s at time t
- p_c = probability of single point crossover operator
- p_m = probability of mutation operator
- l = length of single bit strings
- $o(s)$ number of defined (non "*") bits in s
- $d(s)$ = distance between leftmost, rightmost defined bits in s

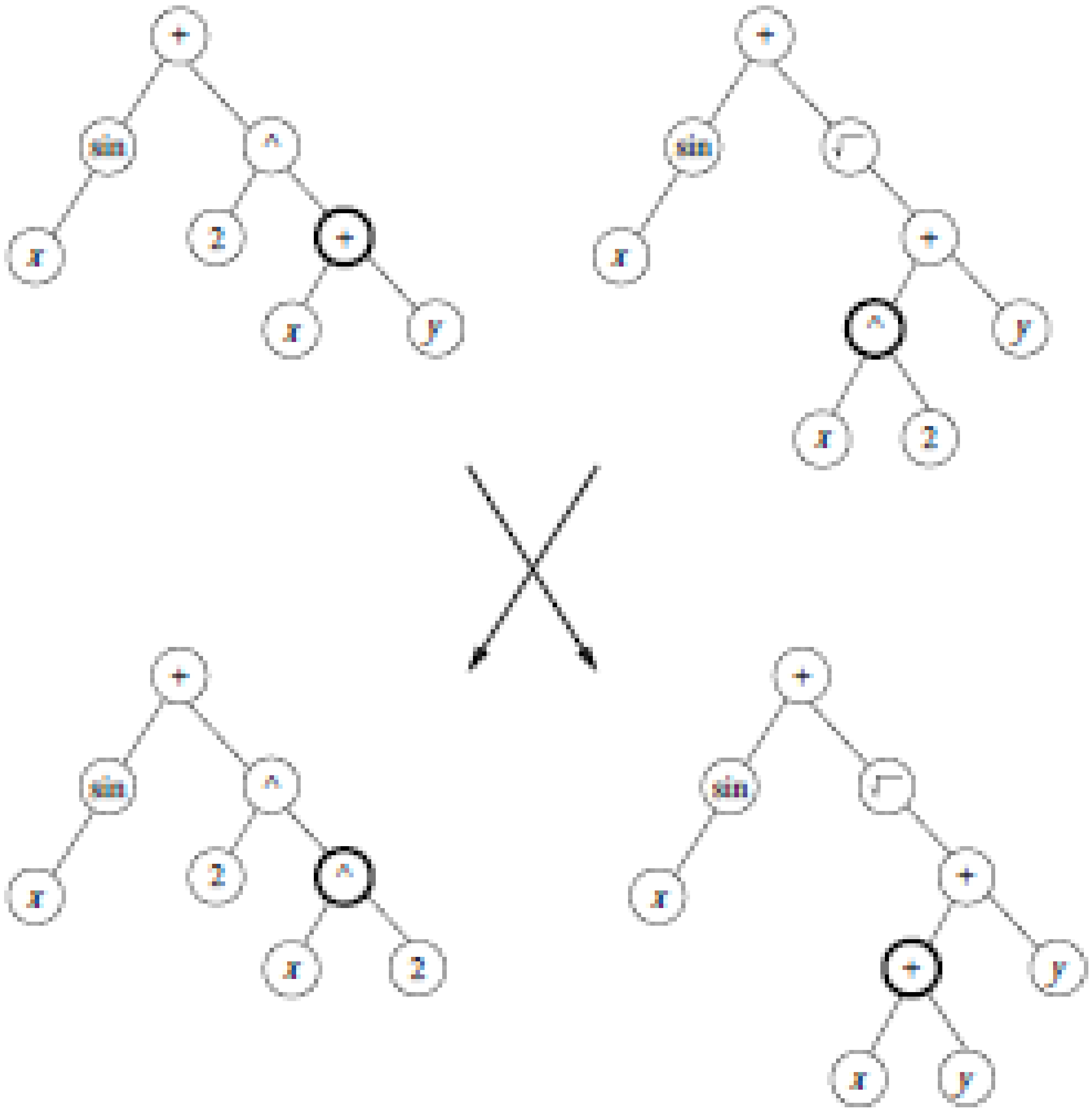
Genetic Programming

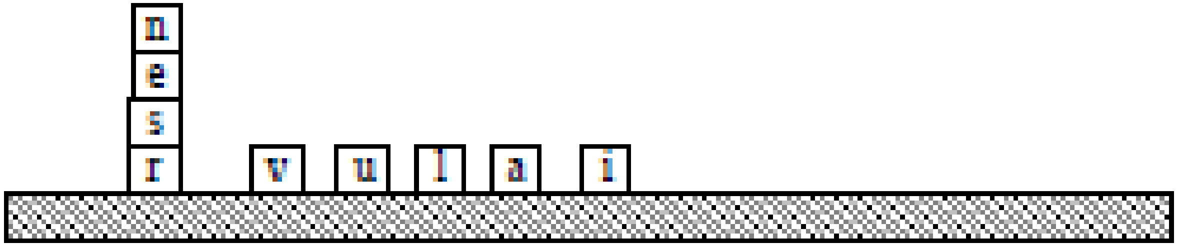
Population of programs represented by trees

$$\sin(x) + \sqrt{x^2 + y}$$



Crossover





Goal: spell UNIVERSAL

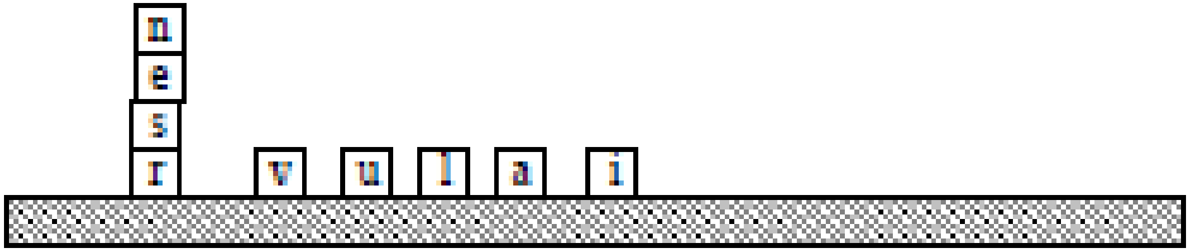
Terminals:

- CS ("current stack") = name of the top block on stack, or F.
- TB ("top correct block") = name of topmost correct block on stack
- NN ("next necessary") = name of the next block needed above TB in the stack

Primitive functions:

- (MS x): ("move to stack"), if block x is on the table, moves x to the top of the stack and returns the value T. Otherwise, does nothing and returns the value F.
- (MT x): ("move to table"), if block x is somewhere in the stack, moves the block at the top of the stack to the table and returns the value T. Otherwise, returns F.
- (EQ x y): ("equal"), returns T if x equals y, and returns F otherwise.
- (NOT x): returns T if $x = F$, else returns F
- (DU x y): ("do until") executes the expression x repeatedly until expression y returns the value T

Genetic Programming



Goal: spell UNIVERSAL

Trained to fit 166 test problems

Using population of 300 programs, found this after 10 generations:

(EQ (DU (MT CS)(NOT CS)) (DU (MS NN)(NOT NN)))

More interesting example: design electronic filter circuits

- Individuals are programs that transform begining circuit to final circuit, by adding/subtracting components and connections
- Use population of 640,000, run on 64 node parallel processor
- Discovers circuits competitive with best human designs

Lamark, 19th century

- Believed individual genetic makeup was altered by lifetime experience
- But current evidence contradicts this view

What is the impact of individual learning on population evolution?

Baldwin Effect

Assume

- Individual learning has no direct influence on individual DNA
- But ability to learn reduces need to "hard wire" traits in DNA

Then

- Ability of individuals to learn will support more diverse gene pool
  - Because learning allows individuals with various "hard wired" traits to be successful
- More diverse gene pool will support faster evolution of gene pool

→ individual learning (indirectly) increases rate of evolution

Baldwin Effect

Plausible example:

1. New predator appears in environment
2. Individuals who can learn (to avoid it) will be selected
3. Increase in learning individuals will support more diverse gene pool
4. resulting in faster evolution
5. possibly resulting in new non-learned traits such as instintive fear of predator

Baldwin Effect

[Hinton and Nowlan, 1987]

Evolve simple neural networks:

- Some network weights fixed during lifetime, others trainable
- Genetic makeup determines which are fixed, and their weight values

Results:

- With no individual learning, population failed to improve over time
- When individual learning allowed
  - Early generations: population contained many individuals with many trainable weights
  - Later generations: higher fitness, while number of trainable weights decreased