DESIGNING NEURAL NETWORKS USING GENE EXPRESSION PROGRAMMING

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PLAN

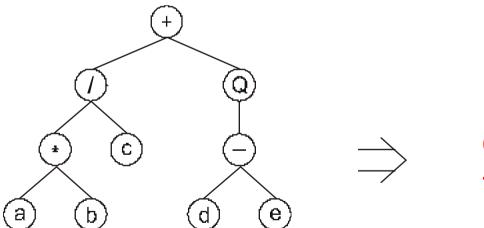
- 1. Representing trees in GEP
- 2. GEP genes
- 3. Multigenic chromosomes
- 4. Representing ANNs in GEP
- 5. Evolving the neural network architecture
- 6. Example: Intragenic two-point recombination
- 7. Fine-tuning the weights/thresholds
- 8. Example: Domain-specific transposition
- 9. XOR: Parameters and performance
- 10. XOR: Two perfect solutions
- 11. 6-Multiplexer: Parameters and performance
- 12. 6-Multiplexer: A perfect unigenic solution
- 13. 6-Multiplexer: A perfect multigenic solution

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REPRESENTING TREES IN GEP

$$\frac{a \cdot b}{c} + \sqrt{d - e}$$



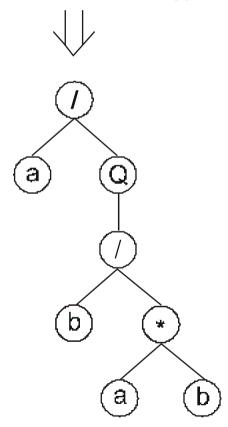


0123456789 +/Q*c-abde

GEP GENES

0123456789012345678901234567890 /aQ/b*ab/Qa*b*-ababaababbabbba

head



tail

$$t = h (n-1) + 1$$

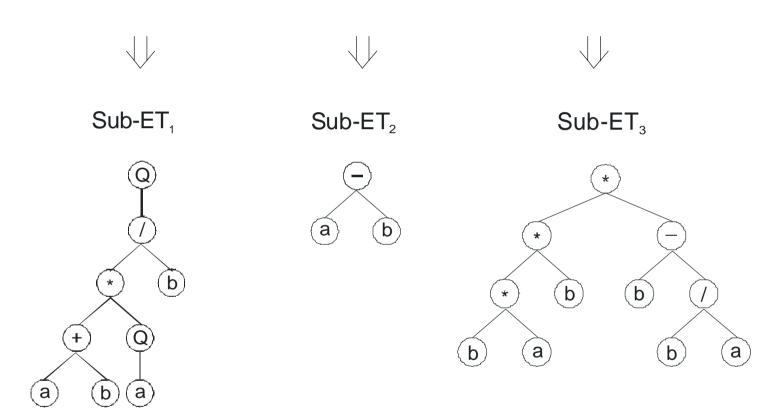
h - head length

t - tail length

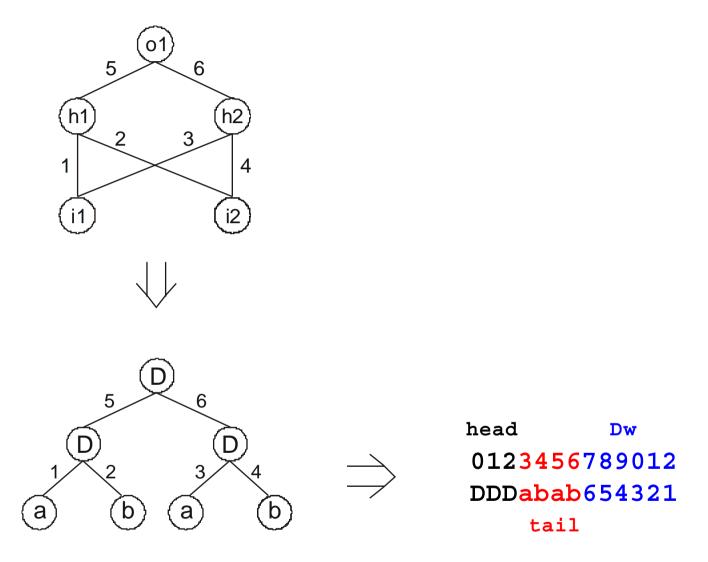
n - max arity

MULTIGENIC CHROMOSOMES

012345678901234012345678901234012345678901234 Q/*b+Qababaabaa-abQ/*+bababbab**-*bb/babaaaab



REPRESENTING ANNS IN GEP



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EVOLVING THE NEURAL NETWORK ARCHITECTURE

Genetic Operators:

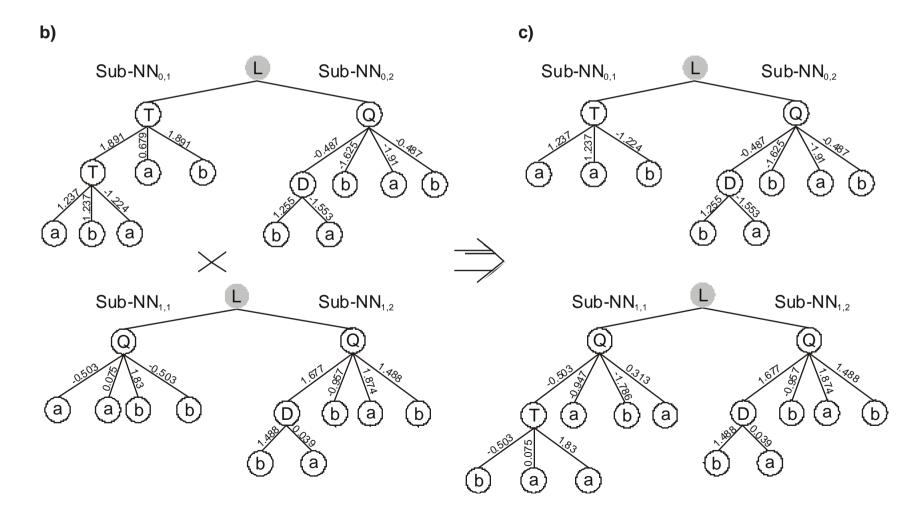
- » Mutation
- » Transposition
 - » IS Transposition
 - » RIS Transposition
 - » Gene Transposition
- » Recombination
 - » One-point Recombination
 - » Intragenic Two-point Recombination

Example: Intragenic Two-point Recombination

a) 0123456789012345601234567890123456 TTababaab14393255QDbabbabb96369304-[0] Qaabbbabb97872192QDbabbaaa81327963-[1]

0123456789012345601234567890123456 Taabbbabb97893255QDbabbabb96369304-[0] QTababaab14372192QDbabbaaa81327963-[1] $W_{0.1} = \{-0.78, -0.521, -1.224, 1.891, 0.554, 1.237, -0.444, 0.472, 1.012, 0.679\}$ $W_{0.2} = \{-1.553, 1.425, -1.606, -0.487, 1.255, -0.253, -1.91, 1.427, -0.103, -1.625\}$

 $\begin{aligned} W_{_{1,1}} &= \{-0.148, 1.83, -0.503, -1.786, 0.313, -0.302, 0.768, -0.947, 1.487, 0.075\} \\ W_{_{1,2}} &= \{-0.256, -0.026, 1.874, 1.488, -0.8, -0.804, 0.039, -0.957, 0.462, 1.677\} \end{aligned}$



FINE-TUNING THE WEIGHTS/THRESHOLDS

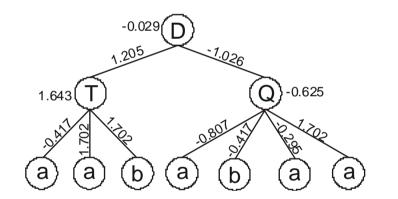
Genetic Operators:

- » Domain-specific Mutation
- » Domain-specific Transposition
- » Direct Mutation of Weights/Thresholds

Example: Domain-specific Transposition

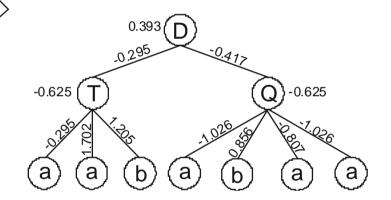
01234567890123456**7890123456789012**3456 DTQaababaabbaabba**0571745736284668**2867

$$\begin{split} W_{\scriptscriptstyle m} &= \{\text{-1.64, -1.834, -0.295, 1.205, -0.807, 0.856, 1.702,} \\ &\quad -1.026, \text{-0.417, -1.061} \} \\ T_{\scriptscriptstyle m} &= \{\text{-1.14, 1.177, -1.179, -0.74, 0.393, 1.135, -0.625,} \\ &\quad 1.643, \text{-0.029, -1.639} \} \end{split}$$



01234567890123456**7890123456789012**3456 DTQaababaabbaabba**0571466827457362**8466

$$\begin{split} W_d &= \{-1.64, -1.834, -0.295, 1.205, -0.807, 0.856, 1.702, \\ &-1.026, -0.417, -1.061\} \\ T_d &= \{-1.14, 1.177, -1.179, -0.74, 0.393, 1.135, -0.625, \\ &1.643, -0.029, -1.639\} \end{split}$$



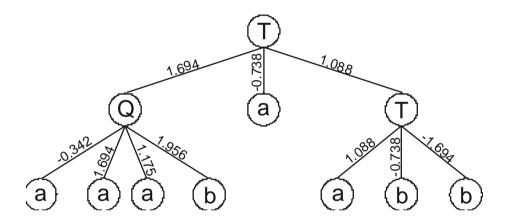
XOR: PARAMETERS AND PERFORMANCE

	Redundant System	Compact System
Number of runs	100	100
Number of generations	50	50
Population size	30	30
Number of fitness cases	4	4
Function set	DTQ	DTQ
Terminal set	аb	a b
Weights array length	10	10
Weights range	[-2, 2]	[-2, 2]
Head length	4	2
Number of genes	1	1
Chromosome length	33	17
Mutation rate	0.061	0.118
One-point recombination rate	0.7	0.7
IS transposition rate	0.1	
IS elements length	1	
RIS transposition rate	0.1	
RIS elements length	1	
Dw specific transposition rate	0.1	0.1
Dw specific IS elements length	2,3,5	2,3,5
Success rate	77%	30%

XOR: Two Perfect Solutions

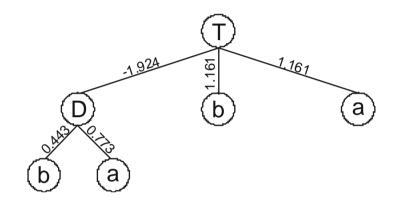
1.

012345678901234567890123456789012 TQaTaaababbbabaaa6085977238275036 W = {1.175, 0.315, -0.738, 1.694, -1.215, 1.956, -0.342, 1.088, -1.694, 1.288}



2.

 $\begin{array}{l} 01\,23\,45\,678\,9012\,3456 \\ \text{TDbabaabb}\,88\,39\,98\,37 \\ W = \{0.713,\,-0.774,\,-0.221,\,0.773,\,-0.789,\,1.792,\,-1.77,\,\\ 0.443,\,-1.924,\,1.161\} \end{array}$

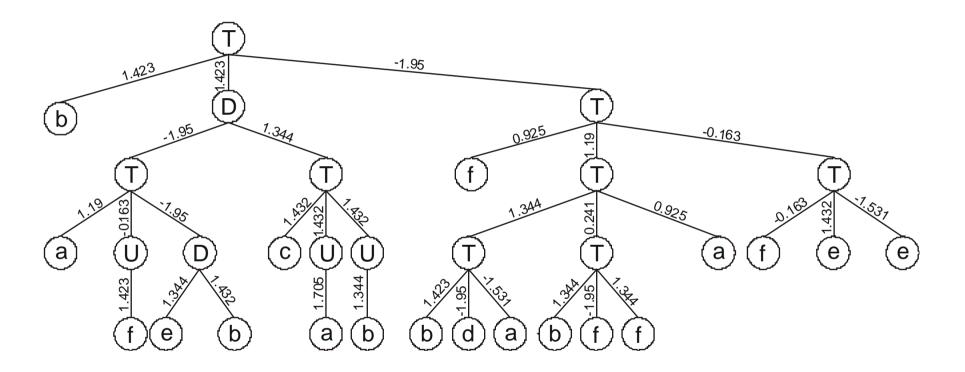


6-Multiplexer: Parameters and Performance

	Unigenic System	Multigenic System
Number of runs	100	100
Number of generations	2000	2000
Population size	50	50
Number of fitness cases	64	64
Function set	3U 3D 3T	3U 3D 3T
Terminal set	abcddef	abcddef
Linking function		0
Weights array length	10	10
Weights range	[-2, 2]	[-2, 2]
Head length	17	5
Number of genes	1	4
Chromosome length	103	124
Mutation rate	0.044	0.044
Intragenic two-point recombination rate	0.6	0.6
Gene recombination rate		0.1
Gene transposition rate		0.1
IS transposition rate	0.1	0.1
IS elements length	1,2,3	1,2,3
RIS transposition rate	0.1	0.1
RIS elements length	1,2,3	1,2,3
Weights mutation rate	0.002	0.002
Dw specific transposition rate	0.1	0.1
Dw specific IS elements length	2,3,5	2,3,5
Success rate	4%	6%

6-Multiplexer: A Perfect Unigenic Solution

$$\label{eq:decomposition} \begin{split} \text{TbDTTTfTTaUDcUUTTafeefebabbdabffddfcfeeeabcabfabdcfe...} \\ \text{...} 709761631479459597193997465381760511137453583952159} \\ W = \{0.241, 1.432, 1.705, -1.95, 1.19, 1.344, 0.925, -0.163, -1.531, 1.423\} \end{split}$$

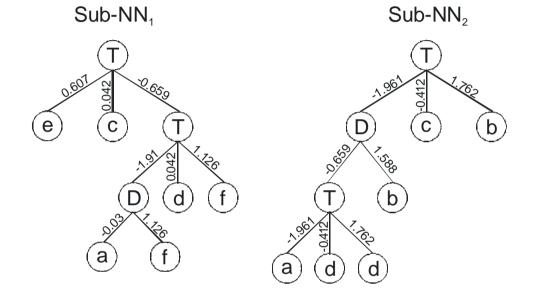


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6-Multiplexer: A Perfect Multigenic Solution

TecTDdfafabdddfa487674791701403 TDcbTbadddfceacc501702156029560 TfTTUbadbcdffdce593993321226318 TDTbaceaaeeacacd072636270049968

$$\begin{split} W_1 &= \{1.126, 0.042, 1.588, -0.03, -1.91, 1.83, -0.412, 0.607, -0.294, -0.659\} \\ W_2 &= \{-1.961, 1.161, 1.588, -0.03, -1.91, 1.762, -0.412, -0.121, -0.294, -0.659\} \\ W_3 &= \{1.558, -0.69, 0.921, 0.134, 0.468, -1.534, 0.966, 1.399, 0.023, 0.915\} \\ W_4 &= \{1.558, 0.767, 0.076, 0.071, 0.468, -1.534, 1.387, -1.857, -1.88, 0.331\} \end{split}$$



Note: Sub-NNs linked by OR

