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Enhancements to a hybrid genetic programming technique applied to symbolic regression

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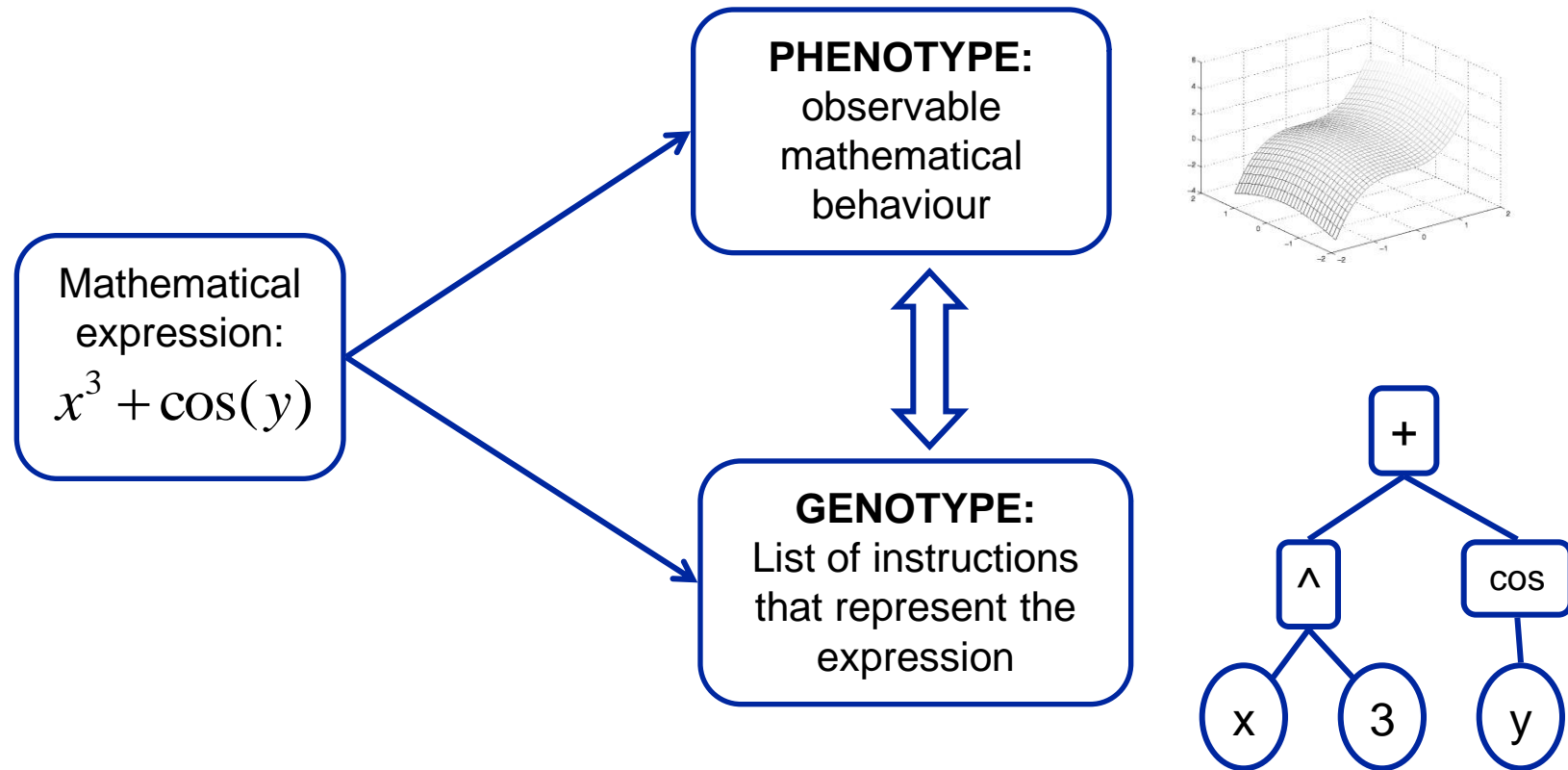
A brief reminder: tree-based hybrid GP applied to symbolic regression

Symbolic Regression:



Tree-based GP:

- individuals are represented by the expressions' syntax trees
- genetic modifications are performed on syntax trees

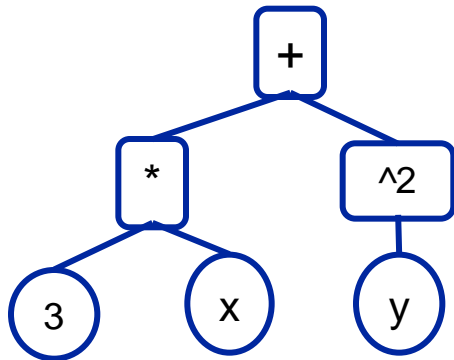


Conventional GP and Hybrid GP : Genotype

Conventional GP:

- constants are treated like common nodes and do participate in genetic operations.

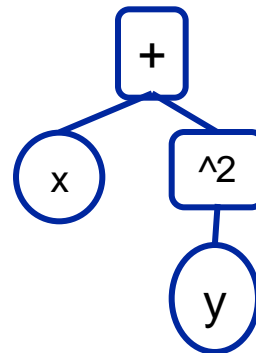
Genotype = individual



Hybrid GP:

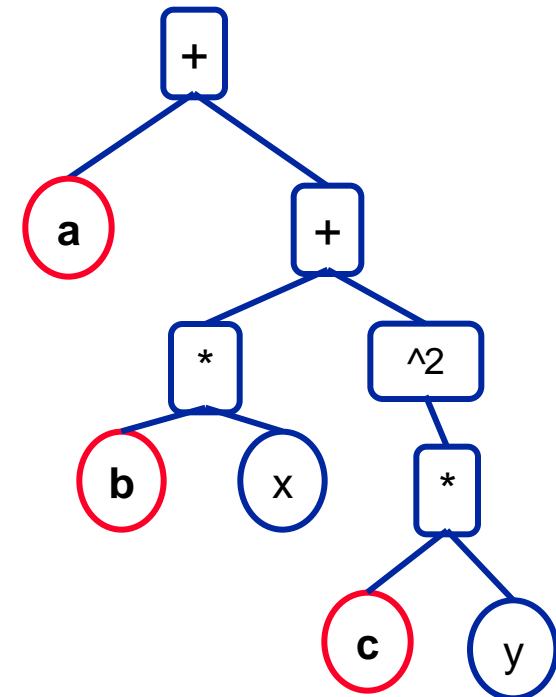
- constants do not participate in genetic operations. They are added afterwards, their location and their values being optimised (see **a**, **b**, **c** below).
- a “**structure**”, or individual without parameters, represents a family of expressions

Genotype

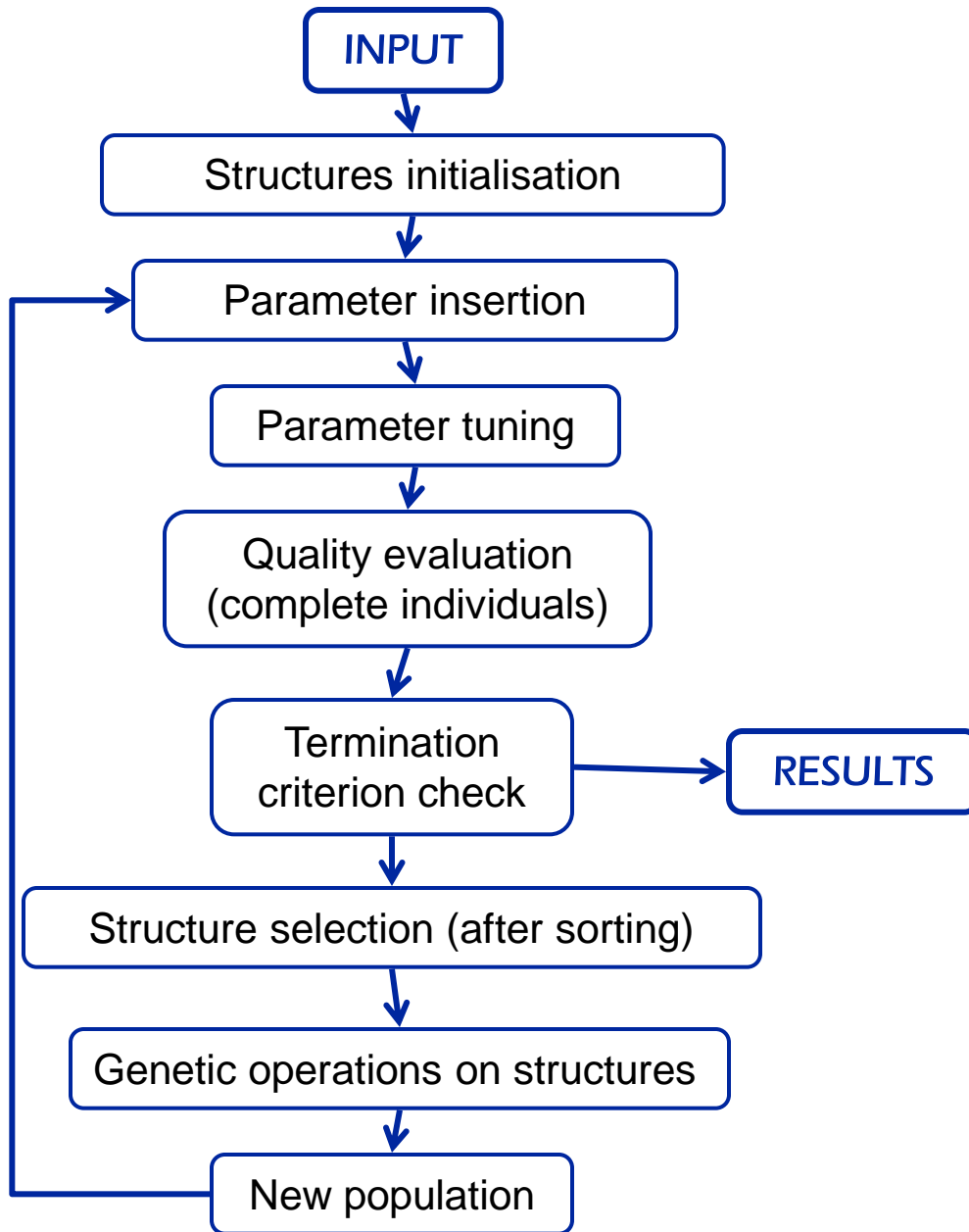


≠

individual



Hybrid Genetic Programming Algorithm



Functions (cos(), ^, +,...), Variables (x,y, ...)
training data set (and **validation set**)

"Structures": trees without parameters
(ramped half and half method is used)

Deterministic algorithm: the number of parameters is reduced to the minimum

Deterministic algorithm (SQP)

Fitness value: weighted sum of different objectives (RMSE, no of singularities, no of tuning parameters, no of nodes)

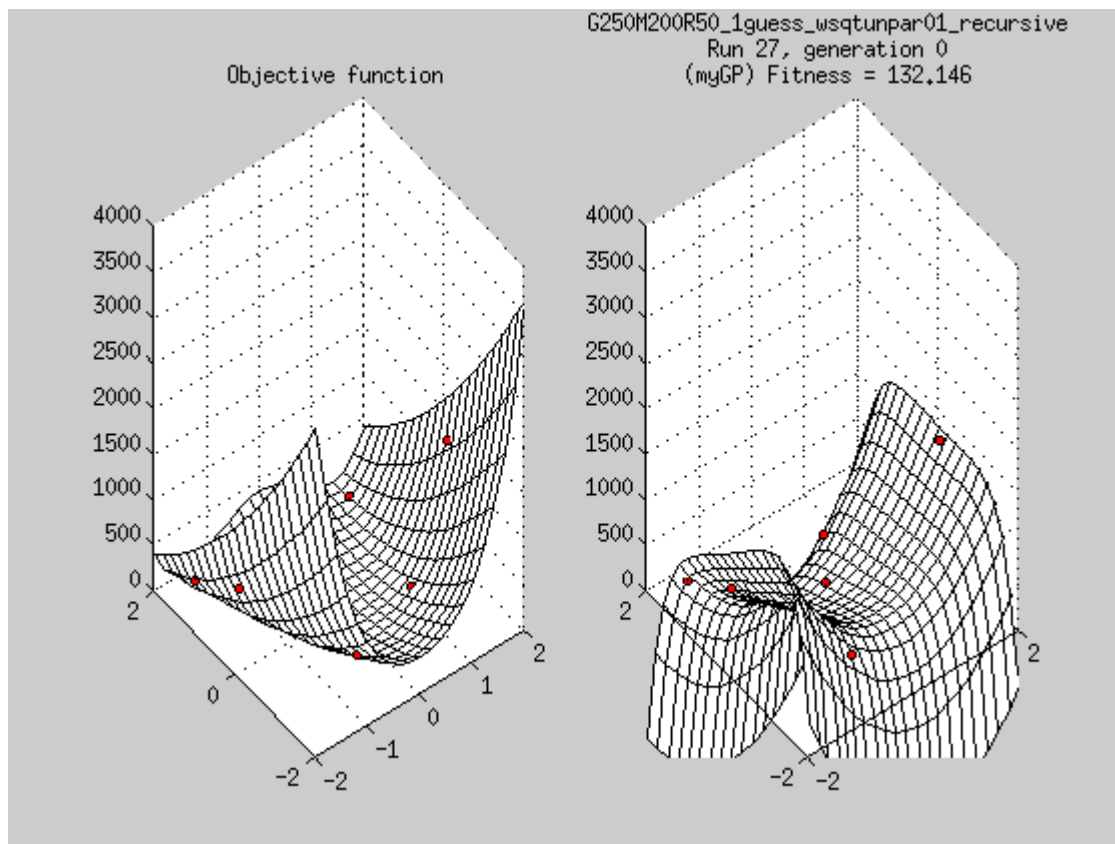
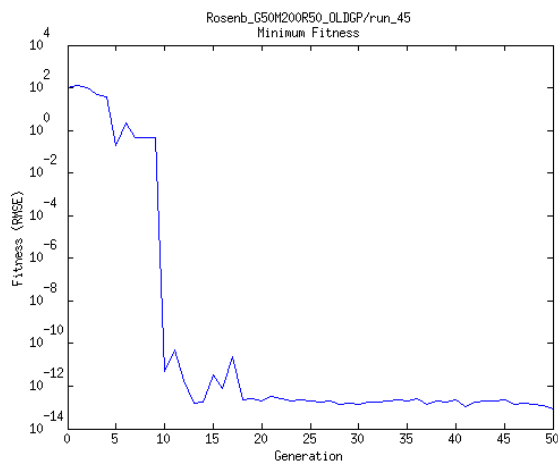
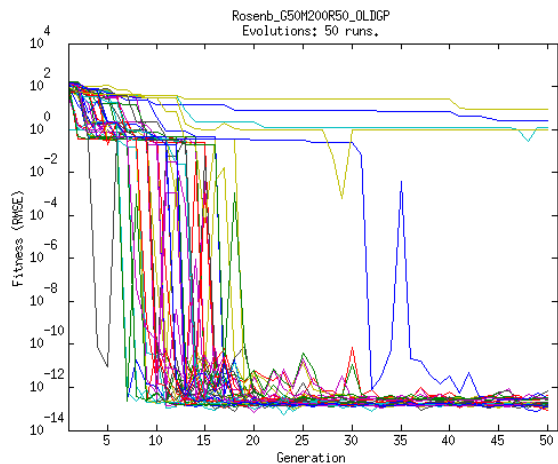
The **fitness value** is inherited from the corresponding tree with parameters

Variation of the structure of the syntax trees (no parameters)

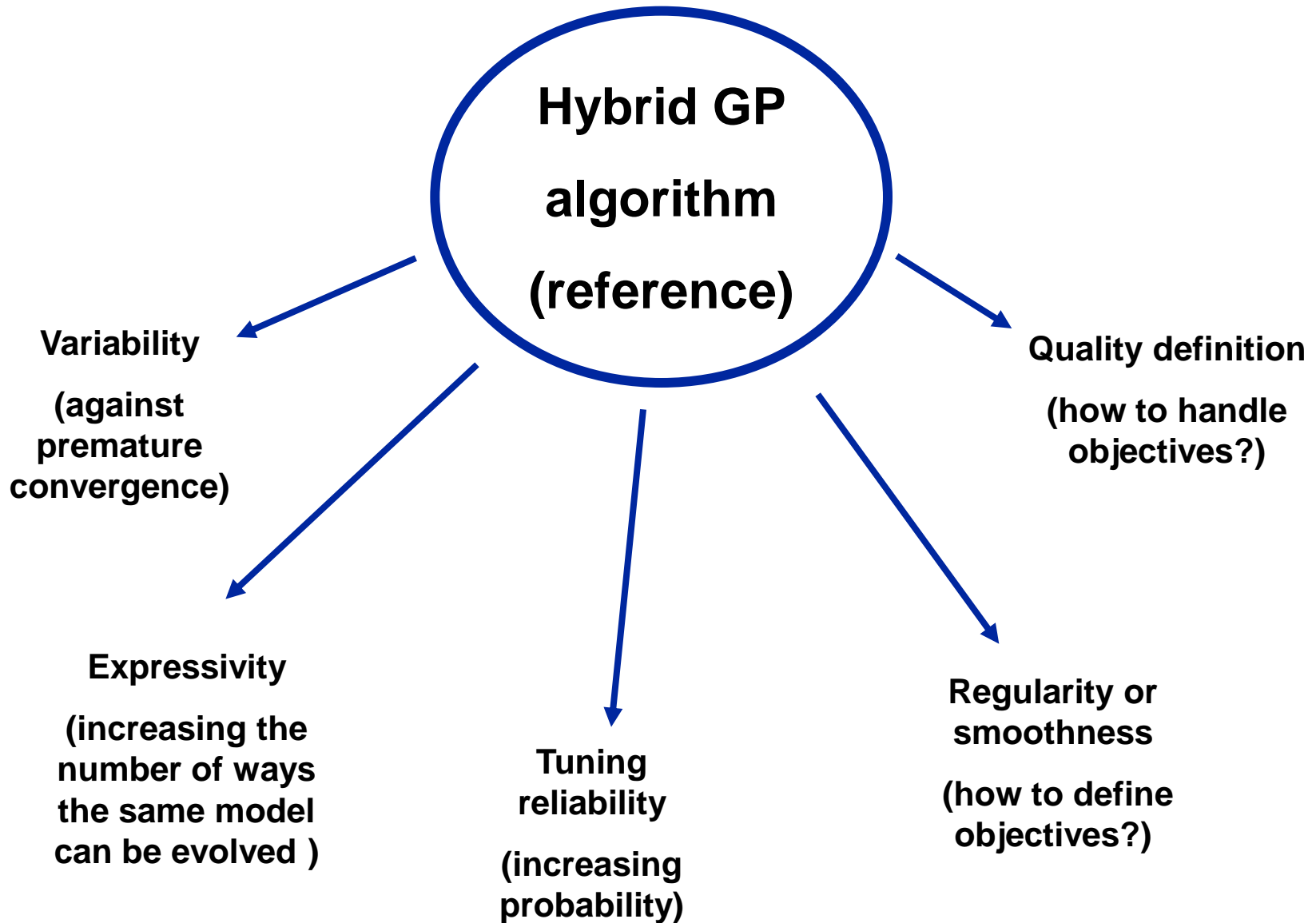
A few inspiring graphical results

Rosenbrock function: $f(z_1, z_2) = 100(z_2 - z_1^2)^2 + (1 - z_1)^2$

Expression returned by hybrid GP: $1.000000 + 1.000000Z1^2 - 2.000000Z1 + (-10.000000Z1^2 + 10.000000Z2)^2$



Can hybrid GP be further improved?



New hybrid GP implementations – 1

With_COPIES : copies are removed from the elite of individuals copied to the new generation

10guesses : increased number of initial guesses for SQP algorithm (10 vs. 2 used normally)

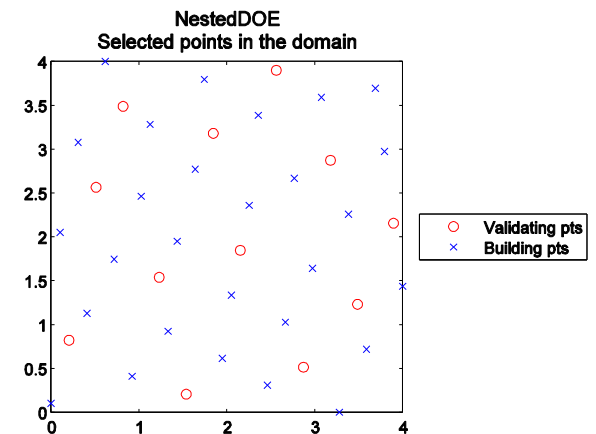
KILLandFILL : periodical elimination of 60% of the population. Empty places are filled with newly generated or “joined” individuals

Shift : added a new operation that can be selected by GP. It introduces a translation of the argument, increasing the number of ways the same model or surrogate can be built:

$$z_1 * z_2 \Rightarrow a_0 + a_1 z_1 z_2$$

$$z_1 * \text{shift}(z_2) \Rightarrow a_0 + z_1(a_1 + a_2 z_2)$$

NestedDOE : training data set is split in two subsets: one used for model building, the other for model evaluation. The split is made in order to have optimal latin hypercube distribution in the subsets and in the merged set.



New hybrid GP implementations – 2

normFIT : normalisation of the main objective of the fitness function:

$$F_1(i, t) = RMSNE(i, t) \quad RMSNE(i, t) = \sqrt{\frac{1}{m} \sum_{j=1}^m \left(\frac{\hat{f}_j(i, t) - f_j}{f_j} \right)^2}$$

normFITdiv : as normFIT, by the main objective is divided by the average RMSNE at the previous generation:

$$F_1(i, t) = RMSNE(i, t) / \overline{RMSNE}(t-1)$$

MinMax : redefinition of the fitness function:

$$F(i, t) = \max \left\{ 10a_1 F_1(i, t), a_2 F_2(i, t), 10^6 F_3(i, t), a_4 F_4(i, t) \right\}$$

$$a_1 + a_2 + a_3 + a_4 = 1$$

Omegalim: an additional algorithm recognises “pulsations” and prevents “high-pulsation” noise:

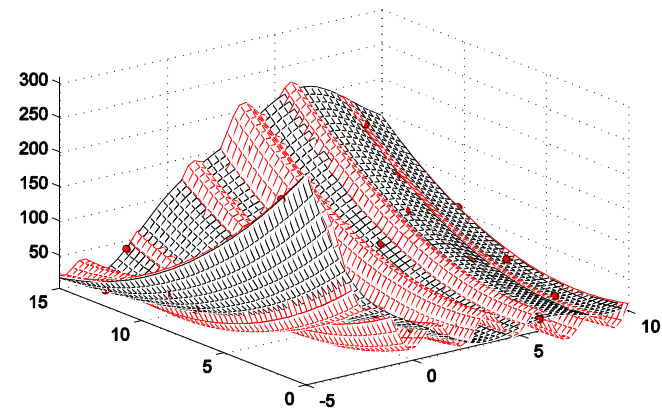
$$\sin(cz_i) \Rightarrow a_{k,i} = c$$

$$\cos(cz_i) \Rightarrow a_{k,i} = c$$

Penalisation if

$$a_{i,k} \notin [-\omega_{i,\text{lim}}, \omega_{i,\text{lim}}]$$

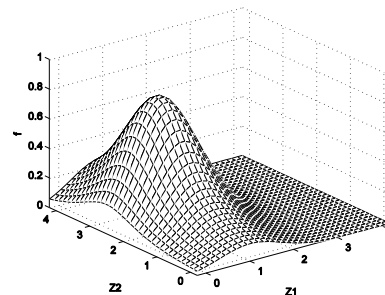
$$NP_{\text{max}} \rightarrow \omega_{i,\text{lim}} = \frac{2\pi * NP_{\text{max}}}{r_i}$$



Test problems

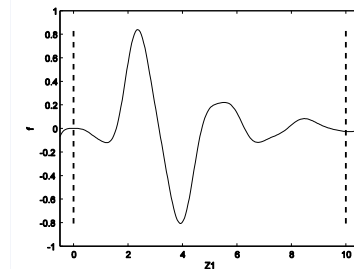
- Kotanchek function:

$$f(x_1, x_2) = e^{-x} x^3 \cos(x) \sin(x) [\cos(x) \sin^2(x) - 1]$$



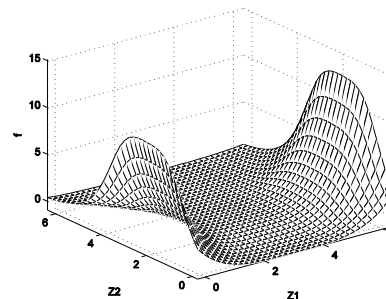
- Salustowicz function:

$$f(x_1, x_2) = e^{-x} x^3 \cos(x) \sin(x) [\cos(x) \sin^2(x) - 1]$$



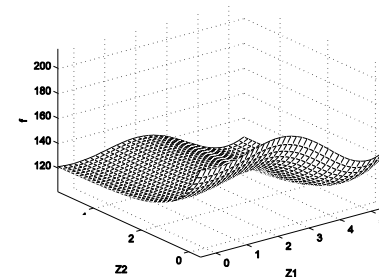
- RatPol2D function:

$$f(x_1, x_2) = \frac{(x_1 - 3)^4 + (x_2 - 3)^3 - (x_2 - 3)}{(x_2 - 2)^4 + 10}$$



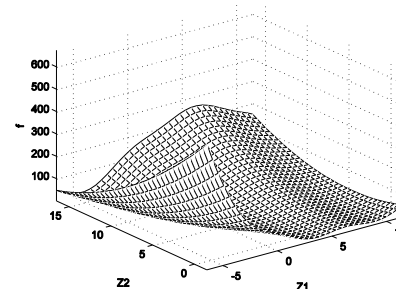
- Hock function:

$$f(x_1, x_2) = [30 + x_1 \sin(x_1)] [4 + \exp(-x_2)]$$

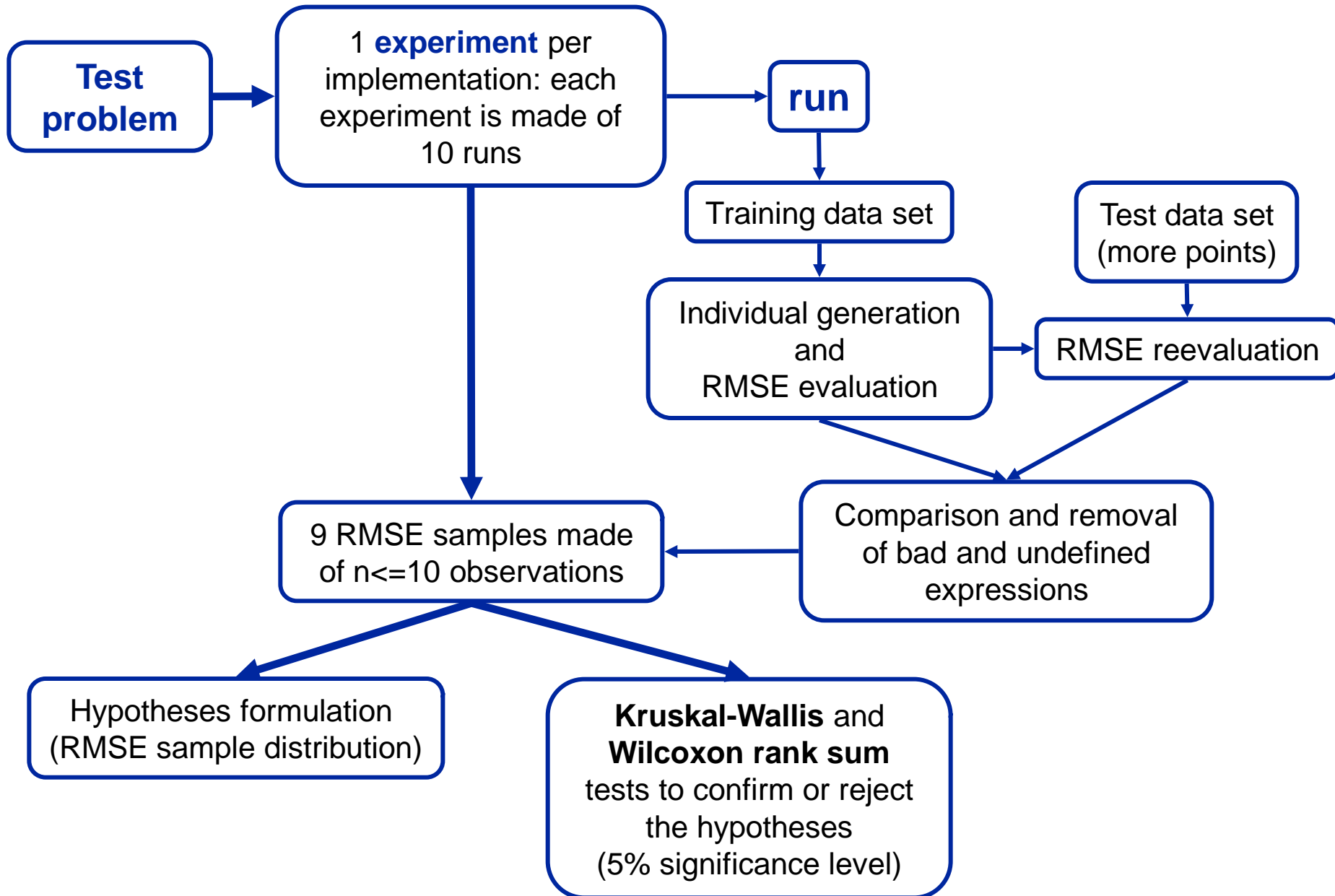


- Branin-Hoo function:

$$f(x_1, x_2) = \left(x_2 - \frac{5.1x_1^2}{4\pi^2} + \frac{5x_1}{\pi} - 6 \right)^2 + 10 \left(1 - \frac{1}{8\pi} \right) \cos(x_1) + 10$$



How results are analysed



Are copies beneficial to the evolution?

P-values from the comparison of Reference vs. with_COPIES on the five test problems (Wilcoxon rank sum test):

NULL hypothesis: reference and with_COPIES have the same median	<i>p</i> -values	
	ANOVA	Wilcoxon
Kotanchek	0.9053	0.2775
Salustowicz	0.1806	0.6667
RatPol2D	0.6072	0.5490
Hock	0.1100	0.0640
Branin-Hoo	0.5576	0.6064

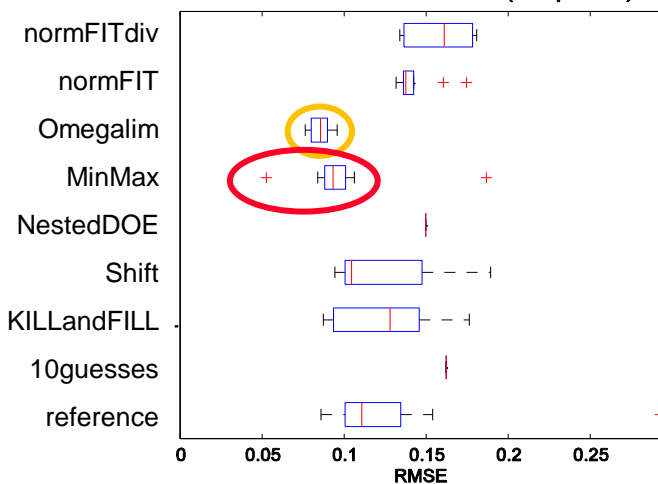
Salustowicz and Branin-Hoo:
high percentage (90% and
50%) of individuals generated
by **reference** are undefined

NO significant evidence of a
difference in RMSE median
according to ANOVA and Wilcoxon
rank sum test. Larger samples are
needed!

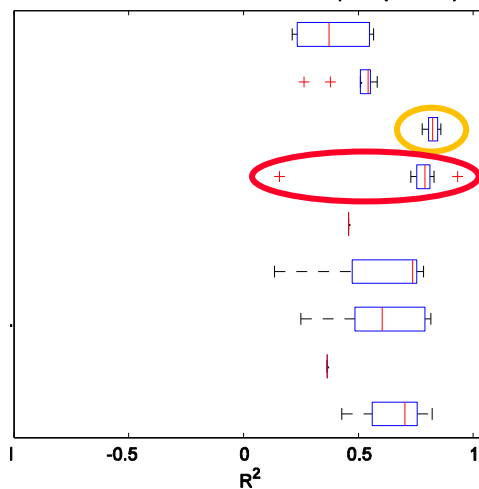
However, in all the
following
experiments copies
are removed from
the elite!

Kotanchek test problem

RMSE on test data
Distribution of best individuals (one per run)



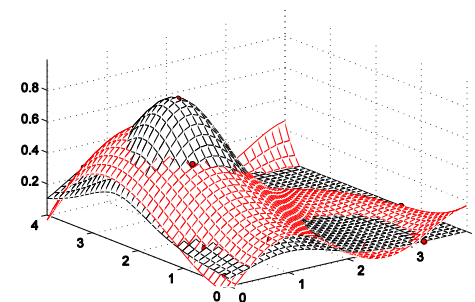
R² on test data
Distribution of best individuals (one per run)



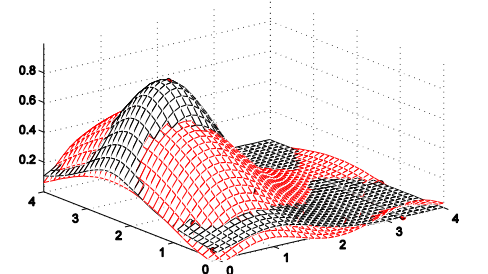
NestedDOE: 9 out of 10 expressions not defined on the test data set!

p-value from Kruskal-Wallis = 4.7E-7

omegalim

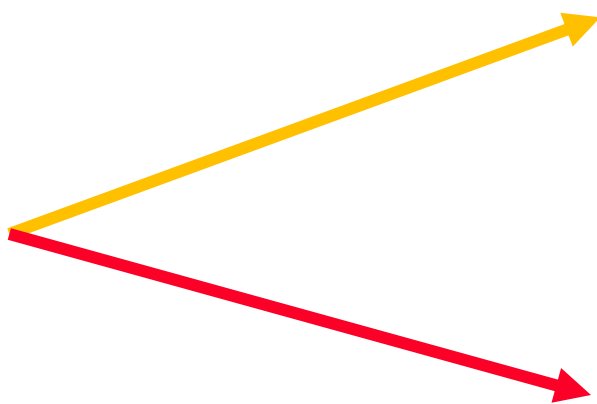
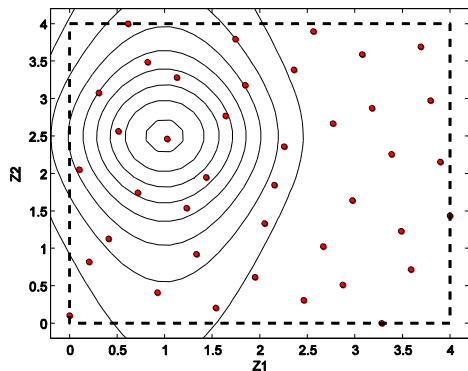


MinMax



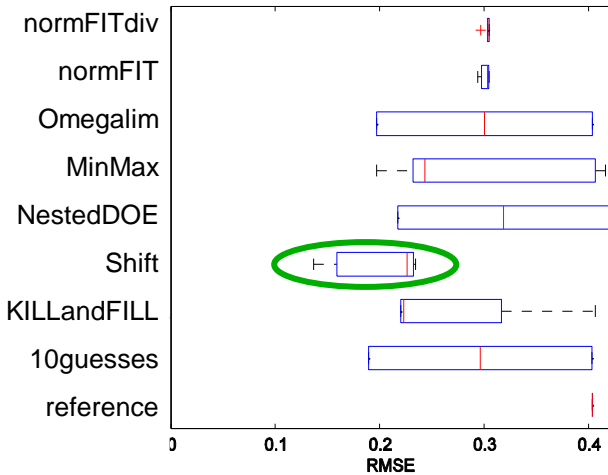
Training data set: 40 points

Test data set: 2025 points

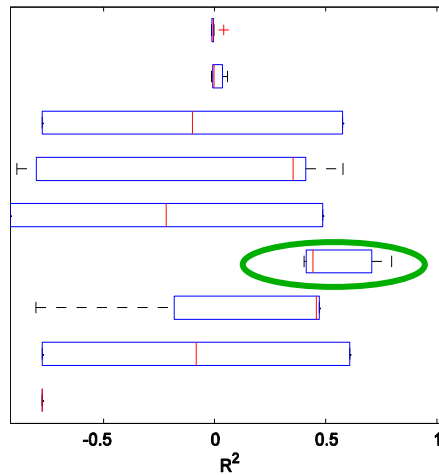


Salustowicz problem

RMSE on test data
Distribution of best individuals (one per run)



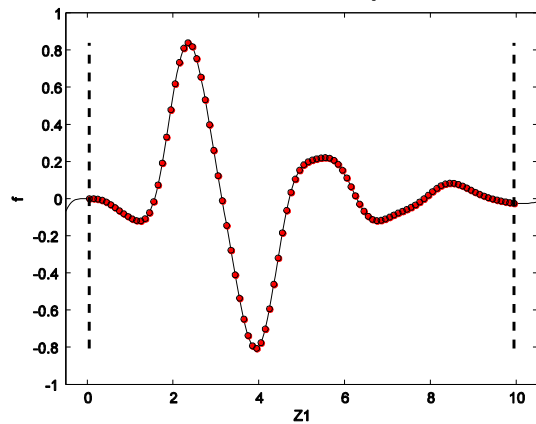
R^2 on test data
Distribution of best individuals (one per run)



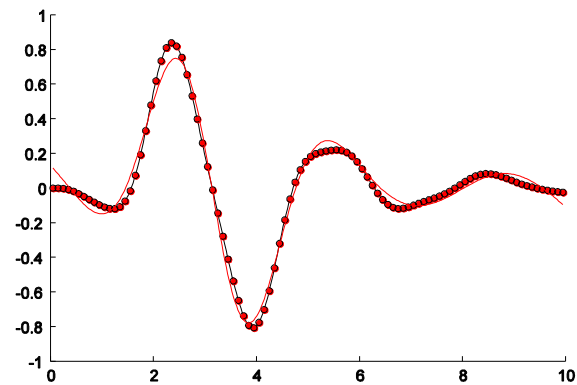
On average 60% of the expressions generated by each implementation are not defined on the test data set!
p-value from Kruskal-Wallis = 0.5675

Training data set: 100 points

Test data set: 221 points

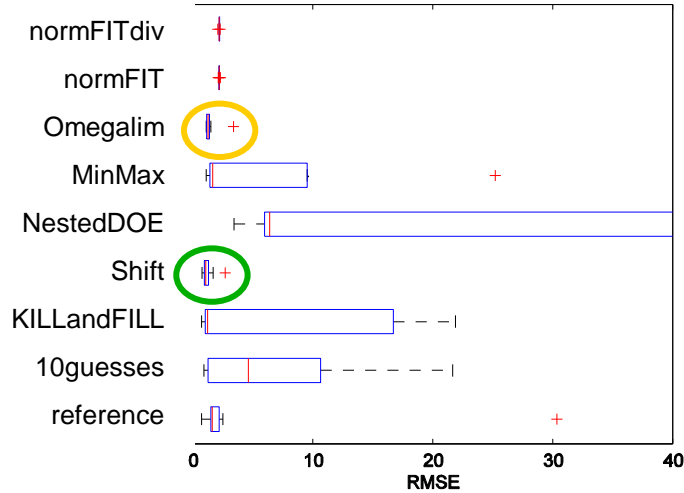


shift

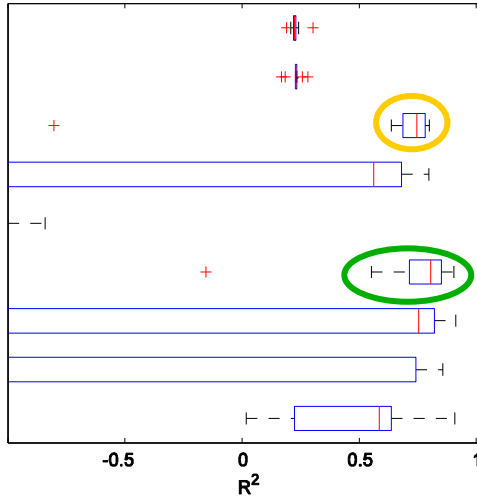


RatPol2D problem

RMSE on test data
Distribution of best individuals (one per run)



R² on test data
Distribution of best individuals (one per run)

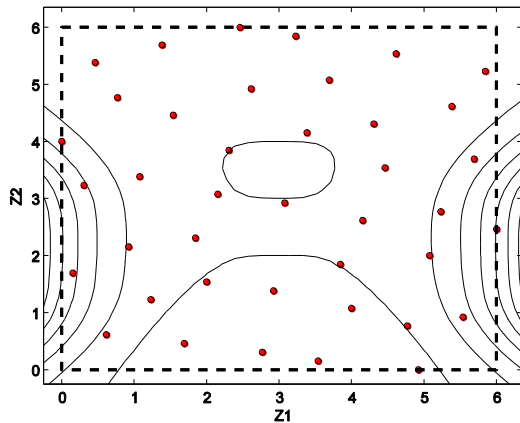


All the expressions generated are defined on the test data set.

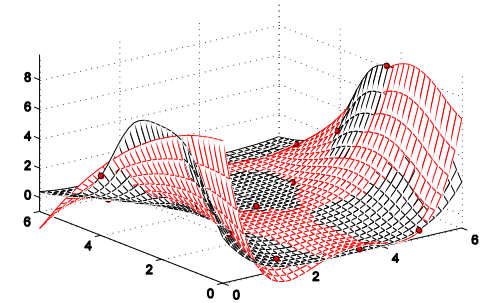
p-value from Kruskal-Wallis =
5.97E-5

Training data set: 40 points

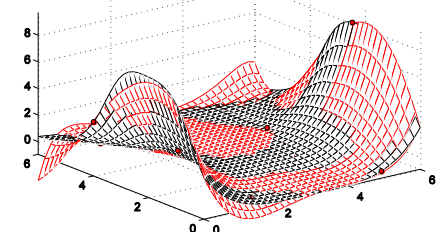
Test data set: 1156 points



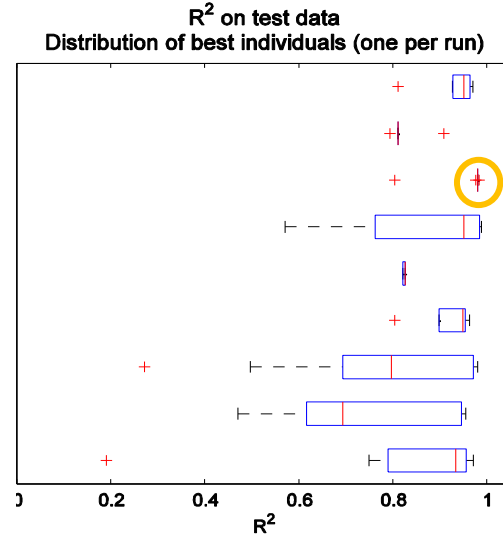
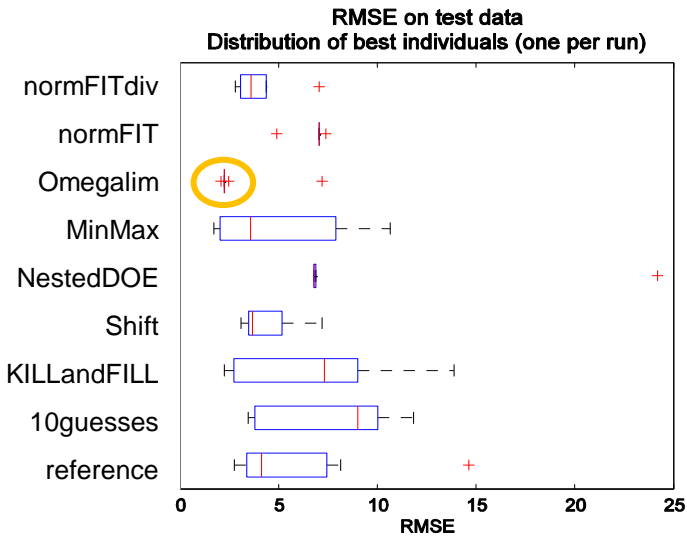
omegalim



shift



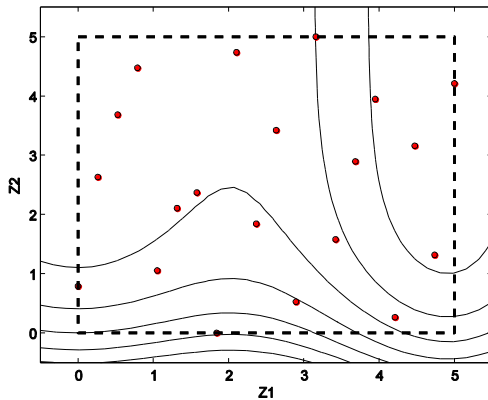
Hock problem



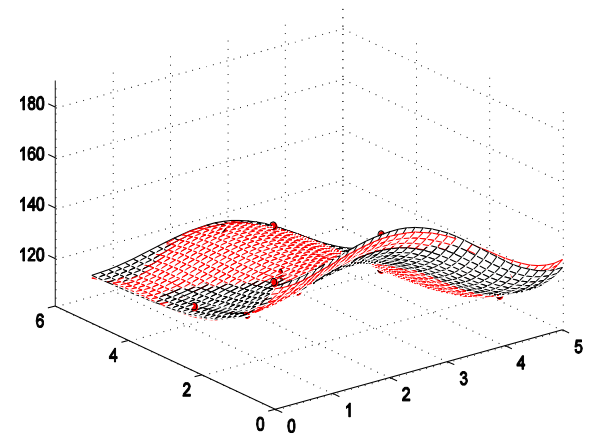
All the expressions generated are defined on the test data set.
p-value from Kruskal-Wallis = 4.58E-4

Training data set: 20 points

Test data set: 441 points

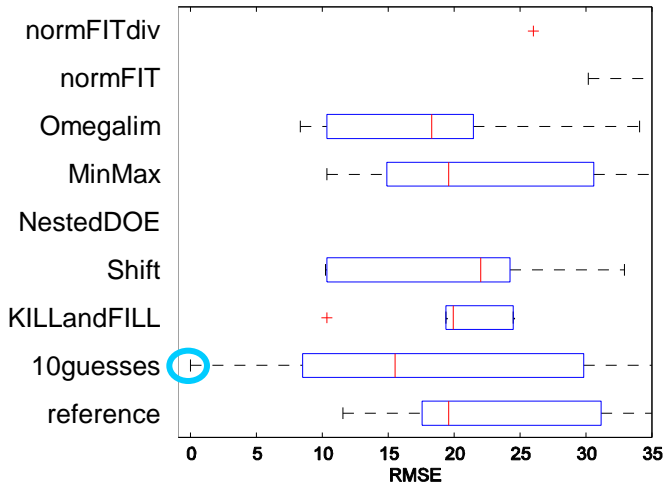


omegalim

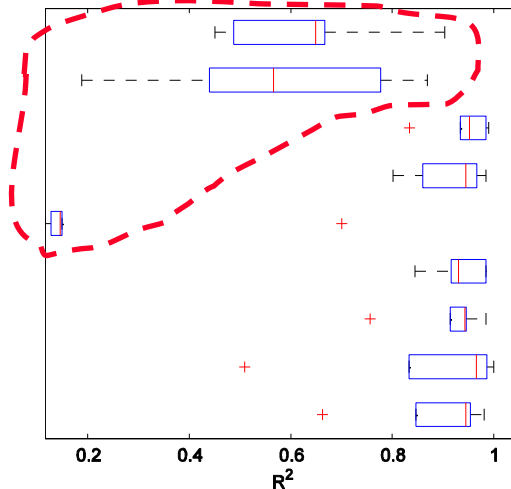


Branin-Hoo problem

RMSE on test data
Distribution of best individuals (one per run)



R^2 on test data
Distribution of best individuals (one per run)



On average 36% of the expressions generated by each implementation are not defined on the test data set!

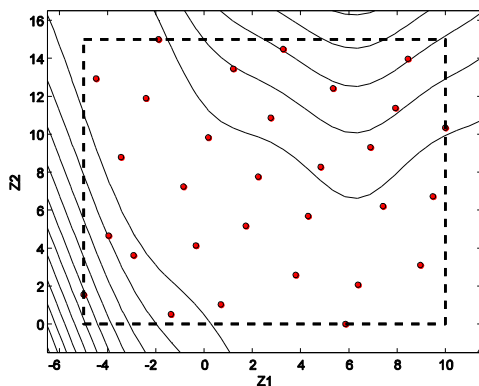
p-value from Kruskal-Wallis = $2.3E-5$



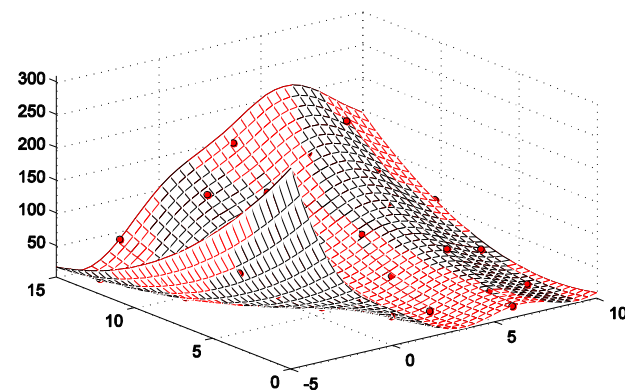
NestedDOE, normFIT and normFITdiv return the worst expressions.

Training data set: 30 points

Test data set: 1369 points



10guesses



Conclusions

- For **reference** implementation, there is not a definitive evidence that deleting copies improves the search.
- **NestedDOE**, **normFIT** and **normFITdiv** show poor performances.
- Increasing the number of initial guesses for SQP does not pay off: a huge increase in computational cost does not result in better regression quality.
- **Omegalim** performs consistently better than the other implementations in all the test problems

Future work:

- Extension of the pulsation control (**omegalim**) to recognise entire expressions as pulsations (interval arithmetics)
- Exploitation of derivative values in fitness evaluation and tuning (smoothing technique)
- Further research to understand why GP encourages the generation of linear combination of primitives as opposed to nested functions (that could explain the general poor performances on Salustowicz test problem)

A few references...

- Standard GP algorithm:

J. R. Koza, “*Genetic programming: on the programming of computers by means of natural selection*” MIT press, Cambridge, MA, USA, sixth edition, 1992

R. Poli, W. B. Langdon, and N. F. McPhee, “*A field guide to genetic programming*” published via <http://lulu.com> and freely available at <http://www.gp-field-guide.org.uk>, 2008. (With contributions by J. R. Koza)

W. Banzhaf, Frank D. Francone, Robert E. Keller, and Peter Nordin, “*Genetic programming: an introduction: on the automatic evolution of computer programs and its applications*” Morgan Kaufmann Publishers Inc., San Francisco, CA, USA, 1998.

- Integration of deterministic methods in standard GP algorithm:

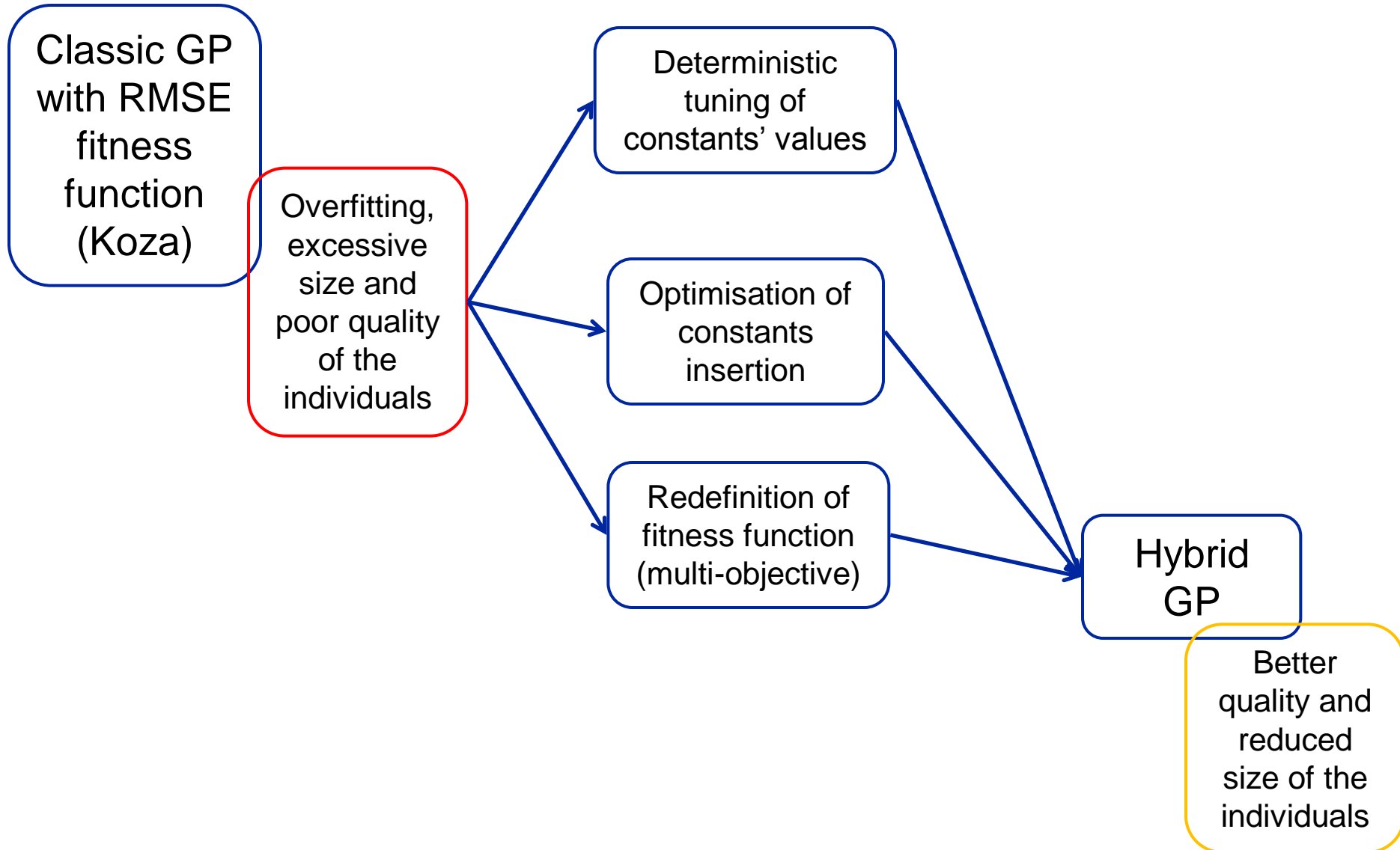
Topchy and W. F. Punch, “*Faster genetic programming based on local gradient search of numeric leaf values*” in Lee Spector, Erik D. Goodman, Annie Wu, W. B. Langdon, Hans-Michael Voigt, Mitsuo Gen, Sandip Sen, Marco Dorigo, Shahram Pezeshk, Max H. Garzon, and Edmund Burke, editors, Proceedings of the Genetic and Evolutionary Computation Conference (GECCO-2001), pages 155-162, San Francisco, California, USA, 7-11 July 2001. Morgan Kaufmann.

Alvarez, L. F., Design optimization based on genetic programming, Ph.D. thesis, University of Bradford, Bradford, UK, 2000.

Vladislavleva, E., Model-based Problem Solving through Symbolic Regression via Pareto Genetic Programming, Ph.D. thesis, Tilburg University, Tilburg, the Netherlands, 2008.

Hornby, G. S., “ALPS: the age-layered population structure for reducing the problem of premature convergence,” GECCO '06: Proceedings of the 8th annual conference on Genetic and evolutionary computation, ACM, New York, NY, USA, 2006, pp. 815–822.

Direction of current research: hybrid GP



Redefinition of Fitness Function in hybrid GP

- Fitness evaluation : **weighted approach**.

$$F(k, t) = a_1 F_1 + a_2 F_2 + a_3 F_3 + a_4 F_4 \quad a_1 + a_2 + a_3 + a_4 = 1$$

$$F_1 = \frac{RMSE(i, t)}{RMSE(t-1)} \quad RMSE(i, t) = \sqrt{\frac{1}{m} \sum_{j=1}^m (\hat{f}_j(i, t) - f_j)^2}$$

$F_2 =$ number of tuning parameters

$F_3 =$ number of singularities

$F_4 =$ number of nodes

$a_1 = 0.989$ $a_2 = 0.01$ $a_3 = 0.1$ $a_4 = 0.001$ for example