

# Surrogate Model for Mixed-Variables Evolutionary Optimization based on GLM and RBF Networks

Lukáš Bajer<sup>1,2</sup>    Martin Holeňa<sup>2</sup>

<sup>1</sup>Faculty of Mathematics and Physics, Charles University, and

<sup>2</sup>Institute of Computer Science, Czech Academy of Sciences

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- 1 Optimization of empirical functions
- 2 Regression model
  - Involved methods
  - Our model
- 3 Experimental results
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# Optimization of empirical functions

optimization:

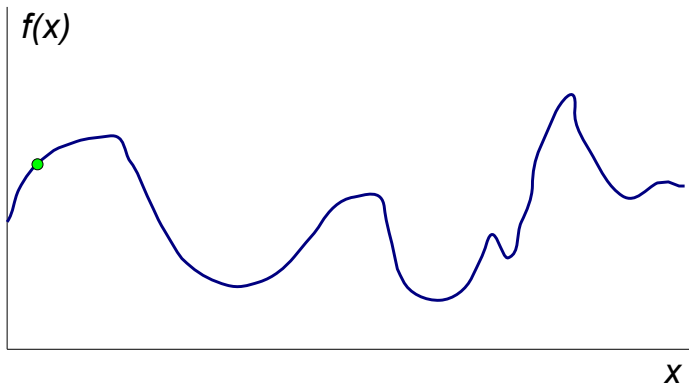
- $S$  – set of feasible solutions,  $f(x)$  – objective function
- **optimization** (minimization) is finding such  $x^* \in S$  that

$$f(x^*) = \min_{\forall x \in S} f(x)$$

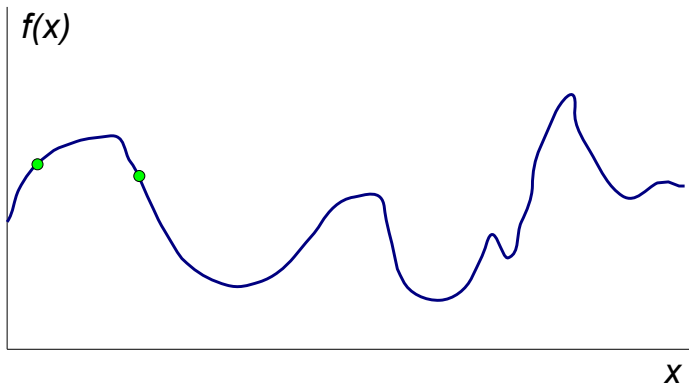
empirical objective functions:

- costly and/or time demanding evaluation of suggested solutions
- **cost** of the whole optimization measured by the resources spent on evaluations (time, money,...)
- discrete and continuous variables expected:  
 $S = (\mathbf{S}^{(D)}, \mathbf{S}^{(C)})$

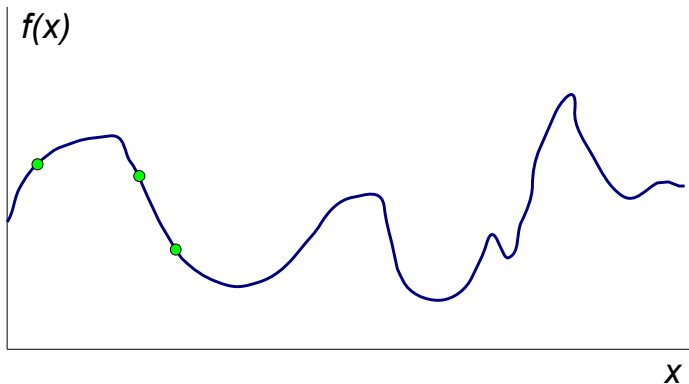
# Optimization of empirical functions



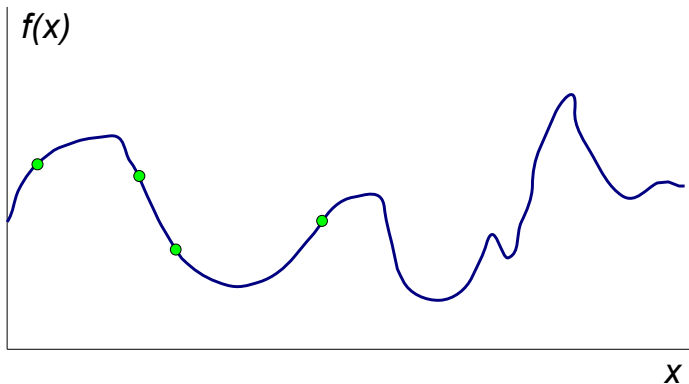
# Optimization of empirical functions



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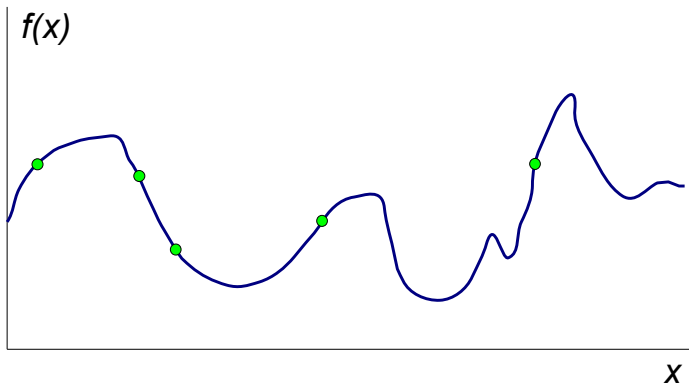


# Optimization of empirical functions

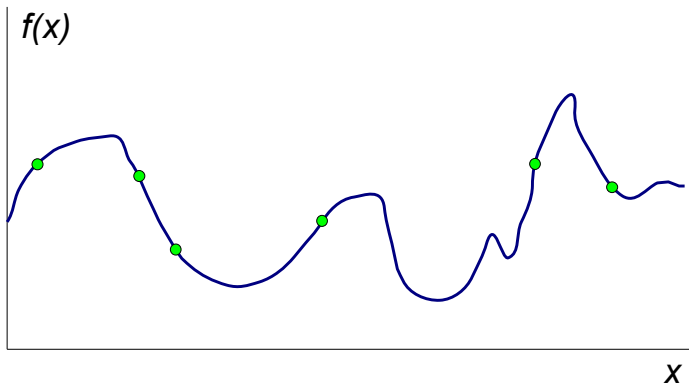




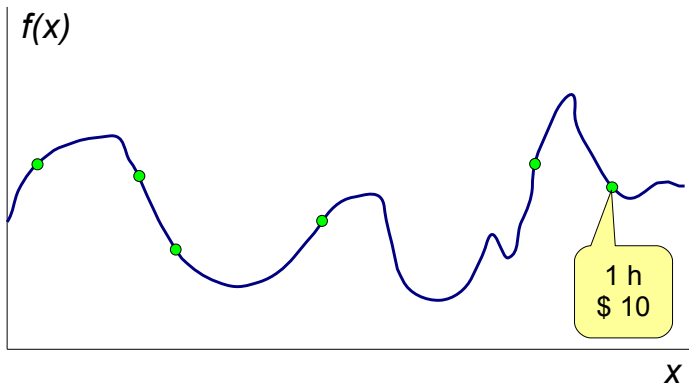
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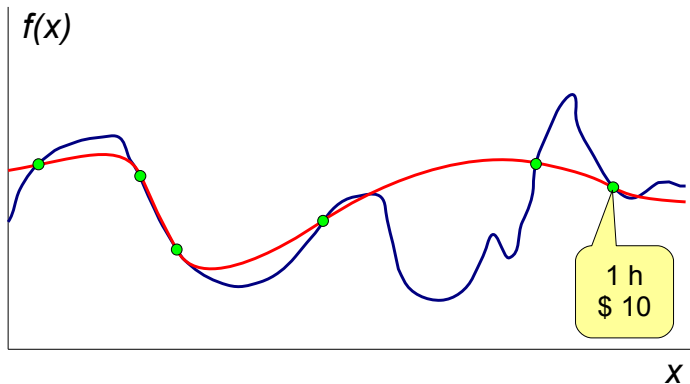
# Optimization of empirical functions



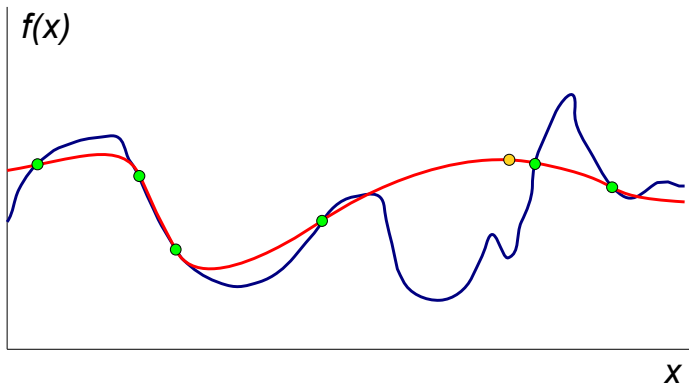
# Optimization of empirical functions



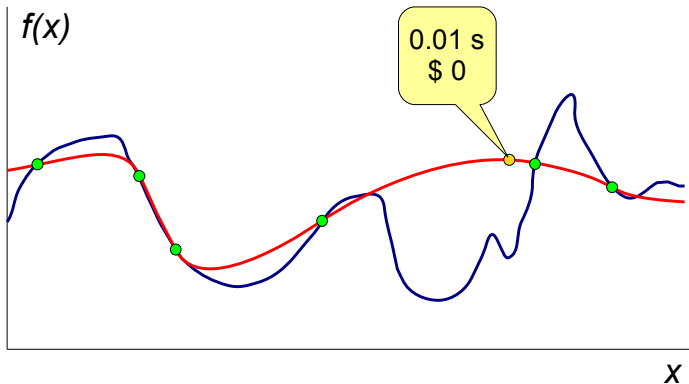
# Optimization of empirical functions



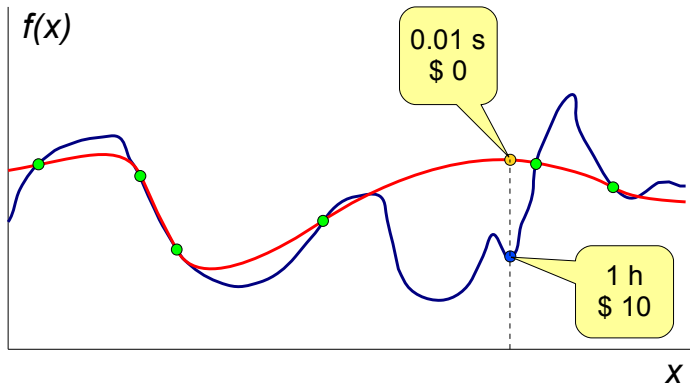
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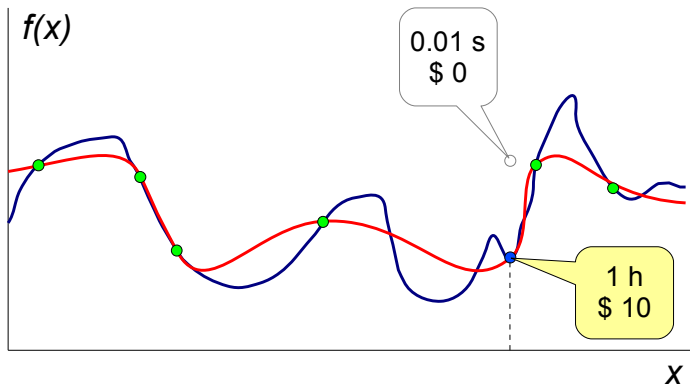
# Optimization of empirical functions



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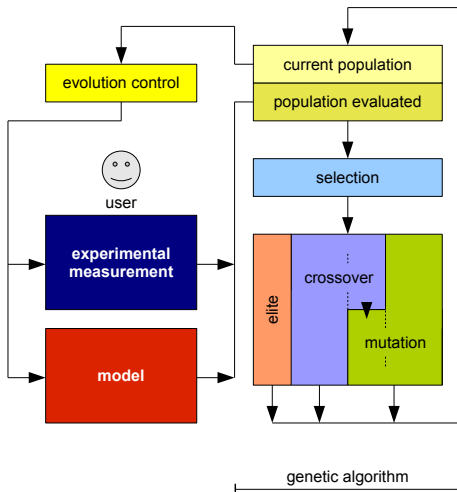
# Surrogate models of objective functions

## General idea

- usually evaluate suggested solutions with a cheap regression model
- use the original measurements to focus the search and ensure the true evaluation of the best found solution
- (–) surrogate model is an approximation of the original fitness – almost always more or less **inaccurate**
- (+) very fast and **cheap**
- **learning** from new measured results of experiments

# Genetic algorithm and surrogate model

- genetic algorithm used as an optimization technique
- two kinds of fitness evaluation
  - experimental measurement (blue)
  - model fitness (red)



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# Regression model

**requirement:** both for **continuous** ( $S^{(D)}$ ) and **discrete** ( $S^{(D)}$ ) variables

- **continuous variables:** RBF network(s)
- **discrete variables:** GLM

# RBF networks

## RBF network

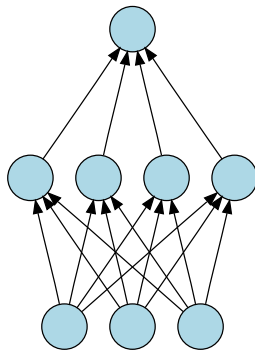
$$f(\mathbf{x}) = \sum_{i=1}^g \pi_i f_i(\|\mathbf{x} - \mathbf{c}_i\|)$$

composed of

- $g$  Gaussian radial components  $f_1, \dots, f_g$  with variable widths  $w_i$

$$f_i(\|\mathbf{x} - \mathbf{c}_i\|) = e^{-w_i(\mathbf{x} - \mathbf{c}_i)}$$

- variable centers  $\mathbf{c}_i \in \mathbb{R}^n$
- components' weights  $\pi_1, \dots, \pi_g$



# (Generalized) Linear Models

## GLM

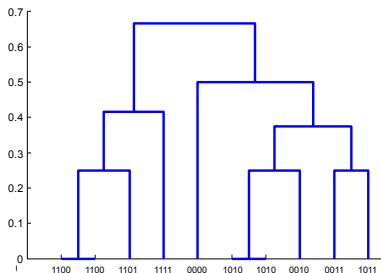
$$\hat{y} = g^{-1} \left( \sum_{j=0}^d x_j \beta_j \right)$$

- independent observed values  $Y$ ;  
assumed from an exponential-family distribution
- explanatory variables  $(x_1, x_2, \dots, x_d)$  transformed through a linear model with parameters  $\beta_1, \dots, \beta_d$
- link function  $g$  connects the random and systematic component, depends on the distribution

# Model construction – (1) clustering

## clustering of the discrete data (in $S^{(D)}$ )

- similar discrete combinations are grouped into the same cluster
- hierarchical clustering with guaranteed minimal size
- $m$  – the number of clusters



# Model construction – (2) RBF networks

## RBF networks

- trained on continuous parts of each such a cluster
- for  $k = 1, \dots, m$

$$\hat{f}_{\text{DSCL}}^{(k)} : \mathbf{S}^{(\text{C})} \rightarrow \mathbf{R}$$

- the best number of components  $g^*$  chosen by cross-validation
- for evaluation on a new  $\mathbf{x}$ 
  - the nearest cluster  $k^*$  is identified (from discrete part)
  - its RBF network's value is computed (from continuous part):

$$\hat{f}_{\text{DSCL}}^{(k^*)}(\mathbf{x}^{(\text{C})}) = \sum_{i=1}^{g^*} \pi_{k^*,i} f_{k^*,i}(\|\mathbf{x}^{(\text{C})} - \mathbf{c}_{k^*,i}\|)$$



# Model construction – (3) GLM model

## GLM model

- model of the residuals

$$\hat{f}_{\text{GLM}} : \mathbf{x}^{(D)} \rightarrow (y - \hat{f}_{\text{DSCL}}(\mathbf{x}^{(C)}))$$

- trained on the discrete variables (explanatory variables)

$$\hat{f}_{\text{GLM}} : \mathbf{S}^{(D)} \rightarrow \mathbf{R}$$

- dummy or integer coding of discrete variables
- residuals assumed from Gaussian, inverse Gaussian or gamma distribution – the best option is chosen via cross-validation

# Model construction

## final model

$$\hat{f} : (\mathbf{S}^{(D)}, \mathbf{S}^{(C)}) \rightarrow \mathbf{R}$$

- sum of the responses of the two previous models

$$\hat{f}(\mathbf{x}) = \hat{f}_{\text{DSCL}}^{(k)}(\mathbf{x}^{(C)}) + \hat{f}_{\text{GLM}}(\mathbf{x}^{(D)}).$$

## evaluation of the final model:

- 1 identify the nearest cluster  $k^*$
- 2 compute response of the corresp.  $k^*$ -th RBF network  $\hat{y}_{\text{DSCL}}$
- 3 get the value of the GLM model  $\hat{y}_{\text{GLM}}$
- 4 sum these two values  $\hat{y} = \hat{y}_{\text{DSCL}} + \hat{y}_{\text{GLM}}$

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# Experimental results

## Task 1: Data from HCN production

- results from a real application of genetic algorithms:  
finding the best catalyst for production of HCN
- 11 continuous, 1 discrete and 11 binary variables
- 555 different discrete combinations within 696 datapoints
- training of the model only

# Experimental results

## Task 2: Benchmark function

- individuals from the first 10 generations of a run of GA
- modified Schwefel's benchmark function

$$y = \frac{1}{p} \sum_{i=1}^p -x_i \sin(\sqrt{|x|})$$

- discrete variables added

$$(x_1^{(D)}, \dots, x_p^{(D)}) \in \{-10, -9, \dots, 10\}$$

- easy to compute for any arbitrary point – possible to test with genetic algorithm

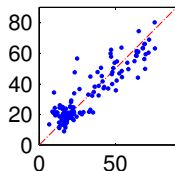
# Experimental results

**Table:** Surrogate-models' regression results on HCN and Schwefel dataset, average results from 50 trainings. RMSE on the testing and training set.

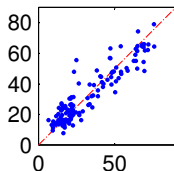
dataset	model	RMSE (test set)	RMSE (train set)
HCN	DSCL	$8.2918 \pm 0.4373$	7.6337
	<b>RESID</b>	<b><math>7.6212 \pm 0.3187</math></b>	6.6131
	SUMO	$115.196 \pm 34.1387$	<b>0.5711</b>
Schwefel	DSCL	$62.712 \pm 3.4248$	83.553
	<b>RESID</b>	<b><math>55.605 \pm 5.4867</math></b>	73.468
	SUMO	$64576 \pm 1.9e+05$	<b>33.964</b>

# Model fitting

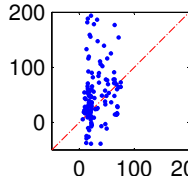
HCN: DSCL model



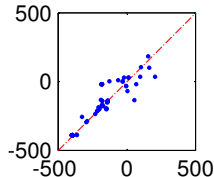
HCN: RESID model



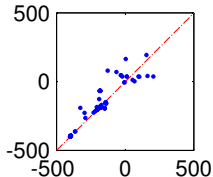
HCN: SUMO model



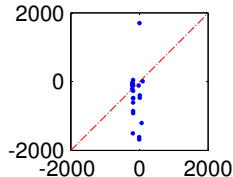
Schwefel: DSCL model



Schwefel: RESID model

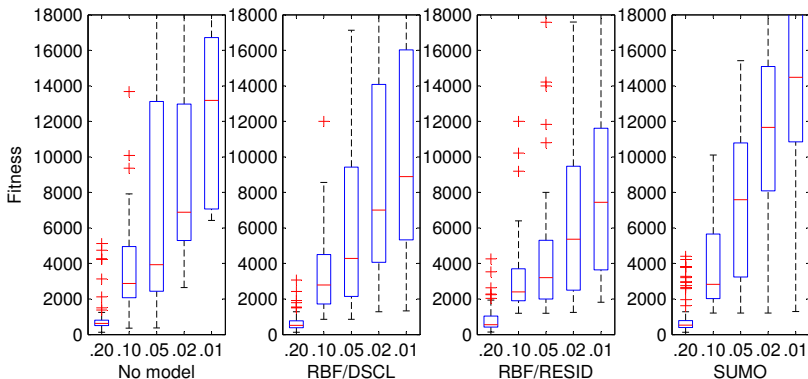


Schwefel: SUMO model



Scatter plots of the DSCL, RESID and SUMO's RBF models on testing data

# Benchmark fitness: genetic optimization



The numbers of original evaluations needed to reach 1.2-, 1.1-, 1.05-, 1.02- and 1.01-multiple of minimum, measured on 100 GA runs



# Conclusion

## Contributions of the work

- detailed description of a surrogate model for genetic optimization
- surrogate model with RBF networks and GLMs, for both continuous and discrete values

## Experimental results

- model exhibits significantly lower testing error than competing RBF networks from SUMO toolbox
- utilizing the model on the benchmark fitness saved up to 35 per cent of empirical function evaluations

# Conclusion

Thank you for your attention.

bajeluk@matfyz.cz  
<http://bajeluk.matfyz.cz>