Genetic synthesis of cascade structures for particle classification

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Abstract

The goal of precise and reliable separation of a product into useful and useless parts demands the cooperation of a set of separating elements. The grouping of them in a cascade allows us to obtain an especially refined product. When the number of the elements is large, characteristics of the cascade depend more on its structure than on the quality of an individual separation element (classifier). The search of the optimal structure becomes a difficult task because of a large number of possible variants of interconnection between the elements. The genetic method of synthesis allows us to determine a nearly optimal structure of a classifier cascade. Particularly, a set of non-trivial structures was synthesized, with a better quality of separation, compared with the cascades from the previous works on particle classification[1, 4].

1 Introduction

A classification of particles is a separation of them into fractions according to size. In the simplest case the separation results in two fractions: fine and coarse. A border between them corresponds to some particular size (boundary size). The apparatus making the separation—classifier—is characterized by the selective function, that shows the dependence of probability φ of a particle passing through the classifier upon the size of that particle δ. In particular, this function may be linear, as on fig. 1. The selective function reflects the quality of separation. Ideally, it could be expressed as $\varphi(\delta) = 1 - u(\delta - \delta_0)$, where u — unitary step function.

At the beginning of this work there was an idea of synthesis of effective classification cascades by the grouping of ineffective separation elements into a structure. In the search for effective structures many methods were used: raw force combinatorial search, Monte-Carlo method, enthropy-based methods. These researches found the regular structure of a cascade (fig. 3) that was fairly efficient. Some authors considered it optimal [1, 4]. In this work I tried to breed new structures, selecting the fittest with respect to the devised criterion. As a result, the genetic synthesis method was devised, akin to the one which is used in similar situation by Nature.

2 The model of a cascade

The task of determining the selective function of an arbitrary classifier cascade can be reduced to solving the linear equation system for every fraction under consideration. Let us assume that N classifiers are grouped into a classifier cascade. Let φ_i be the probability of a particle passing through the i th classifier, depending on size of the particle (selective function); ρ_i , ρ_i^- , ρ_i^+ are flows of a particular fraction in the input, the coarse and fine outputs of the i th classifier, respectively; ρ_i^* is the

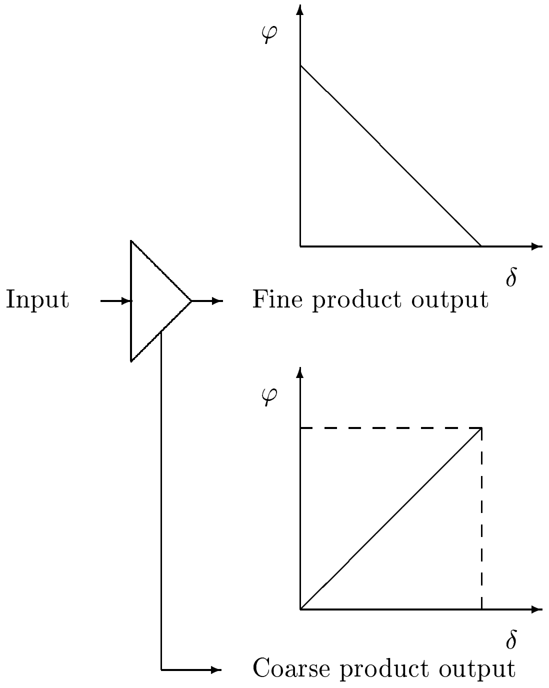

Figure 1: The example of individual classifier and its selective function

inflow of that fraction, going from the outside of the cascade into the input of the i th classifier.

For every classifier, two relationships follow: the equation of material balance

$$\rho_i = \rho_i^+ + \rho_i^- \tag{1}$$

and expression for fractional flow in the fine output

$$\rho_i^+ = \varphi_i \rho_i. \tag{2}$$

Therefore, the fractional flow in the coarse output is

$$\rho_i^- = (1 - \varphi_i)\rho_i. \tag{3}$$

The system of material balance equations for a particular fraction can be written in the matrix form:

$$\begin{pmatrix} 0 & a_{12} & \dots & a_{1n} \\ a_{21} & 0 & \dots & a_{1n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \dots & 0 \end{pmatrix} \begin{pmatrix} \rho_1 \\ \rho_2 \\ \vdots \\ \rho_n \end{pmatrix} + \begin{pmatrix} \rho_1^* \\ \rho_2^* \\ \vdots \\ \rho_n^* \end{pmatrix} = \begin{pmatrix} \rho_1 \\ \rho_2 \\ \vdots \\ \rho_n \end{pmatrix} \tag{4}$$

In shorter terms, $\mathbf{A} \times \bar{\rho} + \bar{\rho}^* = \bar{\rho}$. Here a_{ij} shows the probability of penetration of a particle of the fraction from the input of the j th element into the input of the i th element. This value depends on the size of the particle, the selective function of the j th classifier, and the structure of connections in the cascade:

$$a_{ij} = \begin{cases} 1 - \varphi_j(\delta) & \text{if the coarse output of the } j\text{th element goes into the } i\text{th one;} \\ \varphi_j(\delta) & \text{if the fine output of the } j\text{th element goes into the } i\text{th one;} \\ 0 & \text{otherwise.} \end{cases} \tag{5}$$

When solving the system (4) the cumulative flows of fractions in inputs of all classifiers are determined. Since output flows also become known according to (2) and (3), we can determine the probability of passing a particle of given fraction through the cascade. The fractional flow in the output of the cascade can be written as follows $\rho = \Phi(\varphi_1, \varphi_2, \ldots, \varphi_N)\rho^*$, where function $\Phi(\varphi_1, \varphi_2, \ldots, \varphi_N)$ is the selective function of the cascade.

If we define matrix $\mathbf{B}$ as

$$\mathbf{B} = \mathbf{A} - \mathbf{E} = \begin{pmatrix} -1 & a_{12} & \ldots & a_{1n} \\ a_{21} & -1 & \ldots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \ldots & -1 \end{pmatrix} \tag{6}$$

where $\mathbf{E}$ is the identity matrix, the system (4) can be rewritten as $\mathbf{B} \times \bar{\rho} = -\bar{\rho}^*$. The similar approach is given in [4].

Here we suppose that the input product will always go to the input of the first element, and the output product will be taken from the fine output of the N th element. This condition does not restrict the possible structures, because all elements are interchangeable. Also we assume that the input flow of the considered fraction is one unit. Then $\bar{\rho}^* = (1, 0, \ \ldots \ , 0)^T$ и $\Phi = \rho/\rho^* = \varphi\rho_n$. In order to find the value of Φ for the fraction we have to solve the following system

$$\begin{pmatrix} -1 & a_{12} & \ldots & a_{1n} \\ a_{21} & -1 & \ldots & a_{1n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \ldots & -1 \end{pmatrix} \begin{pmatrix} \rho_1 \\ \rho_2 \\ \vdots \\ \rho_n \end{pmatrix} = \begin{pmatrix} -1 \\ 0 \\ \vdots \\ 0 \end{pmatrix} \tag{7}$$

Since we are only interested in the variable ρ_n , we can skip the back substitution step in the method of Gauss. It is sufficient only to reduce the matrix to the triangle type. It takes as many as $\sim N^3/3$ operations. Thus we saved $\sim N^2/2$ operations on back substitution.

3 Structure synthesis

3.1 Representation

To use the genetic algorithm[2] for the task of cascade synthesis, it is necessary to construct the genome in such a way that every possible cascade would have a constant length genome, encoding the information about the cascade structure. Redundant or irrelevant information must be reduced to the minimum. For a classifier cascade having N elements, the following method of genome construction is suggested. It is not perfect, but workable.

The cascade structure is defined by the consecutive indication of indices of the elements, where coarse and fine outputs of each classifier are connected. According to our assumption, a product will go to the first element initially, and the fine output of N th classifier will be the output of the whole cascade. It takes $n = \lceil \log_2(N+1) \rceil$ bits to represent one output information and $(2N-1)n$ bits to represent the whole structure in such a way. The particular genome can be written as a sequence of numbers, delimited pairwise with a period. We use hexadecimal numbers here. For example, the specification `"23.01.1"` corresponds to a structure, in which the coarse output of the first element goes to the input of the second, the fine output goes to the third; the coarse output of the second is not connected to any element, the fine one goes to the first; the third element has its coarse output connected to the first classifier and the fine one going out of the system. The corresponding cascade is drawn on fig. 2.

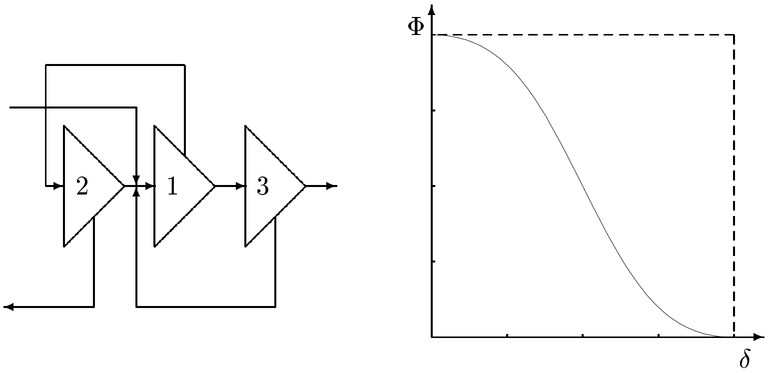

Figure 2: The cascade with specification "23.01.1" and its selective function

We get the selective function of the cascade, solving the system (7) consecutively for characteristic size of every fraction under consideration. For simplicity we assume the selective function of each individual classifier to be linear as shown on fig. 1.

Now, to finish the statement of the problem of genetic synthesis, we need to define the fitness function of an arbitrary structure.

3.2 Evaluation

Traditionally, the separation precision ratio is used as the quality criterion. It equals the ratio of the values of δ corresponding to $\Phi_1 = 1/4$ and $\Phi_2 = 3/4$. However, using this criterion in the synthesis is inefficient, since the process goes too slowly. It is necessary to solve the non-linear equation numerically twice for every structure. What makes the task really difficult is that we don't know the selective function that happen to be in the equation. To obtain one value of this function, we have to solve the equation system of order N. After some uneventful experiments, this criterion was replaced by the following, more workable one:

$$\Phi(1/4) - \Phi(3/4). \tag{8}$$

The latter criterion needs to calculate only two values of selective function. It reduces the time of structure estimation drastically. The meaning of this criterion—maximizing the difference between the penetration of the two fractions—agrees well with the purpose of the separation cascade construction.

The suggested criterion can be viewed as a difference of crude estimates of integrals $\int_0^{\frac{1}{2}} \Phi(\delta)\, d\delta$ and $\int_{\frac{1}{2}}^1 \Phi(\delta)\, d\delta$ according to the rectangle method with one interval of decomposition. It is possible to apply the finer decomposition to obtain the more accurate fitness function, although it will be more time-consuming.

The criterion suggested can be easily generalized for more than two fractions. It can also be used in the structure synthesis of selector or rejecter cascades as well as cascades with a given selective function. For example, to construct the filter for selecting a particular fraction $\delta \in [\delta_0 - \psi, \delta_0 + \psi]$, it is necessary to maximize the difference between $\int_{\delta_0-\psi}^{\delta_0+\psi} \Phi(\delta)\, d\delta$ and $\int_0^{\delta_0-\psi} \Phi(\delta)\, d\delta + \int_{\delta_0+\psi}^1 \Phi(\delta)\, d\delta$, calculated by the rectangle method with the necessary precision.

3.3 Genetic synthesis

The synthesis incorporates the recombination of genetic material and the selection of it according to the criterion of the fitness function maximum. When repeated, these processes lead to finding of the genomes corresponding to more optimal structures [3, 2].

Using the genome construction suggested earlier, it is easy to determine the recombination operation for two genomes. In this work, two-point crossover was used. It assumes cutting the two genomes in two arbitrary points and exchanging the contents between the two cuts. For example, the result of crossover of the genomes drawn on fig. 3, 4 could be the following genome

$$\overbrace{\texttt{29.31.4}}^{\text{fig. 3}}\underbrace{\texttt{2.2A.02.54.EB.C1.8E}}_{\text{fig. 4}}\overbrace{\texttt{9B.AC.BD.CE.DF.E}}^{\text{fig. 3}}$$

The synthesis algorithm is implemented in a program. First 250 genomes generated randomly fill the initial population. For every genome the fitness function is calculated. For this purpose, matrices (7) are calculated for the two fractions from (8), according to the rules (5). These matrices are reduced to the triangle form according to the method of Gauss, in order to find the two values of Φ , which difference is to be maximized according to (8). The genome is then inserted in the list of population ordered by the decreasing values of the fitness function.

Then, on every successive step, the worst genome in the population is replaced by a recombination of arbitrarily selected genomes. The newly created genome is estimated and placed in the population corresponding to its fitness. With a probability of 0.01 a mutation takes place that changes an arbitrarily selected number in the specification of the genome.

The top ten genome specifications are displayed along with their fitness values. The corresponding structures and the selective functions can be viewed upon request.

4 Results

Experiments with the genetic synthesis method were made for the population size of 250 structures. The selective function of every element was assumed linear, as shown in fig. 1. The probability of error of classification of an individual element in this case is $p_{err} = 0.25$. Although the experiments were made with such elements, the method of synthesis does not impose any restrictions on the form of the selective function of an individual classifier.

For the cascades with two to five elements, the structures similar to the known regular scheme with recycling were generated. Some authors proposed it as an optimum for any number of elements. In fact, the more effective structures were found for six to fifteen elements.

Thus, for the cascade of 15 elements, the algorithm came to the regular scheme with recycling (fig. 3). However, as a result of the further evolution, the structure with better fitness was found (fig. 4). The corresponding selective functions are shown on fig. 5.

Additional experiments demonstrated that for cascades that consist of six elements or more, cascade structures exist, which overcome the known regular scheme by the precision of separation. The advantage in effectiveness is negligible in the case of six elements, but it becomes larger for more complex structures.

The dependence of the suboptimal structure of a cascade on the form of the selective function of an individual classifier was researched. The experiments showed that the suboptimal structure is not invariant with respect to the form of the selective function of a classifier, i.e. there is no structure that is optimal for any kind

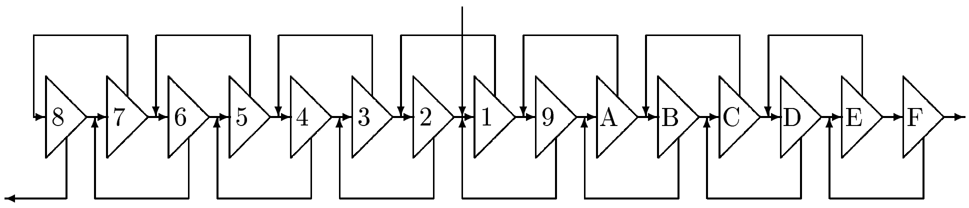

Figure 3: The regular cascade with recycling of 15 elements with specification `29.31.42.53.64.75.86.07.1A.9B.AC.BD.CE.DF.E`

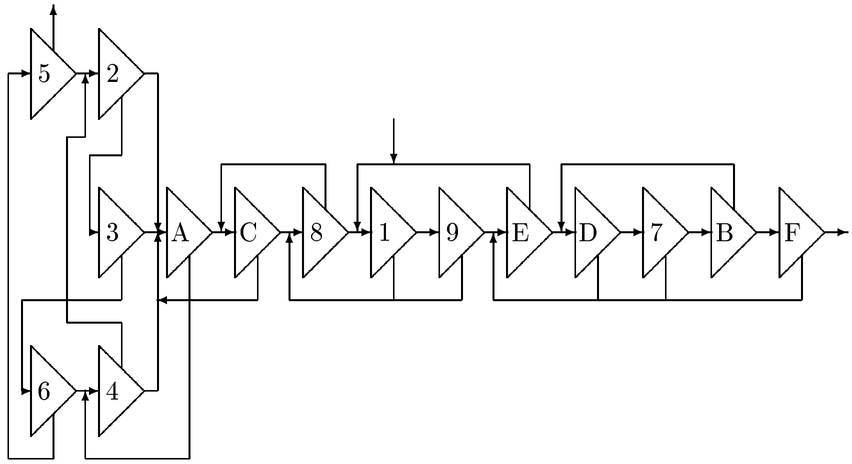

Figure 4: The genetically synthesized cascade of 15 elements, with specification `89.3A.6A.2A.02.54.EB.C1.8E.4C.DF.A8.E7.1D.E`

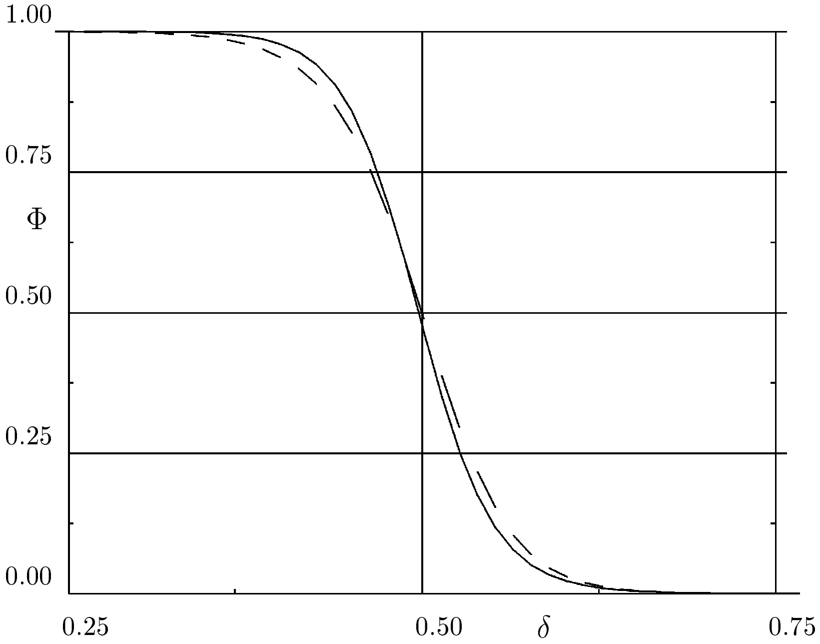

Figure 5: The selective function of regular cascade with recycling (dashed line) and genetically synthesized (solid line)

of elementary classifier. Nevertheless, the genetic synthesis allows us to construct nearly optimal structures for any particular kind of elementary classifiers.

5 Conclusion

This paper has described the successful application of a recently developed genetic algorithm for the design of irregular structures of classification cascades. It has reported better results than previously published for large-sized classification cascades.

There are several areas for the future research. One of these is the refinement of the genetic algorithm to reduce the number of necessary fitness function evaluations, so that problems with a larger number of elements can be tackled in reasonable computing times. Another research area is the optimal design of cascades that remain functional when the failure of some elements takes place inside of them.

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