

Library Evolutionary Algorithms for Clustering (LEAC)

User guide
for LEAC version 1.8
7 March 2016

Hermes Robles-Berumen,
Amelia Zafra,
Sebastian Ventura.

This user guide is for Library LEAC (version 1.8, 7 March 2016), and documents commands for clustering analysis.

Copyright © 2015-2017 Hermes Robles-Berumen, Amelia Zafra, Sebastian Ventura. Knowledge Discovery and Intelligent Systems in Biomedicine Laboratory. Maimoindes Institute of Biomedicine, Córdoba, Spain

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1 Introduction

Library Evolutionary Algorithms for Clustering (LEAC) is a library for the implementation of evolutionary algorithms to solve the problem of *partitional clustering*, the purpose is to find an optimal partition of a dataset X having n d -dimensional *objects*¹. $X = \{x_1, x_2, \dots, x_n\}$ in k subsets C_1, C_2, \dots, C_k ($k \leq n$). So that the objects that are in the same group are more similar between them and the objects of the other groups are the most different. Formally under the partitioning approach the problem of clustering is defined by NP14 as

$$\begin{aligned} C_j &\neq \emptyset \quad \forall j = 1, 2, \dots, k; \\ C_j \cap C_{j'} &= \emptyset \quad \forall j, j' = 1, \dots, k \quad \text{and} \quad \bigcup_{j=1}^k C_j = X. \end{aligned} \tag{1.1}$$

Clustering is useful in areas, such as exploratory *pattern-analysis*, *grouping*, *decision-making*, and *machine-learning* and *data mining* JMF99.

LEAC library it is based on a *layered software architecture* and is conceptually composed of four layers, each of which consists of a set of related packets as shown in the [Figure 1.1](#). The description of each layer is described below:

Algorithm

It consists of evolutionary algorithms, which use the layer based on the operator EA.

EA

Implement what you need to configure GA: encoding criterion, initialization of population, criterion for selecting parents, crossover and mutation operators. Along with the support of the lower layers to achieve scheme of evolution.

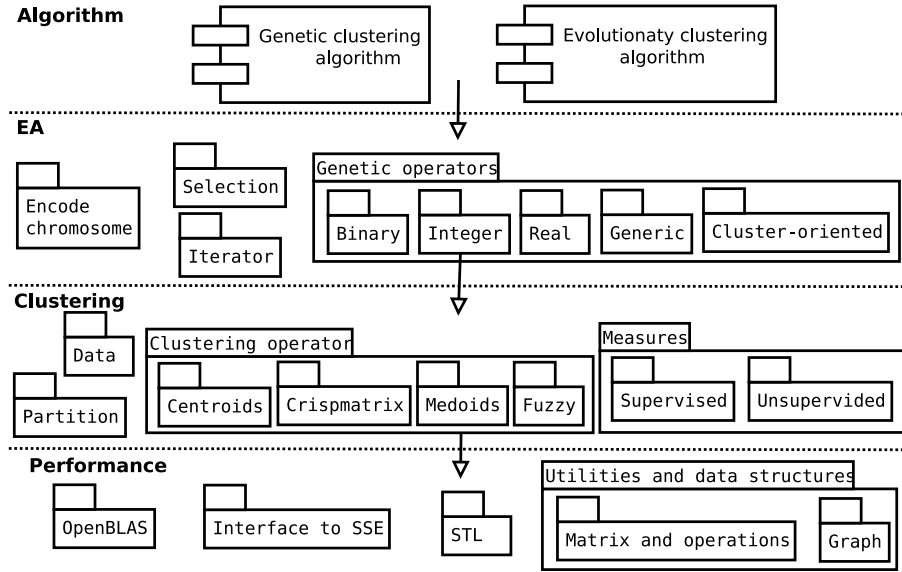
Clustering

It refers to the domain of the problem and implements all specific clustering operators, such as, supervised and unsupervised performance measures and clustering operators based on centroids, crisp matrix or medoids. It is the layer referring to the domain of the problem.

Performance

It consists of low-level functions programmed under the current CPU architectures. For example, Data Alignment and Streaming SIMD Extensions (SSE) Int10. It allows top layers to work with high performance.

¹ The terms *object*, *instance*, *points* or *prototype* usually have the same meaning in the literature on *clustering analysis* and will be freely interchanged in this document

Figure 1.1: *Layered software architecture* of LEAC library

Encode	Fixed-K	Variable-K
	gaclustering_fklabel, MC96	gga_vklabeledbindex and gga_vklabelsilhouette, ABSSJF+12
	gka_fklabel, KM99	cga_vklabel, HE03
	igka_fklabel, LLF+04b	eac_vklabel, HCdC06
Label	fgka_fklabel, LLF+04a	eaci_vklabel, eacii_vklabel, eaciii_vklabel and feac_vklabel, ACH06
Crisp matrix	gaclustering_fkcrispmatrix, BBHB94	gcuk_vkcentroid, BM02b
	gas_fkcentroid, MB00	tgca_vkcentroid, HT12
	kga_fkcentroid, BM02a	
Centroids	gagr_fkcentroid, CZZ09	
	cbga_fkcentroid_int and cbga_fkcentroid, FKKN97	
Medoid	gaprototypes_fkmedoid, KB97	
	hka_fkmedoid, SL04	
	gca_fkmedoid, LDK93	
Tree		gaclustering_vktreebinary, CdLM03
Sub-cluster		clustering_vksubclusterbinary, TY01

Table 1.1: List of evolutionary algorithms implemented with the LEAC library, described by the taxonomy proposed by HCFdC09

LEAC is a modular library which make easier to develop new evolutionary algorithm proposals for solving the partitional clustering. Moreover, it contains the most representative proposals of Evolutionary Algorithms for partitional clustering. Following the taxonomy set by HCFdC09 a first classification of these algorithms is carried out according to the use of fixed or variable number initial of clusters, as well as to the representation of the clusters of a data set. Concretely, 20 state-of-art EA proposals are included, of which 23 programs are implemented see [Table 1.1](#).

LEAC is based on the current standards of the C++ language, as well as on Standard Template Library (STL) and also OpenBLAS to have a better performance. Taking advantage of the characteristics of the C++ language as hybrid language, generic programming, multi-paradigms and lambda function and the C++11 versions and C++14. It allowed the implementation of different evolutionary algorithms. The approach of LEAC to implement the particular characteristics of each algorithm is to encode the diversity of the proposed genetic operators and to use the containers and interpliers of STL to evolve the population according to the flowchart of the algorithms.

2 Get and Install LEAC software

For Windows[®] systems, perform steps 1 through 7 and 12. For GNU/Linux systems and Mac OS X[®], perform steps 1, 2 and 8 through 12.

1. Download the leac project from <https://github.com/kdis-lab/leac>.
2. Unzip the file `leac.zip`, we recommend you in the directory `c:\leac` for Windows[®] and `/home/user/leac` for GNU/Linux and Mac OS X[®]. Verify that the following directories exist within the main directory.

<code>bin</code>	This is the directory to store all EAC binary or executable programs, which result from the compilation of using LEAC.
<code>data</code>	Directory used to store the data sets to be processed.
<code>doc</code>	In the ‘ <code>doc</code> ’ directory you will find all the necessary documentation for the use of LEAC.
<code>eac</code>	It contains the source files of the implementations of the EAC algorithms implemented by the LEAC library.
<code>include</code>	Contains LEAC library header files and source code.
<code>include_inout</code>	Contains the modules for the input of parameters and output of the EAC programs.
<code>openblas</code>	Contains only the header files needed to compile a program with some functionality of the OpenBlas library.
<code>sse_kernel</code>	<code>sse_kernel</code> is a module based on OpenBlas and GotoBLAS2 , own of LEAC. The functionality of this module together with that of OpenBlas is the best performance for the processing of high-dimensional data sets. For now it only works for x86-64 architecture.

For GNU/Linux and Mac OS X go to [Step 8], page 7.

3. Download and install one of the two IDE with the MinGW option [Dev-C++](#) or [Code::Blocks](#)
4. Check the `PATH` where MinGW is installed, it can be `C:\Program Files (x86)\Dev-Cpp\MinGW64\bin` or `C:\Program Files (x86)\CodeBlocks\MinGW\bin` and add it to the `PATH` environment variable using the following instructions

Warning: Adding entries to the `PATH` is normally harmless. However, if you delete any existing entries, you may mess up your `PATH` string, and you could seriously compromise the functioning of your computer. Please be careful. Proceed at your own risk.

- a. Right-click on your **My Computer** icon and select **Properties**.
- b. Click on the **Advanced** tab, then on the **Environment Variables** button ([Figure 2.1](#)).

You should be presented with a dialog box with two text boxes. The top box shows your user settings. The `PATH` entry in this box is the one you want to modify. Note that the bottom text box allows you to change the system `PATH`

variable. You should not alter the system path variable in any manner, or you will cause all sorts of problems for you and your computer!

- c. Click on the PATH entry in the TOP box, then click on the Edit button
 - d. Scroll to the end of the string and at the end add
`'C:\Program Files (x86)\Dev-Cpp\MinGW64\bin'`
 - e. press OK -> OK -> OK and you are done.
5. Download and install [gnuplot](#). The recommendation for the installation is to use the file [gp530-20170911-win64-mingw.zip](#). Unzip in the `c:\gnuplot` directory and add `c:\gnuplot\bin` in the environment variable PATH in the same way as in [\[Step 4\]](#), [page 5](#).
 6. Optionally install the [epsviewer](#) file viewer, to visualize the data sets and the clusters created by the different programs
 7. With the compiler installed See [\[Step 4\]](#), [page 5](#), you can now compile the EAC applications. Open a cmd, you must change the directory to the `leac` directory, For example: `'cd c:\leac\leac'` and execute any of the following three options:

```
'mingw32-make -k -f Makefile DEBUG=yes VERBOSE=yes'
```

To debug and analyze the detailed execution of the programs. These options allow software engineering ilities of correctness and reliability.

```
'mingw32-make -k -f Makefile DEBUG=no VERBOSE=no WITHOUT_PLOT_STAT=no'
```

Optimize and obtain the evolutionary behavior of the population from the fitness function (option WITHOUT_PLOT_STAT) in the execution of the programs.

```
'mingw32-make -k -f Makefile DEBUG=no VERBOSE=no WITHOUT_PLOT_STAT=yes'
```

Versions of optimized programs to have a good performance in the data set processing.

The compilation time of all programs varies according to the capabilities of the computers, but it can be approximately 20 minutes.

To install the applications `'mingw32-make -k -f Makefile install'`

And to eliminate the applications and use another option `'mingw32-make -k -f Makefile clean'`

Go to step [\[Step 12\]](#), [page 8](#).

8. Verify that the compiler is installed, on `terminal` type, if you do not install the missing packages as system administrator (root):

```
'gcc -v'    (>=4.8.5),
```

```
'g++ -v'    (>=4.8.5),
```

```
'make -v'   (>=4.0),
```

If you can not find the packages, install the missing ones as system administrator (root), with your package manager.

For GNU/Linux, e.g. run `'apt-get install gcc-4.9 g++-4.9 make'` or `'zypper install gcc gcc-c++ make'`

For Mac OS X, if you do not have a version ($\geq 4.8.5$), install through MacPorts or Homebrew. The procedure using MacPorts is described below:

- a. Running in a terminal ‘xcode-select --install’ and ‘sudo xcodebuild -license’
- b. Install [XQuartz](#)
- c. Install [MacPorts](#) for your version of the Mac operating system with pkg installer [High Sierra](#), [Sierra](#) or [El Capitan](#).
- d. Add to the PATH variable, where MacPorts is located, e.g, typing the command ‘export PATH=/opt/local/bin/port:\$PATH’
- e. Install the gcc compiler by typing the following commands ‘sudo port -v selfupdate’, ‘sudo port install gcc5’.

For Mac OS X go to [\[Step 10\], page 8](#).

9. If you want to use compile your applications with high-performance modules OpenBLAS and `sse_kernel`, for now this option only works on the x86-64 architecture with GNU/Linux. If you do not want this option, go to [\[Step 10\], page 8](#), and compile with the option `WITH_OPEN_BLAS = no`.

First verify that you have a Fortran compiler installed

```
‘gfortran -v’
    (>=4.8.5),
```

```
‘gfortran -print-file-name=libgfortran.so’
```

To verify that the libgfortran library is installed

If you can not find the packages, install the missing ones as system administrator (root), with your package manager, e.g. run ‘apt-get install gfortran-4.9 libgfortran-4.9-dev’ or ‘zypper gcc-fortran libgfortran3’.

Then you need to compile and get the static libraries of each of the components.

OpenBLAS

- a. From the <http://www.openblas.net/> page, download the source code of the latest version of OpenBLAS.
- b. Unzip the file with the ‘tar zxvf OpenBLAS-0.2.20.tar.gz’ command.
‘cd OpenBLAS-0.2.20’
- c. After editing Makefile.rule ‘NO_CBLAS=1, NO_LAPACK=1, NO_LAPACKE=1’ and run ‘make FC=gfortran’
- d. Copy libopenblas.a static library from the OpenBLAS-0.2.20 directory to the openblas directory of leac, e.g. ‘cp libopenblas.a leac/openblas’

CBLAS, LAPACK and LAPACKE

- a. Download [lapack-3.8.0.tar.gz](http://www.netlib.org/lapack/lapack-3.8.0.tar.gz) from <http://www.netlib.org/lapack/>
- b. ‘tar zxvf lapack-3.8.0.tar.gz’, ‘cd lapack-3.8.0’
- c. ‘cp make.inc.example make.inc’
- d. After editing make.inc, and change the variables ‘CFLAGS = -O3 -march=native -m64 -fomit-frame-pointer -fPIC -pthread’ and the compilers that you are using ‘CC’ and ‘FORTRAN’.

- e. Then you must execute the ‘make cblaslib’, ‘make lapacklib’ and ‘make lapackelib’.
- f. Copy static libraries ‘cp libcblas.a leac/openblas/’, ‘cp liblapack.a leac/openblas/’ and ‘cp liblapacke.a leac/openblas/’

sse_kernel

- a. Change to sse_kernel directory, within leac
 - b. Just type make to compile the library and get libssekernel.a
10. Install gnuplot, as a system administrator (root), for GNU/Linux run ‘apt-get install gnuplot-x1’. For Mac OS X ‘sudo port install gnuplot’.
 11. You can now compile the EAC applications, change to the eac inside the leac home directory ‘cd leac/eac’.

First edit the Makefile file and change the name of the compiler you are using in the CXX variable, (e.g. g++-mp-5), by default it is g++

Select one of the following compilation options:

‘make -k -f Makefile DEBUG=yes VERBOSE=yes’

To debug and analyze the detailed execution of the programs. These options allow software engineering utilities of correctness and reliability.

‘make -k -f Makefile DEBUG=no VERBOSE=no WITHOUT_PLOT_STAT=no’

Optimize and obtain the evolutionary behavior of the population from the fitness function (option WITHOUT_PLOT_STAT) in the execution of the programs.

‘make -k -f Makefile DEBUG=no VERBOSE=no WITH_OPEN_BLAS=yes WITHOUT_PLOT_STAT=yes’

For the processing of the high dimensionality data set, this option is recommended to obtain good performance, for this you must complete See [Step 9], page 7,

12. The API documentation of LEAC was written for Doxygen. For generate the LEAC library API documentation, download a version Doxygen (>= 1.8.13) or with your package manager, install it.

For Windows download [doxygen-1.8.14.windows.x64.bin.zip](#), unzip the file in c:\.

For GNU/Linux download [doxygen-1.8.13](#), ‘tar zxvf doxygen-1.8.13.linux.bin.tar.gz’. You must also install the dependency ‘apt-get install graphviz’.

For Mac OS X ‘sudo port install graphviz’ and ‘sudo port install doxygen’.

To obtain the documentation in a terminal, type ‘doxygen Doxyfile’ in the leac directory, or with the full path where the doxygen command is located, e.g. ‘C:\doxygen-1.8.14.windows.x64.bin\doxygen Doxyfile’ or ‘~/doxygen-1.8.13/bin/doxygen Doxyfile’.

If you do not want to install Doxygen and generate the documentation, we recommend that you use the integrated documentation contained in the html.zip file of the doc directory.

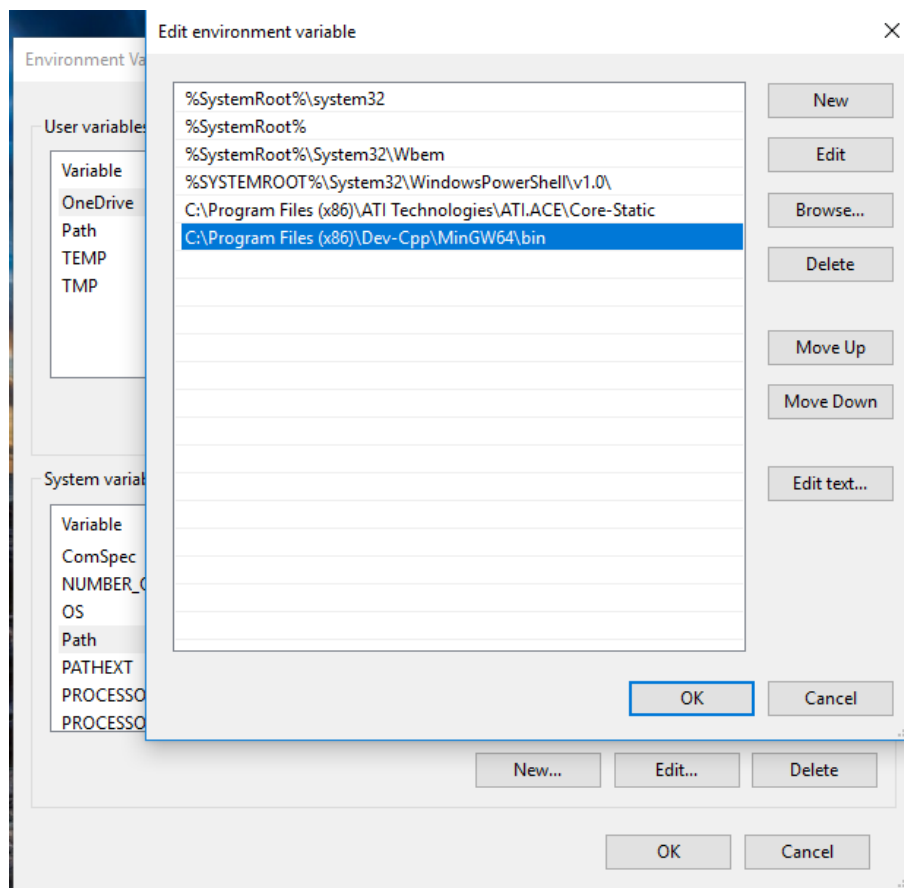


Figure 2.1: Dialog to add the MinGW compiler to the PATH environment variable

3 LEAC Software

In this chapter it is composed of three sections. The first section describes the steps to implement an evolutionary algorithm with the components provided by LEAC, documented with two examples included in [Appendix A \[Example source code\]](#), page 69. The complete documentation of the LEAC components can be found in the [doc/html](#) folder.

If you want to build a new algorithm, you must select the components and put them together in a source file and in the next [Section 3.2 \[Make an executable for a new algorithm\]](#), page 34, we describe how to create the executable file. The third section ([Section 3.3 \[Using implemented algorithms\]](#), page 40) describes how to use the algorithms implemented with LEAC as the end user. If you want to use the implementations of the algorithms listed in [Table 1.1](#), you can omit the first two sections.

3.1 Implementation of an algorithm

LEAC provides the necessary components to implement an evolutionary algorithm to solve the clustering problem. The following subsections describe the order of the steps to construct an evolutionary algorithm and some of the functions and classes provided by LEAC for each step.

3.1.1 Encoding criterion

There are different coding schemes proposed, for the case of the clustering problem traditional encoding string as *binary*, *integer* or *real*. You can also use others based on a partition of the objects in the dataset as pair of *partitioning table and cluster centroids*. The output of an evolutionary algorithms depends on the type of coding used by each for the chromosomes and its associated phenotype: *centroid*, *medoid*, *label*, *tree*, or *graph-based* representations. The terms genotype, chromosome, and individual usually have the same meaning in the literature on evolutionary algorithms.

The different encodings are implemented in the LEAC chromosome class hierarchy shown in [Figure 3.1](#).

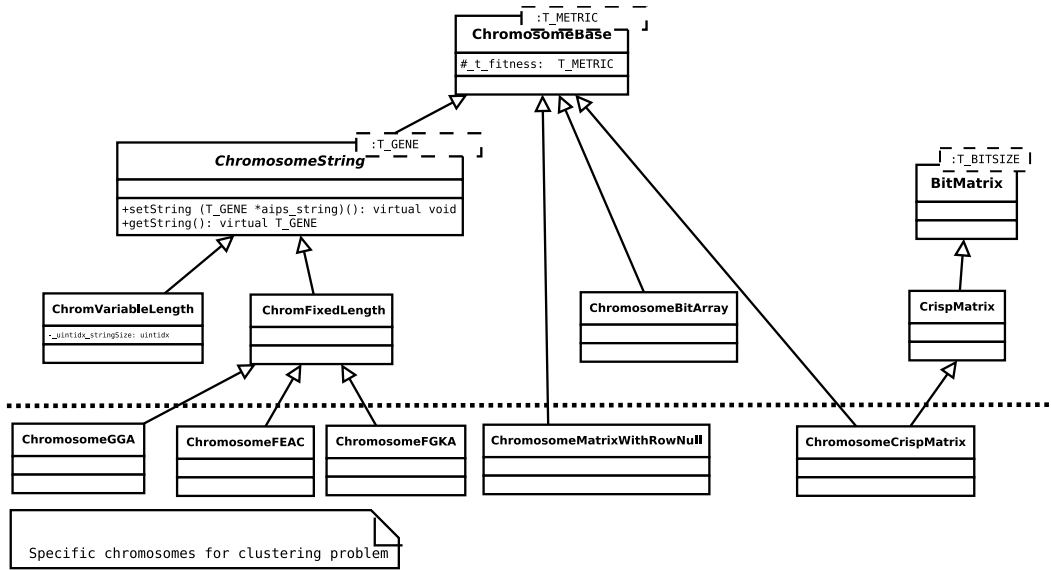


Figure 3.1: Class diagrams of the Chromosomes used for encoding

In LEAC there are three general chromosomes that can be used to implement a large part of the encodings that are:

1. **ChromFixedLength**. Chromosomes with a string of characters, integer or real of fixed length. All instantiated chromosomes will have a fixed length during evolution. The constructor method is:

```
[Constructor on gaencode::ChromFixedLength]
ChromFixedLength <T_GENE, T_METRIC>()
    Where T_GENE it is the type of data of each gene,
    T_METRIC it es the type of data for fitness function
```

Before creating the objects, you must specify the length that each chromosome will have with the following method:

```
[Method on gaencode::ChromFixedLength]
static void setStringSize (uintidx aiuintidx_stringSize)
    See [Example], page 71
```

2. **ChromVariableLength**. It is similar to the previous one, with the difference that the length of each chromosome can vary and can also change in evolution.

```
[Constructor on gaencode::ChromVariableLength]
ChromVariableLength<T_GENE,T_METRIC>(const uintidx aiuintidx_stringSize)
    Where T_GENE it is the type of data of each gene,
    T_METRIC it es the type of data for fitness function
```

3. **ChromosomeBitArray**. To model the binary chromosomes. The above chromosomes could be used with the **T_GENE** parameter equal to **bool**, but to have a better efficiency in storage and performance in the application of genetic operators, bit-level management is performed.

```
[Constructor on gaencode::ChromosomeBitArray]
ChromosomeBitArray<T_BITSIZE,T_METRIC>(const uintidx aiuintidx_numBits)
    Where T_BITSIZE size of the variable to store the bits,
    T_METRIC it es the type of data for fitness function
```


A classification based on the meaning of the coding (phenotype-genotype), used in different algorithms found in the literature on clustering is described in the following subsections.

3.1.1.1 Cluster labels

a. String-of-group-numbers encoding

It consists of an integer vector of length n , where n is the number of instances. The possible values in the vector are from 1 to k and the i th element establishes a relation of belonging from the i th instance to a cluster.

To instantiate the *string-of-group-numbers* chromosomes, you can use the class of use `<undefined> [gaencode::ChromFixedLength]`, page `<undefined>`, where `T_GENE` is integer type.

b. Matrix-based binary encoding

A $k \times n$ binary matrix can also be used to specify a partition of instances in clusters. Formally defined by BEF84 called *crisp partition* or *hard partition*:

$$M_c = \{U_{k \times n} | u_{ji} \in \{0, 1\}; \sum_{i=1}^n u_{ji} > 0, \text{ for all } j, \sum_{i=1}^n u_{ji} = 1, \text{ for all } i\} \quad (4.1)$$

In which the rows represent clusters and the columns represent instances. In this case, if the i^{th} object belongs to the j^{th} cluster, then 1 is assigned to element j^{th} rows and i^{th} columns of the genotype, whereas the other elements of the same column receive 0. You can use the following class:

```
[Constructor on gaencode::ChromosomeCrispMatrix]
ChromosomeCrispMatrix
    <T_BITSIZE, T_CLUSTERIDX, T_METRIC>
    (const uintidx aiuintidx_numRows,
     const uintidx aiuintidx_numColumns)
Where T_BITSIZE size of the variable to store the bits,
T_CLUSTERIDX is integer index for clusters,
T_METRIC it es the type of data for fitness function
See [Example ChromosomeCrispMatrix], page 87.
```

3.1.1.2 Centroid-based

- a. **Real encoding** A chromosome in this encoding is a vector of real numbers that contains the coordinates of each centroid consecutively of the clusters. For an d -dimensional space, the length of a genotype is $d \times k$ words, where the first d positions (or, genes) represent the d dimensions of the first cluster centre, the next d positions represent those of the second cluster centre, and so on:

$$Ch = [g_{11} \ g_{12} \ \dots \ g_{1d} \ g_{21} \ g_{22} \ \dots \ g_{2d} \ \dots \ g_{k1} \ g_{k2} \ \dots \ g_{kd}]$$

To encode a chromosome based on a centroid you can use the same class See `<undefined> [gaencode::ChromFixedLength]`, page `<undefined>`, parameterized for real numbers. See `[Example gaencode::ChromFixedLength]`, page 71.

When a *centroid-based* partition is used, it can be derived by the *nearest object rule* into account the proximities between objects and centroids such a way that the i th

object is assigned to the cluster represented by the closer (i.e., the most similar). With the centroids of the groups μ_j , so the object x_i belongs to the cluster C_j if:

$$x_i \in C_j \leftrightarrow \|x_i - \mu_j\| \leq \min_k \|x_i - \mu_{j'}\|, j' = 1, 2, \dots, k, \quad (3.2)$$

b. **Binary encoding**

Another algorithm based centroids, and with a binary coding is proposed by TY01. First a data reduction procedure is used, which consists in calculating an adjacency matrix $A_{n \times n}$ and subsequently the *connected components*. The result is blocks $\{B_1, B_2, \dots, B_m\}$, with centroid $\{V_1, V_2, \dots, V_m\}$ respectively, So every V_i is used as a seed to generate a higher level cluster.

The length of each chromosomes is m , where the i^{th} position of the string will be ‘1’ therefore, centroid V_i is used as a seed to group those who have a ‘0’ gene and are closer to it.

3.1.1.3 Medoid-based

Another way to partition a data set is by selecting the most *representative object* of each cluster. In the literature there are two proposals for integer and binary encoding, which are described in the following subsections.

a. **Integer encoding**

Integer encoding scheme involves using an array of k elements to provide a medoid-based representation of the dataset. In this case, each array element represents the index of the object x_i , where $i = 1, 2, \dots, n$.

For implementation you can use `gaencode::ChromFixedLength` with `T_GENE` as index data type. See [\[gaencode::ChromFixedLength\]](#), page [\[undefined\]](#).

b. **Binary encoding**

KB97 they use binary encoding to define a medoid-based partition. Each chromosome has a length equal to the number of objects n . A bit on with index i indicates that object x_i is a prototype of a cluster C_j . The members of C_j will be determined by rule (3.2), changing the centroid μ_j by the medoid m_j .

For implementation you can use `gaencode::ChromosomeBitArray`. See [\[gaencode::ChromosomeBitArray\]](#), page [\[undefined\]](#).

3.1.1.4 Graph-based

a. **Binary encoding**

CdLM03 use graph-based coding, for objects they get *minimum spanning tree* (MST). The genes represent the edges of the graph, and the vertices the data set objects. As the MST have $n - 1$ edges. This is the length of the chromosomes. In the binary chromosome a value of “0” means that this edge remains, While a gene with value “1” means that this edge is eliminated. The number of elements with value “1” represents the value of $k - 1$.

3.1.2 Initialization of population

Before initializing the population, you must create a container from the STL library, such as `std::vector` or `std::list`. See [\[Example a vector of chromosomes\]](#), page 71, to represent the population or pool mating.

Several approaches are proposed for the initialization of the population, The simplest procedure to initialize the population is random, objects are randomly assigned to a cluster. Such an initialization strategy usually results in unfavorable initial partitions, since the initial clusters are likely to be mixed up to a high degree. However, it constitutes an effective approach to test the algorithms against hard evaluation scenarios HCFdC09.

In the case studies of this document see [Section A.2 \[GA algorithm\]](#), page 85, and [Section A.1 \[KGA algorithm\]](#), page 69. They use an initialization of seed centroids, selected randomly from the instances and all instances are distributed in groups around these centroids by *nearest object rule*.

For the particular case of population initialization in the GA algorithm ([Section A.2 \[GA algorithm\]](#), page 85), the following two functions are used:

With non-repeated instance indices, the centroids of the clusters can be constructed:

```
void clusteringop::randomInitialize
    (mat::MatrixBase<T_FEATURE> &aomatrixt_centroids,
     const INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast)
    See \[Example clusteringop::randomInitialize\], page 90
```

And finally with the centroids is created an initial partition:

```
void clusteringop::getPartition
    (mat::CrispMatrix<T_BITSIZE,T_CLUSTERIDX> &aobcrispmatrix_partition,
     mat::MatrixRow<T_FEATURE> &aimatrixt_instances,
     mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     dist::Dist<T_DIST,T_FEATURE> &aifunc2p_dist)
    See \[Example clusteringop::getPartition\], page 90
```

For the initialization of the other partition representations, LEAC provides equivalent functions, found in the header files:

- clustering_operator_centroids.hpp
- clustering_operator_crispmatrix.hpp
- clustering_operator_fuzzy.hpp
- clustering_operator_medoids.hpp

3.1.3 Fitness function

The evolutionary algorithms are based on the optimization of some objective function that guides the evolutionary search, his function is known *fitness function*. In the clustering problem different measures are used for *fitness function*, these are classified as *unsupervised measures* ([Section 3.1.3.2 \[Unsupervised measures\]](#), page 18) and *supervised measures* ([Section 3.1.3.3 \[Supervised measures\]](#), page 28). Unsupervised measures usually use a distance, to describe relationships *inter cluster* and *intra cluster*. The following section lists the most common distances and their functions that implement them.

3.1.3.1 Distances

Distance measures is the key in clustering to find the similarity between two objects x_i and x'_i . The most common is the *Euclidean distance* $\|x_i - x'_i\|$. LEAC offers a module in the `dist_euclidean.hpp` file to calculate the distances and the class diagram is shown in [Figure 3.2](#).



Figure 3.2: Class diagrams of the Distances

All classes derived from `Dist` define the *function call operator* that allows you to find the distance between two x_i and $x_{i'}$ objects:

[Method on `dist::Dist`]

```
T_DIST operator()(const T_FEATURE*, const T_FEATURE*, const uintidx)
```

To instantiate a `dist::Dist` object the following constructors are used

1. Euclidean distance

[Constructor on `dist::Euclidean`]

```
Euclidean<T_DIST, T_FEATURE>()
```

2. Euclidean square distance

[Constructor on `dist::Induced`]

```
Induced<T_DIST, T_FEATURE>(const mat::MatrixRow<T_DIST>& aimatrix_weight)
```

See [Example `dist::Induced`], page 17

3. Induced distance

The *induced distance* is a generic measure obtained by multiplying the transposed vector of point x_i to $x_{i'}$ by the *matrix of weight* A and with the vector not transposed (3.3).

$$D_{Ind}(x_i, x_{i'}) = (x_i - x_{i'})^T A (x_i - x_{i'}) \quad (3.3)$$

To calculate the *matrix of weights* A we have the following functions

- a. Identity matrix

[Function]

```
mat::MatrixRow<T_FEATURE> mat::getIdentity (const uintidx aiui_dimension)
```

If the *identity matrix* is used the induced distance is equivalent to the *Square Euclidean distance* ($A = I$)

See [Example `mat::getIdentity`], page 17

b. Mahalanobis matrix

[Function]

```
mat::MatrixRow<T_FEATURE> dist::getMatrixMahalonobis
    (INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast)
```

It is the inverse of the *covariance matrix* C_x of the data set X . When used as an matrix of weights at the *induced distance* is equivalent to *Mahalanobis distance* ($A = C_x^{-1}$). See [Example `dist::getMatrixMahalonobis`], page 17

c. Diagonal matrix

[Function]

```
mat::MatrixRow<T_FEATURE> dist::getMatrixDiagonal
    (T_FEATURE* aiarrrayt_varianceFeatures)
```

It is the inverse matrix of the variance of the attributes in the main diagonal ($A = D_x^{-1}$). See [Example `dist::getMatrixDiagonal`], page 17

The following is an example taken from the `main_gas_clustering.cpp` file, which shows how you can create an instance of a distance and select one of them at run time.

```
dist::Dist<DATATYPE_REAL,DATATYPE_FEATURE>
    *pfunct2p_distAlg = NULL;

switch ( linparam_ClusteringGA.getOpDistance() ) {
case INPARAMCLUSTERING_DISTANCE_EUCLIDEAN:
    pfunct2p_distAlg =
        new dist::Euclidean<DATATYPE_REAL,DATATYPE_FEATURE>();
    break;
case INPARAMCLUSTERING_DISTANCE_EUCLIDEAN_SQ:
    pfunct2p_distAlg =
        new dist::EuclideanSquared<DATATYPE_REAL,DATATYPE_FEATURE>();
    break;
case INPARAMCLUSTERING_DISTANCE_EUCLIDEAN_INDUCED:

    pfunct2p_distAlg =
        new dist::Induced<DATATYPE_REAL,DATATYPE_FEATURE>
            (mat::getIdentity
             <DATATYPE_REAL>
             (data::Instance<DATATYPE_FEATURE>::getNumDimensions()));
    break;
case INPARAMCLUSTERING_DISTANCE_DIAGONAL_INDUCED:

    pfunct2p_distAlg =
        new dist::Induced<DATATYPE_REAL,DATATYPE_FEATURE>
            (stats::getMatrixDiagonal<DATATYPE_FEATURE>
             (larray_desvstdFeactures)
             );
    break;
case INPARAMCLUSTERING_DISTANCE_MAHALONOBIS_INDUCED:

    pfunct2p_distAlg =
        new dist::Induced<DATATYPE_REAL,DATATYPE_FEATURE>
            (stats::getMatrixMahalonobis
             (lvectorptinst_instances.begin(),
              lvectorptinst_instances.end()
             )
            );
    break;
default:
```

```

    throw std::invalid_argument("main_gas_clustering: undefined norm");
    break;
}

```

3.1.3.2 Unsupervised measures

This type of evaluation tries to determine the quality of a given obtained partition of the data without any external information available. This is why this unsupervised measure are sometimes called as internal measures ABSSJF+12. All *unsupervised measures* function of the library are defined in the header file `unsupervised_measures.hpp`, to do calculations of metrics you can include files or simply the `leac.hpp` library, which contains all the header files.

The measures used in the evolutionary algorithms are described below.

1. Sum of quadratic errors (SSE)

A common clustering criterion or quality indicator is the *sum of squared error* (SSE), defined in CZZ09 as

$$\text{SSE} = \sum_{C_j} \sum_{x_i \in C_j} (x_i - \mu_j)^T (x_i - \mu_j) = \sum_{C_j} \sum_{x_i \in C_j} \|x_i - \mu_j\|^2 \quad (3.4)$$

Where x_i represents the instance i th of the dataset. We use the following convention for subscripts i ; $i \in \{1, 2, \dots, n\}$, for the instances. The subscript for the groups is j ; $j \in \{1, 2, \dots, k\}$ and the centroid of cluster C_j is denoted as μ_j .

SSE is also defined in KM99, using [Crisp Partition], page 13, and calling it *total within-cluster variation* (TWCV)

$$\text{TWCV} = \sum_{j=1}^k \text{WCV}^{(j)} = \sum_{j=1}^k \sum_{i=1}^n u_{ij} \sum_{l=1}^d (x_{il} - \mu_{jl})^2 \quad (3.5)$$

To refer to the dimensions of the objects we use l : $l \in \{1, 2, \dots, d\}$, so l th denotes the dimension of x_{il} .

Or with some slight variation *Sum of Euclidean Distance* SED:

$$\text{SED} = \sum_{C_j} \sum_{x_i \in C_j} \|x_i - \mu_j\| \quad (3.6)$$

This is probably the most straightforward and popular evaluation distance in the literature. It only considers cohesion of clusters in order to evaluate the quality of a given partition data ABSSJF+12.

This metric generally used by different algorithms when the number of clusters k is known and is used by BM02a CZZ09.

For the calculation of SSE you have three functions. Different distances can be passed as parameter *aifunc2p-dist* (See Section 3.1.3.1 [Distances], page 15), to obtain the variations of the metric:

```

                                                                    [Function]
std::pair<T_METRIC,bool> um::SSE
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
```

```

INPUT_ITERATOR aiiterator_instfirst,
const INPUT_ITERATOR aiiterator_instlast,
const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

The partition is derived by *aimatrixt_centroids*. See [Equation (3.2)], page 14.
See [Example um::SSE], page 76

Other functions for the calculation of *SSE* that depend on the way to specify the membership of an object to a cluster, are the following:

```

T_METRIC um::SSE
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     T_CLUSTERIDX *aiarraymidx_memberShip,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

```

std::pair<T_METRIC,bool> um::SSE
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const partition::Partition<T_CLUSTERIDX>
     &aipartition_clusters,
     dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

Depending on the encoding used, you have a set of partition clusters classes (*partition::Partition*) for calculating metrics generically. See Figure 3.3. For example, a partition based on (3.2), the constructor you can use is

```

PartitionCentroids<T_FEATURE,T_CLUSTERIDX,T_DIST,INPUT_ITERATOR>
    (mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     const INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const dist::Dist<T_DIST,T_FEATURE>& aifunc2p_dist)

```

And for one based on a crisp matrix (4.1):

```

PartitionCrispMatrix<T_BITSIZE,T_CLUSTERIDX>
    (const mat::CrispMatrix<T_BITSIZE,T_CLUSTERIDX> &aibitcrisp_matrix)

```

See [Example partition::PartitionCrispMatrix], page 93

To avoid defining the template parameters for the case of a partition, you can use the *makePartition*:

```

T_METRIC partition::makePartition
    (mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     const INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const T_CLUSTERIDX aimcidx_numClusters,
     const dist::Dist<T_DIST,T_FEATURE> &aifunc2p_dist)

```

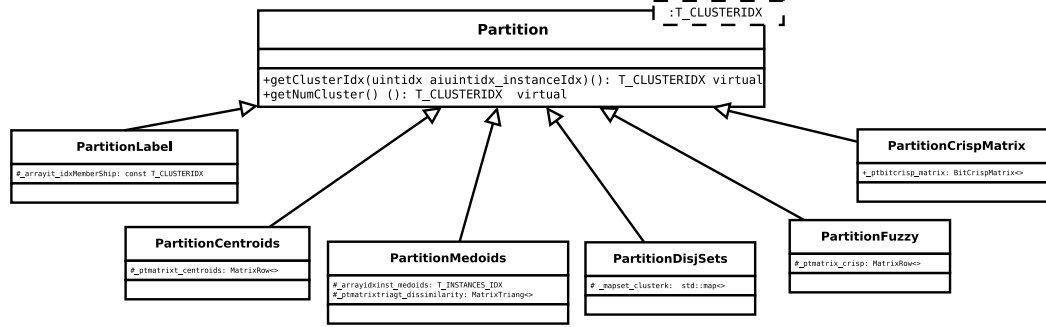


Figure 3.3: Class diagram of the partitions used to calculate the metrics

2. Distortion

The distortion of the clusters is a measure define by FKKN97. Similar to SSE but considers the number of instances and attributes:

$$\text{distortion}(C) = \frac{1}{n \cdot d} \sum_{i=j}^n D(x_i, f_C(x_i))^2 \quad (3.7)$$

Where D is the Euclidean distance, $f_C(x_i)$ be a mapping which gives the closest centroid in solution C for a instance x_i , n is the number of instances, and d number of attributes of the instances.

The function that allows to calculate the measure of the distortion is:

```

std::pair<T_METRIC,bool> um::distortion
(const mat::MatrixBase<T_FEATURE> &aimatrixt_centroids,
 INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 T_CLUSTERIDX *aiarraycidx_memberShip,
 const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist,
 const FUNCINSTFREQUENCY func_instfrequency)
[Function]

```

3. Sum of Euclidean Distance for Medoid

For k -medoid, replacing the centroids by the most representative instance in equation (3.6), we obtain the cost function sum of Euclidean distances to the most representative instance:

$$\text{SEDmedoid} = \sum_{C_j} \sum_{x_i \in C_j} \|x_i - m_j\| \quad (3.8)$$

Where m_j represents the *medoid* or *prototype* of cluster C_j

```

T_METRIC um::SSEMedoid
(const uintidx *aiarrayidxinst_medoids,
 const T_CLUSTERIDX aimcidx_numClustersK,
 const mat::MatrixTriang<T_METRIC> &aimatrixtriagt_dissimilarity)
[Function]

```


The `medoids::getMatrixDissimilarity` function calculates and returns the triangular distance matrix using a specified distance measure. Used to get other measures for example `um::SSEMedoid`. This is in `medoids_clustering.hpp` file.

[Function]

```
mat::MatrixTriang<T_DIST> medoids::getMatrixDissimilarity
(INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 const dist::Dist<T_DIST,T_FEATURE> &aifunc2p_dista)
```

4. Least-squared errors functional

A *fuzzy c-partitions* is represented by a matrix (BEF84):

$$M_{fc} = \{U_{k \times n} | u_{ji} \in [0, 1]; \sum_{i=1}^n u_{ji} > 0, \text{ for all } j, \sum_{i=1}^n u_{ji} = 1, \text{ for all } i\}, \quad (3.9)$$

Several clustering criteria have been proposed for identifying optimal fuzzy c-partitions in X , the most popular and well-studied criterion is associated with matrices M_{fc} equation (3.9) is called *least-squared errors functional*, described in BEF84

$$J_m(U, \mu) = \sum_{i=1}^n \sum_{j=1}^k u_{ji}^m D_{Ind}(x_i - \mu_j), \quad (3.10)$$

Where

$U \in M_{fc}$ (3.9) fuzzy c-partition of X ;

$\mu = [\mu_1, \mu_2, \dots, \mu_k]$ centroids,

m weighting exponent; $1 \leq m < \infty$

$D_{Ind}(x_k, \mu_i)$ is one of the *induced distances* from x_i to μ_j . See [\[Induced distance\]](#), page 16,

[Function]

```
T_METRIC um::jm
(mat::MatrixRow<T_METRIC> &aimatrixt_u,
 mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
 INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 T_METRIC aif_m,
 dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

For hard clustering will be based on $J_m(U, \mu)$ from (3.10), we will rewrite J_1 as:

$$J_1(U, \mu) = \sum_{i=1}^n \sum_{j=1}^k u_{ji} D_{Ind}(x_i - \mu_i) \quad (3.11)$$

[Function]

```
T_METRIC um::j1
(mat::BitMatrix<T_BITSIZE> &aimatrix_crisp,
 mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
 INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

See [\[Example um::j1\]](#), page 90

5. Davis-Bouldin Index

Davies–Bouldin index (DB) DB79, is a function of the ratio of the sum of *within-cluster scatter* to *between-cluster separation*, DB index for the partitioning of k clusters is defined as

$$DB = \frac{1}{k} \sum_j R_{C_j, C_{1 \leq j' \leq k}}, \quad j' = 1, 2, \dots, k \quad \text{and} \quad j \neq j' \quad (3.12)$$

in which the index for the j^{th} cluster against all clusters least the same $R_{C_j, C_{1 \leq j' \leq k}}$ is given by

$$R_{C_j, C_{1 \leq j' \leq k}} = \max_{j', j' \neq j} R_{C_j, C_{j'}}$$

where $R_{C_j, C_{j'}}$ is a measure between a pair of cluster defined by

$$R_{C_j, C_{j'}} = \frac{S_{q, C_j} + S_{q, C_{j'}}}{d_{jj', t}}$$

and the scatter S_{q, C_j} within for j^{th} cluster, is computed as

$$S_{q, C_j} = \left(\frac{1}{|C_j|} \sum_{x_i \in C_j} \{|x_i - \mu_j|_2^q\} \right)^{1/q}$$

S_q is the q^{th} root of the q^{th} moment of the points in cluster j with respect to their mean, and is a measure of the dispersion of the points in cluster j . $d_{jj', t}$ is the Minkowski distance of order t between the centroids that characterize clusters j and j' .

DB use in BM02b.

[Function]

```
T_METRIC um::DBindex
(const mat::MatrixBase<T_FEATURE> &aimatrixt_centroids,
 INPUT_ITERATOR aiterator_instfirst,
 const INPUT_ITERATOR aiterator_instlast,
 const partition::Partition<T_CLUSTERIDX> &aipartition_clusters,
 const dist::Dist<T_METRIC, T_FEATURE> &aifunc2p_dist)
```

6. Silhouette

This metric known as silhouette was proposed by KR90. Consider an object x_i belonging to cluster C_j . So, the average dissimilarity of x_i to all other objects of C_j . is denoted by $a(x_i)$. Now let us take into account cluster $C_{j'}$. The average dissimilarity of x_i to all objects of $C_{j'}$, will be called $D(x_i, C_{j'})$. After computing $D(x_i, C_{j'})$, for all clusters $C_j \neq C_{j'}$, the smallest one is selected, i.e. $b(x_i) = \min D(x_i, C_{j'})$. This value represents the dissimilarity of x_i to its neighbor cluster, and the silhouette $s(x_i)$ given by (ACH06):

$$s(x_i) = \frac{b(x_i) - a(x_i)}{\max \{a(x_i), b(x_i)\}}, \quad (3.13)$$

The higher $s(x_i)$ is better the assignment of the object x_i to a given cluster and

$$-1 \leq s(x_i) \leq 1$$

Use in HE03 and ABSSJF+12.

[Function]

```
T_METRIC um::silhouette
(mat::MatrixTriang<T_METRIC> &aimatrixtriagrt_dissimilarity,
 ds::PartitionLinkedNumInst<T_CLUSTERIDX,
 T_INSTANCES_CLUSTER_K> &aipartlinknuminst_memberShip)
```

7. Simplified Silhouette

The silhouette proposed in KR90 depends on the computation of all distances between objects, leading to a computational cost of $O(n^2)$, which is often not sufficiently efficient for real-world clustering applications (e.g. data mining, text mining, gene-expression data analysis). To circumvent this limitation, a simplified silhouette can be employed. The simplified silhouette is based on the computation of distances between objects and cluster centroids, which are the mean vectors of the clusters. More specifically, the term $a(i)$ of equation (3.13) becomes the dissimilarity of object x_i to the centroid of its cluster (C_j). Similarly, instead of computing $D(x_i, C'_j)$ as the average dissimilarity of x_i to all objects of C'_j , $C_j \neq C'_j$, only the distance between x_i and the centroid of C'_j must be computed. While these modifications reduce the computational cost from $O(n^2)$ to $O(n)$ ACH06.

[Function]

```
std::vector<T_METRIC> um::simplifiedSilhouette
(const mat::MatrixBase<T_FEATURE> &aimatrixt_centroids,
 INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 const partition::Partition<T_CLUSTERIDX> &aipartition_clusters,
 const std::vector<T_INSTANCES_CLUSTER_K> &aivectorit_numInstClusterK,
 const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

8. CS measure

The *CS* measure CSL04 DAK08 is defined as

$$CS(C) = \frac{\frac{1}{k} \sum_{j=1}^k \left\{ \frac{1}{|C_j|} \sum_{x_i \in C_j} \max_{x_{i'} \in C_j} \{D(x_i, x_{i'})\} \right\}}{\frac{1}{k} \sum_{j=1}^k \left\{ \min_{j \in k, j \neq j'} \{D(\mu_j, \mu_{j'})\} \right\}} \quad (3.14)$$

Where

D is a distance function,

x_i and $x_{i'}$ are instances in the same cluster,

μ_j and $\mu_{j'}$ are the centroids of two different cluster.

CSL04 Establish that this measure is a function of the ratio of the sum of within-cluster scatter to between-cluster separation. The smallest $CS(C)$ indicates a valid optimal partition. The *CS* measure has the same rationale as the *DI* (See [Dunn's index], page 24) and the *DB* (See [Davis-Bouldin Index], page 22).

[Function]

```
T_METRIC um::CSmeasure
(INPUT_ITERATOR aiiterator_instfirst,
 const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
 const ds::PartitionLinkedNumInst<T_CLUSTERIDX,T_INSTANCES_CLUSTER_K>
```

```

    &aipartlinknuminst_memberShip,
    const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

9. Dunn's index

A well-established hard cluster validity measure is the Dunn's index (DI) that identifies sets of clusters that are well separated. Dunn's index is defined as (CSL04)

$$DI(C) = \min_{j \in C} \left\{ \min_{j' \in C, j' \neq j} \left\{ \frac{\delta(C_j, C_{j'})}{\max_{j'' \in C} \{\Delta(C_{j''})\}} \right\} \right\} \quad (3.15)$$

Where

$$\delta(C_j, C_{j'}) = \min \{D(x_i, x_{i'}) | x_i \in C_j, x_{i'} \in C_{j'}\},$$

$$\Delta(C_j) = \max \{D(x_i, x_{i'}) | x_i, x_{i'} \in C_j\},$$

and x_i and $x_{i'}$ are instances.

The main drawback with the direct implementation of Dunn's index is its computational load because calculating $DI(C)$ becomes computationally very expensive as k and n increase. The largest $DI(C)$ indicates a valid optimal partition CSL04.

[Function]

```

T_METRIC um::DunnIndex
(INPUT_ITERATOR aiiterator_instfirst,
 const ds::PartitionLinked<T_CLUSTERIDX> &aipartlink_memberShip,
 const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

To avoid calculating distance between instances again and improve performance in the DI evaluation To avoid calculating the distance between the instances and improving performance in the evaluation, use the following function:

[Function]

```

T_METRIC um::DunnIndex
(mat::MatrixTriang<T_METRIC> &aimatrixtriagrt_dissimilarity,
 ds::PartitionLinked<T_CLUSTERIDX> &aipartlinknuminst_memberShip)

```

10. Simplified Dunn's index

Just as the [silhouette], page 22, can also simplify [Dunn's measure], page 24, to reduce the computational cost of $O(n^2)$ to $O(n)$ using the centroids. This measure will be called *Simplified Dunn's index (SDI)*.

$$SDI(C) = \min_{j \in C} \left\{ \min_{j' \in C, j' \neq j} \left\{ \frac{\delta(C_j, C_{j'})}{\max_{j'' \in C} \{\Delta(C_{j''})\}} \right\} \right\} \quad (3.16)$$

Where

$$\delta(C_j, C_{j'}) = \min \{D(\mu_j, \mu_{j'}) | j \neq j'\}$$

$$\Delta(C_j) = \max \{D(x_i, \mu_j) | x_i \in C_j\}$$

And the function to calculate *Simplified Dunn's index*

[Function]

```
T_METRIC um::simplifiedDunnIndex
    (const mat::MatrixBase<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const ds::PartitionLinked<T_CLUSTERIDX> &aipartlink_memberShip,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

11. Variance ratio criterion

The *variance ratio criterion* (*VRC*) sometimes called *Calinski–Harabasz index* initially proposed by CH74 is based on the internal cluster cohesion and the external cluster isolation. The corresponding internal cohesion is calculated by the within-group sum of square distances HT12.

The index is defined as:

$$VRC_k = \frac{SS_B}{SS_W} \cdot \frac{(n - k)}{(k - 1)} \quad (3.17)$$

Where SS_B is the overall between-cluster variance, SS_W is the overall within-cluster variance, k is the number of cluster, and n is the number of instances.

The overall between-cluster variance SS_B is defined as

$$SS_B = \sum_{j=1}^k |C_j| \|\mu_j - M\|^2$$

Where μ_j is the centroid of cluster j , M is the overall mean of the instances. The overall within-cluster variance SS_W is defined as

$$SS_W = \sum_{j=1}^k \sum_{x_i \in C_j} \|x_i - \mu_j\|^2$$

The VRC should be maximized. Use in CdLM03 and HT12.

[Function]

```
T_METRIC um::VRC
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const partition::Partition<T_CLUSTERIDX> &aipartition_clusters,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

12. Intra- and inter-cluster distance

The definition of *intra- and inter-cluster distance* (DIIC) (TY01) is given by the equation:

$$DIIC = \sum_{i=1}^k D_{inter}(C_j)w - D_{intra}(C_j) \quad (3.18)$$

Where $D_{intra}(C_j)$ is the intra-cluster distance

$$D_{intra}(C_j) = \sum_{B_l \subset C_j} \|v_l - \mu_j\| \cdot |B_l|$$

and $D_{inter}(C_j)$ is the inter-cluster distance

$$D_{inter}(C_j) = \sum_{B_l \subset C_j} \left(\min_{j \neq k} \|v_l - \mu_j\| \right) \cdot |B_l|$$

And w is a weight. If the value of w is small, we emphasize the importance of $D_{intra}(C_j)$. This tends to produce more clusters and each cluster tends to be compact. If the value of w is chosen to be large, we emphasize the importance of $D_{inter}(C_j)$. This tends to produce fewer clusters and each cluster tends to be loose. TY01.

[Function]

```
T_METRIC um::Dintra
    (const mat::MatrixRow<T_FEATURE> &aimatrixrowt_S,
     const mat::MatrixRow<T_FEATURE> &aimatrixrowt_Vi,
     const std::vector<T_INSTANCES_CLUSTER_K> &aivectort_numInstBi,
     const partition::Partition<T_CLUSTERIDX> &aipartition_clustersBkinCi,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

[Function]

```
T_METRIC um::Dinter
    (const mat::MatrixRow<T_FEATURE> &aimatrixrowt_S,
     const mat::MatrixRow<T_FEATURE> &aimatrixrowt_Vi,
     const std::vector<T_INSTANCES_CLUSTER_K> &aivectort_numInstBi,
     const partition::Partition<T_CLUSTERIDX> &aipartition_clustersBkinCi,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)
```

This metric can only be calculated when having subgroups. For a clustering C_1, C_2, \dots, C_k each C_j with S_j centroid, is constructed from the subgroups B_i with V_i centroid. This way of clustering is a characteristic particular feature of the algorithm described in TY01.

13. Validity index I

The *validity index I* or simply *Index I* described in MB02 and BM07. It is used as a metric to measure clustering performance. It was proposed as a measure to indicate the (goodness) validity of the solution in the cluster. It is defined as follows:

$$I(k) = \left(\frac{1}{k} \cdot \frac{E_1}{E_k} \cdot D_k \right)^p, \quad (3.19)$$

Where k is the number of clusters

$$E_k = \sum_{j=1}^k \sum_{i=1}^n u_{ji} \|x_i - \mu_j\|,$$

and

$$D_k = \max_{j,j'=1}^k \|\mu_{j'} - \mu_j\|$$

n is the total number of objects x_i . $U(X) = [u_{ji}]_{k \times n}$ is a partition matrix of the objects and μ_j is the centroid of cluster j^{th} . The value of k that maximizes $I(k)$ is considered the correct number of clusters.

[Function]

```

T_METRIC um::indexl
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const partition::Partition<T_CLUSTERIDX> &aipartition_clusters,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist,
     const T_METRIC airt_p = 2.0)

```

14. Xie-Beni index

The index of Xie-Beni (XB) XB91 is defined for *fuzzy c-partitions*. See [Definition fuzzy c-partitions], page 21. This index can be extended to a crisp partition. See [crisp partition], page 13. Note that M_c is imbedded in M_{fc} .

The Xie-Beni index is defined as the quotient of the total variance σ , and minimal separation of groups d_{min} .

$$XB = \frac{\sigma}{n \cdot (d_{min})^2} \quad (3.20)$$

In detail

$$\sigma = \sum_{j=1}^k \sum_{x_i}^n u_{ji}^2 \|x_i - \mu_j\|^2,$$

$$d_{min} = \min_{j,j'=1,j \neq j'}^k \|\mu_j - \mu_{j'}\|$$

$$XB = \frac{\sum_{j=1}^k \sum_{x_i}^n u_{ji}^2 \|x_i - \mu_j\|^2}{n \cdot (d_{min})^2}$$

[Function]

```

T_METRIC um::xb
    (mat::MatrixRow<T_METRIC> &aimatrixt_u,
     mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

And the function to calculate the XB to a hard partition (See [partition::Partition], page 19).

[Function]

```

T_METRIC um::xb
    (const mat::MatrixRow<T_FEATURE> &aimatrixt_centroids,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const partition::Partition<T_CLUSTERIDX> aipartition_clusters,
     const dist::Dist<T_METRIC,T_FEATURE> &aifunc2p_dist)

```

3.1.3.3 Supervised measures

1. Rand Index

The *Rand Index* [Ran71](#) is defined for two partitions of the same data set X , C in k cluster and R in k' known classes. [ACH06](#) indicate that these measures can be seen as an absolute criterion or referential standard that allows the use of classification data sets for performance assessment not only of *classifiers* with the same number of clusters and class ($k = k'$), if not also different ($k \neq k'$). In the same article they write it as follows:

$$\Omega(R, C) = \frac{a + d}{a + b + c + d} \quad (3.21)$$

Where:

- a : Number of pairs of data objects belonging to the same class in R and to the same cluster in C .
- b : Number of pairs of data objects belonging to the same class in R yet to different clusters in C .
- c : Number of pairs of data objects belonging to different classes in R yet to the same cluster in C .
- d : Number of pairs of data objects belonging to different classes in R and to different clusters in C .

The function that obtains the rand index is

```
[Function]
T_METRIC sm::randIndex
    (const sm::ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K>
     &aimatchmatrix_confusion)
```

To obtain the Rand Index, you must first obtain the confusion matrix:

```
[Function]
sm::ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K> sm::getConfusionMatrix
    (INPUT_ITERATOR aiterator_instfirst,
     const INPUT_ITERATOR aiterator_instlast,
     const partition::Partition<T_CLUSTERIDX> &aipartition_clusters,
     const FUNCINSTFREQUENCY func_instfrequency,
     const FUNCINSTCLASS func_instclass)
```

See [\[Example sm::getConfusionMatrix\]](#), page 93

2. Purity

Purity is a simple and transparent evaluation measure each cluster is assigned to the class which is most frequent in the cluster, and then the accuracy of this assignment is measured by counting the number of correctly assigned objects and dividing by n [MRS08](#).

$$\text{purity}(C, R) = \frac{1}{n} \sum_j \max_{j'} |C_j \cap R_{j'}| \quad (3.22)$$

Where C and R two partitions of the same data set X , of k cluster and k' known classes respectively.

[Function]


```
T_METRIC sm::purity
    (const sm::ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K>
     &aimatchmatrix_confusion)
```

3. Precision

To calculate the accuracy, we use the pairs of the R and C partitions, and based on Faw06.

$$\text{precision} = a/(a + c) \quad (3.23)$$

[Function]

```
T_METRIC sm::precision
    (const ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K>
     &aimatchmatrix_confusion)
```

4. Recall

Based on Faw06.

$$\text{recall} = a/(a + b) \quad (3.24)$$

[Function]

```
T_METRIC sm::recall
    (const ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K>
     &aimatchmatrix_confusion)
```

3.1.4 Stop Criterion

There exists no stopping criterion in the literature which ensures the convergence in the evolutionary algorithms, to an optimal solution. Usually, two stopping criteria are used. In the first, the process is executed for a fixed number of iterations and the best string obtained is taken to be the optimal one. In the other, the algorithm is terminated if no further improvement in the fitness value of the best string is observed for a fixed number of iterations, and the best string obtained is taken to be the optimal one MC96.

3.1.5 Select individuals

In this step, the individuals of the population are selected in a mating group to apply the crossing and mutation operators. In LEAC has implemented three schemes of individual selection.

1. Roulette wheel. Based on the concept of survival used in natural genetic systems. To apply this selection after having evaluated the fitness function, the probability distribution is calculated with the function:

[Function]

```
std::vector<T_REAL> prob::makeDistRouletteWheel
    (INPUT_ITERATOR aiiterator_instfirst,
     INPUT_ITERATOR aiiterator_instlast,
     const FITNESSOPERATION fitness_func)
See [Example prob::makeDistRouletteWheel], page 80
```

With the probability distribution, the indices of the individuals to be selected are generated:

[Function]

```
T_INTIDX gaselect::getIdxRouletteWheel
    (const std::vector<T_PROBABILITY> &aivectorrt_probDist,
     const T_INTIDX aiuintidx_begin)
```

2. Tournament. Involves running several “tournaments” between a small number of individuals specified by the variable `aiuintidx_orderTournament` chosen at random from the population, the individual with the best fitness of each tournament is selected:

[Function]

```
INPUT_ITERATOR gaselect::tournament
    (const INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
     const uintidx aiuintidx_orderTournament,
     const FITNESSOPERATION fitness_func)
```

3. Elitism. Some algorithms select the best individuals to be used in the crossing, as in BEF84 (See [Section A.2 \[GA algorithm\]](#), page 85). In BM02a elitism has been implemented in each generation by replacing the worst chromosome (select the worst and replace it with the best chromosome See [\[Example elitism replace the worst\]](#), page 77) of the population with the best one seen up to the previous generation (See [\[Example elitism select the best\]](#), page 78).

The `<algorithm>` header of the library STL Algorithms defines a collection of functions specially designed to be used in ranges of elements, such as `std::max` and `std::sort` that are used to implement elitism.

3.1.6 Crossover operator

To apply the crossover operator LEAC has two functions to iterate over the population and mating pool:

[Function]

```
void gaiterator::crossover
    (INPUT_ITERATOR aiiterator_instfirstParent,
     const INPUT_ITERATOR aiiterator_instlastParent,
     INPUT_ITERATOR aiiterator_instfirstChild,
     const INPUT_ITERATOR aiiterator_instlastChild,
     const GENETIC_OPERATOR genetic_operator)
    Select a pair of parents and children consecutively from their containers.
    See \[Example gaiterator::crossover\], page 80
```

[Function]

```
void gaiterator::crossoverRandSelect
    (INPUT_ITERATOR aiiterator_instfirstParent,
     const INPUT_ITERATOR aiiterator_instlastParent,
     INPUT_ITERATOR aiiterator_instfirstChild,
     const INPUT_ITERATOR aiiterator_instlastChild,
     const GENETIC_OPERATOR genetic_operator)
    Select a pair of parents and children randomly and consecutively respectively from their
    containers.
    See \[Example gaiterator::crossoverRandSelect\], page 95
```

Within the iterator function, the crossover operator is applied. In LEAC has implemented several operators of crossover and mutation proposed in the literature. These are organized by packages as shown in the [Figure 3.4](#). The way in which genetic operators are classified in LEAC is *cluster-oriented* or *nonoriented operators*. They are also classified according to their coding *binary*, *integer*, or *real* encodings. For a classification of operators see HCFdC09. From the point of view of the implementation, it is also possible to classify those that are programmed in a generic way and those that depend on the type of data.

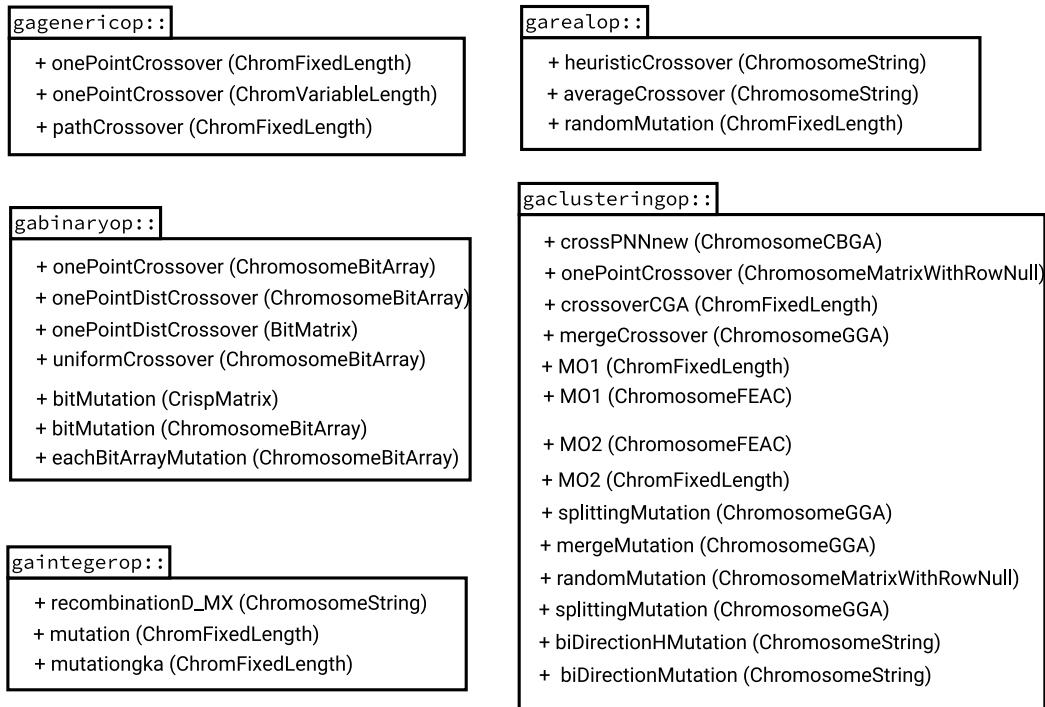


Figure 3.4: Packages of genetic operators provided by LEAC. The type of chromosome received by the operator is indicated in parentheses

The crossover operators used by the algorithms implemented in section [Appendix A \[Example source code\]](#), page 69, they use Single-point and Two-point Crossover described below:

[Function]

```
void gagenericop::onePointCrossover
(gaencode::ChromFixedLength<T_GENE,T_METRIC> &aochrom_child1,
 gaencode::ChromFixedLength<T_GENE,T_METRIC> &aochrom_child2,
 const gaencode::ChromFixedLength<T_GENE,T_METRIC> &aichrom_parent1,
 const gaencode::ChromFixedLength<T_GENE,T_METRIC> &aichrom_parent2)
```

This crossover operator is parameterized for a chromosome of any type of data, internally generates a random number in the interval [1,length of chromosome -2], which is used to make the combination. See [\[Example gagenericop::onePointCrossover\]](#), page 81

[Function]

```
void gabinaryop::onePointDistCrossover
(mat::BitMatrix<T_BITSIZES> &aobitmatrix_child1,
 mat::BitMatrix<T_BITSIZES> &aobitmatrix_child2,
 mat::BitMatrix<T_BITSIZES> &aibitmatrix_parent1,
 mat::BitMatrix<T_BITSIZES> &aibitmatrix_parent2)
```

This is the extension of operator two-point crossover for the case of Bit-Matrix. See [\[Example gabinaryop::onePointDistCrossover\]](#), page 95

3.1.7 Mutation operator

Several operators for mutation are proposed in the literature on evolutionary algorithms for clustering. In the [Figure 3.4](#), in the same way that the crossover operators are grouped, the mutation operators are also grouped by packets.

To illustrate how the mutation operator is applied, the two operators that are used in the illustrative examples in [Appendix A \[Example source code\]](#), [page 69](#), are described below.

BBHB94 use a mutation operator to change the one bit from one row to another in an aleatory manner in a *crisp matrix*:

[Function]

```
void gabinaryop::bitMutation
    (mat::CrispMatrix<T_BITSIZE,T_CLUSTERIDX> &aiobitcrispmatrix_chrom)
    See \[Example gabinaryop::bitMutation\], page 96.
```

In BM02a they propose a mutation operator for (4.2) chromosomes (See [\[centroid-based\]](#), [page 13](#)). It is located in the file `ga_clustering_operator.hpp` and called here as `gaclusteringop::biDirectionHMutation`:

$$\text{mutate}(g_{jl}) = \begin{cases} g_{jl} + \delta \times (\max(x_l) - g_{jl}) & \text{if } \delta \geq 0, \text{ for } j = 1, 2, \dots, k \text{ and } l = 1, 2, \dots, d, \\ g_{jl} + \delta \times (g_{jl} - \min(x_l)) & \text{if } \delta < 0. \end{cases}$$

Where δ is a random number in the interval $[-R, +R]$:

$$R = \begin{cases} \frac{M - M_{\min}}{M_{\max} - M_{\min}} & \text{if } M_{\max} > M, \\ 1 & \text{if } M_{\min} = M_{\max}. \end{cases}$$

M_{\min} and M_{\max} be the minimum and maximum values of the clustering metric, respectively, in the current population. M is the clustering metric value of the current chromosome that must be mutated.

[Function]

```
void gaclusteringop::biDirectionHMutation
    (gaencode::ChromosomeString<T_GENE,T_METRIC> aochrom_offspring,
     const T_METRIC airt_minObjectiveFunc,
     const T_METRIC airt_maxObjectiveFunc,
     const T_GENE* aiaarrayt_minFeatures,
     const T_GENE* aiaarrayt_maxFeatures)
    See \[Example gaclusteringop::biDirectionHMutation\], page 83
```

3.1.8 Other parameters

It is common for GAs and EAs for clustering to use local search. The k-means algorithm is more popular, this is a procedure of fine-tuning of maximum descent, thus speeding up its convergence. The way they apply it varies. LEAC includes an extensive list of functions for local search, some of which are discussed below:

[Function]

```
void clusteringop::updateCentroids
    (T_CLUSTERIDX &aocidx_numClusterNull,
     mat::MatrixRow<T_FEATURE> &aomatixt_centroids,
     mat::MatrixRow<T_FEATURE_SUM> &aomatixt_sumInstancesCluster,
     std::vector<T_INSTANCES_CLUSTER_K> &aovectort_numInstancesInClusterK,
     INPUT_ITERATOR aiiterator_instfirst,
     const INPUT_ITERATOR aiiterator_instlast,
```

```
const dist::Dist<T_DIST,T_FEATURE> &aifunc2p_dist)
```

With rule (3.2) each point is assigned x_i a the clusters C_j See [Equation (3.2)], page 14. Update the centroids $\mu_i^* = 1/n_j \sum_{x_i \in C_j} x_i$, $j = 1, 2, \dots, k$, where n_j is the number of points in cluster C_j . Returns the new centroids, the sum of instances and their number per cluster.

See [Example clusteringop::updateCentroids], page 75

Other algorithms propose to use the k-means algorithms as an operator (KM99)

[Function]

```
T_CLUSTERIDX clusteringop::kmeansoperator
(T_CLUSTERIDX *aioarrayidx_memberShip,
 mat::MatrixRow<T_FEATURE> &aomatrixt_centroids,
 mat::MatrixRow<T_FEATURE_SUM> &aomatrixt_sumInstancesCluster,
 std::vector<T_INSTANCES_CLUSTER_K> &aovectort_numInstancesInClusterK,
 INPUT_ITERATOR aiiterator_instfirst,
 const INPUT_ITERATOR aiiterator_instlast,
 dist::Dist<T_DIST,T_FEATURE> &aifunc2p_dist)
```

For a given partition in an array of labels, it performs an update using the k-means algorithm. Returns the membership labels, centroids, sum of instances and number of instances in each cluster.

For *k-medoids* SL04 proposes a heuristic search:

For each cluster C_j finds the most representative object

1. Assign each object in x_i to the cluster C_j with the closest medoid
2. For each cluster C_j , repeat until the medoid does not change
 - Choose a subset C_{subset} in C_j the corresponds to m_j and its p nearest neighbors of m_j .
 - Calculate the new medoid

$$m_j^* = \arg \min_{x_i \in C_{subset}} \sum_{x'_i \in C_j} \|x_i - x'_i\|$$

- if m_j is different from m_j^* replace with the new medoid
3. Repeat step 1 and 2 until k medoids do not change

The function that implements the local heuristic search for *k-medoids* is the following function:

[Function]

```
void clusteringop::updateMedoids
(uintidx      aioarrayuidx_medoids,
 T_CLUSTERIDX aicidx_numClusterK,
 uintidx      aiuiidx_nearestNeighborsP,
 mat::MatrixTriang<T_DIST> &aimatrixtriagt_dissimilarity)
Update k-medoids, based on SL04
```

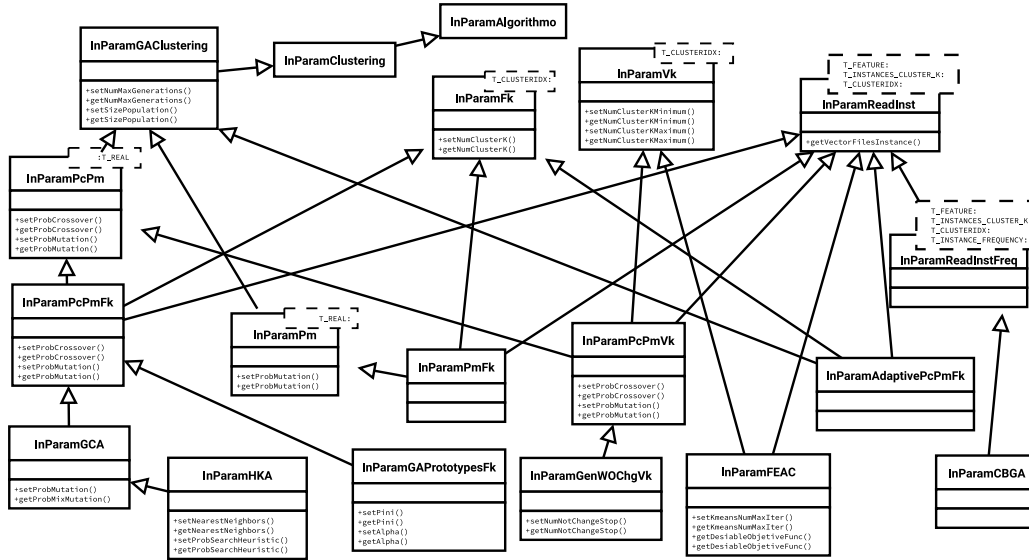


Figure 3.5: Classes used for the input of parameters for the implementation of an algorithm, Nomenclatura, crossover probability (Pc), mutation probability (Pm), fixed k-clusters (Fk), variable k-clusters (Vk). The classes in the lower level correspond to the specific parameters of some algorithms encoded with LEAC.

3.2 Make an executable for a new algorithm

There are two options to make an implementation of a new algorithm. The first is simply to include all the necessary operations in the main file. The second option is to use the scheme followed in the implementations included in the `eac` directory, you must create a file with a structure similar to the one included in Annex (Section A.1 [KGA algorithm], page 69). In both cases, the configuration scheme of an evolutionary algorithm must be followed see Section 3.1 [Implementation of an algorithm], page 11. The steps you need to compile the executable file for a new algorithm are described below:

1. Create the source file and include the LEAC library `#include <leac.hpp>`
2. Select the type of data with which you will work. The `datatype_instance_real.hpp` and `datatype_instance_integer.hpp` files suggest the types of data you can use for the selection of variable types, include in source file one for the real `'#include <datatype_instance_real.hpp>'` or integer `'#include <datatype_instance_integer.hpp>'` domain respectively or define your own data types.
3. Select a class from Figure 3.5 to read the parameters of the new algorithm or define a new class with the parameters specified in the algorithm to be implemented, you can extend from an existing class. For example for `InParamPcPmFk` include the file `'#include <inparam_pcpmfk.hpp>'`.

```

[Constructor on inout::InParamPcPmFk]
InParamPcPmFk<T_CLUSTERIDX,T_REAL,T_FEATURE,T_FEATURE_SUM,T_INSTANCES_CLUSTER_K>
(const std::string& ais_algorithmName,

```

```
const std::string& ais_algorithmoAuthor,
InParam_algTypeOut aiato_algTypeOut,
int aii_opNorm)
```

4. Instance the parameter entry class and assign the default values.

```
/*INPUT: PARAMETER
*/
inout::InParamPcPmFk
<DATATYPE_CLUSTERIDX,
  DATATYPE_REAL,
  DATATYPE_FEATURE,
  DATATYPE_FEATURE_SUM,
  DATATYPE_INSTANCES_CLUSTER_K
>
linparam_ClusteringGA
("Acronym of the algorithm",
 "Algorithm Authors",
 inout::CENTROIDS,
 INPARAMCLUSTERING_DISTANCE_EUCLIDEAN
);

linparam_ClusteringGA.setNumMaxGenerations(1000);
linparam_ClusteringGA.setSizePopulation(50);
linparam_ClusteringGA.setProbCrossover(0.8);
linparam_ClusteringGA.setProbMutation(0.001);
```

When an instance of the `InParamPcPmFk` object is created, the data types used to perform all the calculations are defined, so it is not necessary to specify the data types for the functions that this `InParamPcPmFk` object is used, allowing you to avoid possible errors or redundancies.

5. Assign the default values or simply use this way to read the parameters, for example:

```
linparam_ClusteringGA.setNumMaxGenerations(1000);
linparam_ClusteringGA.setSizePopulation(50);
linparam_ClusteringGA.setProbCrossover(0.8);
linparam_ClusteringGA.setProbMutation(0.001);
```

6. Optionally, if you wish, you can read the input parameters online using the functions provided in the LEAC library. Declare the sentence `'#include <inparamclustering_getparameter.hpp>'` after the file of the parameter class.

If you are using a class of the class diagram ([Figure 3.5](#)), go to [\[Step 7\], page 38](#). Otherwise do the following. Define the directive to the preprocessor in the file of your new parameter class. The name of the directive must be different from the ones that are defined, for example:

```
#define __INPARAM_MY_PCPMFK__
```

If you extend your parameter class from an existing one in [Figure 3.5](#), you must override the definition of the directive that is defined in the base class, for example, instead of simply including the previous statement, you must include the following two statements in your file of parameter class:

```
#undef __INPARAM_PCPMFK__
#define __INPARAM_MY_PCPMFK__
```

Include similar code blocks in the [inparamclustering_getparameter.hpp](#) file, as shown in the following paragraphs, to print the help and read the parameters of the new algorithm.

- a. Find the region of the `inparamclustering_usage` functions, add your directive that was previously defined, and include your definition of the function with the parameter of the new class defined by you (in bold), as shown in the following example:

```
#ifdef __INPARAM_MY_PCPMFK__
template<typename T_CLUSTERIDX,
        typename T_REAL,
        typename T_FEATURE,
        typename T_FEATURE_SUM,
        typename T_INSTANCES_CLUSTER_K
        >
void
inparamclustering_usage
(char *argv0,
 InParamMyClassPcPmFk
<T_CLUSTERIDX,
T_REAL,
T_FEATURE,
T_FEATURE_SUM,
T_INSTANCES_CLUSTER_K
>
&aoipc_inParamClustering
)
#endif
```

- b. Search the area to print help messages and write a block of code similar to the following:

```
#ifdef __INPARAM_MY_PCPMFK__
std::cout << "      --number-clusters[=NUMBER]\n"
          << "                      number of clusters [NUMBER="
          << aoipc_inParamClustering.getNumClusterK() << "]\n";
std::cout << "      --generations[=NUMBER]  number of generations or iterations\n"
          << "                      [NUMBER="
          << aoipc_inParamClustering.getNumMaxGenerations()
          << "]\n";
std::cout << "      --population-size[=NUMBER]\n"
          << "                      size of population [NUMBER="
          << aoipc_inParamClustering.getSizePopulation()
          << "]\n";
std::cout << "      --crossover-probability[=NUMBER]\n"
          << "                      real number in the interval [0.25, 1]\n"
          << "                      [NUMBER="
          << aoipc_inParamClustering.getProbCrossover()
          << "]\n";
std::cout << "      --mutation-probability[=NUMBER]\n"
          << "                      real number in the interval [0, 0.5]\n"
          << "                      [NUMBER="
          << aoipc_inParamClustering.getProbMutation()
          << "]\n";

#endif
```

- c. Find the `inparamclustering_getParameter` functions and defines its own function similar to the previous one:

```
#ifdef __INPARAM_MY_PCPMFK__
template<typename T_CLUSTERIDX,
        typename T_REAL,
        typename T_FEATURE,
        typename T_FEATURE_SUM,
        typename T_INSTANCES_CLUSTER_K
```



```

>
void
inparamclustering_getParameter
(InParamMyClassPcPmFk
<T_CLUSTERIDX,
T_REAL,
T_FEATURE,
T_FEATURE_SUM,
T_INSTANCES_CLUSTER_K
>
&aoipc_inParamClustering,
int argc,
char **argv
)
#endif

```

- d. In the `inparamclustering_getParameter` function, find the array where the parameter labels are defined and define a new array with the labels of the parameters for the new algorithm, as shown in the following example:

```

#ifdef __INPARAM_MY_PCPMFK__
const char *lastr_myInParamPcPmFk[] =
{
    "number-clusters",
    "population-size",
    "crossover-probability",
    "mutation-probability",
    "generations",
    (char *) NULL
};
#endif

```

- e.

In `long_options` array, define your parameters with the options shown below

```

#ifdef __INPARAM_MY_PCPMFK__
{
    "number-clusters",          required_argument, 0, 0},
    "population-size",         required_argument, 0, 0},
    "crossover-probability",    required_argument, 0, 0},
    "mutation-probability",     required_argument, 0, 0},
    "generations",             required_argument, 0, 0},
};
#endif

```

- f. Finally, add the necessary code to obtain the parameters

```

#ifdef __INPARAM_MY_PCPMFK__
else if ( strcmp /*number-clusters*/
(long_options[option_index].name,
lastr_inParamPcPmFk[0] ) == 0 )
{
    T_CLUSTERIDX lmcidxT_numClusterK;
    liss_stringstream.clear();
    liss_stringstream.str(optarg);
    liss_stringstream >> lmcidxT_numClusterK;
    aoipc_inParamClustering.setNumClusterK(lmcidxT_numClusterK);
}
else if ( strcmp /*population-size*/
(long_options[option_index].name,
lastr_inParamPcPmFk[1] ) == 0
)
{

```

```

        liss_stringstream.clear();
        liss_stringstream.str(optarg);
        liss_stringstream >> luintidx_read;
        aoipc_inParamClustering.setSizePopulation(luintidx_read);
    }
    else if ( strcmp /*crossover-probability*/
              (long_options[option_index].name,
               lastr_inParamPcPmFk[2]) == 0
            )
    {
        T_REAL  lT_readProbabilityCrossover;

        liss_stringstream.clear();
        liss_stringstream.str(optarg);
        liss_stringstream >> lT_readProbabilityCrossover;
        aoipc_inParamClustering.setProbCrossover(lT_readProbabilityCrossover);
    }
    else if ( strcmp /*mutation-probability*/
              (long_options[option_index].name,
               lastr_inParamPcPmFk[3]) == 0
            )
    {
        T_REAL  lT_readProbabilityMutation;

        liss_stringstream.clear();
        liss_stringstream.str(optarg);
        liss_stringstream >> lT_readProbabilityMutation;
        aoipc_inParamClustering.setProbMutation(lT_readProbabilityMutation);
    }
    else if ( strcmp /*generations*/
              (long_options[option_index].name,
               lastr_inParamPcPmFk[4]) == 0
            )
    {
        COMMON_IDOMAIN lT_readNumMaxGenerations;

        liss_stringstream.clear();
        liss_stringstream.str(optarg);
        liss_stringstream >> lT_readNumMaxGenerations;
        aoipc_inParamClustering.setNumMaxGenerations(lT_readNumMaxGenerations);
    }
    else {
        aoipc_inParamClustering.errorArgument
            (argv[0],
             long_options[option_index].name,
             lastr_inParamPcPmFk
            );
    }
}
#endif

```

7. If you completed the previous step, you can now invoke the `inparamclustering_getParameter` function, to modify or complete the parameters online:

```
inparamclustering_getParameter(linparam_ClusteringGA, argc, argv);
```

Otherwise just read the parameters as in [\[Step 5\], page 35](#).

8. Read the data set to be processed with any of the following functions:

```
std::pair<std::vector<data::Instance<T_FEATURE>*>, [Function]
```

```

std::vector<data::Instance<T_FEATURE>* > > dataSetRead
(inout::InParamReadInst<T_FEATURE,T_INSTANCES_CLUSTER_K,T_CLUSTERIDX>
&aipri_inParamReadInst)

[Function]

std::pair<std::vector<data::Instance<T_FEATURE>* >,
std::vector<data::Instance<T_FEATURE>* > > dataSetReadWithFreq
(inout::InParamReadInstFreq
<T_FEATURE,T_INSTANCES_CLUSTER_K,T_CLUSTERIDX,T_INSTANCE_FREQUENCY>
&aipri_inParamReadInstWithFreq)

```

The following example shows how to read a data set, which can have a class attribute and also test data

```
auto lpairvec_dataset = inout::dataSetRead(linparam_ClusteringGA);
```

9. Directly include genetic operators in the main function or invoke directly the function that has the implementation of the new algorithm in the main function. At the end of writing your source code, your `main` function should have something similar to the following code:

```

#include <leac.hpp>
#include <datatype_instance_real.hpp>
#include <inparam_pcpmfk.hpp>
#include <inparamclustering_getparameter.hpp>
#include <instances_read.hpp>

#include "kga_fkcentroid.hpp"

int main(int argc, char **argv)
{
    /*INPUT: PARAMETER
    */
    inout::InParamPcPmFk
    <DATATYPE_CLUSTERIDX,
    DATATYPE_REAL,
    DATATYPE_FEATURE,
    DATATYPE_FEATURE_SUM,
    DATATYPE_INSTANCES_CLUSTER_K
    >
    linparam_ClusteringGA
    ("KGA",
    "Bandyopadhyay and Maulik 2002",
    inout::CENTROIDS,
    INPARAMCLUSTERING_DISTANCE_EUCLIDEAN
    );

    linparam_ClusteringGA.setNumMaxGenerations(1000);
    linparam_ClusteringGA.setSizePopulation(50);
    linparam_ClusteringGA.setProbCrossover(0.8);
    linparam_ClusteringGA.setProbMutation(0.001);

    inparamclustering_getParameter(linparam_ClusteringGA, argc, argv);

    auto lpairvec_dataset = inout::dataSetRead(linparam_ClusteringGA);

    dist::Euclidean<DATATYPE_REAL,DATATYPE_FEATURE> funct2p_dist;

    inout::OutParamGAC
    <DATATYPE_REAL,
    DATATYPE_CLUSTERIDX>

```

```

        loop_outParamGAC(inout::SSE);

    auto lchrom_best =
        eac::kga_fkcentroid
        (loop_outParamGAC,
         linparam_ClusteringGA,
         lpairvec_dataset.first.begin(),
         lpairvec_dataset.first.end(),
         funct2p_dist
        );

    std::cout << "chrom_best: " << lchrom_best << std::endl;

    return 0;
}

```

10. With the source files completed, compile your new algorithm, with the following command

```

'g++ -std=c++11 -D __VERBOSE_YES -I ../include -I ../include_inout/
-fopenmp kga_main.cpp -o kga'

```

The '-D __VERBOSE_YES' option is optional to debug your program. You can also compile your application with the other evolutionary algorithms provided by LEAC, adding the commands in the [Makefile](#) file for your new algorithm.

3.3 Using implemented algorithms

This section shows how to use the programs located in the `eac` directory to find a solution to the problem of clustering. For the use and obtain better results, the algorithms on which the programs are based, we categorize them into three aspects: if the number the clusters is fixed or variable, the coding of the solution by the algorithm (See [Section 3.1.1 \[Encoding criterion\]](#), page 11) and the similarity function (See [Section 3.1.3.2 \[Unsupervised measures\]](#), page 18).

To complete the practical examples, you should have completed the installation described in the [Chapter 2 \[Get and Install LEAC software\]](#), page 5, and have access to the directory `bin` directory with the command '`cd c:\leac\bin`' for Windows® or '`cd leac/bin`' for GNU/Linux from a `cmd` or `terminal` respectively.

The nomenclature used for the name of the programs is based on the three aspects described above. Name of the algorithm on which the program is based, fixed or variable k and the coding used.

`name_[fk|vk]coding`

All EAC programs are executed from a terminal with online parameters. With the parameter '`--help`', You will get a description of the different options, there are two types of options, those that are common for all the programs and the particular ones of each algorithm, these last ones are shown after the message [\[Particular options of the algorithm: \[Name\]\]](#), page 42,

For example, here are some realistic execution '`kga_fkcentroid --help`'. This is the output of the command

```

Usage: ./kga_fkcentroid [OPTION]
        About groups of instances for a set K as well as statistics
        of the algorithm used

```

```

-i, --instances=FILE or DIRECTORY
                                file or directory containing data of instances
                                to be clustered
-x, --select-instances[=PREFIX]
                                if instances is directory search files with
                                prefix for training (eg. iris-10-1tra.dat,
                                iris-10-2tra.dat,... PREFIX=tra.dat)
-t, --test[=FILE or PREFIX] if instances is directory search files with
                                prefix for test (eg. iris-10-1tst.dat,
                                iris-10-2tst.dat,... PREFIX=tst.dat),
                                in other case only name file
-b --format-file[=NAME]         uci, or keel, by default uci
-h, --with-header[=yes/no]     file contains names of instances or a header,
                                by default is no
-u, --number-instances[=NUMBER]
                                the number of instances the file contains
                                instances, if not specified file is obtained
-a, --select-attributes[=ARG]
                                select the attributes to be processed for
                                example, "1-2,4" by default all. Also
                                used to specify the number of dimensions
                                of the instances, unless specified file is
                                obtained instances
-d, --delimit-attributes=[ARG]
                                separated file by default ","
-c, --class-column[=NUMBER] input file of instances has a class assigned
                                in the column [NUMBER=undefined]
-e, --cluster-column[=NUMBER]
                                input file of instances has a cluster assigned
                                in the column [NUMBER=undefined]
-l, --idinstances-column[=NUMBER]
                                the input file instance is assigned a column
                                instance identifier [NUMBER=undefined]
-f, --freq-instances-column[=NUMBER]
                                the input file instance is assigned a column
                                frequency instances [NUMBER=undefined]
-r, --number-runs[=NUMBER] number of runs or repetitions of the algorithm
                                (by default [NUMBER=1])
-R, --runtime-filename=[FILE]
                                out file of times run
-n --distance[=NAME]           euclidean, euclidean_sq, euclidean_induced,
                                diagonal_induced, or mahalonobis_induced,
                                by default euclidean
-z, --random-seed[=NUMBER] string with integer number seed by, default
                                is random
-w, --max-execution-time[=NUMBER]
                                real number for max execution time in seconds
                                by default is 36000
-C, --centroids-outfile=[FILE]
                                print centroids, standard output FILE=stdout
    --centroids-format[=yes/no]
                                print the matrices by rows and columns,
                                by default is no
-M, --membership-outfile=[FILE]
                                print membership of the instances,
                                standard output FILE=stdout
-T, --partitionstable-outfile=[FILE]

```

```

                                print partitions table of the instances,
                                standard output FILE=stdout
--table-format[=yes/no]
                                print the partitions table by rows and
                                columns, by default is no
-P, --gnuplot=FILE             file of gnuplot to graphics result
                                (compiling only with WITHOUT_PLOT_STAT)
-y, --gnuplot-styles=WORD      plot graphics with: points, lines,
                                linespoints, and dot [ARG=linespoints]

Particular options of the algorithm KGA
based on Bandyopadhyay and Maulik 2002
--number-clusters[=NUMBER]     number of clusters [NUMBER=3]
--generations[=NUMBER]         number of generations or iterations
                                [NUMBER=1000]
--population-size[=NUMBER]     size of population [NUMBER=50]
--crossover-probability[=NUMBER] real number in the interval [0.25, 1]
                                [NUMBER=0.8]
--mutation-probability[=NUMBER] real number in the interval [0, 0.5]
                                [NUMBER=0.001]

-v, --verbose[=NUMBER]         explain what is being done (compiled with
                                VERBOSE=yes)
                                NUMBER=[-1,..,9999] Quiet level -1 not,
                                verbose, default=-1
-q, --bar-progress             progress bar printing, default is not
-?, --help                     help

```

For all the evolutionary algorithm studied in this work, the parameters they share are:

```
--generations
--population-size
```

they only vary in the number of generations and in the number of chromosome proposed by the different authors.

The following sections describe the evolutionary algorithm currently implemented with the LEAC library, based on taxonomy proposed by HCFdC09, *k-fixed* vs. *k-variable* and the coding they use to represent the chromosomes, see [Table 1.1](#). We also include practical examples of clustering applications with real data sets provided by [UC Irvine Machine Learning Repository](#).

3.3.1 Genetic algorithms for fixed k-clusters

3.3.1.1 Based on cluster label

The genetic algorithms in this section use an [\[string-of-group-numbers encoding\]](#), [page 13](#). The algorithms included in LEAC are the following:

- `gaclustering_fklabel`

Based on [MC96](#), optimize to [\[SED\]](#), [page 18](#), the operators that use are `gagenericop::onePointCrossover` and `gaintegerop::mutation` (change a random gene). The classification of these operators can be considered *object-oriented*, that

randomly moves objects among clusters. They propose a small population size, which makes a guided exploration around the best solution, with a fixed crossing probability and a mutation probability with a default value high 0.5 and decreasing in each generation until reaching $1/n$.

Parameters:

```
--crossover-probability[=NUMBER]
    real number in the interval [0.25, 1] [NUMBER=0.8]

--mutation-probability[=NUMBER]
    real number in the interval [0, 0.5] [NUMBER=0.5]
```

- **gka_fklabel**

Based on [KM99](#), Optimize to [\[TWCV\]](#), page 18. The authors of this document propose not to use the crossover operator, instead they use the **k-means algorithm**. HCFdC09 state that this algorithm must be an evolutionary algorithm rather than a genetic algorithm. LEAC implements several variants of the **k-means algorithm**, including the algorithm used by this algorithm (`<undefined> [clusteringop::kmeansoperator]`, page `<undefined>`). Mutation change an gene value depending on the distances of the cluster centroids from the corresponding instance. It can be assigned to another group by the following probability distribution associated with each gene.

Parameters:

```
--mutation-probability[=NUMBER]
    real number in the interval [0, 1.0] [NUMBER=0.05]
```

- **igka_fklabel** based on [LLF+04b](#), and **fgka_fklabel** based on [LLF+04a](#). optimize to [\[SSE\]](#), page 18,

```
--mutation-probability[=NUMBER]
    real number in the interval [0, 1.0] [NUMBER=0.05]
```

fgka_fklabel

Based on [LLF+04a](#), optimize to [\[SSE\]](#), page 18,

```
--mutation-probability[=NUMBER]
    real number in the interval [0, 1.0] [NUMBER=0.05]
```

3.3.1.2 Based on the centroids

The algorithms in this section seek to find the centroids of the cluster for a user-defined k . If you are looking for precision to locate the centroid of the clusters, these algorithms are a good option. The way they encode the solutions as a string with the coordinates of the centroids consecutively, see See [\[real encoding\]](#), page 13. The genetic algorithms implemented in this class are listed below:

- **gas_fkcentroid**

Based on [MB00](#), optimize to [\[SED\]](#), page 18,

```
--crossover-probability[=NUMBER]
    real number in the interval [0.25, 1] [NUMBER=0.8]
```

```
--mutation-probability[=NUMBER]
    real number in the interval [0, 0.5] [NUMBER=0.001]
```

- `kga_fkcentroid`
Based on [BM02a](#), optimize to [\[SED\]](#), page 18,
`--crossover-probability[=NUMBER]`
 real number in the interval [0.25, 1] [NUMBER=0.8]
`--mutation-probability[=NUMBER]`
 real number in the interval [0, 0.5] [NUMBER=0.001]
- `gagr_fkcentroid`
Based on [CZZ09](#), optimize to [\[SSE\]](#), page 18,
- `cbga_fkcentroid_int` and `cbga_fkcentroid`
Based on [FKKN97](#), optimize to [\[Distortion\]](#), page 20,
`--mutation-probability[=NUMBER]`
 real number in the interval [0, 1.0] [NUMBER=0.01]
`--select-method[=NAME]`
 roulette, elitist1, elitist2, or zigzag, by default elitist1
`--gla-iterations[=NUMBER]`
 number of GLA iterations [NUMBER=0]

Next, we describe the steps to execute KGA algorithm base on BM02a and discuss the parameters that can be used to carry out an experimental study. Something similar would be included for all the algorithms.

For the following example we will analyze the [wine data set](#). First you must download the [wine.data](#) file and store it in the `data` directory, all data sets used in the following illustrative examples should be stored in this directory.

Since the domain of the attributes is different for the [wine.data](#), it is convenient to standardize them, for this the program `stdvar_milligan_cooper1988` Based on (MC88) is available as support for the normalization of the data set.

```
'stdvar_milligan_cooper1988 -i ../data/wine.data -a "2-14" -c 1 --std-var Z1
> ../data/wine_std.data'
```

The Wine data set includes 13 variables from column 2 to column 14 and the column from class 1, therefore, the `-a` or `--select-attributes` parameter is "2-14", the class is in column 1, the parameter `-c` or `--class-column` it must be assigned to 1. The transformation that applies to the variables in this case is *z-score* $Z_1 = (x_{il} - \bar{x}_{*l})/s_{*l}$, where x_{il} is the original data value, and \bar{x}_{*l} and s_{*l} are the sample mean and standard deviation, respectively.

Next, algorithm KGA BM02a will be run, for the normalized data

```
'kga_fkcentroid -i ../data/wine_std.data -a "1-13" -c 14 --number-clusters 3
-C stdout --centroids-format yes -M stdout'
```

The attributes are now in columns "1-13" and the class in column 14, because the `stdvar_milligan_cooper1988` program in the output file writes the class in the last column. Parameters with uppercase letters are used for the output. '`-C stdout`' indicates that the output of the centroids found by the program is terminal and formatted with '`--centroids-format yes`'. The parameter '`-M stdout`' generates a string of the membership labels of the instances in a cluster calculated with equation (3.2)

A possible result for a partition of three clusters ('--number-clusters 3') by the KGA algorithm is

IN:

Algorithm name: KGA
Based on: Bandyopadhyay and Maulik 2002
Metric used: SSE

Data set: ../data/wine_std.data

Number of instances: 178

Dimensions: 13

Random seed: 605281295 2141350197 2332488985 1350226326 4001754309
1842645844 2127210415 1490264447

OUT:

CHROMOSOME: BEST: objective, 449.524, fitness, 0.00222458: 0.875627, -0.30372, 0.318045,
-0.662654, 0.563299, 0.87404, 0.940985, -0.583943, 0.580146, 0.166718, 0.482367,
0.764896, 1.15509, 0.164444, 0.869095, 0.186373, 0.522892, -0.0752605, -0.976575,
-1.21183, 0.724021, -0.777513, 0.93889, -1.16151, -1.28878, -0.405943, -0.936362,
-0.390863, -0.437966, 0.2084, -0.462469, -0.0531982, 0.0667156, -0.0197664, 0.0646097,
-0.879594, 0.451708, 0.288923, -0.753899

Cluster number (K): 3

SSE: 449.524

DB-index: 1.39179

Silhouette: 0.285942

VRC: 70.8369

CS measure: 0.437609

Dunn's index: 0.176897

Execution time (seg): 2.03319

Generations find the best: 7

Centroids:

Col:	0	1	2	3	4
Row					
0:	0.875627	-0.30372	0.318045	-0.662654	0.563299
1:	0.164444	0.869095	0.186373	0.522892	-0.0752605
2:	-0.936362	-0.390863	-0.437966	0.2084	-0.462469

Col:	5	6	7	8	9
Row					
0:	0.87404	0.940985	-0.583943	0.580146	0.166718
1:	-0.976575	-1.21183	0.724021	-0.777513	0.93889
2:	-0.0531982	0.0667156	-0.0197664	0.0646097	-0.879594

Col:	10	11	12
Row			
0:	0.482367	0.764896	1.15509
1:	-1.16151	-1.28878	-0.405943
2:	0.451708	0.288923	-0.753899

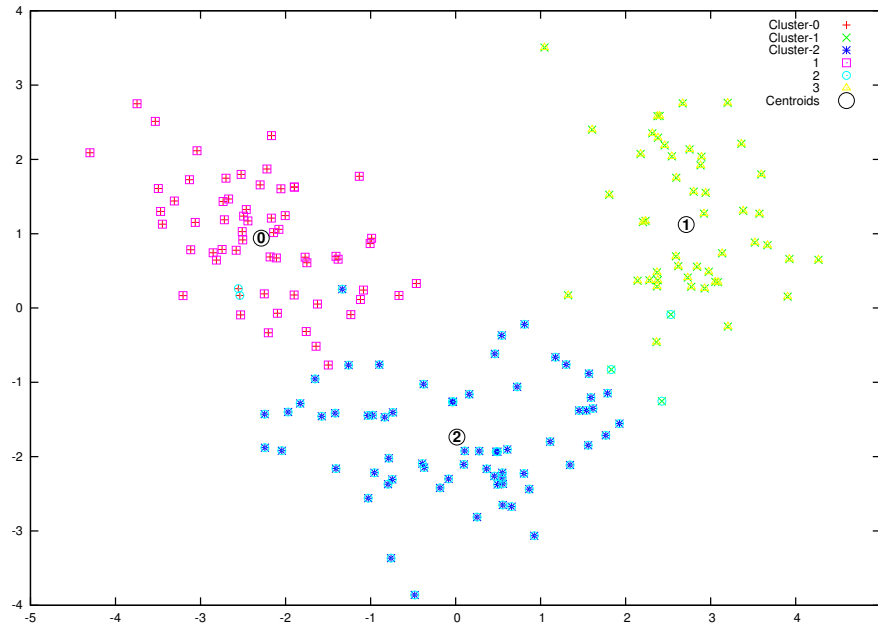


Figure 3.6: Clusters of Wine data set, obtained with `kga_fkcentroid`

In all programs, it is possible to use part of the data set for *training* and another part for *test*, to make easier to carry out an experimental study. To determine the ownership of the test data, the equation of the nearest centroid-instance is used (3.2).

To demonstrate how to process a data set with training and test data, you can use the [Libras Movement Data Set](#), with the [movement_libras.data](#) and [movement_libras_1.data](#) files.

To obtain better results in the data mining process, it is important to have knowledge about the data set. Libras Movement data set is formed by the coordinates of a two-dimensional curves of the movement of the hand with domain and range to be between -1 and 1 . To have better accuracy, we center on $(0.5, 0.5)$ each of the curves of the training data set, with the following awk script:

```
#run:
# 'awk -f movement_libras_trans.awk -F "," -v OFS=","
  movement_libras.data > movement_libras_trans.data'

for(i=1;i< NF;i++) sumcoord1+=$i; i++; sumcoord2+=$i ;
numpoint = (NF-1) / 2.0;
xd = 0.5 - sumcoord1/numpoint;
yd = 0.5 - sumcoord2/numpoint;
sumcoord1=0; sumcoord2=0;
for(i=1;i< NF;i++) $i += xd; i++; $i += yd ;
for(i=1; i<=NF; i++) printf "%s",$i (i==NF?ORS:OFS)
```

The `movement_libras_trans.awk` file of the script can be found in the `data` folder. To run the script, type:

```
'awk -f movement_libras_trans.awk -F "," -v OFS="," movement_libras.data >
movement_libras_trans.data'
```

With the transformed dataset we apply the KGA algorithm:

```
'kga_fkcentroid -i ../data/movement_libras_trasn.data -t ../data/movement_libras_1.data
-a "1-90" -c 91 -C c_movement_libras.data -T stdout --table-format yes
--number-cluster 15'
```

A possible result of the program is the following:

IN:

Algorithm name: KGA

Based on: Bandyopadhyay and Maulik 2002

Metric used: SSE

Data set: ../data/movement_libras_trasn.data

Number of instances: 360

Dimensions: 90

Data set test: ../data/movement_libras_1.data

Number of instances: 45

Random seed: 2127474194 2277915873 2997828778 567204173 2395445691
1861208675 35718978 101314263

OUT:

CROMOSOME: BEST: objective, 209.665, fitness, 0.00476951: 0.545241, 0.779453,
0.544903, 0.779338, 0.542145, 0.778586, 0.539438, 0.776675, 0.534216, 0.773666,
...
0.462735, 0.320573, 0.457353, 0.311718, 0.452307, 0.306383, 0.451046, 0.302055

Cluster number (K): 15

SSE: 209.665

DB-index: 1.15626

Silhouette: 0.284789

VRC: 87.1936

CS measure: 1.36284

Dunn's index: 0.0855026

Test data SSE: 52.8738 Has group without objects

Test data DB-index: 3.59388

Test data Silhouette: -0.103324

Test data VRC: 0.721814

Test data CS measure: 1.76497

Test data Dunn's index: 0.0650252

Execution time (seg): 85.0431

Generations find the best: 56

Partition table:

Cluster: 0	1	2	3	4
Class				
1: 0	0	10	0	0
2: 0	0	11	0	0
3: 0	0	0	0	0
4: 0	0	0	0	0

5: 0	6	0	0	17
6: 0	0	0	7	0
7: 0	0	0	0	0
8: 14	0	0	0	0
9: 0	0	0	0	0
10: 0	0	0	0	0
11: 11	0	0	0	0
12: 0	0	0	0	0
13: 15	0	0	0	0
14: 0	6	0	14	1
15: 0	0	0	0	0
sum: 40	12	21	21	18
Cluster: 5	6	7	8	9
Class				
1: 0	0	0	8	0
2: 0	0	0	5	0
3: 0	0	23	0	0
4: 0	12	0	0	3
5: 1	0	0	0	0
6: 0	7	0	0	0
7: 0	0	0	0	20
8: 0	0	0	0	0
9: 0	0	0	0	0
10: 7	0	0	0	15
11: 0	0	0	0	0
12: 0	0	0	0	24
13: 0	0	0	0	0
14: 0	0	0	0	3
15: 12	0	0	0	4
sum: 20	19	23	13	69
Cluster: 10	11	12	13	14
Class				
1: 6	0	0	0	0
2: 6	0	0	2	0
3: 0	0	0	1	0
4: 0	0	8	1	0
5: 0	0	0	0	0
6: 0	0	9	1	0
7: 0	0	0	4	0
8: 0	0	0	1	9
9: 0	0	0	24	0
10: 0	0	0	2	0
11: 0	9	0	0	4
12: 0	0	0	0	0
13: 0	7	0	0	2
14: 0	0	0	0	0
15: 0	0	0	0	8
sum: 12	16	17	36	23
Cluster: sum				
Class				
1: 24				
2: 24				

```

3: 24
4: 24
5: 24
6: 24
7: 24
8: 24
9: 24
10: 24
11: 24
12: 24
13: 24
14: 24
15: 24
sum: 360

```

```

Rand index: 0.915877
Purity: 0.552778
Precision: 0.385553
Recall: 0.527295

```

Partition table test:

Cluster: 0	1	2	3	4
Class				
1: 0	0	2	0	0
2: 0	0	1	0	0
3: 0	0	0	0	0
4: 0	0	0	0	0
5: 0	1	0	0	2
6: 0	0	0	0	0
7: 0	0	0	0	0
8: 1	0	0	0	0
9: 0	0	0	0	0
10: 0	0	0	0	0
11: 1	0	0	0	0
12: 0	0	0	0	0
13: 0	0	0	0	0
14: 0	0	0	0	0
15: 0	0	0	0	0
sum: 2	1	3	0	2

Cluster: 5	6	7	8	9
Class				
1: 0	0	0	1	0
2: 0	0	0	2	0
3: 0	0	3	0	0
4: 0	1	0	0	0
5: 0	0	0	0	0
6: 0	2	0	0	0
7: 0	0	0	0	3
8: 0	0	0	0	0
9: 0	0	0	0	0
10: 0	0	0	0	3
11: 0	0	0	0	0
12: 0	0	0	0	3

13: 0	0	0	0	0
14: 0	0	0	0	3
15: 0	0	0	0	3
sum: 0	3	3	3	15

Cluster: 10	11	12	13	14
Class				
1: 0	0	0	0	0
2: 0	0	0	0	0
3: 0	0	0	0	0
4: 0	0	2	0	0
5: 0	0	0	0	0
6: 0	0	1	0	0
7: 0	0	0	0	0
8: 0	0	0	0	2
9: 0	0	0	3	0
10: 0	0	0	0	0
11: 0	2	0	0	0
12: 0	0	0	0	0
13: 0	3	0	0	0
14: 0	0	0	0	0
15: 0	0	0	0	0
sum: 0	5	3	3	2

Cluster: sum
Class
1: 3
2: 3
3: 3
4: 3
5: 3
6: 3
7: 3
8: 3
9: 3
10: 3
11: 3
12: 3
13: 3
14: 3
15: 3
sum: 45

Test data Rand index: 0.879798
Test data Purity: 0.577778
Test data Precision: 0.227941
Test data Recall: 0.688889

With the option ‘-T, --partitionstable-outfile’, you get the confusion matrix and with the ‘-t’ option for training and testing, as well as measures related to the previous classification of the objects, called supervised measures.

The centroids, besides serving to represent the centers of the clusters, also have a meaning that depends on the domain of the problem, in the libras data set, represent the mean movement of the hand in a two-dimensional curve made in a period of time. The centroids obtained in the execution are shown in [Figure 3.7](#).

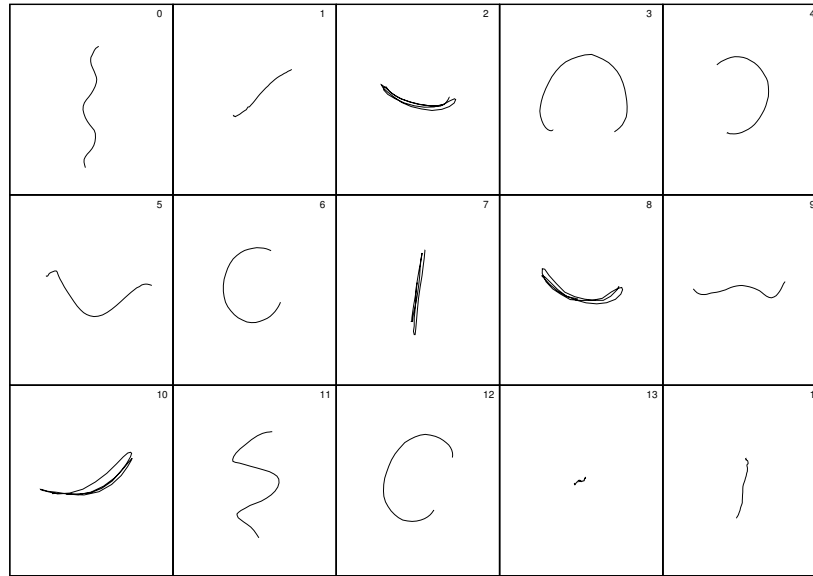


Figure 3.7: Average of the movements of the libras data set obtained with the program `kga_fkcentroid`

3.3.1.3 Based on the most representative

K-medoid algorithms attempt to partition the data by assigning each object to a representative and then optimizing a unsupervised measures (Section 3.1.3.2 [Unsupervised measures], page 18).

- `gaprototypes_fkmedoid`

Based on KB97, optimize to $[J_1]$, page 21,

`--crossover-probability[=NUMBER]`

real number in the interval $[0.25, 1]$ [NUMBER=0.5]

`--mutation-probability[=NUMBER]`

real number in the interval $[0, 0.5]$ [NUMBER=0.015]

`--probability-ini[=NUMBER]`

real number in the interval $[0.01, 0.1]$ depending n and k , if -1 is eq k/n [NUMBER=-1]

`--alpha[=NUMBER]`

real number $\alpha > 0$ to force the algorithm desired number cluster [NUMBER=10]

- `gca_fkmedoid`

Based on LDK93, optimize to $[SEDmedoid]$, page 20,

`--mix-recombination-probability[=NUMBER]`

real number in the interval $[0.5, 0.9]$ [NUMBER=0.9]


```

--point-mutation-probability[=NUMBER]
    real number in the interval [0.2, 0.4] [NUMBER=0.4]

--mix-mutation-probability[=NUMBER]
    real number in the interval [0, 0.125] [NUMBER=0.125]
• hka_fkmedoid
    Based on SL04, optimize to \[SEDmedoid\], page 20,

--mix-recombination-probability[=NUMBER]
    real number in the interval [0.5, 0.9] [NUMBER=0.95]

--point-mutation-probability[=NUMBER]
    real number in the interval [0.2, 0.4] [NUMBER=0.02]

--mix-mutation-probability[=NUMBER]
    real number in the interval [0, 0.125] [NUMBER=0.05]

--order-tournament[=NUMBER]
    order of tournament [NUMBER=2]

--nearest-neighbors[=NUMBER]
    number of the nearest neighbors (p) [NUMBER=3]

--search-heuristic-probability[=NUMBER]
    real number in the interval [0.0, 1.0] [NUMBER=0.2]

```

As an illustrative example of algorithms that finds the most representative instances for each cluster, we describe the `hka_fkmedoid` program based on the HKA algorithm (SL04)

Now let's illustrate how to find the most representative instances of the [iris.data](#) data set. You can run the program with the following parameters

```
'hka_fkmedoid -i ../data/iris.data -a "1-4" -c 5 --number-clusters=3 -C
c_hka_iris.dat -M m_hka_iris.dat'
```

A possible exit from the program would be:

```

IN:
    Algorithm name: HKA
        Based on: Weiguo Sheng and Xiaohui Liu
        Metric used: SSE

        Data set: ../data/iris.data
    Number of instances: 150
        Dimensions: 4

    Random seed: 4253005715 70818531 1631842517 1223368670 2252683652
                1178029056 3404574059 1048346743

```

OUT:

```
CROMOSOME: BEST: objective, 98.2137, fitness, 0.0101819: 7, 78, 112
```

```

Cluster number (K): 3
    SSE: 98.2137
    DB-index: 0.811606
    Silhouette: 0.552592
    VRC: 494.895

```

```

CS measure: 0.155418
Dunn's index: 0.0988074
Execution time (seg): 0.072937
Generations find the best: 69

```

For this execution, the most representative instances for each Iris cluster are:

ID	SepalLength	SepalWidth	PetalLength	PetalWidth	Class
7	5	3.4	1.5	0.2	Iris-setosa
78	6	2.9	4.5	1.5	Iris-versicolor
112	6.8	3	5.5	2.1	Iris-virginica

To visualize the results:

```

'plot_clustering -i ../data/iris.data -a "1-4" -c 5 --centroids-infile
c_hka_iris.dat --member-infile m_hka_iris.dat --centroids-title "Medoid"
--graphics-outfile hka_iris'

```

And graphically show the prototypes and groups in [Figure 3.8](#).

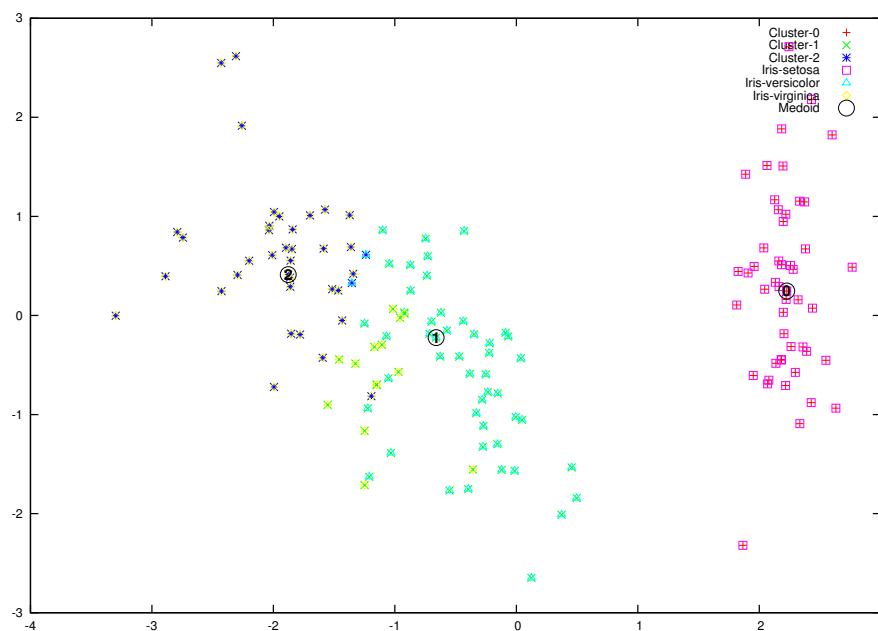


Figure 3.8: The most representative instances of the Iris data set, obtained with the program 'hka_fkmedoid'

3.3.2 Genetic algorithms for variable k-clusters

The genetic algorithms described in the following sections direct the search both to find the best cluster number (k^*) and cluster formation, in which the objects belonging to the same clusters are similar and with the objects of the other different clusters. In this case, there is no information about the most appropriate value in the data set.

The clustering is an exploratory technique, which can be used to make the automatic classification. To do this, you can use an algorithm that finds the appropriate number of

clusters, when an expert is not available, or also compare the clusters obtained against the predefined classes.

The parameters that are common in these algorithms are:

```
--k-minimum[=NUMBER]
    number of clusters by default [NUMBER=2]

--k-maximum[=NUMBER]
    Some authors leave it to the user's criteria, others propose a predetermined
    value based on the size of the data set, such as  $n/2$  or  $n^{1/2}$ , most agree with
    the latter.
```

3.3.2.1 Based on the centroids

The genetic algorithms in this section use an See [\[real encoding\]](#), page 13, with some variant to allow the search for the optimum k . The algorithms included in LEAC are the following:

- **gcuk_vkcentroid**

Based on [BM02b](#), optimize to [\[DB\]](#), page 22. Encodes the chromosomes as strings of real numbers that represent the coordinates of the centroids, combined with # symbols, allow the diversity of chromosomes with different k , through the application of genetic operators `onePointCrossover` and `randomMutation`.

Parameters:

```
--crossover-probability[=NUMBER]
    real number in the interval [0.25, 1] [NUMBER=0.8]

--mutation-probability[=NUMBER]
    real number in the interval [0, 0.5] [NUMBER=0.001]
```

- **tgca_vkcentroid**

Based on [HT12](#), optimize to [\[VRC\]](#), page 25. It is a novel genetic algorithm, called by its authors as a *two-stage genetic clustering algorithm*. First, the TGCA focuses on the search of the best number of clusters, and then gradually transfers towards finding the globally optimal cluster centers. Furthermore, a maximum attribute range partition approach is used in the population initialization so as to overcome the sensitivity of clustering algorithms to initial partitions (HT12).

Parameters:

```
--num-subpopulations-cross[=NUMBER]
    number of subpopulations for parallel crossover. It must be less than half
    the size compared to the population [NUMBER=4]

--crossover-probability[=NUMBER]
    real number in the interval [0.25, 1] [NUMBER=0.8]

--kmeans-iterations[=NUMBER]
    maximum number of iterations for k-means algorithm [NUMBER=100]

--kmeans-threshold[=NUMBER]
    threshold value for k-means algorithm [NUMBER=0]
```

With the `gcuk_vkcentroid` program, you will find an automatic classification of the Zoo data set. The data set [zoo.data](#) has 7 classes with 17 attributes. All attributes are binary, with the exception of number 14, which can be seen as nominal.

To process it can be transformed into binary with the following `awk` script:

```
#run:
# awk -f zoo_binary.awk -F ',' -v OFS=',' zoo.data > zoo_bin.csv
BEGIN {

    h1 = "animalname";
    h2 = "hair";
    h3 = "feathers";
    h4 = "eggs";
    h5 = "milk";
    h6 = "airborne";
    h7 = "aquatic";
    h8 = "predator";
    h9 = "toothed";
    h10 = "backbone";
    h11 = "breathes";
    h12 = "venomous";
    h13 = "fins";
    h14 = "legs_0,legs_2,legs_4,legs_5,legs_6,legs_8";
    h15 = "tail";
    h16 = "domestic";
    h17 = "catsize";
    h18 = "type";

    print h1,h2,h3,h4,h5,h6,h7,h8,h9,h10,h11,h12,h13,h14,h15,h16,h17,h18;
}

{
# legs:Numeric (set of values: 0,2,4,5,6,8)
    if ( $14 == 0)
        $14 = "1,0,0,0,0,0";
    else if ( $14 == 2)
        $14 = "0,1,0,0,0,0";
    else if ( $14 == 4)
        $14 = "0,0,1,0,0,0";
    else if ( $14 == 5)
        $14 = "0,0,0,1,0,0";
    else if ( $14 == 6)
        $14 = "0,0,0,0,1,0";
    else if ( $14 == 8)
        $14 = "0,0,0,0,0,1";
    print $1,$2,$3,$4,$5,$6,$7,$8,$9,$10,$11,$12,$13,$14,$15,$16,$17,$18
}
```

```
'awk -f zoo_binary.awk -F ',' -v OFS=',' zoo.data > zoo_bin.csv'
```

```
'gcuk_vkcentroid -i ../data/zoo_bin.csv -h yes -a "2-22" -c 23 --k-minimum=2
--k-maximum=20 -C c_zoo_gcuk.data -M m_zoo_gcuk.data -T stdout --table-format
yes'
```

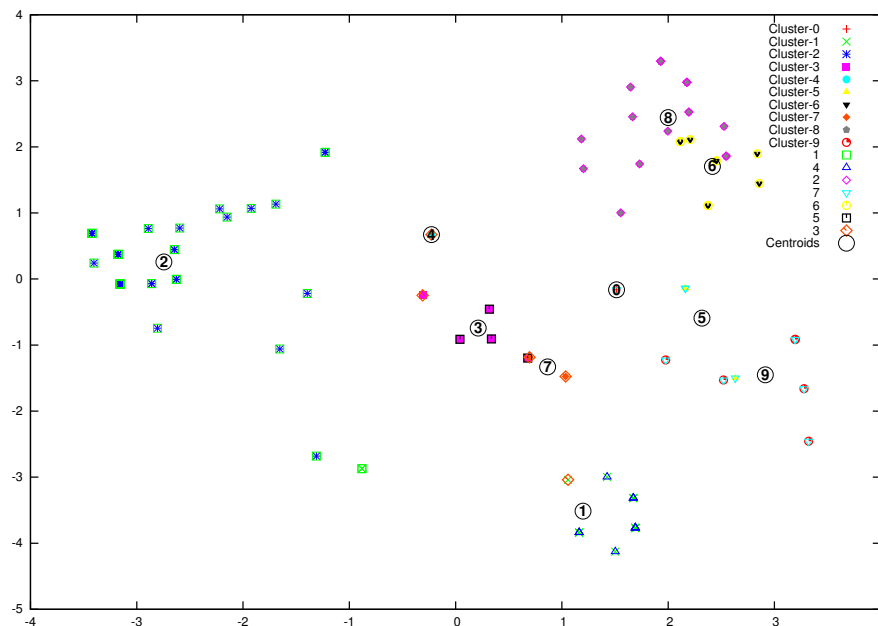


Figure 3.9: Clusters obtained in the data set Zoo with gcuk_vkcentroid

IN:

Algorithm name: GCUK

Based on: Bandyopadhyay and Maulik 2002

Metric used: DB-index

Data set: ../data/zoo_bin.csv

Number of instances: 101

Dimensions: 21

Random seed: 728997733 111590912 682175903 3140775393 958797699
412503851 3032481805 703125621

OUT:

CROMOSOME: BEST: rows, 9, columns, 21 > 0, 1, 1, 0, 0.8, 0.3, 0.45, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0.15, 0.3; 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0; 0.0588235, 0, 0.764706, 0.176471, 0, 1, 0.764706, 1, 1, 0.176471, 0.117647, 0.941176, 1, 0, 0, 0, 0, 0, 0.941176, 0.0588235, 0.411765; 1, 0, 0.0263158, 1, 0.0526316, 0.0789474, 0.5, 0.973684, 1, 1, 0, 0.0263158, 0.0.184211, 0.815789, 0, 0, 0.868421, 0.210526, 0.763158; 0, 0, 1, 0, 0, 0.8, 0.8, 1, 1, 1, 0.2, 0, 0, 1, 0, 0, 0.4, 0, 0; 0.4, 0, 1, 0, 0.6, 0, 0.1, 0, 0, 1, 0.2, 0, 0.2, 0, 0, 0.8, 0, 0, 0.1, 0; 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1; 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 0.5, 0, 1, 0, 0, 0, 0, 1, 0, 0; 0, 0, 1, 0, 0.857143, 1, 0, 0, 0.142857, 0, 0.285714, 0, 0.142857, 0.142857, 0.285714, 0.142857, 0, 0, 0.142857

Cluster number (K): 9

DB-index: 0.855135

SSE: 98.3379

Silhouette: 0.355542

VRC: 26.5558

CS measure: 1.72969

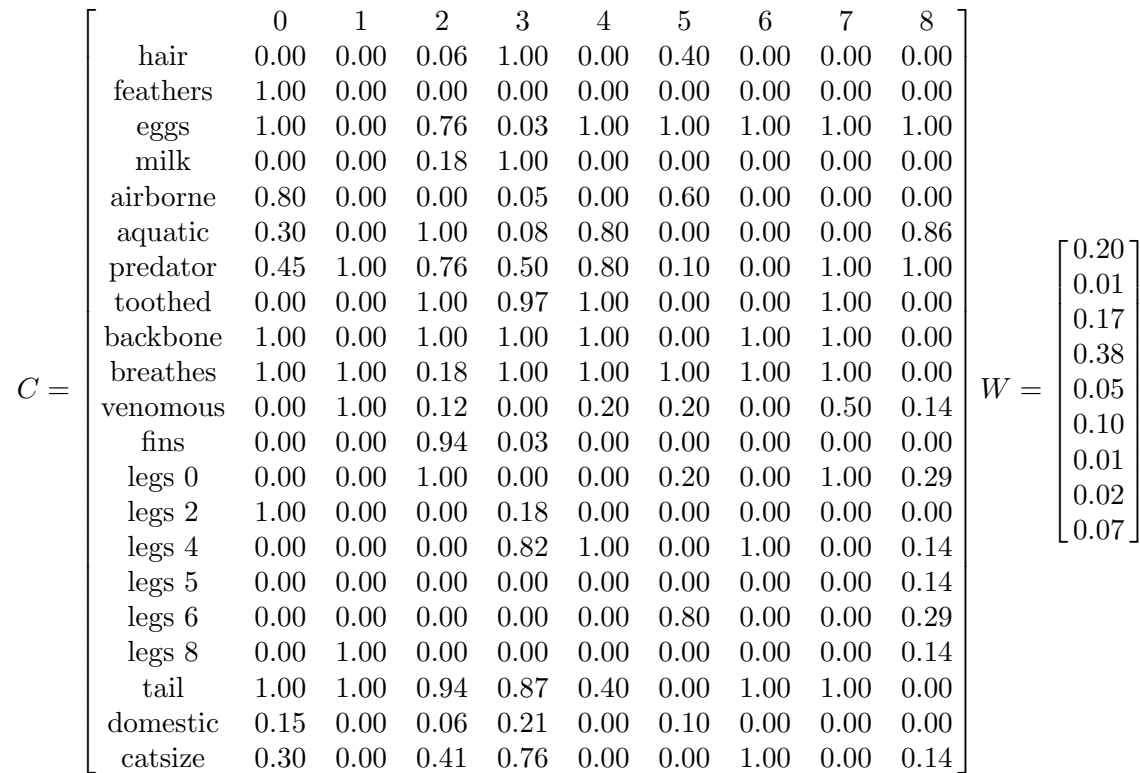
Dunn's index: 0.57735

Execution time (seg): 0.354636
 Generations find the best: 53

Partition table:

Cluster: 0	1	2	3	4
Class				
1: 0	0	3	38	0
4: 0	0	13	0	0
2: 20	0	0	0	0
7: 0	1	0	0	0
6: 0	0	0	0	0
5: 0	0	0	0	4
3: 0	0	1	0	1
sum: 20	1	17	38	5
Cluster: 5	6	7	8	sum
Class				
1: 0	0	0	0	41
4: 0	0	0	0	13
2: 0	0	0	0	20
7: 2	0	0	7	10
6: 8	0	0	0	8
5: 0	0	0	0	4
3: 0	1	2	0	5
sum: 10	1	2	7	101

Rand index: 0.956238
 Purity: 0.930693
 Precision: 0.932188
 Recall: 0.875956

Figure 3.10: Zoo Clusters with `gcuk_vkcentroid`

From the run of the program, 9 clusters were obtained, using the *DB-index* similarity measure, with very good measured values obtained. For this data set it is possible to use the centroids to obtain an association between items in the same row (AIS93, HPY00) as shown in the [Figure 3.10](#) And the summary in the [Table 3.1](#).

```
'plot_clustering -i ../data/zoo_bin.csv -h yes -a "2-22" -c 23
--centroids-infile c_zoo_gcuk.data --member-infile m_zoo_gcuk.data
--graphics-outfile zoo_gcuk'
```

C_j	W_j	Frequent dimension	Outliers
0	20%	95-100%: feathers eggs backbone breathes legs 2 tail 80-90%: airborne	
1	1%	90-100%: predator breathes venomous legs 8 tail	
2	17%	90-100%: aquatic backbone fins legs 0 tail	{eggs hair domestic}
3	38%	90-100%: hair milk toothed backbone breathes legs 4	{eggs airborne fins legs 4}
4	5%	90-100%: eggs toothed backbone breathes legs 4 80-90%: aquatic predator	
5	10%	90-100%: eggs breathes 80-90%: legs 6	{legs 6 domestic}
6	1%	90-100%: eggs backbone breathes legs 4 tail catsize	
7	2%	90-100%: eggs predator toothed backbone breathes legs 0 tail	
8	7%	90-100%: eggs predator 80-90%: aquatic	{aquatic venomous legs 4 legs 5 legs 8 catsize }

Table 3.1: Zoo clusters summary table

3.3.2.2 Based on cluster label

The genetic algorithms in this section use an See [string-of-group-numbers encoding], page 13, with some variant to allow the search for the optimum k . The algorithms included in LEAC are the following:

- `gga_vklabeledbindex` and `gga_vklabelsilhouette`

Based on ABSSJF+12, optimize to [DB], page 22, and [Silhouette], page 22. Chromosome is formed by two section [*element* | *group*]. The element section each position (gene) corresponds to the belongings of the object to a cluster. The group section corresponds to the alphabet of possible values of the genes $\{1, 2, 3, \dots, k\}$. An island model, where operators `mergeCrossover`, `mergeMutation` and `splittingMutation` are applied

```
--sub-population-size[=NUMBER]
    size of sub-populations (islands) [NUMBER=20]

--number-island[=NUMBER]
    number of sub-populations or islands [NUMBER=4]

--pe[=NUMBER]
    probability of migration good individuals between islands [0,1]
    [NUMBER=0.5]

--pci[=NUMBER]
    initial probability crossover, real number in the interval [0,1] must be
    high in the first stages [NUMBER=0.8]
```


- `--pcf [=NUMBER]`
 final probability crossover, real number in the interval $[0,1]$ must moderate in the last stages `[NUMBER=0.4]`
- `--pci [=NUMBER]`
 initial probability mutation, real number in the interval $[0,1]$ is smaller in the first generations `[NUMBER=0.05]`
- `--pcf [=NUMBER]`
 final probability mutation, real number in the interval $[0,1]$ is larger in the last ones `[NUMBER=0.2]`
- `--pbi [=NUMBER]`
 initial probability local search, real number in the interval $[0,1]$ must be high in the first stages `[NUMBER=0.1]`
- `--pbf [=NUMBER]`
 final probability local search, real number in the interval $[0,1]$ must moderate in the last stages `[NUMBER=0.05]`
- `cga_vklabel`
 Based on [HE03](#) optimize to [\[Silhouette\]](#), page 22,
 String of label of $(n + 1)$ positions. Each position corresponds to an instance, i.e., the i -th position (gene) represents the i -th object, whereas the last gene represents the number of clusters (k).

`--crossover-probability [=NUMBER]`
 real number in the interval $[0.25, 1]$ `[NUMBER=0.5]`

`--mutation-probability [=NUMBER]`
 for operator 1 and 2 real number in the interval $[0, 0.5]$ `[NUMBER=0.25]`
- `eac_vklabel`
 Based on [HCdC06](#) optimize to

`--desiable-objfunc [=NUMBER]`
 value desiable of objetive function (eg. silhouette $[-1,1]$ rand index $[0,1]$)
`[NUMBER=1]`

`--kmeans-iterations [=NUMBER]`
 maximum number of iterations for k-means algorithm `[NUMBER=5]`

`--kmeans-difference [=NUMBER]`
 maximum absolute difference between centroids in two consecutive iterations is less than or equal to `[NUMBER=0.001]`
- `feac_vklabel`, and its variants `eaci_vklabel`, `eacii_vklabel` and `eaciii_vklabel`
 Based on [ACH06](#)

`--desiable-objfunc [=NUMBER]`
 value desiable of objetive function (eg. silhouette $[-1,1]$ rand index $[0,1]$)
`[NUMBER=1]`

`--kmeans-iterations [=NUMBER]`
 maximum number of iterations for k-means algorithm `[NUMBER=5]`


```

Class

g: 225
b: 126
sum: 351

Rand index: 0.612291
Purity: 0.840456
Precision: 0.707252
Recall: 0.477702

'plot_clustering -i ../data/ionosphere.data -a "1-34" -c 35 --member-infile
m_gga_ionosphere.data --graphics-outfile gga_ionosphere'
```

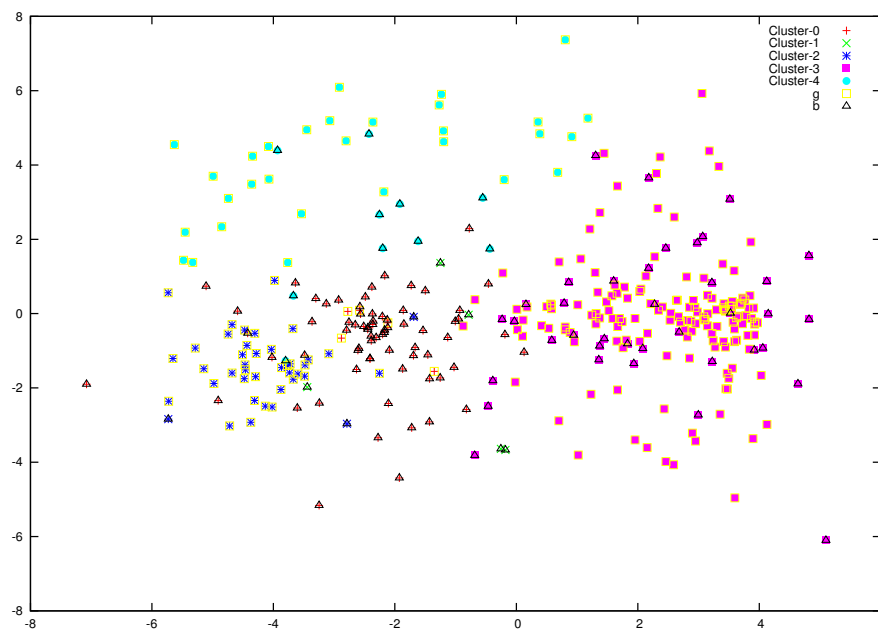


Figure 3.11: Clusters obtained with gga_vklabellsilhouette

3.3.2.3 Based on other encoding schemes

- gacustering_vktreebinary

Based on [CdLM03](#) optimize to [VRC], [page 25](#), Adopt an encoding scheme based on minimum spanning tree (MST), the tree nodes represent the n instances of the data set and the edges $(n - 1)$ correspond to the nearest instances. The algorithm first calculates the MST and creates the partitions of the data set by preserving or deleting the edges, represented by a binary string. The value 0 means that the corresponding edge remains, while the value 1 means that it is deleted. The number of elements with value 1 is equal to $(k - 1)$, where k is the number of clusters.

Parameters:

`--notchangestop [=NUMBER]`

after a number x of iterations, the best chromosome does not change. (We have fixed $x = 3$) [NUMBER=3].


```

          DB-index: 0.976877
        Silhouette: 0.39575
          CS measure: 0.0297727
        Dunn's index: 0.038597
    Execution time (seg): 12.9314
Generations find the best: 10

```

Partition table:

Cluster: 0	1	2	sum
Class			
cp: 142	0	1	143
im: 7	68	2	77
imS: 0	1	1	2
imL: 0	2	0	2
imU: 1	34	0	35
om: 0	1	19	20
omL: 0	5	0	5
pp: 5	1	46	52
sum: 155	112	69	336

```

Rand index: 0.86672
  Purity: 0.761905
Precision: 0.687857
  Recall: 0.927444

```

And the results can be visualized with the following command. [Figure 3.12](#)

```

'plot_clustering -i ../data/ecoli.data -a "2-8" -c 9 -d " " --centroids-infile
ecoli_centroids.data --member-infile ecoli_membership.data --graph-infile
ecoli_tree.data --graphics-outfile ecoli_tree --centroids-size 1.5
--member-size 0.5 --size-instance 0.6'

```

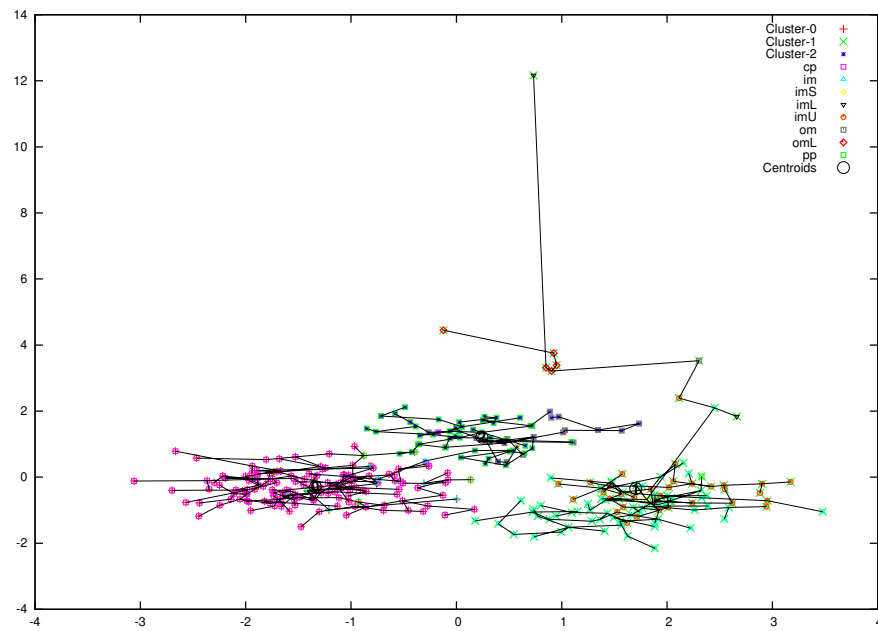


Figure 3.12: Minimum spanning tree (MST) and clusters obtained with `gaclustering_vktreebinary` program for the *ecoli* data set

4 Reporting Bugs

If you find a bug in LEAC, please send electronic mail to hermes@uaz.edu.mx.

Appendix A Example source code

The following source code show the use of the LEAC library. The files are in `eac` directory.

A.1 KGA algorithm

The following encoded algorithm is the KGA (`kga_fkcentroid.hpp`), described in the paper BM02a.

```

/#!/ \file kga_fkcentroid.hpp
*
* \brief KGA \cite Bandyopadhyay:Maulik:GAclustering:KGA:2002
*
* \details This file is part of the LEAC.\n\n
* Implementation of the KGA algorithm based on the paper:\n
* S. Bandyopadhyay and U. Maulik. An evolutionary technique based\n
* on k-means algorithm for optimal clustering in rn. Inf. Sci. Appl.,\n
* 146(1-4):221--237, 2002.\n
* URL: http://www.sciencedirect.com/science/article/pii/S0020025502002086,\n
* <a href="http://dx.doi.org/10.1016/S0020-0255(02)00208-6">\n
* doi:http://dx.doi.org/10.1016/S0020-0255\(02\)00208-6</a>\n.
* \n
* Library Evolutionary Algorithms for Clustering (LEAC) is a library\n
* for the implementation of evolutionary algorithms\n
* focused on the partition type clustering problem. Based on the\n
* current standards of the <a href="http://en.cppreference.com">C++</a>\n
* language, as well as on Standard\n
* Template Library <a href="http://en.cppreference.com/w/cpp/container">STL</a>\n
* and also <a href="http://www.openblas.net/">OpenBLAS</a> to have a better performance.\n
* \version 1.0
* \date 2015-2017
* \authors Hermes Robles-Berumen <hermes@uaz.edu.mx>\n
* Sebastian Ventura <sventura@uco.es>\n
* Amelia Zafra <azafra@uco.es>\n
* <a href="http://www.uco.es/kdis/">KDIS</a>\n
* \copyright <a href="https://www.gnu.org/licenses/gpl-3.0.en.html">GPLv3</a> license
*/

#ifndef __KGA_FKCENTROID_HPP__
#define __KGA_FKCENTROID_HPP__

#include <vector>
#include <algorithm>

#include <leac.hpp>
#include "inparam_pcpmfk.hpp"
#include "outparam_gac.hpp"

#include "plot_runtime_function.hpp"

/#!/ \namespace eac
\brief Evolutionary Algorithms for Clustering
\details Implementation of evolutionary algorithms used to solve the clustering problem

\version 1.0
\date 2015-2017
\copyright GPLv3 license
*/

```

```

namespace eac {

/*! \fn gaencode::ChromFixedLength<T_FEATURE,T_REAL> kga_fkcentroid
    (inout::OutParamGAC<T_REAL,T_CLUSTERIDX> &aoop_outParamGAC,
    inout::InParamPcPmFk<T_CLUSTERIDX,T_REAL,T_FEATURE,T_FEATURE_SUM,T_INSTANCES_CLUSTER_K>
    &aiinp_inParamPcPmFk,
    const INPUT_ITERATOR aiiterator_instfirst,
    const INPUT_ITERATOR aiiterator_instlast,
    const dist::Dist<T_REAL,T_FEATURE> &aifunc2p_dist)
    \brief KGA \cite Bandyopadhyay:Maulik:GAclustering:KGA:2002
    \details Implementation of the KGA algorithm based on
    \cite Bandyopadhyay:Maulik:GAclustering:KGA:2002.
    \returns A partition of a data set, encoded on a chromosome where
    each gene is the coordinate of a centroid. Base to following equation:
    \f[
    x_i \in C_j \rightarrow \mid x_i - \mu_j \mid \begin{array}{c} \mid \\ \mid \end{array} k \end{array}
    \mid x_i - \mu_k \mid, \mid; j=1,2,..k,
    \f]
    where \f\mu_j\f$, represents the centroid of cluster \fC_j\f$
    \param aoop_outParamGAC a inout::OutParamGAC with the
    output parameters of the algorithm
    \param aiinp_inParamPcPmFk a inout::InParamPcPmFk parameters
    required by the algorithm
    \param aiiterator_instfirst an InputIterator to the initial
    positions of the sequence of instances
    \param aiiterator_instlast an InputIterator to the final positions
    of the sequence of instances
    \param aifunc2p_dist an object of type dist::Dist to calculate distances
*/
template < typename T_FEATURE,
            typename T_REAL,
            typename T_FEATURE_SUM,
            typename T_INSTANCES_CLUSTER_K,
            typename T_CLUSTERIDX, //-1, 0, 1, ..., K
            typename INPUT_ITERATOR
            >
gaencode::ChromFixedLength<T_FEATURE,T_REAL>
kga_fkcentroid
(inout::OutParamGAC
<T_REAL,
T_CLUSTERIDX> &aoop_outParamGAC,
inout::InParamGACClusteringProbCProbMFixedK
<T_CLUSTERIDX,
T_REAL,
T_FEATURE,
T_FEATURE_SUM,
T_INSTANCES_CLUSTER_K> &aiinpcgaprobfixedk_inParamKGA,
const INPUT_ITERATOR aiiterator_instfirst,
const INPUT_ITERATOR aiiterator_instlast,
const dist::Dist<T_REAL,T_FEATURE> &aifunc2p_dist
)
{
    const uintidx lconstui_numClusterFixedK =
        (uintidx) aiinpcgaprobfixedk_inParamKGA.getNumClusterK();

/*Defines the size of the chromosome

```

Specifically, each chromosome is described by a sequence of $length(Ch) = l \times k$ real-valued numbers where l is the dimension of the instances, and k is the number of clusters. That is to say, the chromosome of the algorithm is written as (4.2) (See [\[centroid-based\]](#), page 13)

```

*/

/*ASSIGN SIZE FOR ALL CHROMOSOMES
*/

gaencode::ChromFixedLength<T_FEATURE,T_REAL>::setStringSize
( lconstui_numClusterFixedK * data::Instance<T_FEATURE>::getNumDimensions() );

gaencode::ChromFixedLength<T_FEATURE,T_REAL> lochromfixleng_best;

/*VARIABLE NEED FOR POPULATION AND MATINGPOOL GENETIC
*/

/*POPULATION CREATE-----
*/

std::vector<gaencode::ChromFixedLength<T_FEATURE,T_REAL> >
    lvectorchromfixleng_population
    (aiinpcgaprobfixdk_inParamKGA.getSizePopulation());

/*CREATE SPACE FOR STORE MATINGPOOL-----
*/

std::vector<gaencode::ChromFixedLength<T_FEATURE,T_REAL> >
    lvectorchromfixleng_matingPool
    (aiinpcgaprobfixdk_inParamKGA.getSizePopulation());

std::uniform_real_distribution<T_REAL> uniformdis_real01(0, 1);

#ifdef __VERBOSE_YES

/*ID PROC
*/
geverboseui_idproc = 1;

++geiinparam_verbose;
const char* lpc_labelAlgGA = "kga_fkcentroid";
if ( geiinparam_verbose <= geiinparam_verboseMax ) {
    std::cout
        << lpc_labelAlgGA
        << ": IN(" << geiinparam_verbose << ")\n"
        << "\t(output Chromosome: lochromfixleng_best["
        << &lochromfixleng_best << "]\n"
        << "\t output outparam::OutParamGAC&: "
        << "aoop_outParamGAC["
        << &aoop_outParamGAC << "]\n"
        << "\t input InParamGACClusteringProbCProbMFixedK&: "
        << "aiinpcgaprobfixdk_inParamKGA["
        << &aiinpcgaprobfixdk_inParamKGA << "]\n"
        << "\t input aiiterator_instfirst[" << *aiiterator_instfirst << "]\n"
        << "\t input aiiterator_instlast[" << &aiiterator_instlast << "]\n"
        << "\t input dist::Dist<T_REAL,T_FEATURE> &aifunc2p_dist["
        << &aifunc2p_dist << ']'

```

```

    << "\n\t\tPopulation size = "
    << aiinpcgaprobfixedk_inParamKGA.getSizePopulation()
    << "\n\t\tProbCrossover = "
    << aiinpcgaprobfixedk_inParamKGA.getProbCrossover()
    << "\n\t\tProbMutation = "
    << aiinpcgaprobfixedk_inParamKGA.getProbMutation()
    << "\n\t)"
    << std::endl;
}
#endif /*__VERBOSE_YES*/

runtime::ListRuntimeFunction<COMMON_IDOMAIN>
llfh_listFuntionHist
(aiinpcgaprobfixedk_inParamKGA.getNumMaxGenerations(),
 "Iterations",
 "Clustering metrics"
);

/*DECLARATION OF VARIABLES: COMPUTING STATISTICAL AND METRIC OF THE ALGORITHM*/
#ifndef __WITHOUT_PLOT_STAT
std::ofstream lfileout_plotStatObjectiveFunc;
runtime::RuntimeFunctionValue<T_REAL> *lofh_SSE = NULL;
runtime::RuntimeFunctionStat<T_REAL>
*lofhs_statObjectiveFunc[STATISTICAL_ALL_MEASURES];
std::vector<T_REAL> lvectorT_statfuncObjectiveFunc;

if ( aiinpcgaprobfixedk_inParamKGA.getWithPlotStatObjectiveFunc() ) {

    lvectorT_statfuncObjectiveFunc.reserve
    ( aiinpcgaprobfixedk_inParamKGA.getSizePopulation());
    //DEFINE FUNCTION
    lofh_SSE = new runtime::RuntimeFunctionValue<T_REAL>
    ("SSE",
     aiinpcgaprobfixedk_inParamKGA.getAlgorithmName(),
     RUNTIMEFUNCTION_NOT_STORAGE
    );

    llfh_listFuntionHist.addFuntion(lofh_SSE);

    //DEFINE FUNCTION STATISTICAL
    for (int li_i = 0; li_i < STATISTICAL_ALL_MEASURES; li_i++) {
        lofhs_statObjectiveFunc[li_i] =
            new runtime::RuntimeFunctionStat<T_REAL>
            ( (char) li_i,
              aiinpcgaprobfixedk_inParamKGA.getAlgorithmName(),
              RUNTIMEFUNCTION_NOT_STORAGE
            );
        llfh_listFuntionHist.addFuntion(lofhs_statObjectiveFunc[li_i]);
    }

    //OPEN FILE STORE FUNCTION
    aoop_outParamGAC.setFileNameOutPlotStatObjectiveFunc
    (aiinpcgaprobfixedk_inParamKGA.getFileNamePlotStatObjectiveFunc(),
     aiinpcgaprobfixedk_inParamKGA.getTimesRunAlgorithm()
    );

    lfileout_plotStatObjectiveFunc.open
    (aoop_outParamGAC.getFileNameOutPlotStatObjectiveFunc().c_str(),

```

```

        std::ios::out | std::ios::app
    );

    lfileout_plotStatObjectiveFunc.precision(COMMON_COUT_PRECISION);

    //FUNCTION HEADER
    lfileout_plotStatObjectiveFunc
    << llfh_listFuntionHist.getHeaderFuntions()
    << "\n";
}

#endif /*__WITHOUT_PLOT_STAT*/

/*WHEN CAN MEASURE STARTS AT ZERO INVALID OFFSPRING
*/
aoop_outParamGAC.setTotalInvalidOffspring(0);

/*OUT: GENETIC ALGORITHM CHARACTERIZATION*/
runtime::ExecutionTime let_executionTime = runtime::start();

T_FEATURE *larray_maxFeactures =
    new T_FEATURE[data::Instance<T_FEATURE>::getNumDimensions()];

T_FEATURE *larray_minFeactures =
    new T_FEATURE[data::Instance<T_FEATURE>::getNumDimensions()];

stats::maxFeatures
(larray_maxFeactures,
 aiiterator_instfirst,
 aiiterator_instlast
 );

stats::minFeatures
(larray_minFeactures,
 aiiterator_instfirst,
 aiiterator_instlast
 );

/*INITIALIZE POPULATION-----
3.1.1 POPULATION INITIALIZATION
Chosen distict points from the data set are used to initialize
the K cluster centers encoded in each chorosome.
This is similar to the initialization od the centers
in K-Means algorithm. This process es repeat for each chromosome
in the population BMO2a */
{ /*BEGIN INITIALIZE POPULATION P(t)*/

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "(0) POPULATION INITIAL";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
        << geverbosepc_labelstep
        << ": IN(" << geiinparam_verbose << ')'
        << std::endl;
    }
}
#endif /*__VERBOSE_YES*/

```

```

for ( auto& lchromfixleng_iter: lvectorchromfixleng_population ) {

    /*DECODE CHROMOSOME
    */
    mat::MatrixRow<T_FEATURE>
        lmatrixrowt_centroidsChrom
        (lconstui_numClusterFixedK,
         data::Instance<T_FEATURE>::getNumDimensions(),
         lchromfixleng_iter.getString()
        );

    clusteringop::randomInitialize
        (lmatrixrowt_centroidsChrom,
         aiiterator_instfirst,
         aiiterator_instlast
        );

    lchromfixleng_iter.setFitness
        (-std::numeric_limits<T_REAL>::max());
    lchromfixleng_iter.setObjectiveFunc
        (std::numeric_limits<T_REAL>::max());

}

#ifdef __VERBOSE_YES
    if ( geiinputparam_verbose <= geiinputparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinputparam_verbose << ') '
            << std::endl;
    }
    --geiinputparam_verbose;
#endif /*__VERBOSE_YES*/

} /*END INITIALIZE POPULATION P(t)*/

while ( 1 ) {

    /*BEGIN ITERATION
    */
    llfh_listFuntionHist.increaseDomainUpperBound();

/*3.1.2 CLUSTERING

```

In this step, the cluster are formed according to the center encoded in the chromosome. This is done by assigning each point $x_i, i = 1, 2, \dots, n$ to one of the clusters C_j with center z_i^* such that

$$\|x_i - \mu_j\| \leq \|x_i - \mu_{j'}\|, \quad j' = 1, 2, \dots, k, \quad \text{and} \quad j \neq j'$$

All ties are resolved arbitrarily. As like the K-Means algorithm, for each cluster C_i , its new center μ^* is computed as $\mu_i^* = 1/n_j \sum_{x_i \in C_j} x_i, j = 1, 2, \dots, k$, where n_j is the number of points in cluster C_i . These μ^* now replace the previous μ_i s in the chromosome.

BMO2a
*/

```

    { /*BEGIN CLUSTERING*/
#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "A. THE CLUSTERS ARE FORMED";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": IN(" << geiinparam_verbose << ' '
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    for ( auto& liter_iChrom: lvectorchromfixleng_population ) {

        /*DECODE CHROMOSOME*/
        mat::MatrixRow<T_FEATURE>
            lmatrixrowt_centroidsChrom
            (lconstui_numClusterFixedK,
             data::Instance<T_FEATURE>::getNumDimensions(),
             liter_iChrom.getString()
            );

        mat::MatrixRow<T_FEATURE_SUM>
            llmatrixrowt_sumInstancesCluster
            (lconstui_numClusterFixedK,
             data::Instance<T_FEATURE>::getNumDimensions(),
             T_FEATURE_SUM(0)
            );

        std::vector<T_INSTANCES_CLUSTER_K>
            lvectort_numInstancesInClusterK
            (lconstui_numClusterFixedK,
             T_INSTANCES_CLUSTER_K(0)
            );

        T_CLUSTERIDX lmcidx_numClusterNull;

        clusteringop::updateCentroids
            (lmcidx_numClusterNull,
             lmatrixrowt_centroidsChrom,
             llmatrixrowt_sumInstancesCluster,
             lvectort_numInstancesInClusterK,
             aiiterator_instfirst,
             aiiterator_instlast,
             aifunc2p_dist
            );
    }
#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ' '
            << std::endl;
    }
    --geiinparam_verbose;

```

```

#endif /*__VERBOSE_YES*/

} /*END CLUSTERING*/

/*FITNESS FUNCTION-----

/* 3.1.3 Fitness computation
For each chromosome, the clusters formed in the previous step are utilized
computing the clustering metric, SSE, as follows:


$$SSE = \sum_{j=1}^k \sum_{x_i \in C_j} \|x_i - \mu_j\|$$


For finding the appropriate clusters SSE has to be minimized. The fitness
function of a chromosome is defined as  $1/SSE$ . Therefore, maximization of the
fitness function will lead to minimization of the clustering metric SSE.
*/

{ /*BEGIN COMPUTED METRIC M AND FITNESS*/

#ifdef __VERBOSE_YES
geverbosepc_labelstep = "B. COMPUTED METRIC M AND FITNESS";
++geiinputparam_verbose;
if ( geiinputparam_verbose <= geiinputparam_verboseMax ) {
    std::cout
        << geverbosepc_labelstep
        << ": IN(" << geiinputparam_verbose << ') '
        << std::endl;
    }
}
#endif /*__VERBOSE_YES*/

long ll_invalidOffspring = 0;

for ( auto& lchromfixleng_iter: lvectorchromfixleng_population ) {

    /*DECODE CHROMOSOME*/
    mat::MatrixRow<T_FEATURE>
        lmatrixrowt_centroidsChrom
        (lconstui_numClusterFixedK,
         data::Instance<T_FEATURE>::getNumDimensions(),
         lchromfixleng_iter.getString()
        );

    std::pair<T_REAL,bool> lpair_SSE =
        um::SSE
        (lmatrixrowt_centroidsChrom,
         aiiterator_instfirst,
         aiiterator_instlast,
         aifunc2p_dist
        );

    lchromfixleng_iter.setObjectiveFunc(lpair_SSE.first);
    lchromfixleng_iter.setFitness(1.0 / lpair_SSE.first);
    lchromfixleng_iter.setValidString(lpair_SSE.second);

    if ( lchromfixleng_iter.getValidString() == false )

```



```

        ++ll_invalidOffspring;

#ifdef __WITHOUT_PLOT_STAT
        lvectorT_statfuncObjectiveFunc.push_back
            (lchromfixleng_iter.getObjectiveFunc());
#endif /*__WITHOUT_PLOT_STAT*/

    }

    aoop_outParamGAC.sumTotalInvalidOffspring
        (ll_invalidOffspring);

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ') '
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END COMPUTED METRIC M AND FITNESS*/

/*ELITISM-----
    Elitism has been implemented in each generation by
    replacing the worst chromosome of the population with
    the best one seen up to the previous generation.
    BM02a      */
    { /*BEGIN ELITISM REPLACING THE WORST CHROMOSOME*/

#ifdef __VERBOSE_YES
        geverbosepc_labelstep = "ELITISM REPLACING THE WORST CHROMOSOME";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ') '
                << std::endl;
        }
    }
#endif /*__VERBOSE_YES*/

    auto lit_chromMin =
        std::min_element
            (lvectorchromfixleng_population.begin(),
             lvectorchromfixleng_population.end(),
             [](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& x,
                const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& y
                )
            { return x.getFitness() < y.getFitness(); }
            );

    if ( lit_chromMin->getFitness() < lochromfixleng_best.getFitness() ) {
        *lit_chromMin = lochromfixleng_best;
    }
}

```

```

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ') '
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END ELITISM REPLACING THE WORST CHROMOSOME*/

    /*The best string or chromosome seen up to the last generation
    provides the solution to the clustering problem.
    BM02a */
    { /*BEGIN PRESERVING THE BEST STRING*/

        auto lchromfixleng_iterMax =
            std::max_element
                (lvectorchromfixleng_population.begin(),
                 lvectorchromfixleng_population.end(),
                 [](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& x,
                    const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& y
                 )
                { return x.getFitness() < y.getFitness(); }
            );

#ifdef __VERBOSE_YES
        geverbosepc_labelstep = "ELITISM PRESERVING THE BEST";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ")\tmax fitness = "
                << lchromfixleng_iterMax->getFitness()
                << std::endl;
        }
#endif /*__VERBOSE_YES*/

        if ( lochromfixleng_best.getFitness() <
            lchromfixleng_iterMax->getFitness() ) {

            /*CHROMOSOME ONE WAS FOUND IN THIS ITERATION*/
            lochromfixleng_best = *lchromfixleng_iterMax;

            aoop_outParamGAC.setIterationGetsBest
                (llfh_listFuntionHist.getDomainUpperBound());
            aoop_outParamGAC.setRunTimeGetsBest
                (runtime::elapsedTime(let_executionTime));
        }

#ifdef __VERBOSE_YES
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": OUT(" << geiinparam_verbose << ') '
                << std::endl;
        }
#endif
    }

```

```

    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

} /*END PRESERVING THE BEST STRING*/

/*MEASUREMENT BEST: COMPUTING STATISTICAL AND METRIC OF THE
ALGORITHM
*/
#ifdef __WITHOUT_PLOT_STAT
if ( aiinpcgaprobfixedk_inParamKGA.getWithPlotStatObjectiveFunc() ) {

    lofh_SSE->setValue(lochromfixleng_best.getObjectiveFunc());

    functionhiststat_evaluateAll
        (lofhs_statObjectiveFunc,
         lvectorT_statfuncObjectiveFunc
        );
    lfileout_plotStatObjectiveFunc << llfh_listFuntionHist;
    lvectorT_statfuncObjectiveFunc.clear();
}
#endif /*__WITHOUT_PLOT_STAT*/

/*TERMINATION CRITERION-----
3.1.5 TERMINATION CRITERION
BM02a */
#ifdef __VERBOSE_YES
/*ID PROC
*/
++geverboseui_idproc;

++geiinparam_verbose;
if ( geiinparam_verbose <= geiinparam_verboseMax ) {
    std::cout
        << "TERMINATION CRITERION ATTAINED?: "
        << llfh_listFuntionHist.getDomainUpperBound()
        << std::endl;
}
--geiinparam_verbose;
#endif /*__VERBOSE_YES*/

if ( !(llfh_listFuntionHist.getDomainUpperBound()
        < aiinpcgaprobfixedk_inParamKGA.getNumMaxGenerations() )
    )
    break;

/*3.1.4 GENETIC OPERATIONS
BM02a */

/*SELECTION-----
Selection. The selection process selects chromosomes from the mating pool
directed by the survival of the fittest concept of natural genetic systems.
In the proportional selection strategy adopted in this paper, a chromosome is
assigned a number of copies, which is proportional to its fitness in the pop-
ulation.
BM02a */
{ /*BEGIN SELECTION*/

```

```

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "SELECTION";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": IN(" << geiinparam_verbose << '),'
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    const std::vector<T_REAL>&& lvectorT_probDistRouletteWheel =
        prob::makeDistRouletteWheel
        (lvectorchromfixleng_population.begin(),
         lvectorchromfixleng_population.end(),
         [](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>&
            lchromfixleng_iter) -> T_REAL
         {
             return lchromfixleng_iter.getFitness();
         }
        );

    /*COPY POPULATION TO STRING POOL FOR ROULETTE WHEEL-----
    */
    for ( auto& lchromfixleng_iter: lvectorchromfixleng_matingPool ) {

        uintidx lstidx_chrom =
            gaselect::getIdxRouletteWheel
            (lvectorT_probDistRouletteWheel,
             uintidx(0)
            );

        lchromfixleng_iter = lvectorchromfixleng_population.at(lstidx_chrom);
    }

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << '),'
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END SELECTION*/

/*CROSSOVER-----
Crossover is a probabilistic process that exchanges information between two
parent chromosomes for generating two offspring. Here, single-point crossover
with a fixed crossover probability of  $p_c$  is used. For chromosomes
of length  $l \times k$ , a random integer, called the crossover point,
is generated in the range  $[1, l-1]$ . The portions of the chromosomes
lying to the right of the crossover point are exchanged to produce two
offspring.
*/

```

```

    { /*BEGIN CROSSOVER*/
#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "CROSSOVER";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout << geverbosepc_labelstep
            << ": IN(" << geiinparam_verbose << ')'
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    long ll_invalidOffspring = 0;

    gaiterator::crossover
    (lvectorchromfixleng_matingPool.begin(),
    lvectorchromfixleng_matingPool.end(),
    lvectorchromfixleng_population.begin(),
    lvectorchromfixleng_population.end(),
    [&](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>&
        aichrom_parent1,
        const gaencode::ChromFixedLength<T_FEATURE,T_REAL>&
        aichrom_parent2,
        gaencode::ChromFixedLength<T_FEATURE,T_REAL>&
        aochrom_child1,
        gaencode::ChromFixedLength<T_FEATURE,T_REAL>&
        aochrom_child2
        )
    {

        if ( uniformdis_real01(gmt19937_eng) <
            aiinpcgaprobfixedk_inParamKGA.getProbCrossover() ) {

            gagenericop::onePointCrossover
            (aochrom_child1,
            aochrom_child2,
            aichrom_parent1,
            aichrom_parent2
            );

            /*DECODE CHROMOSOME CHILD1*/
            mat::MatrixRow<T_FEATURE>
            lmatrixrowt_centroidsChromChild1
            (lconstui_numClusterFixedK,
            data::Instance<T_FEATURE>::getNumDimensions(),
            aochrom_child1.getString()
            );

            std::pair<T_REAL,bool>
            lpair_SSE1 =
            um::SSE
            (lmatrixrowt_centroidsChromChild1,
            aiiterator_instfirst,
            aiiterator_instlast,
            aifunc2p_dist
            );
            aochrom_child1.setObjectiveFunc(lpair_SSE1.first);
            aochrom_child1.setFitness(1.0 / lpair_SSE1.first);

```

```

    aochrom_child1.setValidString(lpairs_SSE1.second);

    if ( aochrom_child1.getValidString() == false )
        ++ll_invalidOffspring;

    /*DECODE CHROMOSOME CHILD1*/
    mat::MatrixRow<T_FEATURE>
        lmatrixrowt_centroidsChromChild2
        (lconstui_numClusterFixedK,
         data::Instance<T_FEATURE>::getNumDimensions(),
         aochrom_child2.getString()
        );

    std::pair<T_REAL,bool>
        lpairs_SSE2 =
        um::SSE
        (lmatrixrowt_centroidsChromChild2,
         aiiterator_instfirst,
         aiiterator_instlast,
         aifunc2p_dist
        );

    aochrom_child2.setObjectiveFunc(lpairs_SSE2.first);
    aochrom_child2.setFitness(1.0 / lpairs_SSE2.first);
    aochrom_child2.setValidString(lpairs_SSE2.second);

    if ( aochrom_child2.getValidString() == false )
        ++ll_invalidOffspring;

    } //if Crossover
    else {
        aochrom_child1 = aichrom_parent1;
        aochrom_child2 = aichrom_parent2;
    }
}
);

aop_outParamGAC.sumTotalInvalidOffspring
(ll_invalidOffspring);

#ifdef __VERBOSE_YES
    if ( geiinputparam_verbose <= geiinputparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinputparam_verbose << ') '
            << std::endl;
    }
    --geiinputparam_verbose;
#endif /*__VERBOSE_YES*/

} /*END CROSSOVER*/

/*Mutation. Each liter_Chrom chromosome undergoes mutation with a fixed
probability  $p_m$  (lr_mutationProbability). Let  $M_{min}$  (lchrom_minObjFunc) and  $M_{max}$ 
(lrt_maxClusteringMetric) be the minimum and maximum values of the clustering metric,
respectively, in the current population.
See [Definition gaclusteringop::biDirectionHMMutation], page 32
*/

```

```

    { /*BEGIN MUTATION*/
#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "MUTATION";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout << geverbosepc_labelstep
                    << ": IN(" << geiinparam_verbose << ')'
                    << std::endl;
    }
#endif /*__VERBOSE_YES*/

    auto lchrom_minObjFunc =
        std::min_element
        (lvectorchromfixleng_population.begin(),
         lvectorchromfixleng_population.end(),
         [](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& x,
            const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& y
            )
         { return x.getObjectiveFunc() < y.getObjectiveFunc(); }
        );
    T_REAL lrt_minClusteringMetric =
        lchrom_minObjFunc->getObjectiveFunc();

    auto lchrom_maxObjFunc =
        std::max_element
        (lvectorchromfixleng_population.begin(),
         lvectorchromfixleng_population.end(),
         [](const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& x,
            const gaencode::ChromFixedLength<T_FEATURE,T_REAL>& y
            )
         { return x.getObjectiveFunc() < y.getObjectiveFunc(); }
        );

    T_REAL lrt_maxClusteringMetric =
        lchrom_maxObjFunc->getObjectiveFunc();

    for ( auto& lchromfixleng_iter: lvectorchromfixleng_population ) {

        if ( uniformdis_real01(gmt19937_eng)
            < aiinpcgaprobfixdk_inParamKGA.getProbMutation() )
        { //IF BEGIN MUTATION
            gaclusteringop::biDirectionHMutation
            (lchromfixleng_iter,
             lrt_minClusteringMetric,
             lrt_maxClusteringMetric,
             larray_minFeactures,
             larray_maxFeactures
            );
            lchromfixleng_iter.setFitness
            (-std::numeric_limits<T_REAL>::max());
            lchromfixleng_iter.setObjectiveFunc
            (std::numeric_limits<T_REAL>::max());
        } //END BEGIN MUTATION
    }
#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout

```

```

        << geverbosepc_labelstep
        << ": OUT(" << geiinparam_verbose << ' '
        << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END MUTATION*/

} /*END EVOLUTION While*/

/*FREE MEMORY
*/
delete [] larray_maxFeactures;
delete [] larray_minFeactures;

runtime::stop(let_executionTime);
aop_outParamGAC.setNumClusterK
    (aiinpcgaprobfixdk_inParamKGA.getNumClusterK());
aop_outParamGAC.setMetricFuncRun
    (lochromfixleng_best.getObjetiveFunc());
aop_outParamGAC.setAlgorithmRunTime
    (runtime::getTime(let_executionTime));
aop_outParamGAC.setFitness
    (lochromfixleng_best.getFitness());
aop_outParamGAC.setNumTotalGenerations
    (llfh_listFuntionHist.getDomainUpperBound());

#ifndef __WITHOUT_PLOT_STAT
    if ( aiinpcgaprobfixdk_inParamKGA.getWithPlotStatObjetiveFunc() ) {
        runtime::plot_funtionHist
            (llfh_listFuntionHist,
             aiinpcgaprobfixdk_inParamKGA,
             aop_outParamGAC
            );
    }
#endif /*__WITHOUT_PLOT_STAT*/

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        geverbosepc_labelstep = lpc_labelAlgGA;
        std::cout
            << lpc_labelAlgGA
            << ": OUT(" << geiinparam_verbose << ")\n";
        lochromfixleng_best.print();
        std::cout << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    return lochromfixleng_best;

} /* END kga_fkcentroid */

} /*END eac */

```



```
#endif /*__KGA_FKCENTROID_HPP__*/
```

A.2 GA algorithm

```

/*! \file gaclustering_fkcrispmatrix.hpp
 * This file is part of the LEAC.
 *
 * Implementation of the GA algorithm based on the paper:
 *
 * J.C. Bezdek, S. Boggavarapu, L.O. Hall, and A. Bensaid.
 * Genetic algorithm guided clustering. In Evolutionary Computation,
 * 1994. IEEE World Congress on Computational Intelligence., Proceed-
 * ings of the First IEEE Conference on, pages 34--39 vol.1, Jun 1994.
 * doi:10.1109/ICEC.1994.350046.
 *
 * Library Evolutionary Algorithms for Clustering (LEAC) is a library
 * for the implementation of evolutionary and genetic algorithms
 * focused on the partition type clustering problem. Based on the
 * current standards of the C++ language, as well as on Standard
 * Template Library STL and also OpenBLAS to have a better performance.
 *
 * (c) Hermes Robles-Berumen <hermes@uaz.edu.mx>
 *
 * For the full copyright and license information, please view the LICENSE
 * file that was distributed with this source code.
 */

#ifndef __GACLUSTERING_FKCRISPMATRIX_HPP__
#define __GACLUSTERING_FKCRISPMATRIX_HPP__

#include <iostream>
#include <iomanip>
#include <vector>

#include <leac.hpp>

#include "plot_runtime_function.hpp"
#include "inparam_gaclustering_withoutpcpm.hpp"
#include "outparam_gaclustering.hpp"

/*! \namespace eac
    \brief Evolutionary Algorithms for Clustering
    \details Implementation of genetic and evolutionary algorithms used to solve
           the clustering problem

    \author Hermes Robles-Berumen
    \date   2015-2017
    \copyright GPLv3 license
 */

namespace eac {

/*! \fn gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>
    gaclustering_fkcrispmatrix
    (inout::OutParamGAC<T_REAL,T_CLUSTERIDX> &aoop_outParamGAC,
    inout::InParamGAClusteringWithoutProbCProbM<T_CLUSTERIDX,T_BITSIZE,T_FEATURE,

```

```

T_FEATURE_SUM,T_INSTANCES_CLUSTER_K> &aiinpkbezdekga_inParam,
const INPUT_ITERATOR aiiterator_instfirst,
const INPUT_ITERATOR aiiterator_instlast, dist::Dist<T_REAL,T_FEATURE> &aifunc2p_dist)
    \brief gaclustering_fkcrispmatrix
    \details GA clustering based on BBHB94 Returns a crisp matrix, which encodes a par-
    tition of a data set, for a defined k.
    \param aoop_outParamGAC a inout::OutParamGAC that contains
    information relevant to program execution
    \param aiinpkbezdekga_inParam a inout::InParamGACClusteringWithoutProbCProbM with
    the input parameters for the program configuration
    \param aiiterator_instfirst an InputIterator to the initial positions of the
    sequence of instances
    \param aiiterator_instlast an InputIterator to the final positions of the
    sequence of instances
    \param aipartition_clusters a partition of instances in clusters
    \param aifunc2p_dist an object of type dist::Dist to calculate distances
*/

template < typename T_BITSIZE,
           typename T_REAL,
           typename T_FEATURE,
           typename T_FEATURE_SUM,
           typename T_INSTANCES_CLUSTER_K, //0, 1, ..., N
           typename T_CLUSTERIDX,         //-1, 0, 1, ..., K
           typename INPUT_ITERATOR
           >
gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>
gaclustering_fkcrispmatrix
(inout::OutParamGAC
<T_REAL,
T_CLUSTERIDX>          &aoop_outParamGAC,
inout::InParamGACClusteringWithoutProbCProbM
<T_CLUSTERIDX,
T_BITSIZE,
T_FEATURE,
T_FEATURE_SUM,
T_INSTANCES_CLUSTER_K> &aiinpkbezdekga_inParam,
const INPUT_ITERATOR   aiiterator_instfirst,
const INPUT_ITERATOR   aiiterator_instlast,
dist::Dist<T_REAL,T_FEATURE> &aifunc2p_dist
)
{
#ifdef __VERBOSE_YES
    /*ID PROC
    */
    geverboseui_idproc = 1;

    ++geiinparam_verbose;
    const char* lpc_labelAlgGA = "gaclustering_fkcrispmatrix";
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
        << lpc_labelAlgGA
        << " IN(" << geiinparam_verbose << ")\n"
        << "\t(output outparam::OutParamGAC&: aoop_outParamGAC["
        << &aoop_outParamGAC << "]\n"
        << "\t input InParamClusteringBezdekGA1994&: aiinpkbezdekga_inParam["
        << &aiinpkbezdekga_inParam << "]\n"
        << "\t input aiiterator_instfirst[" << *aiiterator_instfirst << "]\n"

```

```

    << "\t input aiiterator_instlast[" << &aiiterator_instlast << "]" \n"
    << "\t input  dist::Dist<T_REAL,T_FEATURE>  &aifunc2p_dist["
    << &aifunc2p_dist << ']'
    << "\n\t\tPopulation size = "
    << aiinpkbezdekga_inParam.getSizePopulation()
    << "\n\t\tMatingPool size = "
    << aiinpkbezdekga_inParam.getSizeMatingPool()
    << "\n\t\tGenerations = "
    << aiinpkbezdekga_inParam.getNumMaxGenerations()
    << "\n\t\ttrandom-seed = "
    << aiinpkbezdekga_inParam.getRandomSeed()
    << "\n\t)"
    << std::endl;
}
#endif /*__VERBOSE_YES*/

const uintidx  luintidx_numClusterK =
    (uintidx) aiinpkbezdekga_inParam.getNumClusterK();
const uintidx  luintidx_numIntances =
    uintidx(std::distance(aiiterator_instfirst,aiiterator_instlast));

/*CONVERT INSTANCES TO FORMAT MATRIX
*/
mat::MatrixRow<T_FEATURE>&& lmatrixt_y =
    data::toMatrixRow
    (aiiterator_instfirst,
     aiiterator_instlast
    );

std::uniform_int_distribution<T_CLUSTERIDX> uniformdis_mmctxOK
    (0,aiinpkbezdekga_inParam.getNumClusterK()-1);

gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>
    lochrombitcrispmatrix_best(luintidx_numClusterK,luintidx_numIntances);

/*STL container for storing the chromosome population
*/
std::vector<gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* >
    lvectorchrombitcrispmatrix_population;

/*Vector for matingpool
*/
std::vector<gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* >
    lvectorchrombitcrispmatrix_matingPool;

/*Vector for temporary storage when applying generic operators
*/
std::vector<gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* >
    lvectorchromfixleng_childR;

if ( aiinpkbezdekga_inParam.getSizePopulation()
    <= aiinpkbezdekga_inParam.getSizeMatingPool() )
    throw std::invalid_argument
        ("gaclustering_fkcrispmatrix: "
         "size population should be greater than size matingpool"
        );

```

```

runtime::ListRuntimeFunction<COMMON_IDOMAIN>
    llfh_listFuntionHist
    (aiinpkbezdekga_inParam.getNumMaxGenerations(),
     "Iterations",
     "Clustering metrics"
    );

/*Declaration of variables: computing statistical
and metric of the algorithm
*/
#ifdef __WITHOUT_PLOT_STAT
    std::ofstream          lfileout_plotStatObjectiveFunc;
    runtime::RuntimeFunctionValue<T_REAL> *lofh_J1 = NULL;
    runtime::RuntimeFunctionValue<T_INSTANCES_CLUSTER_K>
        *lofh_misclassified = NULL; /*function extra*/
    runtime::RuntimeFunctionStat<T_REAL>
        *lofhs_statObjectiveFunc[STATISTICAL_ALL_MEASURES];
    std::vector<T_REAL>      lvectorT_statfuncObjectiveFunc;

    if ( aiinpkbezdekga_inParam.getWithPlotStatObjectiveFunc() ) {

        lvectorT_statfuncObjectiveFunc.reserve
            ( aiinpkbezdekga_inParam.getSizePopulation());
        //Variable to monitor in the execution of the program
        lofh_J1 = new runtime::RuntimeFunctionValue<T_REAL>
            ("J1",
             aiinpkbezdekga_inParam.getAlgorithmName(),
             RUNTIMEFUNCTION_NOT_STORAGE
            );

        llfh_listFuntionHist.addFuntion(lofh_J1);

        if ( aiinpkbezdekga_inParam.getClassInstanceColumn() ) {
            lofh_misclassified =
                new runtime::RuntimeFunctionValue<T_INSTANCES_CLUSTER_K>
                    ("Misclassified",
                     aiinpkbezdekga_inParam.getAlgorithmName(),
                     RUNTIMEFUNCTION_NOT_STORAGE
                    );
            llfh_listFuntionHist.addFuntion(lofh_misclassified);
        }

        //Statistics of variable J1 in runtime
        for (int li_i = 0; li_i < STATISTICAL_ALL_MEASURES; li_i++) {
            lofhs_statObjectiveFunc[li_i] =
                new runtime::RuntimeFunctionStat
                    <T_REAL>
                    ( (char) li_i,
                     aiinpkbezdekga_inParam.getAlgorithmName(),
                     RUNTIMEFUNCTION_NOT_STORAGE
                    );
            llfh_listFuntionHist.addFuntion(lofhs_statObjectiveFunc[li_i]);
        }

        //OPEN FILE STORE FUNCTION
        aoop_outParamGAC.setFileNameOutPlotStatObjectiveFunc
            (aiinpkbezdekga_inParam.getFileNamePlotStatObjectiveFunc(),
             aiinpkbezdekga_inParam.getTimesRunAlgorithm()
            );
    }

```

```

    );

    lfileout_plotStatObjectiveFunc.open
    (aop_outParamGAC.getFileNameOutPlotStatObjectiveFunc().c_str(),
     std::ios::out | std::ios::app
    );

    lfileout_plotStatObjectiveFunc.precision(COMMON_COUT_PRECISION);

    //Header function
    lfileout_plotStatObjectiveFunc
    << llfh_listFuntionHist.getHeaderFuntions()
    << "\n";
}
#endif /*__WITHOUT_PLOT_STAT*/

runtime::ExecutionTime let_executionTime = runtime::start();

/*Create space for store population
*/
lvectorchrombitcrispmatrix_population.reserve
(aiinpkebezdekga_inParam.getSizePopulation() + 1);
for (uintidx lui_i = 0;
     lui_i < aiinpkebezdekga_inParam.getSizePopulation();
     lui_i++)
{
    lvectorchrombitcrispmatrix_population.push_back
    (new gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>
     (luuintidx_numClusterK,luuintidx_numIntances)
    );
}

/*Space for store matingpool
*/
lvectorchrombitcrispmatrix_matingPool.reserve
(aiinpkebezdekga_inParam.getSizeMatingPool());

/*Space for chromosomes R
*/
lvectorchromfixleng_childR.reserve
(aiinpkebezdekga_inParam.getSizeMatingPool() + 1 );

/*Initialization of population

```

Initial population of size P , consisting of U matrices is pseudo randomly generated such that each has one at least one 1 in every row ($\sum_{j=1}^n U_{ij} \geq 1 \forall i$) and each column sums to 1, i.e. $\sum_{i=1}^c U_{ij} = 1, \forall j$.

The partly random initialization is obtained as follows. For each cluster center v_i , we choose the k^{th} element of the cluster center to be the k^{th} feature of a randomly chosen pattern to be clustered. This is done for each of the s elements of a cluster center. The process is repeated for each cluster center. An initial U matrix is then generated from the cluster centers. For a GA, population P (the population size) U matrices are generated in this manner.

```

*/
{ /*BEGIN INITIALIZE POPULATION*/

```

```

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "POPULATION INITIALIZATION";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": IN(" << geiinparam_verbose << ')'
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    mat::MatrixRow<T_FEATURE>
        lmatrixt_v
        ( luintidx_numClusterK,
          data::Instance<T_FEATURE>::getNumDimensions()
        );

    for ( auto lchrombitcrispmatrix_iter: lvectorchrombitcrispmatrix_population) {

        clusteringop::randomInitialize
            (lmatrixt_v,
             aiiterator_instfirst,
             aiiterator_instlast
            );

        clusteringop::getPartition
            (*lchrombitcrispmatrix_iter,
             lmatrixt_y,
             lmatrixt_v,
             aifunc2p_dist
            );

        T_REAL lT_j1 =
            um::j1
            (*lchrombitcrispmatrix_iter,
             lmatrixt_v,
             aiiterator_instfirst,
             aiiterator_instlast,
             aifunc2p_dist
            );

        lchrombitcrispmatrix_iter->setObjectiveFunc(lT_j1);

    }

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ')'
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

```

```

    } /*END INITIALIZE POPULATION*/
/*Population sort by  $J_1$ 
    The  $U$  matrices are sorted by  $J_1$  value. and the  $R$  with the lowest  $J_1$ ,
    values are choses to reproduce.
*/
    { /*BEGIN POPULATION SORT BY  $J_1$ */

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "SORT POPULATION";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << " : IN(" << geiinparam_verbose << ')'
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    std::sort
        (lvectorchrombitcrispmatrix_population.begin(),
        lvectorchrombitcrispmatrix_population.end(),
        [](const gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* x,
        const gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* y
        )
        { return x->getObjectiveFunc() < y->getObjectiveFunc(); }
        );

#ifdef __VERBOSE_YES

    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {

        for ( auto lchrombitcrispmatrix_iter: lvectorchrombitcrispmatrix_population) {

            lchrombitcrispmatrix_iter->print
                (std::cout,
                geverbosepc_labelstep,
                ', ',
                ', ',
                );
            std::cout << '\n';
        }
    }
    --geiinparam_verbose;

    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << " : OUT(" << geiinparam_verbose << ')'
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

```

```

} /*END POPULATION SORT BY J_1*/

while( true ) {

    /*BEGIN PRESERVING THE CHROMOSOME BEST
    */

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "ELITISM PRESERVING THE BEST";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": IN(" << geiinparam_verbose << ') '
            << std::endl;
    }
#endif /*__VERBOSE_YES*/

    if ( lvectorchrombitcrispmatrix_population[0]->getObjectiveFunc()
        < lochrombitcrispmatrix_best.getObjectiveFunc() ) {
        lochrombitcrispmatrix_best =
            *lvectorchrombitcrispmatrix_population[0];
        /*A better chromosome is found in this iteration
        */
        aoop_outParamGAC.setIterationGetsBest
            (llfh_listFuntionHist.getDomainUpperBound());
        aoop_outParamGAC.setRunTimeGetsBest
            (runtime::elapsedTime(let_executionTime));
    }

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ') '
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END PRESERVING THE CHROMOSOME BEST*/

    /*COMPUTING STATISTICAL OF THE ALGORITHM
    */
#ifdef __WITHOUT_PLOT_STAT

    if ( aiinpkbezdekga_inParam.getWithPlotStatObjectiveFunc() ) {

        for ( auto lchrombitcrispmatrix_iter:
            lvectorchrombitcrispmatrix_population ) {
            lvectorT_statfuncObjectiveFunc.push_back
                (lchrombitcrispmatrix_iter->getObjectiveFunc());
        }

        lofh_J1->setValue
            (lvectorchrombitcrispmatrix_population[0]->getObjectiveFunc());
    }

```



```

if ( lofh_misclassified != NULL ) {

    partition::PartitionCrispMatrix
    <T_BITSIZE,T_CLUSTERIDX>
    lpartitionCrispMatrix_classifierU
    (*lvectorchrombitcrispmatrix_population[0]);

    sm::ConfusionMatchingMatrix<T_INSTANCES_CLUSTER_K>&&
    lmatchmatrix_confusion =
    sm::getConfusionMatrix
    (aiiterator_instfirst,
    aiiterator_instlast,
    lpartitionCrispMatrix_classifierU,
    [] (const data::Instance<T_FEATURE>* ainst_iter )
    -> T_INSTANCES_CLUSTER_K
    {
        return T_INSTANCES_CLUSTER_K(1);
    },
    [] (const data::Instance<T_FEATURE>* ainst_iter )
    -> T_CLUSTERIDX
    {
        data::InstanceClass
        <T_FEATURE,
        T_INSTANCES_CLUSTER_K,
        T_CLUSTERIDX>
        *linstclass_iter =
        (data::InstanceClass
        <T_FEATURE,
        T_INSTANCES_CLUSTER_K,
        T_CLUSTERIDX>*)
        ainst_iter;

        return linstclass_iter->getClassIdx();

    }
    );
    lofh_misclassified->setValue
    (lmatchmatrix_confusion.getMisclassified());
}
functionhiststat_evaluateAll
(lofhs_statObjectiveFunc,
lvectorT_statfuncObjectiveFunc
);
lfileout_plotStatObjectiveFunc << llfh_listFuntionHist;
lvectorT_statfuncObjectiveFunc.clear();
}
#endif /*__WITHOUT_PLOT_STAT*/

#ifdef __VERBOSE_YES

/*ID PROC
*/
++geverboseui_idproc;

++geiinparam_verbose;
if ( geiinparam_verbose <= geiinparam_verboseMax ) {

```

```

        std::cout
            << "END ITERATION: "
            << llfh_listFuntionHist.getDomainUpperBound()
            << "\tobjetivoFunc = "
            << lochrombitcrispmatrix_best.getObjetivoFunc()
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    /*Termination criterion attained?
    */
    if ( (llfh_listFuntionHist.getDomainUpperBound()
        >= aiinpkbezdekga_inParam.getNumMaxGenerations()) ||
        (runtime::elapsedTime(let_executionTime) >
        aiinpkbezdekga_inParam.getMaxExecutiontime())
        )
        break;

    /*Selection
    R matrices with the lowest J_1, values are choses to reproduce.
    */

    /*Selection
    R matrices with the lowest J_1, values are choses to reproduce.
    */

    { /*BEGIN SELECTION
    */
        auto ichrom_population = lvectorchrombitcrispmatrix_population.begin();

        for (uintidx lui_i = 0;
            lui_i < aiinpkbezdekga_inParam.getSizeMatingPool();
            lui_i++) {
            lvectorchrombitcrispmatrix_matingPool.push_back
                (*ichrom_population);
            ++ichrom_population;
        }

        } /*END SELECTION*/

    /*Crossover operator

    The crossover point and number of columns in the two  $U$  matrices chosen
    for reproduction are randomly chosen. The columns of the matrices are
    combined to create the children matrices.

    */

    { /*BEGIN CROSSOVER OPERATORS*/

    #ifdef __VERBOSE_YES
        geverbosepc_labelstep = "CROSSOVER OPERATORS";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ')'
                << std::endl;
        }
    }

```

```

    }
#endif /*__VERBOSE_YES*/

    for (uintidx lui_i = 0;
        lui_i < aiinpkbezdekga_inParam.getSizeMatingPool();
        lui_i++) {
        lvectorchromfixleng_childR.push_back
            (new gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>
                (luiintidx_numClusterK,luintidx_numIntances)
            );
    }

    gaiterator::crossoverRandSelect
    (lvectorchrombitcrispmatrix_matingPool.begin(),
    lvectorchrombitcrispmatrix_matingPool.end(),
    lvectorchromfixleng_childR.begin(),
    lvectorchromfixleng_childR.end(),
    [&](gaencode::ChromosomeCrispMatrix
        <T_BITSIZE,T_CLUSTERIDX,T_REAL>* aichrom_parent1,
        gaencode::ChromosomeCrispMatrix
        <T_BITSIZE,T_CLUSTERIDX,T_REAL>* aichrom_parent2,
        gaencode::ChromosomeCrispMatrix
        <T_BITSIZE,T_CLUSTERIDX,T_REAL>* aochrom_child1,
        gaencode::ChromosomeCrispMatrix
        <T_BITSIZE,T_CLUSTERIDX,T_REAL>* aochrom_child2
    )
    {

        gabinaryop::onePointDistCrossover
        (*aochrom_child1,
        *aochrom_child2,
        *aichrom_parent1,
        *aichrom_parent2
        );

        aochrom_child1->setObjectiveFunc(std::numeric_limits<T_REAL>::max());
        aochrom_child2->setObjectiveFunc(std::numeric_limits<T_REAL>::max());

    }
    );

    lvectorchrombitcrispmatrix_matingPool.clear();

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << " : OUT(" << geiinparam_verbose << ' )'
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    }/*END CROSSOVER OPERATORS*/

    /*Mutation consists of randomly choosing an element of a column to have
    the value 1, such that it is a different element than the one currently

```

having a value of 1.

```

*/
    { /*BEGIN MUTATION OPERATOR*/
#ifdef __VERBOSE_YES
        geverbosepc_labelstep = "MUTATION OPERATOR";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ') '
                << std::endl;
        }
#endif /*__VERBOSE_YES*/

        for ( auto ichrom_childR: lvectorchromfixleng_childR ) {
            gabinaryop::bitMutation(*ichrom_childR);
        }

#ifdef __VERBOSE_YES
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": OUT(" << geiinparam_verbose << ') '
                << std::endl;
        }
        --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*END MUTATION OPERATOR*/

    { /*BEGIN EVALUATE J1 FOR CHILDR*/
#ifdef __VERBOSE_YES
        geverbosepc_labelstep = "EVALUATE J1 FOR CHILDR";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ') '
                << std::endl;
        }
#endif /*__VERBOSE_YES*/

        mat::MatrixRow<T_FEATURE>
            lmatrixt_v
            (luintidx_numClusterK,
             data::Instance<T_FEATURE>::getNumDimensions()
            );

        mat::MatrixRow<T_FEATURE_SUM>
            lmatrixT_sumWX
            (lmatrixt_v.getNumRows(),
             lmatrixt_v.getNumColumns()
            );
        std::vector<T_INSTANCES_CLUSTER_K>
            lvectorT_sumWik(lmatrixt_v.getNumRows());

        for ( auto ichrom_childR: lvectorchromfixleng_childR ) {

            /*Calculate the centroid associated with U_i

```

```

        */
        clusteringop::getCentroids
        (lmatrixt_v,
         lmatrixT_sumWX,
         lvectorT_sumWik,
         *ichrom_childR,
         lmatrixt_y
        );

        T_REAL lT_j1 =
        um::j1
        (*ichrom_childR,
         lmatrixt_v,
         aiiterator_instfirst,
         aiiterator_instlast,
         aifunc2p_dist
        );

        ichrom_childR->setObjectiveFunc(lT_j1);

    }

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ' '
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    } /*EVALUATE J1 FOR CHILDR*/

    /*The R chuild U matrices are added to the population
    with the P-R U matrices with the greatest J1 values
    dropped from the population.
    */
    { /*BEGIN ADD P-R U MATRICES TO POPULATION*/
#ifdef __VERBOSE_YES
        geverbosepc_labelstep = "ADD P-R U MATRICES TO POPULATION";
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << geverbosepc_labelstep
                << ": IN(" << geiinparam_verbose << ' '
                << std::endl;
        }
#endif /*__VERBOSE_YES*/

        std::sort
        (lvectorchromfixleng_childR.begin(),
         lvectorchromfixleng_childR.end(),
         [](const gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* x,
            const gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* y
            )
        { return x->getObjectiveFunc() < y->getObjectiveFunc(); }
        );
    }

```

```

std::vector<gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>* >
    lvectorchrombitcrispmatrix_tmpL;

lvectorchrombitcrispmatrix_tmpL.swap(lvectorchrombitcrispmatrix_population);

/*Insert a sentinel to merge the two vectors
*/
lvectorchrombitcrispmatrix_tmpL.push_back
    (new gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>());
lvectorchromfixleng_childR.push_back
    (new gaencode::ChromosomeCrispMatrix<T_BITSIZE,T_CLUSTERIDX,T_REAL>());

lvectorchrombitcrispmatrix_population.reserve
    (aiinpkbezdekga_inParam.getSizePopulation() + 1);

uintidx luintidx_l = 0;
uintidx luintidx_r = 0;

for (uintidx lui_i = 0;
     lui_i < aiinpkbezdekga_inParam.getSizePopulation();
     lui_i++)
{
    if ( lvectorchrombitcrispmatrix_tmpL[luintidx_l]->getObjectiveFunc() <
        lvectorchromfixleng_childR[luintidx_r]->getObjectiveFunc() )
    {

#ifdef __VERBOSE_YES
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << " lvectorchrombitcrispmatrix_population[" << lui_i << " ]'
                << " <-- lvectorchrombitcrispmatrix_tmpL[" << luintidx_l << " ]'
                << '[' << & lvectorchrombitcrispmatrix_population[luintidx_l] << " ]'
                << " Fitness: "
                << lvectorchrombitcrispmatrix_tmpL[luintidx_l]->getObjectiveFunc()
                << '\n';
        }
        --geiinparam_verbose;
#endif //__VERBOSE_YES

        lvectorchrombitcrispmatrix_population.push_back
            (lvectorchrombitcrispmatrix_tmpL[luintidx_l]);
        lvectorchrombitcrispmatrix_tmpL[luintidx_l] = NULL;
        ++luintidx_l;

    }
    else {

#ifdef __VERBOSE_YES
        ++geiinparam_verbose;
        if ( geiinparam_verbose <= geiinparam_verboseMax ) {
            std::cout
                << " lvectorchrombitcrispmatrix_population[" << lui_i << " ]'
                << " <-- lvectorchromfixleng_childR[" << luintidx_r << " ]'
                << "[" << & lvectorchrombitcrispmatrix_population[luintidx_r] << " ]'
                << " Fitness: "

```

```

        << lvectorchromfixleng_childR[luintidx_r]->getObjectiveFunc()
        << '\n';
    }
    --geiinparam_verbose;
#endif //__VERBOSE_YES

    lvectorchrombitcrispmatrix_population.push_back
        (lvectorchromfixleng_childR[luintidx_r]);
    lvectorchromfixleng_childR[luintidx_r] = NULL;
    ++luintidx_r;

}

}

for (uintidx lui_i = 0;
    lui_i < lvectorchromfixleng_childR.size();
    ++lui_i) {
    if ( lvectorchromfixleng_childR[lui_i] != NULL )
        delete lvectorchromfixleng_childR[lui_i];
}
lvectorchromfixleng_childR.clear();

for (uintidx lui_i = 0;
    lui_i < lvectorchrombitcrispmatrix_tmpL.size();
    ++lui_i) {
    if ( lvectorchrombitcrispmatrix_tmpL[lui_i] != NULL )
        delete lvectorchrombitcrispmatrix_tmpL[lui_i];
}
lvectorchrombitcrispmatrix_tmpL.clear();

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ') '
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/
} /*END ADD P-R U MATRICES TO POPULATION*/

/*The reproduction and survival of fittest process
continues for some set number of generations
*/

llfh_listFuntionHist.increaseDomainUpperBound();

} /*while*/

/*FREE MEMORY*/
{/*BEGIN FREE MEMORY OF POPULATION*/

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = "DELETEPOPULATION";
    ++geiinparam_verbose;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout

```

```

        << geverbosepc_labelstep
        << ": IN(" << geiinparam_verbose << ')'
        << std::endl;
    }
#endif /*__VERBOSE_YES*/

    for (uintidx lui_i = 0;
        lui_i < lvectorchrombitcrispmatrix_population.size();
        ++lui_i) {
        delete lvectorchrombitcrispmatrix_population[lui_i];
    }

#ifdef __VERBOSE_YES
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << geverbosepc_labelstep
            << ": OUT(" << geiinparam_verbose << ')'
            << std::endl;
    }
    --geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    }/*END FREE MEMORY OF POPULATION*/

    runtime::stop(let_executionTime);
    aoop_outParamGAC.setNumClusterK
        (aiinpkbezdekga_inParam.getNumClusterK());
    aoop_outParamGAC.setMetricFuncRun
        (lochrombitcrispmatrix_best.getObjectiveFunc());
    aoop_outParamGAC.setAlgorithmRunTime
        (runtime::getTime(let_executionTime));

    aoop_outParamGAC.setFitness
        (lochrombitcrispmatrix_best.getObjectiveFunc());
    aoop_outParamGAC.setNumTotalGenerations
        (llfh_listFuntionHist.getDomainUpperBound());

    /*FREE: COMPUTING STATISTICAL AND METRIC OF THE ALGORITHM
    */
#ifdef __WITHOUT_PLOT_STAT

    if ( aiinpkbezdekga_inParam.getWithPlotStatObjectiveFunc() ) {
        plot_funtionHist
            (llfh_listFuntionHist,
            aiinpkbezdekga_inParam,
            aoop_outParamGAC
            );
    }

#endif /*__WITHOUT_PLOT_STAT*/

#ifdef __VERBOSE_YES
    geverbosepc_labelstep = lpc_labelAlgGA;
    if ( geiinparam_verbose <= geiinparam_verboseMax ) {
        std::cout
            << lpc_labelAlgGA

```



```

    << " OUT(" << geiinparam_verbose << ")\n";
    std::setprecision(COMMON_COUT_PRECISION);

    mat::MatrixRow<T_FEATURE>
        lmatrixt_vBestChrom
        ( luintidx_numClusterK,
          data::Instance<T_FEATURE>::getNumDimensions()
        );

    mat::MatrixRow<T_FEATURE_SUM>
        lmatrixT_sumWX
        (lmatrixt_vBestChrom.getNumRows(),
         lmatrixt_vBestChrom.getNumColumns()
        );

    std::vector<T_INSTANCES_CLUSTER_K>
        lvectorT_sumWik(lmatrixt_vBestChrom.getNumRows());

    clusteringop::getCentroids
        (lmatrixt_vBestChrom,
         lmatrixT_sumWX,
         lvectorT_sumWik,
         lochrombitcrispmatrix_best,
         lmatrixt_y
        );

    lochrombitcrispmatrix_best.print
        (std::cout,
         geverbosepc_labelstep,
         ', ',
         ', ',
         ');

    std::cout << '\n';
    um::j1
        (lochrombitcrispmatrix_best,
         lmatrixt_vBestChrom,
         aiiterator_instfirst,
         aiiterator_instlast,
         aifunc2p_dist
        );

    std::cout << std::endl;

    std::setprecision(COMMON_VERBOSE_COUT_PRECISION);

}
--geiinparam_verbose;
#endif /*__VERBOSE_YES*/

    return lochrombitcrispmatrix_best;

} /*END gaclustering_fkcrispmatrix */

} /*END namespace alg*/

#endif /*__GACLUSTERING_FKCRISPMATRIX_HPP__*/

```


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