# Master 1 Bioinformatique

# Object-oriented programming

## Hierarchical clustering

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Version 1.4

## 1 Objective

This project's goal is to classify a set of students according to their grades, and to generate the corresponding dendrogram.

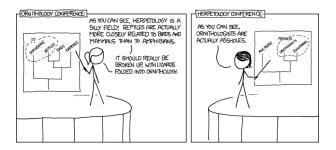


Figure 1: xkcd 867 (http://xkcd.com/867/)

## 2 Representing a class of students

### 2.1 Class Student: methods overload

**Step 1** Create a class **Student** that represents the set of students. Each student has an (assumed) unique identifier (a string) and a grade (a double).

**Step 2** Add a first constructor having for parameters an identifier and a grade. Then add a second constructor having an identifier as single parameter. This is an excellent opportunity to use method overload...

Step 3 Add the methods getIdent(), getGrade() et setGrade(double newGrade).

**Step 4** In the main(...) method, create the following instances and check that the methods from step 3 still work correctly:

```
Student riri = new Student("riri", 12.5);

Student fifi = new Student("fifi", 14.0);

Student loulou = new Student("loulou", 18.5);

Student geo = new Student("geo", 19.5);

Student donald = new Student("donald", 10.5);
```

#### 2.2 Class Promo: inheritance and static methods

Step 5 Create a class Promo that represents a set of students. Promo is a sub-class of java.util.ArrayList<sup>1</sup>. Make sure to read the documentation for ArrayList, you will need it soon. Please note that ArrayList is a generic class, whereas all the elements of a Promo instance are composed of instances of Student, so you will need to state that Promo is a subclass of ArrayList<Student>.

Step 6 In the Promo's main(...) method, create an instance m1bioinfo of Promo, and add the members riri, fifi, geo, donald and loulou (respect this order so that the highest and lowest grades are in the middle of the list. The idea here is to avoid having the students almost sorted for the clustering).

Step 7 Add the methods getMinGrade(), getMaxGrade() et getAverageGrade() to the class Promo. The class java.lang.Math<sup>2</sup> has several useful methods. For iterating over all the students that compose a promotion, you can seek inspiration from the article "Traversing collections"<sup>3</sup>. Feel glad to have declared Promo as a subclass of ArrayList.

**Step 8** In the main(...) method of Promo, add the code for printing the lowest grade, the highest and the average for m1bioinfo.

Step 9 The PromoLoader class (FIXME: fournie sur l'ENT) has a method loadTsvFile(...) that takes as argument a text file (one student per line; its identifier, a tabulation, its grade) for creating an instance of Promo. Why is the method loadTsvFile(...) declared as "static"? Draw the parallel with the methods min(...), max(...) and abs(...) from java.lang.Math.

## 3 Hierarchical clustering

## 3.1 Principle

#### 3.1.1 Agglomerative vs. divisive approaches

Classifying consists in organizing a set of elements in groups based on the elements' similarities or differences.

 $<sup>^{1} \</sup>verb|http://docs.oracle.com/javase/7/docs/api/java/util/ArrayList.html|$ 

<sup>2</sup>http://docs.oracle.com/javase/7/docs/api/java/lang/Math.html

 $<sup>^3</sup>$ http://docs.oracle.com/javase/tutorial/collections/interfaces/collection.html

**Hierarchical clustering** consists in organizing the sets of elements into subsets included in to each others in a tree-like structure. There are two main approaches for determining this organization:

- the **agglomerative approach** (also called ascending) starts by creating one (atomic) cluster for each element, and then iteratively generates new clusters composed of the most similar two, until there only remains one cluster;
- the divisive approach (also called descending) starts by gathering all the elements into a single cluster, and then iteratively decompose the clusters into subclusters until each of them is only composed of a single element.

The divisive approach requires more operations than the agglomerative one and is therefore longer... except when we only need the most general clusters (e.g. to separate a sample into two groups).

#### 3.1.2 Distance measures between elements and between clusters

For both the agglomerative and ther divisive approaches, clustering depends on two main parameters:

- a distance measure between elements (also simply called *distance*). There are several classical ones: euclidian distance, Manhattan distance... In our case, we will consider that the distance between two students is the absolute value of the difference of their grades;
- a distance measure between clusters (also called *linkage*) that relies on the *distance* between elements of the two clusters. There are several classical linkage measures: the average of the distances between all the combinations of elements, their maximum, their minimum... In our case, we will consider that the distance between two clusters of students is the average of the distances between all the elements of the first cluster and all the elements of the second cluster.

#### 3.2 Classe ClusterOfStudents

This section aims at implementing the ClusterOfStudents class for representing a cluster of Student instances. A simple cluster is composed of a single instance of Student. A complex cluster is composed of several sub-clusters which can themselves be either simple or complex clusters. A complex cluster has a tree-like structure where all the leaves are simple clusters.

Initially, a complex cluster is only composed of simple clusters (Fig. 2). After clustering, a complex cluster is composed of sub-clusters that are intermediate complex clusters (Fig. 3)

#### 3.2.1 Initialization

Step 10 Create a ClusterOfStudents with a subclusters attribute that represents the list of its sub-clusters. For simplifying the clustering step (when marshalling the students composing the cluster), add an attribute students that represents the set of students constituting the leaves of the cluster.



Figure 2: Complex cluster in its initial state: it is composed of five simple sub-clusters, each composed of a student.

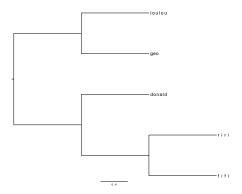


Figure 3: Complex cluster after clustering. It is composed of two intermediate complex sub-clusters. The firt is itself composed of two simple clusters (geo and loulou). The second is composed of a smple sub-cluster (donald) and a complex sub-cluster composed of two simple sub-clusters (riri and fifi).

## **Step 11** Add the following constructors:

- a default constructor ClusterOfStudents() that creates an empty cluster (we do not reaaly need it, but I find it cleaner to have a default constructor);
- a constructor for simple clusters ClusterOfStudents (Student aStudent);
- a constructor for complex clusters before clustering ClusterOfStudents(Promo aPromo).

Step 12 In ClusterOfStudents' main(...) main method, create an instance of a simple cluster geoCluster initialized with geo, and an instance of complex cluster bioCluster initialized with m1bioinfo.

#### 3.2.2 Visualization

The Newick format<sup>4</sup> provides a straightforward representation of trees and dendrograms, and is supported by most visualization tools. You can use the Tree Viewer web server<sup>5</sup> or T-REX<sup>6</sup> or the dedicated softwares FigTree<sup>7</sup>, dendroscope<sup>8</sup> (free use in an academic context; getting a licence is not required for the basic functions). FigTree seems to give the best results.

The dendrogram from Fig. 2 can be represented by ((loulou,geo),(donald,(riri,fifi)));.

NB: for visualizing dendrograms, we could as well have used the R functions via the Java–R binding, but it is more complicated, and writing Newick files makes for an interesting exercice anyway.

Step 13 Add a getNewick() method to the class ClusterOfStudents that returns a string representing the dendrogram in the Newick format. Because of the final semicolon, you may need to introduce an intermediate function (aptly named getNewickIntermediate()). For marshalling the tree, you will make your life easier by considering a recursive approach (but this is not mandatory). Should these methods' visibility be public, protected or private?

Step 14 Generate a Newick representation of bioCluster and check (for example with T-REX or dendroscope) whether you get something similar to Fig. 2.

## 3.2.3 Clustering

Step 15 Ajoutez une méthode linkage (ClusterOfStudents anotherCluster) qui renvoie la distance entre deux clusters. Le plus simple est sans doute de choisir la moyenne des différences des notes entre toutes les combinaisons d'étudiants du cluster courant et de anotherCluster.

Step 16 Dans le main(...) de ClusterOfStudents, créez les clusters simples loulouCluster et donaldCluster et vérifiez que les distances entre geoCluster, loulouCluster et donaldCluster correspondent à ce que vous attendez (pensez à vérifier les six combinaisons).

Step 17 Dans le main(...) de ClusterOfStudents, créez le cluster complexe geoLoulouCluster et vérifiez que sa distance avec donaldCluster correspond à ce que vous attendez. Vérifiez également la distance entre donaldCluster et geoLoulouCluster.

Step 18 Ajoutez la méthode clusterizeAgglomerative(). Clusterisez bigCluster et affichez le résultat au format Newick.

La figure 4 montre le résultat de la classification pour un ensemble d'étudiants. Observez que puisque toutes les branches ont une longueur constante, on a l'impression de distinguer deux clusters principaux. La figure 5 montre qu'en rendant la longueur des branches proportionnelle à la distance séparant les deux clusters que l'on fusionne, ce sont en fait trois clusters principaux qui apparaissent (voir section 4.1).

<sup>&</sup>lt;sup>4</sup>http://evolution.genetics.washington.edu/phylip/newicktree.html

<sup>&</sup>lt;sup>5</sup>http://www.proweb.org/treeviewer/

<sup>6</sup>http://www.trex.uqam.ca/

<sup>7</sup>http://tree.bio.ed.ac.uk/software/figtree/

<sup>8</sup>http://ab.inf.uni-tuebingen.de/software/dendroscope/

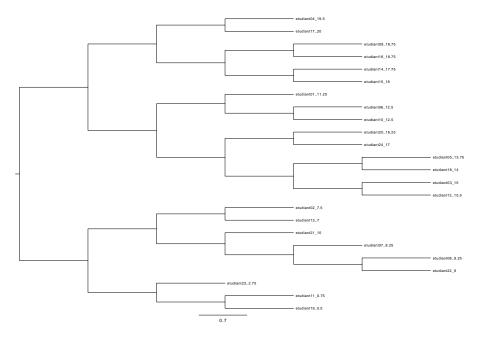


Figure 4: Cluster complexe après clustering.

## 4 Extensions facultatives

## 4.1 Amélioration du dendrogramme

Le format Newick permet d'indiquer la longueur de chacun des branches. Utilisez plutôt l'application FigTree<sup>9</sup> ou le site de Tree Viewer<sup>10</sup> pour la visualisation, les autres outils semblent avoir des problèmes.

Step 19 Améliorez la méthode getNewick() pour que toutes les feuilles soient au même niveau.

Step 20 Améliorez la méthode getNewick() pour que toutes les feuilles soient au même niveau et que la longueur des branche soit proportionnelle à l'écart des notes.

## 4.2 Approche divisive

Step 21 Ajoutez une méthode clusterizeDivisive() à la classe ClusterOfStudents. Clusterisez bigCluster et comparez avec l'approche ascendante.

## 4.3 Modélisation de ClusterOfStudents

Dans la classe ClusterOfStudents, chaque instance d'étudiant apparaît deux fois :

<sup>9</sup>http://tree.bio.ed.ac.uk/software/figtree/

 $<sup>^{10} \</sup>mathtt{http://www.proweb.org/treeviewer/}$ 



Figure 5: Cluster complexe après clustering. La longueur des branches est proportionnelle à la distance séparant les deux clusters fusionnés.

- dans l'attribut subClusters puisque le dendrogramme a autant de sousclusters feuilles que d'étudiants ;
- dans l'attribut students qui permet un parcours plus simple de la liste des étudiants d'un cluster en évitant de devoir parcourir récursivement tout le dendrogramme à chaque fois.

On pourrait penser que cela occupe donc deux fois plus de place en mémoire que nécessaire, même si dans notre cas ce surcoût est acceptable dans la mesure où chaque instance occupe peu de place mémoire et qu'il y a relativement peu d'étudiants. Néanmoins, Java ne duplique évidemment pas les instances de Student dans les deux attributs. Chaque attribut ne contient en fait que les adresses des instances de Student (on appelle ça un passage d'objet par référence). Ainsi, si vous modifiez la note d'un étudiant dans students, cette modification apparaîtra également dans subClusters, et inversement.

Au final, le fait d'utiliser deux attributs qui semblent redondants parce qu'ils contiennent les mêmes objets :

- a l'avantage principal d'améliorer le temps de traitement en évitant un parcours de l'arborescence du dendrogramme chaque fois que l'on souhaite parcourir les étudiants (et cela arrive souvent durant l'étape de clustering);
- a l'avantage secondaire de simplifier l'écriture de la classe en vous dispensant justement d'écrire la fonction de parcours de l'arborescence du

## ${\it dendrogramme}~;$

• a l'inconvénient d'augmenter légèrement la consommation de la mémoire.

Step 22 Écrivez une classe ClusterOfStudentsBis qui ne contient que l'attribut subClusters. Comparez les temps de clusterisation de ClusterOfStudents et de ClusterOfStudentsBis.