Community discovery in Milan

project for the course of Distributed Enabling Platforms

Michele Carignani, Alessandro Lenzi

July 16, 2014

Contents

Abstract

The aim of the project is to analyze and then visualize telecommunication data in order to discover real-world communities basing on the strength of connection between different geographical areas. We implemented a pipeline of map reduce job with the Hadoop distributed computation environment[1]. In 1 and 2 of this report, we describe the original dataset and analyze its properties. Then in 4 we explain how we rearranged the data in order to reduce the noise and improve the tractability and robustness of the community discovery phase. Sections 5, 6 will then briefly describe two different approaches for community discovery (finding strongly connected components and markovian clustering) and in detail describe strategy and implementation of the latter which has proved to give more significant results. Finally 7 will collect results and conclusion of the developed project.

1 Dataset

The dataset on which the analysis has been developed is an aggregated log of mobile phone calls and short text messages with their geographical source and destination points.

The dataset is composed of several files, each one containing information of one specific day within the observation period of two months (november and december 2013).

In each file, a row describes the connection strength between two geographical areas in the area surrounding Milan (Italy) during a time period of 10 minutes within the day.

The concept of connection strength between two areas is not formally defined: it is a decimal value proportional to the number of calls and sms sent from one area to another one.

Geographic areas are identified by a logical a grid of 10.000 squared areas (with area $10.000m^2$) identified by an integer number $i \in [0, 9999]$ where the $i/100$ and $i\%100$ are respectively the x and y coordinates of the node.

Therefore the format of each line is:

```
timestamp \t sourceNode \t  destNode \t strength
```

where timestamp is the time in milliseconds describing the first millisecond of the period described. To sum up, the dataset describes a number of directed weighted graphs over the nodes of the geopgraphical grid, one for each 10-minutes long interval in the 2 months observation period. The total size of the dataset is around 345GB.

2 Data distributions analysis

In order to understand the possibility of finding such communities, we run some analysis on the weights of the arcs. This analysis has been done over weights of arcs, neglecting temporarely their probabilisitc nature but considering them just as common random variables. We consider this analysis as executed on a stochastic process with discrete times and discrete values in [0,1].

[1]http://hadoop.apache.org/

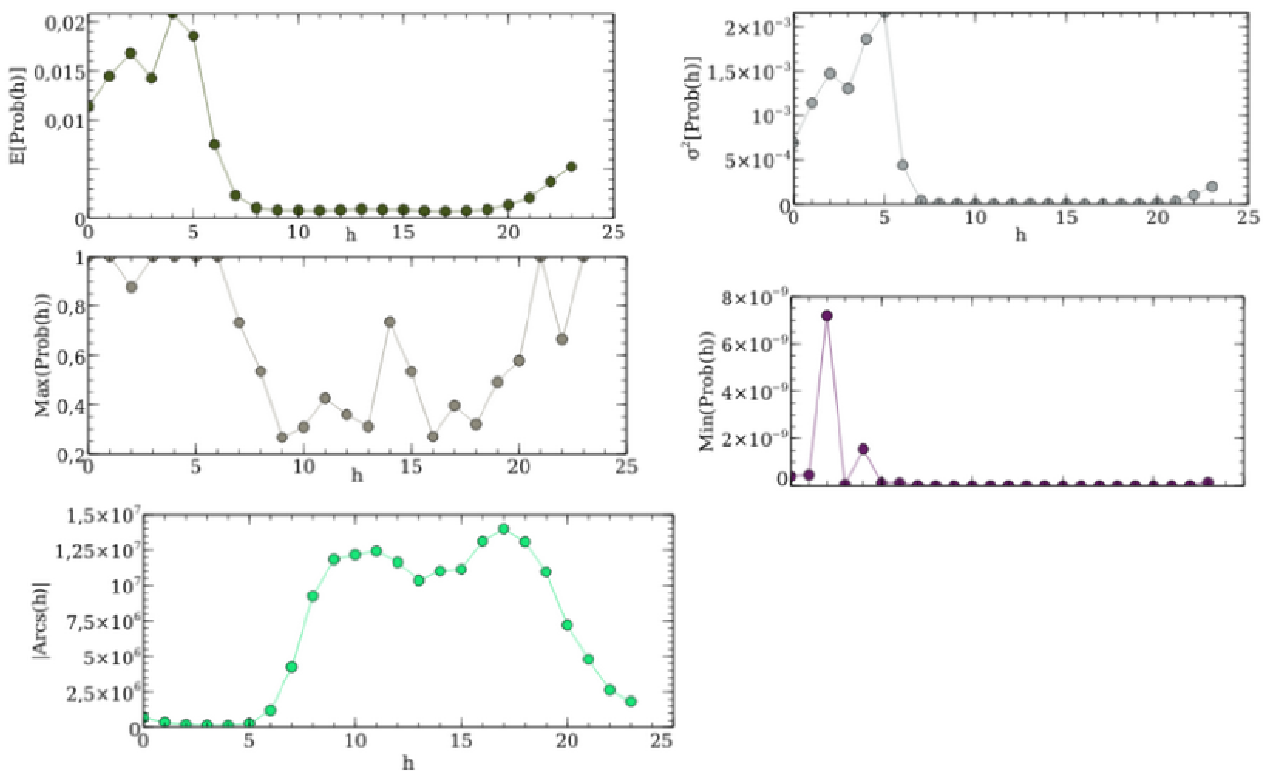


Figure 1: Plots on the probabilities detected in the graph. Subfigures are numberd from (a) to (e) going from left to right and from top to bottom.

In 1 some statistics on the process have been done. Please notice that the analysis has been done over a certain day of the dataset (to be precise, the 15th of november), thus is not comprehensive and is only meant to give an indication of the behaviour of the system.

In (a) we show the empirical mean for every hour of the day taken into consideration. It is possible to notice that, during night hours, the average probability experiences a spike, probably indicating that the number of outgoing arcs in these hours is lower than usual. This hypothesis is confirmed by the plot in (e), in which the total number of non-null arcs for a graph over an hour is shown. Part (b), instead, shows the behaviour of the variance on the probability of the arcs in different hours. While during working hours the variance is very low (with several outgoing arcs converging towards the average), it grows in non-working hours. In (c) and in (d) we show, instead, the maximum and minimum probability values of the arcs for any hour graphs. Particularly interesting is (c), in which it is possible to notice that, in the hours with high traffic, some spikes in traffic exist, while the minima always remain in the order of $10^{-}9$

3 Model

In our model, we started by considering what is a community. In our personal interpretation of this word, we defined a community as a set of individuals with close relationship, meaning high probability to interact or to have someone in common with whom they interact.

Since we're dealing with calls, the idea is that a community can be identified by the frequency of calls between members belonging to the same community.

The idea behind this approach is that, since we're searching for a community, we don't care about their size (i.e. the probability for an individual to be in a certain "community"), but only the probability that two geographical areas (and thus, in our model, their inhabitants) can be correlated by their calls.

The assumptions that we made are:

- People are related to some zones more strongly, meaning that an individual has an higher probability of staying in certain zones (for example, near his work place or near his home) than in random places in the area taken into consideration. This allows to relate calls from certain geographical zones to some people.
- People call more often other people belonging to their community.
- Is not of major interest who is colling whom, since we only care about the existance of a "binding" between the two individuals.
- A person may belong to several communities, however depending on the day and on the time of the call, the probability of communicating with a certain community changes. As an example, during work hours it is more probable that calls will be addressed to people related to the working activity, while outside it will involve more probably family and friends. [2]

This automatically leads to a model in terms of probability of calls outgoing from a certain zone, thus, assuming N_u as the total population considered, we assumed the strength $S_{i,j}$ connecting zone i and zone j in our dataset to be

$$S_{i,j} = P\{call(i,j)\}P\{a\ caller\ is\ in\ i\}N_u$$

As it is possible to see, using the strengths as an indicator "as they are", even though the N_u factor will have no influence, zones with an higher population or with an higher concentration of calls could obfuscate the behaviour of less populated zones, justifying why the probability approach has been followed.

The probability of one call between grid i and grid j can be thus extimated as

$$P_{i,j} = P\{call(i,j\} = \frac{S_{i,j}}{\sum_j S_{i,j}}$$

We can think of the initial dataset as composed of several graphs, one for each 10 minutes slots, in which the strengths $S_{i,j}$ are seen as weights of the arcs connecting

[2]Similarly, Telco operators have been known to distinguish between business traffic and residential traffic

two zones $S_{i,j}$. However notice that using a single 10 minutes graph is not particularly significative, as noise could change significantly the results.

So, to get more realistic results and to deal with the very high level of noise in the dataset, we decided to gather and average the strength of interaction between couples of nodes in several 10-minutes periods considering a semantically meaningful aggregation in time (not alway contiguous, e.g. we aggregated all monday mornings periods), in which we assumed that the behaviour of commmunities would be more or less the same. We called these aggregations *average probability graphs*, in which nodes are cells in the grid of our dataset, arcs represent interaction and their weight the average probability that such an interaction is established

To be more formal, let E be the set of arcs of the initial dataset and $E_{id} \subseteq E$ be the set of arcs belonging to aggregation id composed of k, then the weight $w_{id}(e) = \widehat{P_{i,j}}$ of an arc $e = (i, j)$ of the average graph for aggregation period id will be

$$w_{id}(e) = \frac{\sum_{e' \in E_{id}} w(e')}{k}$$

4 Data aggregation

The aim of this part of the project was to produce aggregated probability graphs as defined in 3 .
We developed a procedure composed by two consecutive logical map reduce computations executable within the Hadoop environment. The input of the *Time Aggregation* phase is the raw dataset, while the output is a graph of probabilities of interaction between zones of the considered area over a certain period of interest.

4.1 Average graph calculation

This logical phase aims to calculate several *average graphs* for a given period of interest. We define an average graph as the graph in which the weight of every arc is the average of the detected strength in input. When no strength is detected in a given 10 minute period, the strength connecting the two areas is considered to be zero. This phase is composed of a map-reduce job, whose pseudo code can be seen in 2 and 3 respectively. The mapper filters only the interesting entries in the dataset, and labels them with an appropriate identifier for the aggregation. The output key is composed by the a triple `AggregationId,SourceId,DestId` while the key is the stength.
In the reducer, we calculate the sum of all such values and then divide it by the number of ten minutes slots in the aggregation.

4.1.1 Implementation details

During the initial executions, our testing environment could not successfully compute aggregations over huge periods, because of **lack of free disk space**.
The problem was due to the fact that, in the first map, even though the filter would reduce in general the size of the input data, this reduction was not enough to fit disks on certain nodes of the cluster before going on with the conseguent reduce phase.
With a worst case calculation, in fact, an input split containing all nodes in a graph

```
FilterMap(key, value):
// input takes in input all dataset files
// implementeted in aggregated_graphs.FilterMapper.java
  d = parse(value)
  for(interesting_period in all_periods)
  if (d.timestamp belongs_to interesting_period)
   k = (interesting_period,d.sourceNode,d.destNode)
   v = d.value
    emit(k, v)
    return;
```

Figure 2: Filter Map pseudo-code

```
AverageReduce(key,values):
// implemented in aggregated_graphs.AverageReducer.java
  sum = count = 0
  for v in values:
   sum += v
   count++
  (id,num,source,dest) = parse(key)
  avg = sum / num
  emit((id,source),(dest,value))
```

Figure 3: Average Reduce pseudo-code

would produce a graph containing 100000000 of arcs, each one with a weight which could be approximated to 24 Bytes, thus achieving approximately an output of 2GB.
To cope with this issue, we went through a number of different approaches, to finally discover that a *"classic"* splitting technique, along with the benefits provided by the combiner, would result in the best solution for our environment.

1. **Combiners** a combiner has been defined to shrink the first map output size. The combiner performs a sum over all strengths in the same aggregation period and, of course, with same source and destination. The output of the combiner is a graph for each aggregation period in which the strength is the sum of all strength. This solution, for an aggregation with containing n 10 minutes slots, could reduce the output of each map task up to $1/n$ of the original size without the combiner. The pseudo-code of the combiner used is depicted below:

   ```
   FilterCombine(key, value):
   sum = 0;
   for v in value
   sum += v
   context.write(key, sum)
   ```

2. **GZip** another approach that we tried, and thereafter discarded, was to use GZip as compression codec for data going out of the map. From experimental results, we noticed that this approach, altough not providing enough benefits to cope with disk utilization issues, slowed down our computation significantly.

3. **Change in split size** thanks to the combiner, the biggest is the number of time slots gathered in a single aggregation, the biggest is the shrinking in data. Therefore, we tried to increase the size of the splits to be given to a single map task to exploit this reduction. We progressively increased split size from 128MB to 1GB and then to contain a single whole file, which was defined as not splittable. However, we noticed that this method, while decreasing the efficiency in the cluster utilization (as only fewer processing units could be used together) and in the completion time of this phase, was still not enough to cope with our disk issues.

4. **Divide and conquer** the latest, and best approach to solve the disk space issue, was to change the logic in the driver so that what was previously the first map-reduce phase, has been decomposed into several little map-reduce phases, each one taking a parametric number of files of the dataset. This partitioning method, in which a partition is processed in parallel and the next partition can be processed only when the previous aggregated graphs have been written on HDFS, can be indeed seen as a generalization of the previous case, but allowing to compute what we called *average graphs* even in a space constrained environment. Sadly, the introduction of this "partitioning" has some drawbacks, since it will make necessary to introduce a sorting phase in the probability reducer, necessary to eliminate duplicates.

5. **Other attempts** we also went through several other ways, among which the decommissioning of the nodes (node 0, node 1 and node 2) with less space, trying to

Partition size	**Execution time**
1 File	2h 20’ 45”
5 Files	1h 11’ 38”
9 Files	1h 06’ 2”

Figure 4: Execution times for generating the average probability graphs with different partition sizes over (about) 56GB of data in 9 files. 10 reducers have been used.

```
IdentityMap(key, value):
  emit(key, value)
```

Figure 5: Identity Map pseudo code

avoid to fill the disk completely. However, this solution (even impreved using the hadoop balancer) was very slow and, as obvious, led to a severe cluster underutilization that we didn’t consider acceptable.

We finally adopted a solution in which the split size was left to 128MB as in the default case, only a partition of files is processed in parallel and a combiner is used in the first phase to reduce both disk and network bandwidth utilization. Counterintuitively, the sequentialization performed with this approach, with an appropriate partition size allowing to exploit fully the parallelism degree of the environment, when operating with huge datasets led to benefits also in terms of completion time. With smaller inputs, however, there’s a degradation in terms of completion time (as shown in 4), even though it is not drammatic.
Our hypothesis is that, after a certain (cluster-dependant) threshold in the size of data is met, the I/O and network bottleneck do not allow to grow in speed, while the huge number of tasks contending the resources would result in a severe slowdown.

4.2 Probability graph calculation

The probability graph calculation follows immediately the phase of average graph calculation.
In this phase we calculate a probability graph in which an arc represents the probability of transition between the two nodes that it connects. This is an average probability in our specific case, since it is achieved receiving as input an average graph. Also this phase is composed of a map-reduce job, whose pseudo code is shown in 5 and 6.

The map is a mere identity, while the reduce calculates the total weight of the arcs belonging to the forward star of a single node, to then rescale in terms of probabilities every arc.

4.3 Driver

The driver takes the following input parameters:

1. **Aggregation file**, the file containing the descriptions of the aggregations to be performed

```
ProbabilityReduce(key, values):
  sum = 0
  a_list = []
  for v in values:
    (dest, weight) = parse(v)
    sum += weight
   a_list.append((dest,weight))
  for a in a_list:
    emit((key.src, a.dest), a.weight / sum)
```

Figure 6: Probability Reduce pseudo code

2. **Input directory**, the directory containing the files with the daily calls measurements
3. **Output directory**, the directory in which the average probability graph will be written
4. **Partition size** in terms of files per partition. The default is 1. To take the whole dataset must be 0.
5. **Number of reducers**, by default corresponds to the number of aggregations to perform.

The driver reads the aggregation file, and then saves the aggregation representation in the context, in order for it to be accessible to map and reduce tasks in the first phase.
Then there's an iteration in the files placed inside the input directory, adding files one by one until the size of the partition is met. Then a single job is executed, calculating the average graph for the given partition before a new partition is calculated and a new average graph calculation starts.
Finally, when average graphs have been calculated for each partition, the second part takes all these files in input and proceeds to write in the output directory the average probability graph. A sketch depicting the driver logic in a dataflow fashion can be found in 7; the code is available at the following address

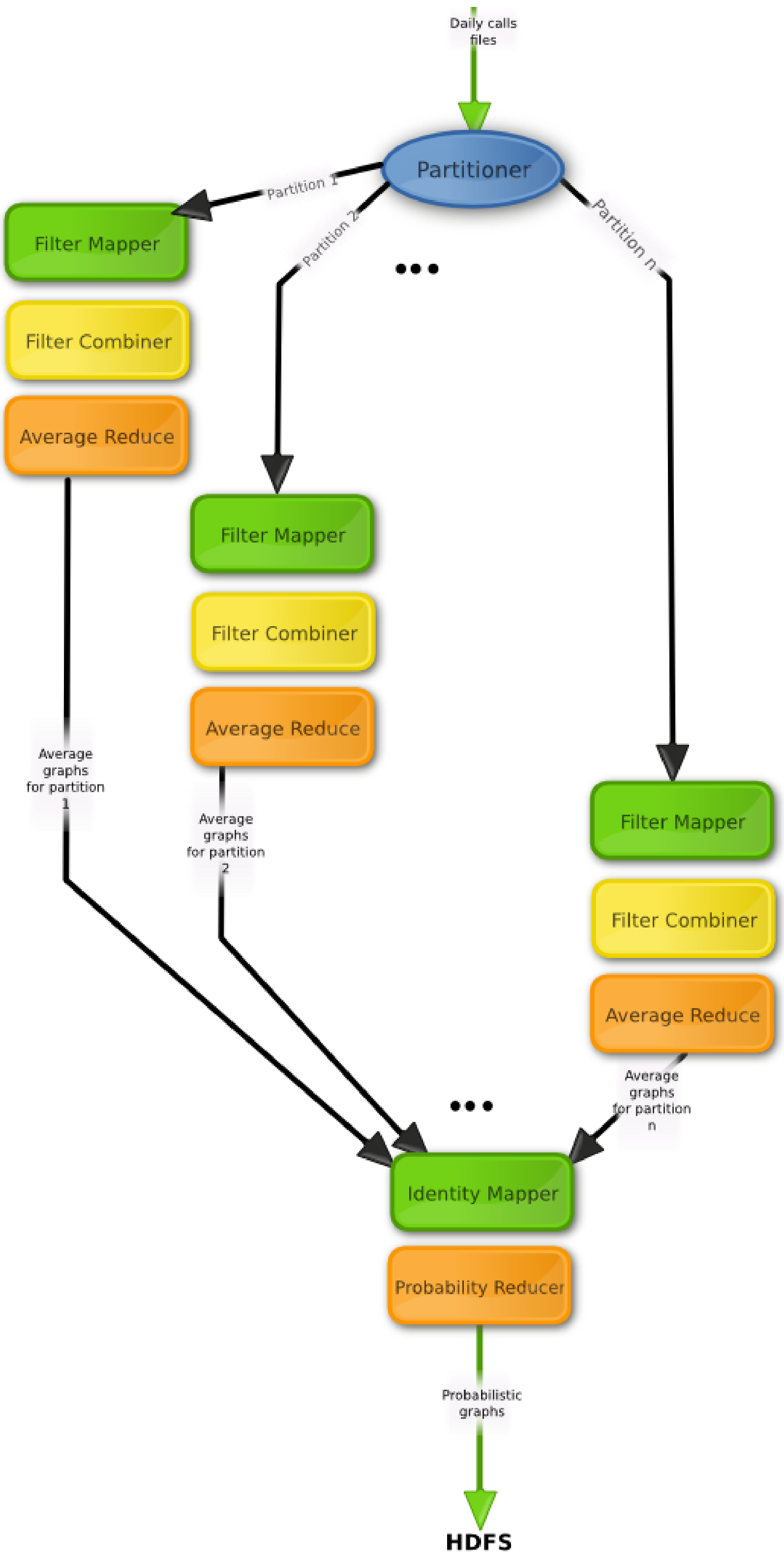


Figure 7: TimeAggregatedGraphs.java logic

5 Communities discovery approaches

Once the aggregated graph is produced (as list of weighted edges) is time to compute the communities (i.e. the clusters) over it.

Two different approaches were developed and tested. As we will see, the second will give the expected results, while the first will fail.

5.1 Tarjan Connected Components algorithm

Defining the communities as connected components onto the graph[3], the first idea was to apply Tarjan's algorithm for connected components, whose pseudo code is in 8.

In our initial approach, a mere visit, ordered on the arc identifier (i.e. `for i = 0 to 10000 do strongconnect(i)`) was performed. This visit, though executed with different cuts over the probability of the arcs, evidenced a strong bias of the order of visit on the found strongly connected components. As an example, with a cut on probability 0.005, a huge SCC is found, containing almost all nodes. Only few nodes remain outside this CFC, and some small aggregations can be found between them. So our second step has been achieving a visiting strategy consistent with the effective traffic measured during the day. To do so, we used the measurements of the total activity of grids in order to establish a visiting order to be followed during the procedure. We performed the following attempts and different visits on our graph:

1. Nodes visited for increasing outgoing hourly traffic, with arcs selected with increasing probability.
2. Nodes visited for decreasing outgoing hourly traffic, with arcs ordered with increasing probability.
3. Nodes visited for decreasing outgoing hourly traffic, with arcs ordered with decreasing probability.
4. Nodes visited for increasing outgoing hourly traffic, with arcs ordered with decreasing probability.

The image 9 shows the found strongly connected components in the most trafficated hours of the analysis. As it is possible to notice by looking to 1, in fact, during these hours arcs values are very concentrated near the mean, and thus most of them will be cutted out, making most of the strongly connected components to disappear in the most trafficated hours of the day. The results are slightly better in less trafficated hours as shown in 10, in which the variance is higher and thus a wider number of arcs will "save himself" from the performed cutting. In other attempts, we tried to modify the threshold so that it would save more arcs for the computation, but we have not been able to find an appropriate threshold leading to a large enough number of clusters and with an acceptable size.
In fact, in most cases, a too low threshold led to few huge connected components whilst too high led to few and very small connected components.

[3]A connected component in a graph $A = (N, E)$ is a subset of nodes $A' \in A$ s.t. each node in A' is connected to all the other nodes in A'

```
input: graph G = (V, E)
output: set of strongly connected components (sets of vertices)
index := 0
S := empty
for each v in V do
if (v.index is undefined) then
strongconnect(v)

function strongconnect(v)
v.index := index
v.lowlink := index
index := index + 1
S.push(v)
for each (v, w) in E do
if (w.index is undefined) then
strongconnect(w)
v.lowlink := min(v.lowlink, w.lowlink)
else if (w is in S) then
v.lowlink := min(v.lowlink, w.index)
if (v.lowlink = v.index) then
start a new strongly connected component
do
w := S.pop()
add w to current strongly connected component
until (w = v)
output the current strongly connected component
end function
```

Figure 8: Tarjan Strongly Connected Components algorithm

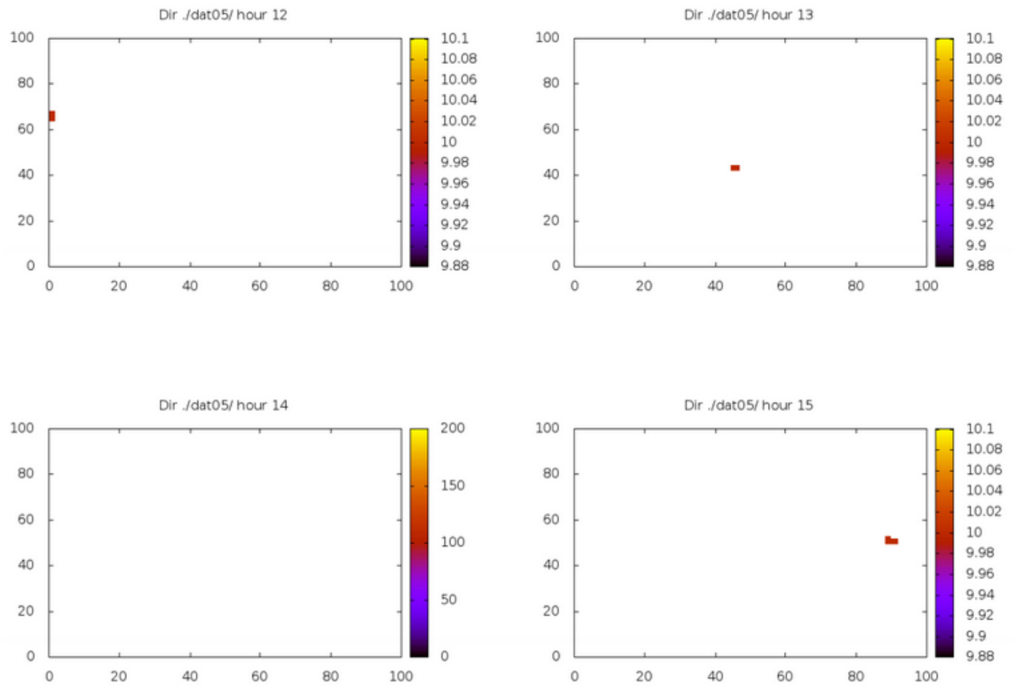


Figure 9: Strongly connected components found with Tarjan Algorithm.From left to right, top to bottom the hours considered are 12, 13, 14, 15. The visit has been performed with increasing hourly traffic and arcs selected with increasing probability. The cut has been performed at value 0.05.

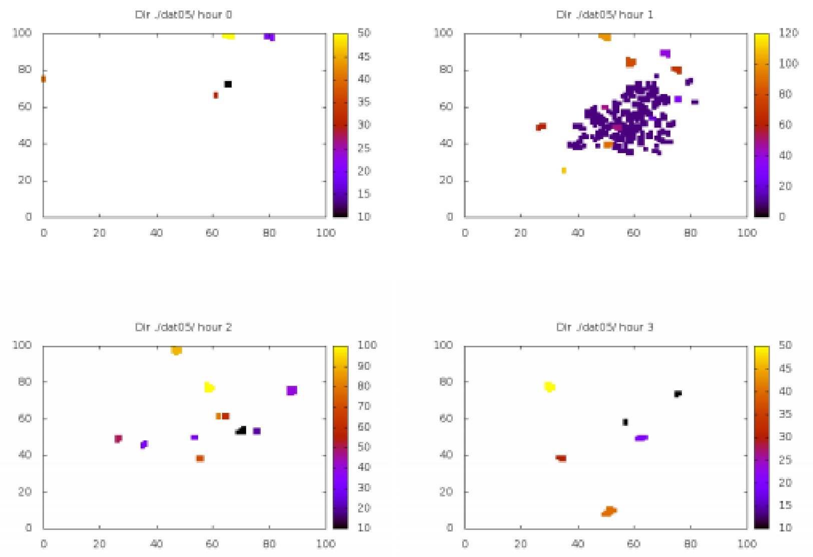


Figure 10: Stronglu connected components found with Tarjan Algorithms. From left to right, top to bottom the hours considered are 0, 1, 2 and 3. The visits have been performed with increasing hourly traffic and arcs selected with increasing probability. Cut performed at value 0.05

The approach described above, in our opinion, could not lead to the desired results because of two reasons:

- First, the visiting order, though more meaningful, was still establishing a bias in the search of the components because of the "paths" eliminated by the original Tarjan algorithm
- and second, the "static" threshold did not adapt well to changing traffic along the days.

To overcome this issues, we decided to implement a small variation of the Tarjan SCC algorithm, in which visited nodes not becoming part of a strongly connected component could be visited again while searching for others, thus increasing the complexity of the algorithm but with the advantage of reducing the visit ordering bias.
The other modification that we implemented was that of percentile-based cuts. In this approach, for every hour, the probability distribution has been calculated and only arc probabilities in a certain percentile have been held, while the others have been cutted as it was done before with a "static" threshold. This allows for a more fine-grained cutting, allowing to keep more arcs also in more trafficated hours of the day.

In 11 this modified algorithm has been tried with a cut on the 99-th precentile. In the plot for the SCC found in this case, it is possible to see that most of them are geographically localized (as we expected), but still their size is very small.
However, only few components were able to "survive" across several hours, and are mostly localized in the outskirts of the city.
Other attempts have been made to find suitable strongly connected components, but also small modification in percentiles led either to very noise results (with almost all zones in the same component) or to empty results. From this approach, we understood that

1. Very high cuts are needed, because of the high connectivity degree of the graph
2. The statistics of arcs probabilities, however, seem to indicate the existance of zones calling themselves significantly more frequently than others.
3. Visiting strategy has a very strong bias, and probably never considering twice the same arc could lead to eliminate some interesting strongly connected components
4. The number of components is almost always lower than the expected one, however they are uniformly spreaded along the space taken into consideration
5. In different hours, the components vary in their positions, possibly indicating different users behaviours in different hours
6. Specially during hours in which we expected less traffic, components tend to move towards the outskirts, possibly denoting clusters belonging to small towns near Milan
7. The found components are not stable during consecutive hours but they appear and disappear. In the beginning we thought this was due to the "static" cut, but the reproposition of this behaviour with the percentile denotes that the reason must be either a very noisy dataset or high variation in the users behaviours during the day.

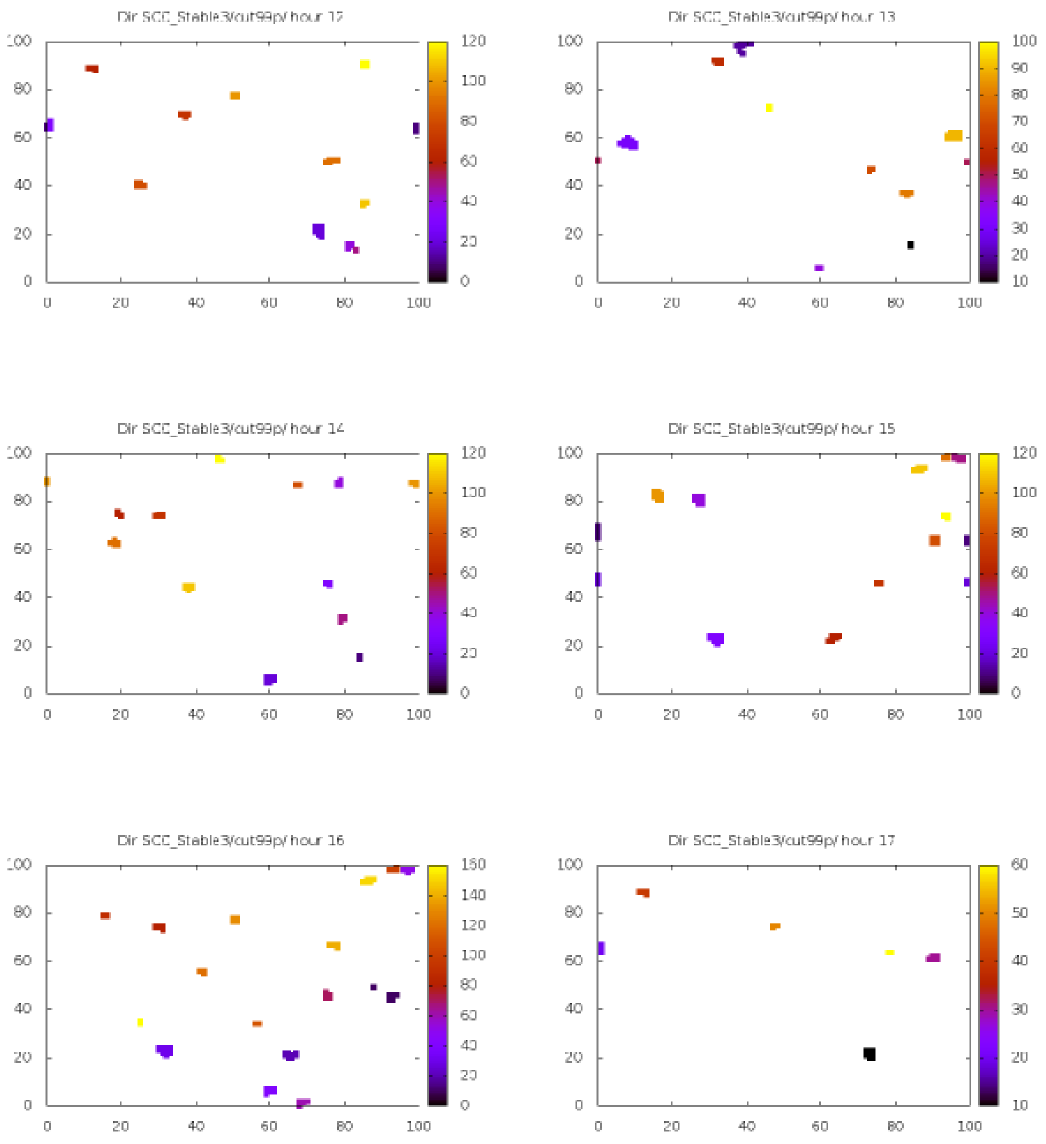


Figure 11: Strongly connected components found cutting at the 99-th percentile. Hours depicted are, from left to right and from top to bottom, 12-17.

Figure 12: Markov Clustering pseudocode

As previously said in Chapter 2, all of this research led us to the conclusion that the best approach was to find a sort of "average behaviour" to analyse and to move to a different approach, in which communities are seen as clusters. To do so, we chose the *Markov Clustering* algorithm, which is known in litterature for the purpose of finding communities in graphs.

For a more complete dissertation on what we did using this approach for discovering communities, we invite you to refer to the attacched file `CfcSuGrafiOrari.pdf`, in Italian.

5.2 Markov Clustering

We then looked at a diffferent approach: Markov Clustering based on the Markov Clustering Algorithm by Stijn van Dongen[4].

The idea was to reduce noise and emphasize relations in a more structured way by multiplying the adjancy matrix of the graph by itself until the number of non-null elements in each row is very low (reduce the number of edges) and with values probability weight close to 1 (taking the most probable connections).

Therefore, the pseudocode of the algorith is:

6 Looking for communities with Markov Clustering

In the next sections we explain in details the implementation of the different phases of MCL.

6.1 Convergency loop

This loop is repeated a number of times, until the convergence is reached or the maximum number of loops is executed. The convergency loop is composed of 3 phases:

1. Matrix Multiplication, in which the current stochastic matrix is multiplied by itself
2. Matrix Inflation, an operation used to fasten convergency and whose aim and implementation will be explained in the following
3. Matrix Convergence Checker, used to compare achieved values with the previous ones.

Given the matrix A of step i, matrix A' output of step $i+1$ has reached the convergency if the following holds:

$$\forall i, j. |A_{i,j} - A'_{i,j}| < \epsilon$$

where ϵ is a parameter of the computation. In order to minimize occupied space, to fasten convergency and to avoid pathological cases to lead to "false convergency" (i.e. if the

[4] `http://micans.org/mcl/`

```
OneStepRowMap(key, value):
    for k = 1 to N:
        emit((value.row, k), ('A', value.column, value.probability))
OneStepColumnMap(key, value)
    for k = 1 to N:
        emit((k, value.column), ('B', value.row, value.probability))
```

Figure 13: RowMap and ColumnMap used in the One-Step matrix multiplication algorithm. N is the size of the matrix, which is assumed to be square.

Markov Chain represented by the matrix is characterized by periodicity), we decided to avoid matrix power method and to make the convergency loop proced as the Fibonacci series, meaning that at step i the matrix calculated in the loop will be $A^{fib(i)}$. In the following, we will explain in detail the various phases in this convergency loop.

6.2 Matrix multiplication

The first phase of the loop is **Matrix Multiplication**. For this part, we followed different approaches for the implementation as map-reduce computations. While the first two approaches revealed themselves to be very effective when dealing with dummy data using for the tests, when real data was fetched both showed significant drawbacks that induced us to search for a third solution, that is the one actually implemented in the delivered project.

Several implementations needed to be developed and tested in order to achieve feasibility (onto the given environment) and improve performances.

6.2.1 One step map-reduce

In the beginning, we started by thinking that a simple approach could be producing all couples to be multiplied of the two matrices with an appropriate index.[5] In this case, we have two different Map functions for two different files. To implement this in Map-Reduce, we exploited the MultipleInputs function provided by the framework indicating for the two matrices a different mapper able to emit different values. The "first" matrix is fetched to the `OneStepRowMap` of fig. **??** while the second to the `ColumnMap` of the same figure. In the pseudocode, there's no consideration for cases in which the value is 0, since the matrix is already memorized neglecting null values. The output of both mappers is fetched to `OneStepReduce` of fig. 14.

As it is possible to understand very easily, with actual data this kind of implementation could not work, since for every matrix element $N = 10^4$ elements are emitted. Elements are themselves 10^8, making the total number of couples emitted by the mapper 10^12.

Approximating the couple (key, value) with the size of its biggest component- the double precision floating point probability values taking 128 bits on 64 word machines -

[5]This algorithm has been readapted and implemented starting from this website: http://importantfish.com/one-step-matrix-multiplication-with-hadoop/

```
OneStepReduce(key, values):
    A[N] = {j: a_ij for (x, j, a_ij) in values if x == A}
    B[N] = {j: b_jk for (x, j, b_jk) in values if x == B}
    result = 0
    for j = 1 to N:
        result += hash_A[j] * hash_B[j]
    emit(key, result)
```

Figure 14: OneStepReduce used in the One-Step matrix multiplication algorithm. The key represents a single element in the matrix

we would have needed a total memory of 128TB, which is much larger than our enviroment total memory space, making impossible to carry on the computation for dense matrices.

This implementation produced on our test environment a runtime expection because of the memory being empty.

In fact, the Mappers writes their output in files but before this is put onto memory and, since for every matrix element the mapper emits $N = 10^4$ elements, and the elements are themselves 10^8 the total number of couples (key, value) written in memory by the mappers to then be written on HDSF to be passed to the reducer was 10^{12}.

Approximating the couple (key, value) with the size of its biggest component- the double precision floating point probability values taking 128 bits on 64 word machines - we would have needed a total memory of 128TB, which would be much larger than our enviroment total memory space.

6.2.2 Two step map-reduce

The second approach has been the one of decomposing the computation further, trying to avoid the explosion of data emitted caused by the algorithm discussed before. In this approach, we have two map reduce steps.[6]

In the mappers shown in fig. 15 used in the first step - again we distinguished between the two matrices using MultipleInputs - rows and columns values are emitted using their index as key. In the reducer in fig. 16the values of the row and column received are distinguished using the "A" and "B" flags. Subsequently, every row value is multiplied for every column value, and this multiplied values are emitted using as key the position of the value of the output matrix to which they will contribute.

The second map-reduce phase of this algorithm implements the identity function in the mapper, and sums up all multiplicated values for a certain value of the final matrix in the reducer shown in fig. 17

Even though this algorithm is way more optimized with respect to the previous one, since it also avoids to emit intermediate couples for possibly null values, it has reveled to be very slow in practice. This is due, in our opinion, to the need of writing intermediate data between the two steps of the job in HDFS, which slows down computation significantly.

[6]Once again, this algorithmhas been readapted and implemented following the post available at http://importantfish.com/two-step-matrix-multiplication-with-hadoop/

```
TwoStepRowMap(key, value):
    emit(value.row, ("A", value.column, value.probability))

TwoStepColumnMap(key, value):
    emit(value.column, ("B", value.row, value.probability))
```

Figure 15: Mappers used in the first phase of the two-step matrix multiplication algorithm.

```
reduce(key, values):
    list_A = {(i, a_ij) for (M, i, a_ij) in values if M == "A"}
    list_B = {(k, b_jk) for (M, k, b_jk) in values if M == "B"}
    for (i, a_ij) in list_A:
        for (k, b_jk) in list_B:
            emit((i, k), a_ij*b_jk)
```

Figure 16: Reducer used in the first phase of the two-step matrix multiplication algorithm.

```
reduce(key, values):
    result = 0
    for value in values:
        result += value
    emit(key, result)
```

Figure 17: Reducer used in the second phase of the two-step matrix multiplication algorithm, summing up al row-by-column values concurring in its calculation.

Also in this case some disk problems could arise, because once again, in the worst case, the intermediate data between the two steps is in general 1/2 of the one emitted by the mapepr in the previous case, making once again this algorithm unfeasible for the data we were dealing with. We will se how we solved this problem, by decomposing in smaller parts the input matrix, in the following part.

6.2.3 Block-wise

With this approach, to cope with the problems related to the disk, we divided the matrix into several blocks. Blocks have been enforced to have always the same size, and the approach discussed below has been used.

Let **A** and **B** be two NxN matrix, and let p be the number of row/column partitions given as input parameter, meaning that p^2 blocks will be produced for each matrix. As an example, we can decompose A as follows:

$$\mathbf{A} = \begin{bmatrix} \mathbf{A_{1,1}} & \mathbf{A_{1,2}} & ... & \mathbf{A_{1,p}} \\ \mathbf{A_{2,1}} & ... & ... & \\ ... & & & \\ \mathbf{A_{p,1}} & ... & ... & \mathbf{A_{p,p}} \end{bmatrix}$$

Now let both **A** and **B** be decomposed as explained before, we can calculate a single block $\mathbf{C_{i,j}}$ of the matrix $\mathbf{C} = \mathbf{A}x\mathbf{B}$ as follows:

$$\mathbf{C_{i,j}} = \sum_{k=1}^{p} \mathbf{A_{i,k}} \times \mathbf{B_{k,j}}$$

This approach allows, with a sufficient decomposition, to prevent any problem related to disk usage and, in the meanwhile, produced with some test matrices a way faster computation in the latest implementation. In fact, the inner multiplication - to be clear, the one between two blocks in the decomposition of the matrices given as input of this phase - has been implemented in three different way:

1. In the first case, we tried the (now promising) one-step matrix multiplication algorithm proposed above. However also in this case the output of the mapper revealed himself as huge, as also for a 1/10-th partition of the matrix (with 1000 values) this approach would produce 10^9 values, which is certainly a manageable size but still big enough to slow down the computation significantly, specially when considering the huge number of such multiplications to perform to calculate the whole **C**.

2. In the second case, to be honest merely for the sake of completeness, we tried also to plug-in as multiplication module the two-step matrix multiplication algorithm. As it could have been foreseen, also this approach - though faster than the previous one - was still not fast enough to meet our requirements.

3. The third case, which is the one used in the final project, revealed himself to be the best both in terms of space and in completion time. This algorithm merely multiplies two blocks using the good old $O(n^3)$ sequential row-by-column matrix multiplication.

As it is possible to understand, the approach that we finally decided to follow is very efficient for several resons. Consider the case in which the number of partitions is 10, thus achieving 100 blocks for each of the two multiplied matrices. The blocks will contain, in a worst case approximaton, 10^6 doubles, meaning that a block multiplication will fit in memory and thus result in better performances, since also the output of each block-by-block multiplication will have size of approximately 32MB each, considering also the indexes.

Notice that this values, on our environment, allow to multiply several blocks in parallel, leading to a very good utilization factor of the machines and nice results in terms of completion time. The detailed implementation of this part is discussed thoroughly in 6.2.4.

6.2.4 Block-wise multiplication implementation

We wanted to develop, in this part, an highly parametrized system so to finely tune our computation to make it faster, given that this is the biggest contributor to the completion time of the convergency loop, which is executed also several times. For this reason, a module, called BlockWiseMatrixMultiplication has been developed, with the aim of allowing parametrized execution.

This module, which implements the `Tool` interface of the Hadoop framework, can be executed specifying the number of blocks of the final matrix $\mathbf{C_{i,j}}$ to be executed in parallel. It takes also in input the directory containing the two input matrices splitted in blocks and the directory in which the results must be written. Partitions are calculated automatically scanning the blocks by horizontal coordinates (by row) and then by column.

For each block multiplication scheduled by this very simple partitioner, a new thread is forked, which is responsible for starting and monitoring all the jobs (running in parallel) consisting of the multiplications $\mathbf{A_{i,k}} \times \mathbf{B_{k,j}}$ needed to calculate $\mathbf{C_{i,j}}$.

In order for them to run in parallel, we used the `JobControl` class of the Hadoop framework, which allows to schedule parallel jobs (and also to define dependencies between jobs). For every output block $\mathbf{C_{i,j}}$ p multiplications of the original matrix blocks are performed as independent jobs running in parallel. These jobs consist of a single map-reduce phase, in which the mappers (as usual, one for the row and one for the column exploiting MultipleInputs) of fig. 18 take care of "joining" and labelling the two blocks to be multiplied. In the reducer, the whole blocks are gathered and saved in a matrix, which is then multiplied before the final values are written in output, as it is possible to see in fig. 19. In the reducer, a slight optimization has been achieved by memorizing the second matrix (accessed k times) by column and not by row, to avoid jumps in memory and to exploit caches and memory in the best possible way.

The second job needed to finally compute $\mathbf{C_{i,j}}$ is the one performing the sum over all partial matrices produced before, in order to achieve the real values in the computed block. This job has, in its configuration, the horizontal and vertical coordinates i and j of the output block. In its mapper of fig. 20, it aggregates by block row id and block column id the elements, so that they can be subsequently summed in the reducer as of fig. 21. This job is dependant of the previous ones, thus starts as soon as all the input data needed has been produced. The thread forked and running the JobControl containing all such "individual block" jobs running in parallel, is checked periodically by another

```
BlockRowMapper(key, value):
    emit(
      value.blockVerticalIndex,
      ('A',value.row_id,value.column_id, value.probability)
    )

BlockColumnMapper(key, value):
    emit(value.blockHorizontalIndex, ('B', value.row_id, value.column_id, value.proba
```

Figure 18: Mappers used in the block-wise matrix multiplication. The block $\mathbf{A_{i,k}}$ is managed by BlockRowMapper, while $\mathbf{B_{k,j}}$ by BlockColumnMapper. This names are given merely for consinstency wrt. previous algorithms

```
MatrixMultiplicationReducer(key, values):
    A[N/p][N/p]
    B[N/p][N/p]
    for v in values
        if v.label = 'A'
            A[v.row_id][v.col_id] = v.probability
        else
            B[v.col_id][v.row_id] = v.probability
    for i in [1, N/p]
        for j in [1, N/p]
            sum = 0
            for k in [1, N/p]
                sum += A[i][k]*B[j][k]
            if sum > 0
                emit((i,j), sum)
```

Figure 19: Reducer used in the block-wise matrix multiplication. It performs the usual row-by-column matrix multiplication algorithm. N is the size of the matrix, p is the number of splits

```
BlockSumMapper(key, value):
    emit((value.row_id, value.col_id), value.probability)
```

Figure 20: The map function used to perform the sum over all partial matrices $\mathbf{A_{i,k}} \times \mathbf{B_{k,j}}$ and thus to calculate $\mathbf{C_{i,j}}$

```
BlockSumReducer(key, values):
    blockIdX = get(block.horizontal_coordinates)
    blockIdY = get(block.vertical_coordinates)
    sum = 0
    for v in values
        sum += v
    emit((blockIdX, blockIdY, key.row_id, key._column_id), sum)
```

Figure 21: The reduce function used to calculate the sum over single values in a position of the block and which writes out the final block.

thread for completion. When this phase terminates, another set of blocks of parametric size is calculated and the related multiplications are run. This approach of not running everything in parallel has been pursued in order to avoid disk space issues and also to be able to avoid too much contention in the system. From experimental results, in fact, we were able to verify that the matrix multiplication can be made very fast by dividing initial matrices in 25 blocks and using partitions of size from 5 (corresponding thus to an entire row).

The drawback of this approach is that some others modules - for decomposing and recomposing the matrix - must be executed, as we wanted our procedure not to affect the final matrix representation.

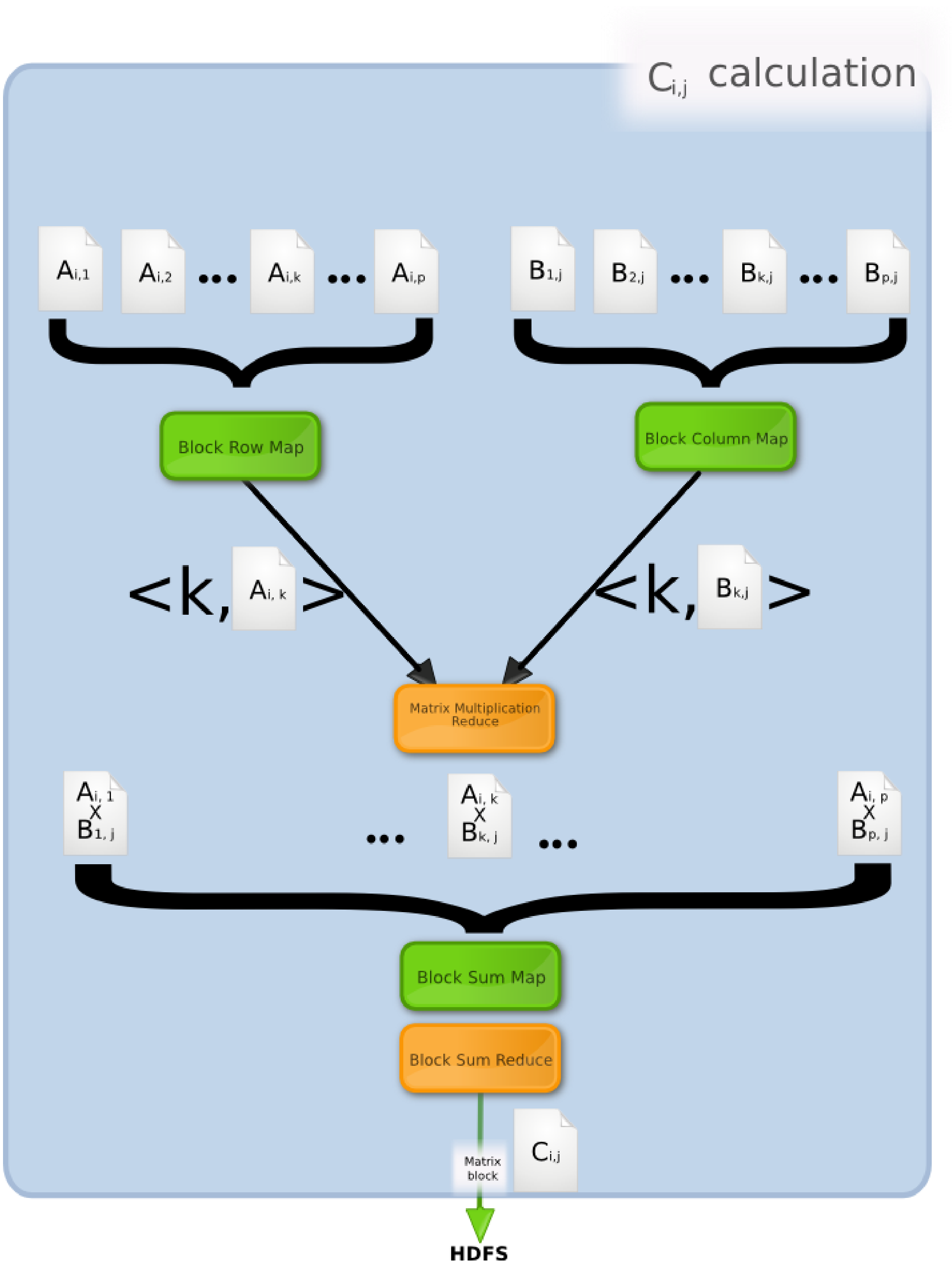
These modules implementation is discussed in 6.5 and 6.6. Finally, the behaviour of a single block multiplication is sketched in fig. 22, while the comprehensive driver of the matrix multiplication procedure that we finally adopted is illustrated in fig. 23, and its source code can be seen on

6.3 Inflation

After multiplying the matrix by the last precedently computed, we apply a strategy called inflation in order to enlarge differences between elements in a row. Using the algorithm author words: "richests get richer, poorests get poorer".

For each row, we compute the sum of all r-th powers of its elements. Then we recompute the element i,j as

$$a_{i,j} = \frac{a_{ij}^r}{\sum_{k=0..N} a_{ik}^r}$$



$C_{i,j}$ calculation
$A_{i,1}$ $A_{i,2}$ ... $A_{i,k}$ ... $A_{i,p}$
$B_{1,j}$ $B_{2,j}$ ... $B_{k,j}$ ... $B_{p,j}$
Block Row Map
Block Column Map
<k, $A_{i,k}$ >
<k, $B_{k,j}$ >
Matrix Multiplication Reduce
$A_{i,1} \times B_{1,j}$ ... $A_{i,k} \times B_{k,j}$ ... $A_{i,p} \times B_{p,j}$
Block Sum Map
Block Sum Reduce
Matrix block
$C_{i,j}$
HDFS

Figure 22: Procedure followed to calculate a single $\mathbf{C_{i,j}}$.

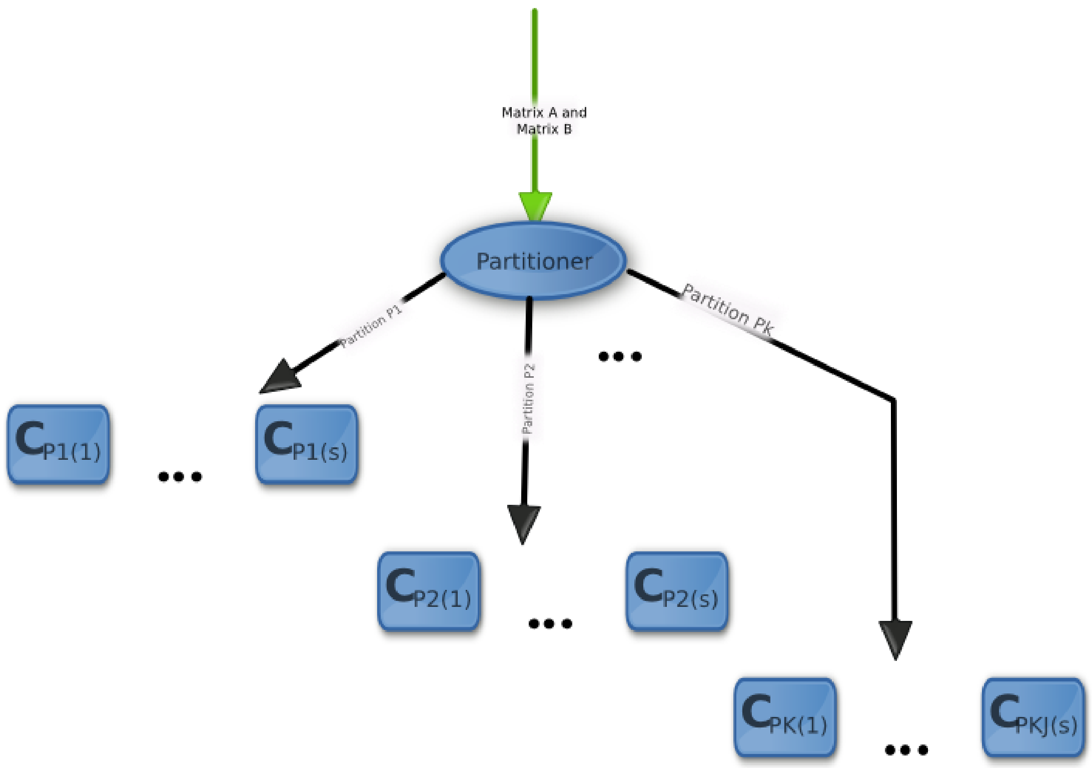


Figure 23: Whole matrix multiplication procedure in a block-wise fashion. S blocks of the matrix are calculated in parallel, while the others wait for the completion of the previous ones before going on. In the image, s is the maximum size of the partition, k is assumed as the number of partitions and Pi(n) is a function returning the index of the n-th block in partition Pi.In the image, the blue blocks titled after the matrix block they are used to compute represent the calculation shown in fig. 22

6.4 Convergency

6.5 Matrix splitter

6.6 Matrix recombiner

6.7 Driver

6.8 Finding clusters

By the definition given in the original paper, given a matrix multiplied until convergency is reached, the clusters are identified as disjoint components in the graph, that means a partition of the set of nodes such that there are no edges linking two nodes which belong two different subsets in the partition.

In the final matrix actually, values that are not 0 are 1 or tend to 1 and since this is stochastic matrix, this means that for each row only one value is different from zero.

This, in turn, means that our aim of reduce the graph density toward a linear number of edges, w.r.t the number of nodes, were actually reached.

In this scenario, it is much more probable to discover disjoint compoments of the graph, i.e clusters, i.e communities.

We implemented the last module of our application, the DisjointComponentVisit class, as a visit of the graph able of recognizing the different disjoint componets, which defines and uses three main actions:

- `new_component()` creates a new subset of nodes,
- `merge_components(c1,c2)` merges two subsets into one,
- `add_to(n,c)` add a node to a subset.

The module, cycles over all edges in the result files, looks for the components containing the head and the tail of the egde, the in case they are the same it continues. If the head and tail belong to different component, they are merged into one. If one of the two nodes does not belong to any components, it is added to the component of the other one (in case none of them are contained in any components, a new component is created and both are added to it).

We used the Java class `java.util.TreeSet` to implement the components which assures logarithmic time for the operations of adding a new element and testing if an element is contained.

Since the expected result of convergency is that all non-zero edges are one, dunring this visit edges with weight values less than 0.9 are discarded. This is due becase of the approximention done by posing a maximum number of iterations to the convergency loop.

After all components are computed, we generate three files:

- a text file called `clusters.txt` with all the components and the list of the nodes within it,
- a PNG file called `clusters.png` displaying all the edges and

- a PNG file called `patchwork.png` displaying the grid where each node is coloured with a different color depending on the cluster it is in.

7 Risultati