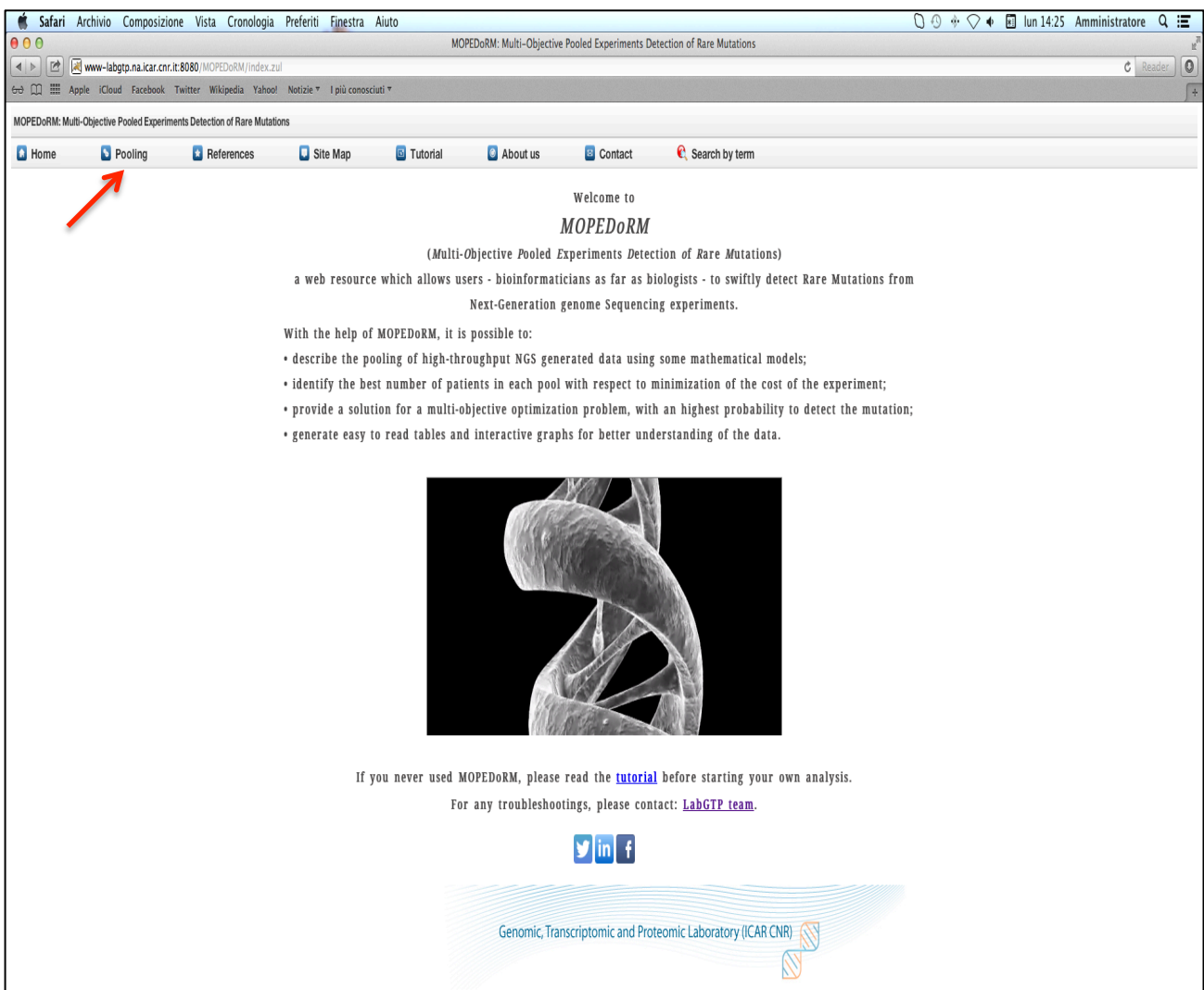


OPENDoRM
USER MANUAL

How to navigate OPENDoRM

The following pages are a schematic representation of how to navigate through OPENDoRM web server in order to extract information of interest. OPENDoRM core is represented by the *Pooling* section. Starting from the *Home page* the user clicks on the related button on the top of the menu bar.



The next page shows a digram portraying the four pooling implemented methods. For sake of simplicity, for the “*Pooling*” section of only examples about “*DiagWalks*” algorithm is shown in the next pages. The “*Without Replica* and *With Replica*” subsection contains the same kind of information, and has been developed with the same rationale.

MOPEDoRM: Multi-Objective Pooled Experiments Detection of Rare Mutations

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Methods Available

In order to plan an NGS pooled experiment, MOPEDoRM provides two distinct mathematical models: Pooling without Replication and Pooling with Replication, this latter in turn divided in Opt and Transposition strategies.

```

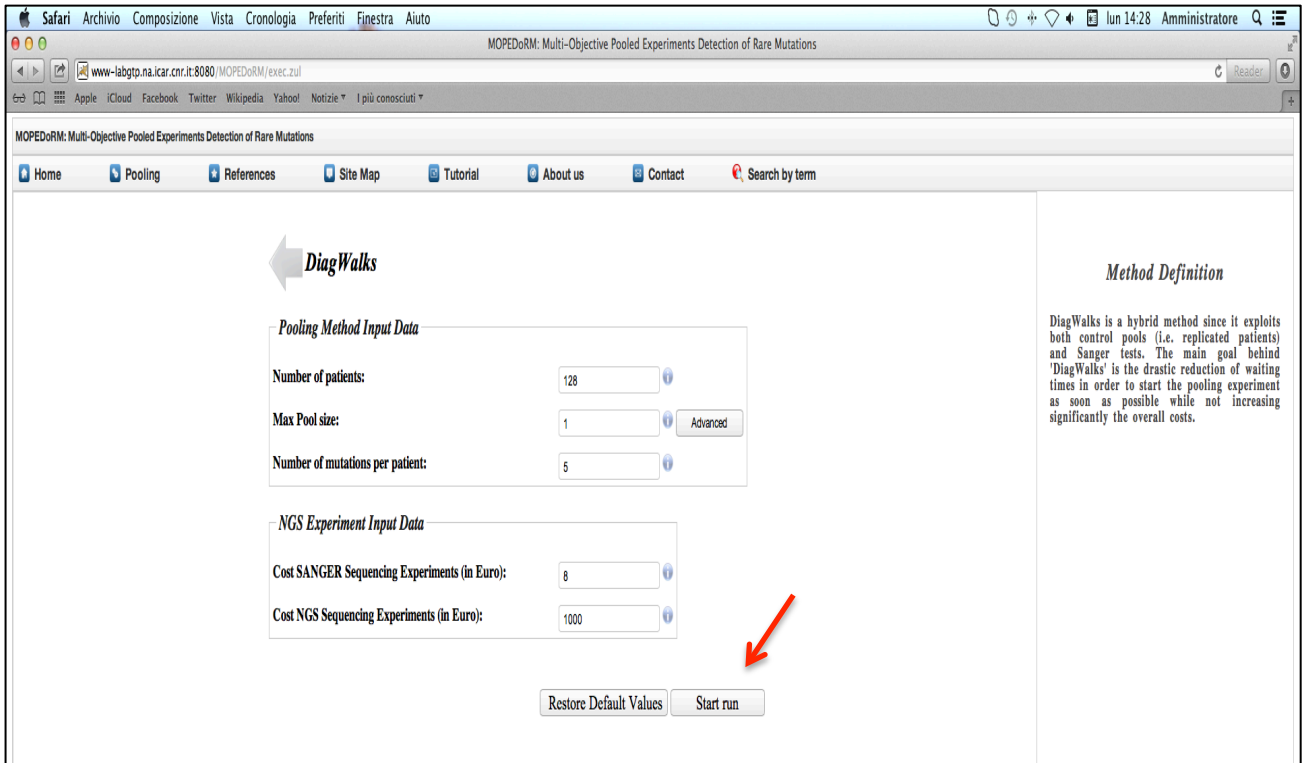
graph TD
    PM[Pooling Methods] --> WR[Without Replica]
    PM --> WR2[With Replica]
    PM --> H[Hybrid]
    WR --> NR[NoReplica]
    WR2 --> OR[OptReplica]
    WR2 --> T[Transposition]
    H --> DW[DiagWalks]
    
```

User can select appropriate model through the buttons displayed above and, according to the need, select numerous options for performing the own experiment. Extensive details of each model are given in the page of selected strategy.

For this case study, the following input data are used:

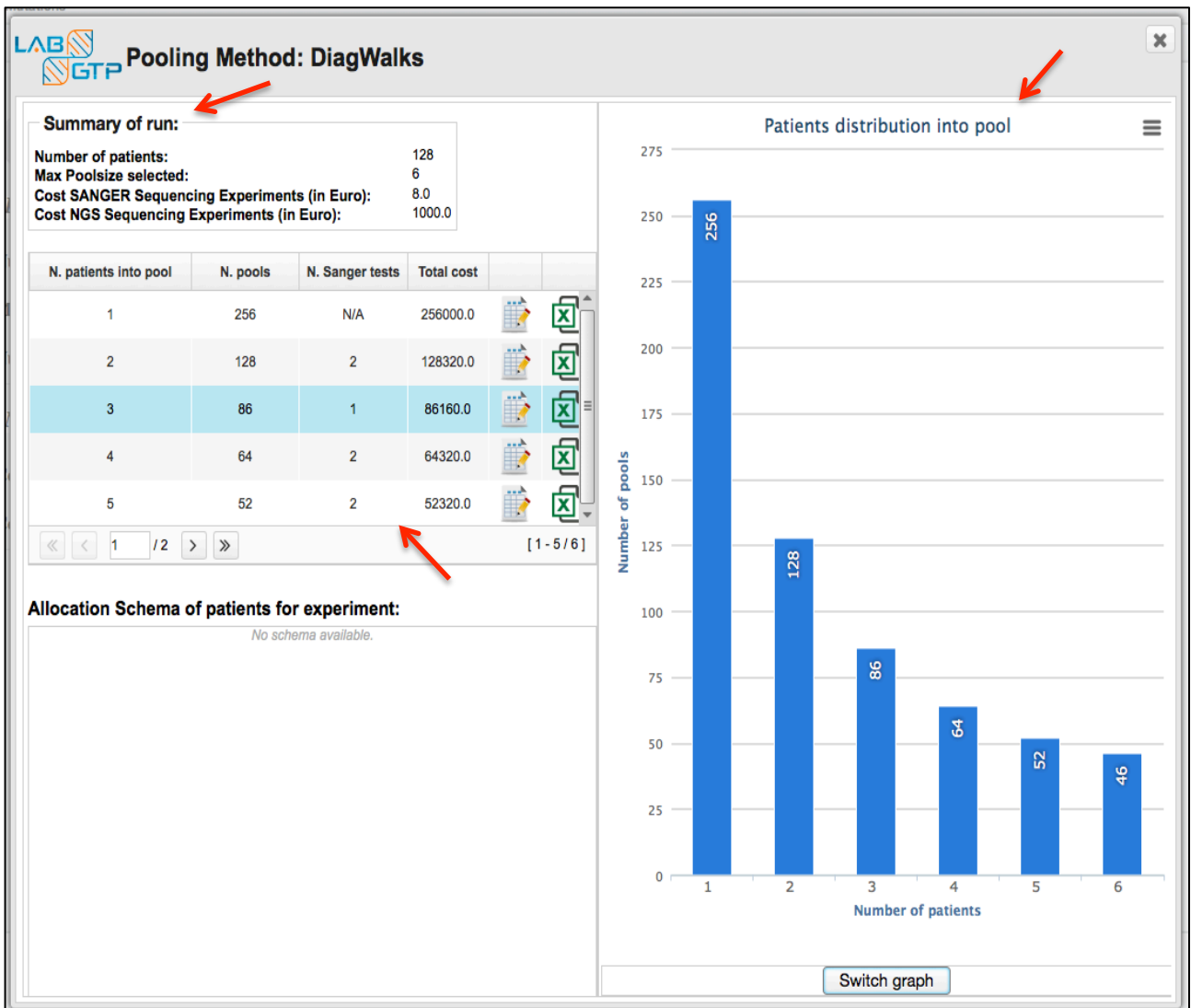
PARAMETERS	EXPLANATIONS	VALUES
<i>Number of patients</i>	Number of patients	128
<i>Max Pool Size</i>	The maximum number of patients allowed in each pool	1 NOTE: When 1 is selected, the program simulates the experiment varying the Max Pool Size for each iteration starting from 1 all the way up to 6.
<i>Number of mutations per patient</i>	How many DNA mutations are expected to be detected	5
<i>Cost SANGER Sequencing Experiments</i>	The price in Euro of each SANGER Sequencing Experiment	8
<i>Cost NGS Sequencing Experiments</i>	The price in Euro of each NGS Sequencing experiment	1000

To start the simulation clicks on the “*Start Run*” button:



You should wait only few seconds before the task will be successfully completed and the screens that show the computed results will appear.

The resulting page is divided in three subdivision. On the left top corner there is the *Summary of run*, which briefly indicates the input parameters selected before. Under the *Summary of run*, there is a grid indicating the results of each simulation of the NGS experiment using the input data provided before. Whereas, on the right side of the window there is a charts section that indicates the Patient's distribution into pool.



Let's analyze the final report in closer detail. In this specific case, 6 rows are displayed.

PARAMETERS	EXPLANATIONS
<i>N. patients into pool</i>	The number of patients allowed in each pool (i.e. the Max Poolsize computed for that specific simulation)
<i>N. pools</i>	The overall number of pools needed.
<i>N. Sanger tests</i>	The required number of Sanger tests
<i>Total cost</i>	The overall cost (in euros) of the experiment. The lowest computed cost is highlighted in green (in this case, 51280 euros).
<i>Build Allocation Schema</i>	It allows the program to compute and display the arrangement of the patients inside the pools according to the specific input data used for the simulation.
<i>Download Excel:</i>	It allows the user to download an Excel file containing the respective Allocation Schema.

Moreover, the grid is divided in six columns

Pooling Method: DiagWalks

Summary of run:

Number of patients:	128
Max Poolsize selected:	6
Cost SANGER Sequencing Experiments (in Euro):	8.0
Cost NGS Sequencing Experiments (in Euro):	1000.0

N. patients into pool	N. pools	N. Sanger tests	Total cost		
1	256	N/A	256000.0		
2	128	2	128320.0		
3	86	1	86160.0		
4	64	2	64320.0		
5	52	2	52320.0		

<< < 1 / 2 > >>



[1 - 5 / 6]

and the best result is reported in green color

LAB GTP Pooling Method: DiagWalks

Summary of run:

Number of patients:	128
Max Poolsize selected:	6
Cost SANGER Sequencing Experiments (in Euro):	8.0
Cost NGS Sequencing Experiments (in Euro):	1000.0

N. patients into pool	N. pools	N. Sanger tests	Total cost		
6	46	1	46160.0		

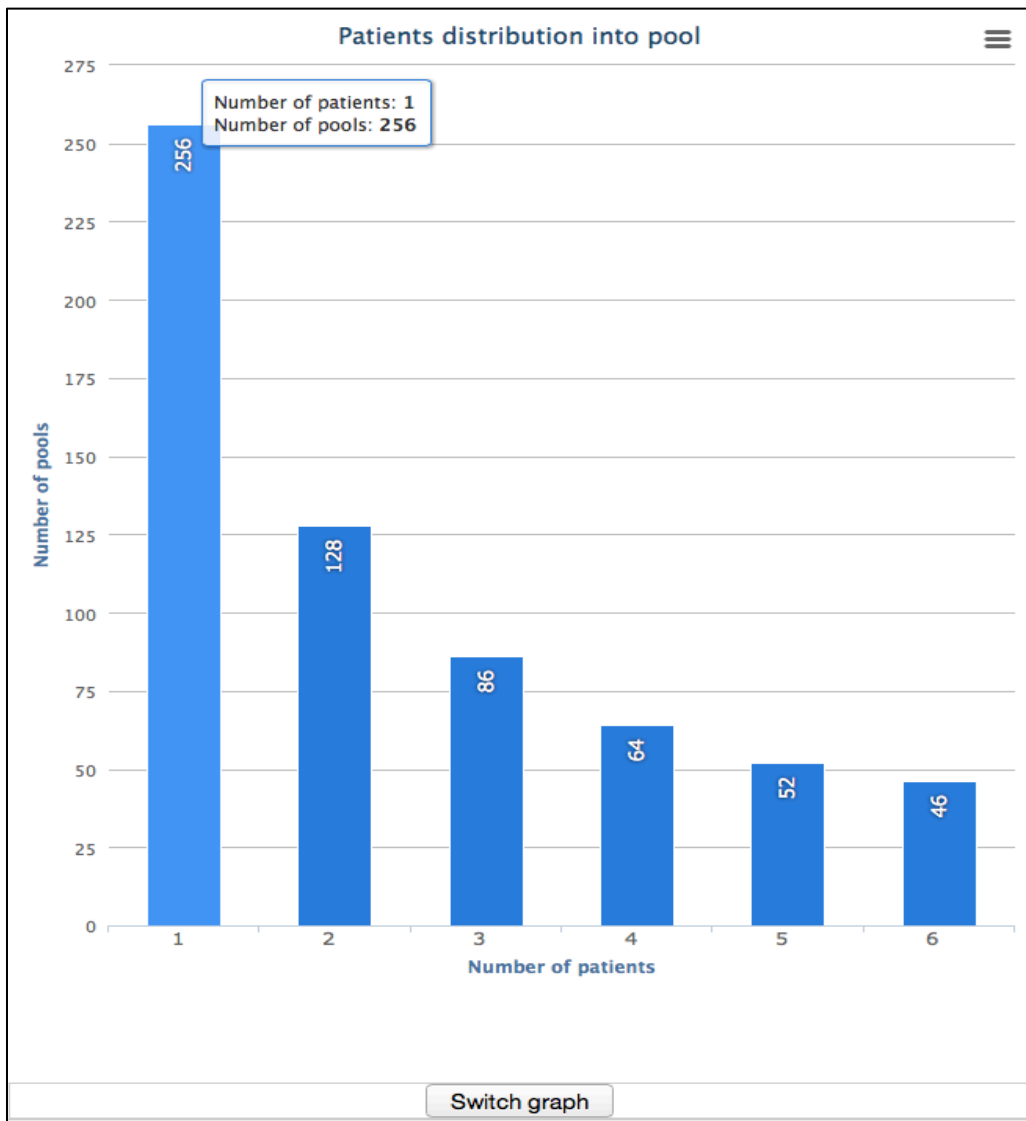
Navigation: << < 2 / 2 > >> [6 - 6 / 6]

Under the grid outlined before, there is the “Allocation Schema of patients for experiment”. Once the user clicks on the built Allocation Schema described before, the program will display the Allocation Schema of the patients in this area of the window.

Allocation Schema of patients for experiment:

P1	P2	P3	P4	P5	P6	P7	P8	P9
#1	#7	#13	#19	#25	#31	#37	#43	#49
#2	#8	#14	#20	#26	#32	#38	#44	#50
#3	#9	#15	#21	#27	#33	#39	#45	#51
#4	#10	#16	#22	#28	#34	#40	#46	#52
#5	#11	#17	#23	#29	#35	#41	#47	#53
#6	#12	#18	#24	#30	#36	#42	#48	#54

On the right side of the window, the program automatically draws a column graph called “Patients distribution into pool”: on the horizontal axis it indicates the number of patients, on the vertical one the number of pools. This graph shows how the number of patients inside each pool and the required number of pools change for each of the simulations of the experiment.



When clicking on the “Switch graph” button, the program draws another graph called “*Trend of NGS cost distribution*”: on the horizontal axis it indicates the number of patients, on the vertical one the cost of the experiment. This graph shows how the cost of the experiment changes, for each of the computed iterations, according to the variation of the number of patients, starting from 1 all the way up to the selected input number (in this case, 128).

