Bioinformatics 2019-2020

Date: 15 January 2020

Project report

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| Bioinformatics@Data Science A.Y. 2019-2020  Malignant Mesothelioma: a study on the interactome  Giulia Cassarà1, Ivan Colantoni1  1Group no. 13 Abstract In this project we will analyze the genes involved in Malignant Mesothelioma disease, the interactions between the diseased genes and those of the human organism. |

Basic introduction about the disease/process

Max 200 words. Add here few basic information about the disease/process under scrutiny.

Seed genes

Explain briefly the methods you followed to get the information about the seed genes and add the related table (see table format below).

Summary on interaction data

Explain briefly the methods you followed to get the information about the interaction data and add the related table. Refer clearly to different files (i.e. when necessary.

1. Sample numbered list, if necessary.
2. The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog.
3. The quick brown fox jumps over the lazy dog.

The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog.

* Sample bullet list, if necessary.
* The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog.
* The quick brown fox jumps over the lazy dog. The quick brown fox jumps over the lazy dog.

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**Table 1.**Sample table. This should be the table format, add/remove columns and rows according to the data to be shown.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| |S| | Predicted cost | Timing | Predicted speed | Speed |
| 1 | S219.20(100%) | 68m43s | 1.00 | 1.00 |
| 2 | 29.10+219.10(~50%) | 35m13s | 2.00 | 1.95 |
| 4 | 219.20(100%) | 68m43s | 1.00 | 1.00 |
| 10 | 29.10+219.10(~50%) | 35m13s | 2.00 | 1.95 |
| 20 | 219.20(100%) | 68m43s | 1.00 | 9.5 |

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# Interactomes data

Explain briefly the methods you followed to build the intersection interactome and add the related tables/charts.

# Enrichment analysis

Explain briefly the methods you followed to carry out the enrichment analysis and add the related tables/charts.

# Notes and comments

References (if any, this is the format to be used)

Alexandrescu,A. (2001) Modern C++ Design: Generic Programming and Design Patterens Applied. Addision Wesley Professional, Boston.

Dormand,J.R. and Prince,P.J. (1980) A family of embedded Runge–Kutta formulae. *J. Comp. Appl. Math.*, **6**, 19–26.