

Bioinformatics as A Tool for Systems Biology

Diego Liberati*

Research Director, National Research Council, Italy

***Corresponding author:** Diego Liberati, Research Director, National Research Council, Italy, Tel: (+39)3480569317, Email: diego.liberati@polimi.it

Received Date: 09th June 2018

Accepted Date: 10th July 2018

Published Date: 20th July 2018

Citation: Diego Liberati (2018) Bioinformatics as A Tool for Systems Biology. Enliven: Bioinfo 4(1): 001.

Copyright: © 2018 Diego Liberati. This is an Open Access article published and distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

The identification of the gene expression for health and sick cells, together with the concentration measurement of the many protein species they are involved in building, is of paramount importance in understanding our functioning. In principle a gene could be considered expressing a protein, in fact epigenetic factors make every gene modify its expression even in health: it is sufficient to take into account that the same genetic heritage works slightly differently in different kind of cells of each of us.

Expression is thus regulated by both other genes, interacting in that very situation, but also by proteins, also expressed by other genes. A complex network of gene and protein actors is thus recruited for every specific task, implying a successful or unsuccessful answer to our need. Such interactions are not so different, in principle, with respect to the neuron interactions in the brain, where every neuron is differently recruited in different teams to face several tasks. They are even not so different with respect to our social interactions, where each of us is in touch with potentially different groups with a possibly different degree of engagement, in order to cope with a variety of desires or needs.

Tools designed to discover, identify, and weight such interactions are thus of paramount importance in investigating pathophysiology at biochemical cellular level. As a matter of example, Page ranking, the famous algorithm rooting Google fortune, is a great font of inspiration, whose drawback is only the computational cost when data increase of magnitude order. A simple randomization approach, nevertheless, would already be able to reduce computation to acceptable computational time and amount of allocated resources, provided that one is able to allow a kind of little “blurry” in the approximate results: there is never free lunch!

On this ground, a variety of approaches could thus be designed to approach such “social” biochemical life within the cell. On the other side, similar math tools could be applied in the study of our real society, thus better paralleling the ancient gap among humanities and sciences, in a true holistic view not against specialization but toward trans-disciplinary integration for the sake of a better grasp of the world in which we live at the different levels of its epiphany

Submit your manuscript at

<http://enlivenarchive.org/submit-manuscript.php>

New initiative of Enliven Archive

Apart from providing HTML, PDF versions; we also provide **video version** and deposit the videos in about 15 freely accessible social network sites that promote videos which in turn will aid in rapid circulation of articles published with us.