International Journal of Computational Bioinformatics and In Silico Modeling
Vol. 2, No. 2 (2013): 87-88
Editorial
Open Access

ISSN: 2320-0634

Editorial

Anwar Rayan

Drug Discovery Informatics Lab, QRC - Qasemi Research Center, Al-Qasemi College, Baka EL-Garbiah 30100, ISRAEL.
email: a_rayan@qsm.ac.il

Bioinformatics continues to be one of the hottest fields in science and due to its growing importance, more and more valuable articles are being produced. Due to that Aizeon Publishers launched recently the "*International Journal of Computational Bioinformatics and In Silico Modeling*". This is an open access journal committed to publish high valuable scientific works, available to all, free of charge. The journal considers research and review articles of all aspects of bioinformatics, chemo-informatics, drug design and discovery techniques, *in silico* genomics, *in silico* proteomics, computational biology, system biology, ADME/Tox predictions, data mining techniques, computational and statistical methods. All submitted manuscripts are subjected to peer review process by at least three renown experts in the field and accepted to publication in the journal if found original, novel and worthwhile to the scientific community.

Editor notes:

The current success rate of a drug developed from conception to market could is estimated to be less than 1% [1]. As well, bringing NME to the market costs in average more than one billion dollars, and it takes at least 10 years to be developed [2]. Further development and heavily application of computational bioinformatics and in silico modeling techniques in drug development process might increase success rate and salvage a vast amount of time and resources required for drug development. The two issues described below in this editorial are hot topics and could have positive impact on the process of drug development.

Mono, bi and multifunctional drugs

Most drugs developed to date are directed toward a single biological target that is responsible for a certain disease. However, in complex diseases such as cancer, there is a complex interaction between multiple signaling pathways with various target molecules. The very limited success in treatment of such diseases could be due to focusing on a single target strategy, either a single gene, gene product, or signaling pathway. The emerging paradigm that suggests the development of multifunctional pharmaceuticals targeting an array of pathological pathways, each of which is believed to contribute to the disease conditions, is currently gaining increasing acceptance [3] and can be an asset in the treatment/ curing of multi-factorial disorders. As well, such multifunctional pharmaceutical may exhibit a more favorable side effect profile than a cocktail of several drugs. Bioinformatics and chemo-informatics techniques could play a central role in pushing the multifunctional drug discovery era forward. Scientists working in this field are encouraged to submit research and review articles dealing with this topic to the "International Journal of Computational Bioinformatics and In Silico Modeling".

Application of *in silico* tools in the natural product-based drug discovery

Natural product-based medicines, particularly, herbal-based drugs represent 60-80% of all drugs in use today. Although computational methods are well established in drug discovery and molecular design, their application in the field of natural products is still in its infancy. Only few works reported application of *in silico* tools in the natural product-based drug discovery. In order to accelerate identification of bioactive natural-based products, maximizing their efficacy and minimizing potential side effects of drug candidates, we need to do more in this era. Our journal is interested in pushing this field forward and encouraging scientists to submit research and review articles related to this hot topic.

Editorial update:

We are pleased to welcome Prof. Salvatore Guccione (Catania University, Italy) and Prof. Omar Deeb (Al-Quds University, Palastine) for joining the editorial board staff at the beginning of 2013. We continue to welcome suggestions for more editorial board members, so if you are a specialist/ renowned scientist in one of the journal topics and interested in joining, please let us know. The editorial board members should support the journal in different ways: review and evaluate manuscripts, writing editorials and reviews, help to raise awareness of the journal and

contribute ideas as to how to develop the journal to be a key medium for computational bioinformatics & modeling.

By Anwar Rayan
Editor-In-Chief

REFERENCES

1. Bennani YL. (2012). Drug discovery in the next decade: innovation needed ASAP. Drug discovery today, 175: 531-544
2. Rayan A, Marcus D and Goldblum A. (2010). Predicting oral druglikeness by iterative stochastic elimination. Journal of chemical information and modeling, 50(3): 437-445
3. Hopkins AL. (2008). Network pharmacology: the next paradigm in drug discovery. Nature chemical biology, 4(11): 682-690

Short Biography:

Dr. Anwar Rayan Studied Chemistry (degree awarded with distinction) followed by a Ph.D. in Computational Chemistry with Prof. Amiram Goldblum. Postdoctoral Studies on Bioinformatics at the school of pharmacy in Jerusalem. Research fellow in FMP, Berlin, Germany.

Dr. Anwar Rayan is currently CEO of GeneArrest LTD company and head of the Drug Discovery Informatics Lab at the QRC – Al Qasemi Academic College. Founder of five companies (IDD therapeutics , Pepticom, Sensotrade, GeneArrest and RAND Biotechnologies). Having more than 37 papers in peer-reviewed journals and 5 patents.

*****