

Open Access Research in Biological Networks Will Facilitate Advances in Network-Based Paradigms for Biomedicine and Biofuel Production

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Editorial

The evolving field of systems biology involves characterizing and modeling biological systems as biophysical and biochemical networks, based on experimental data, so that the behavior of these model networks can be simulated and verified by further experiments [1,2]. This holistic approach of underlying biological systems has recently gained prominence, since it is now well established that disease states, such as cancer or diabetes or the infection of a host by a bacteria or a virus result from malfunctioning or compromised gene-gene interaction and protein-protein interaction networks rather than individual genes and proteins. In order to cure the disease, it is important to disrupt the cellular networks that result in a diseased state, while maintaining the cellular interactions necessary for the cell to survive. Drug agents that target only single genes or proteins might not disable the disease-causing network, since many cellular networks, including disease causing ones, can be quite robust, so that there is no major change in the output from the network if a single node in the network is removed [3]. In such cases, a network-based drug design paradigm [3] becomes necessary, which identifies multiple nodes in the network that should be targeted to render the disease causing network(s) dysfunctional. In case of bacterially and virally infected cells, the network-based approach to biomedicine would target the cellular interaction networks in the diseased cells without affecting the non-infected cells.

Similarly, in the field of metabolic engineering microbes to produce biofuel or biofuel-precursor molecules [4], it is important to understand the networks of genes and proteins that regulate the metabolism [5]. Metabolic engineering of microbes to produce non-endogenous biofuel/biofuel-precursor molecules [6-8] or to produce endogenous bio-fuel like metabolites more efficiently would involve inserting and/or knocking out genes. It becomes essential to gain an understanding of how the relevant metabolic network is regulated at the mRNA and protein levels, since the goal is to divert the metabolic flux from once channel to another more conducive to metabolic production of biofuel or biofuel-precursor molecules. This is because inserting or knocking out single genes might not significantly alter the outputs of the metabolic network. As in the field of network medicine, a holistic systems biology approach would help indicate the multiple genes in a microbial organism that should be targeted by metabolic engineering to effectively channel the metabolic flux to the desired metabolites, while allowing the organism to survive.

The systems approach to understanding cell signaling and metabolism requires access to not only the experimental data at gene, protein and metabolite levels but also to the models that are based on these data and attempt to incorporate the interplay between different levels of the data. One way to make these data and model accessible to the worldwide community of systems biologists is by utilizing the open access model.

Open access (OA) is the practice of providing unrestricted access to peer-reviewed scholarly journal articles via the internet [9]. Theses, scholarly monographs and book chapters are increasingly being

published using the OA model as vehicle. Making articles openly accessible helps to maximize their research impact [10]. A citation impact advantage for the OA model was first reported in 2001 [11]. Since then, there have been multiple studies [12], varying in methodological rigor, that have established that an OA article is more likely to be read and cited than the same article, the access to which is hindered by subscription barriers. It has been reported in a 2006 PLoS Biology article [13], that articles published as immediate open access in PNAS were thrice as likely to be cited than non-open access papers. For scholars, a published article is the peer-reviewed report of the research they have done. The more the article is read, cited and built upon, the better it is for the researcher's career and the more is the advancement of the research initiated by the scholar [9,14,15]. Also, open access publication helps to reduce publication delays [9]. Not only that, such open access publication drastically increases the viewership of the article and might seed collaborations with other research groups across the world. In this respect, it should be mentioned that the OMICS Publishing Group (<http://www.omicsonline.org/>) has endeavored to facilitate worldwide collaboration by allowing translation of articles from English to more than 50 languages and by allowing authors to popularize and advertise their research through common social networking sites [16]. The OA publishing model will extend the readership to less affluent countries in which researchers might not afford paid journal subscriptions [9]. Also, increasing the accessibility of the research will reduce the probability that any research group will not invest in investigating what some other research group has already found.

Open access publication of articles in the specific research area of network-based models of living systems, linked to the underlying data sets, would enable a broad readership to contribute to the models, thereby evolving the models towards a more complete understanding of complex phenotypes [17] relevant to disease states and production of biofuels. Such publication will make accessible not only the models but also the relevant underlying data. For example, in case of an outbreak of a new viral infection, experimental data locally harvested at the geographical origin of the infection might be easily made accessible worldwide via open access publications. This might be very useful to researchers in other countries who might have to overcome bureaucratic red tape to perform experiments in a foreign country. Such availability of data will also be of immense importance

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to theoretically skilled scientists in less affluent countries who do not have enough resources to carry out the relevant experiments. Thus open access publication of network biology research will facilitate the contribution of scientists from all over the world to the network-based paradigms of drug design and metabolic engineering.

It is important that more and more journals allow for open access publication of systems biology research results. This will usher in an era of unprecedented worldwide scientific collaboration which is expected to result in significant advances in the fields of biomedicine and metabolic engineering, so that future generations will be better protected against diseases and will have access to a sustainable energy economy.

References

1. <http://ieeecs.org/sites/ieeecs.org/files/documents/loCT-Part44BiophysicalNetworks-LR.pdf>
2. [No authors listed] (2012) Abstracts. *Pharmacoepidemiol Drug Saf* 21: 788-798.
3. Csermely P, Agoston V, Pongor S (2005) The efficiency of multi-target drugs: the network approach might help drug design. *Trends Pharmacol Sci* 26: 178-182.
4. Lee SK, Chou H, Ham TS, Lee TS, Keasling JD (2008) Metabolic engineering of microorganisms for biofuels production: from bugs to synthetic biology to fuels. *Curr Opin Biotechnol* 19: 556-563.
5. Brynildsen MP, Liao JC (2009) An integrated network approach identifies the isobutanol response network of *Escherichia coli*. *Mol Syst Biol* 5: 277.
6. Hanai T, Atsumi S, Liao JC (2007) Engineered synthetic pathway for isopropanol production in *Escherichia coli*. *Appl Environ Microbiol* 73: 7814-7818.
7. Atsumi S, Cann AF, Connor MR, Shen CR, Smith KM, et al. (2008) Metabolic engineering of *Escherichia coli* for 1-butanol production. *Metab Eng* 10: 305-311.
8. Atsumi S, Hanai T, Liao JC (2008) Non-fermentative pathways for synthesis of branched-chain higher alcohols as biofuels. *Nature* 451: 86-89.
9. <http://en.wikipedia.org/wiki/Openaccess>
10. Swan A (2006) The culture of Open Access: researchers' views and responses, in *Open access: key strategic, technical and economic aspects*, N. Jacobs, Editor. Chandos.
11. Lawrence S (2001) Free online availability substantially increases a paper's impact. *Nature* 411: 521.
12. <http://opcit.eprints.org/oacitation-biblio.html>
13. Eysenbach G (2006) Citation advantage of open access articles. *PLoS Biol* 4: e157.
14. <http://openaccess.eprints.org/index.php?archives/28-guid.html>
15. <http://www.garfield.library.upenn.edu/essays/v11p354y1988.pdf>
16. <http://www.omicsonline.org/special-features.php>
17. <http://www.opennetworkbiology.com/about>