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Omics for Metabolic Reconstruction Engineering: The Current Trend

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After a long debate on computational biology as scientific discipline or just a tool for the other biological science related discipline, this branch has oozes with huge potential; therefore without any hesitation scientific community is accepting this as a discipline of science. In last editorial article I had focused on the need of this branch and respective deed. Broadly computational biology used two vibrant and energetic fields, i.e. bioinformatics and system biology. The system biology, a well being dynamic field of science mainly related to analysis of biological data, and a main objective is to process the measurements for any biological system under study to describe the functions and behavior of the system [1,2]. The transition from macro to nano level measurements in the biological system is rapid and can be regarded as a story of two decades, and thus resulting in the generation of a huge data base of physiochemical properties of individual molecules along their physiological role. Progress in the measurements of the rates and interactions of molecular and cellular processed has initiated a revolution in our understanding of dynamic phenomena in cells [2]. The multi-domain proteins which could bind to several other biomolecules either simultaneously or at different points in the cell cycle or in different cell types and their analysis open a new hope for targeted bioengineering. The molecular interaction and specific binding event in various metabolic pathways has been archived in various literatures. Still there is a strong need to develop the tools can deal with consecutive network analysis, as the biological-system is too complex to resolve the same [3,4]. These metabolic networks form conventional signaling cascades, classical metabolic pathways, transcription activation complexes, vesicle mechanisms, and cellular growth and differentiation systems, indeed all of the systems that make cells work. Interaction information is based on the experimental observation of a specific interaction between two or more molecules, augmenting rapidly [5].

The ultimate manifestation of gene function is through intermolecular interactions. It is impossible to disentangle the mechanistic description of the function of a biomolecule from a description of other molecules with which it interacts. One of the best forms of the annotation of a gene's function, from the perspective of a machine readable archive, is information linking specific molecular interactions together, an interaction database [1,5-8]. Thus, interactions, defining molecular function and interaction databases are critical components as we move toward complete and dynamic functional description of the cell at a molecular level of detail. Interaction databases are essential to the future of bioinformatics as a new science. In this review, what can be achieved through integration of current interaction information into a common framework is broadly considered, and a number of databases that contain interaction information are examined, an example the Kyoto Encyclopedia of Genes and Genomes (KEGG) database, a server dedicated to deal with genomes, enzymatic pathways, and biological chemicals [6-10]. The PATHWAY database records networks of molecular interactions in the cells, and variants of them specific to particular organisms. In last seventeen years this online database grew tremendously, now it is holding 200,285 pathways map with 428 referral maps. This database and collective information about related gene, proteins and corresponding interactions, empowers the researcher to plan a bigger, predictive and percussive biotechnology. To organize and structure this information so that it can offer a rationally coherent biological picture is both extremely exciting and truly intimidating [1,2,4,7,10].

Therefore the analysis, inference, modeling and simulation of these data to develop the model for further applications are required. Just understand the role of Omics or bioinformatics in enhanced production or introduction of novel properties in specific product. I had searched the some keywords in PUBMED and the trends are really endeavoring for the strong association between biotechnologists to system biologist and bioinformaticians [1,2,4,7]. The increasing trend of metabolic pathway analysis and metabolic reconstruction for metabolic engineering and drug design can easily understand by publications archived in PUB Med. The KEGG has been used in about 1100 archived literatures since it came in existence i.e. from 1097. From the very first only published paper on KEGG pathways in 1997, the 2012 has been honored with 133 publications in 2012 itself, with a total 579 all-time papers. Figure 1 and 2 repenting the application of KEGG pathways information and scholarly output on metabolic pathways reconstruction. This reconstruction engineering studies need to keep track of the metabolism that is being engineered.

Among the researcher dealing with metabolic engineering, there is

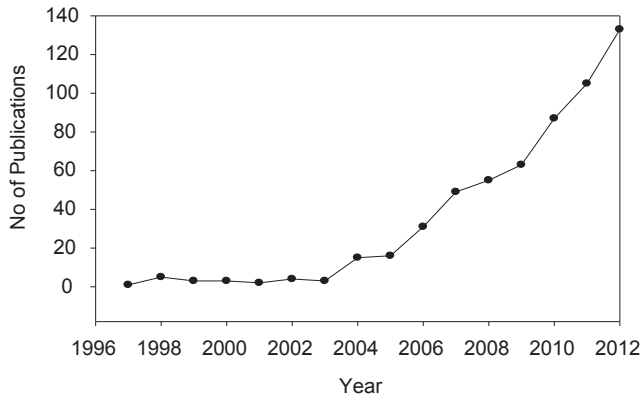

Figure 1: Research Papers archived in PUBMED, used KEGG Pathways for experimental designs at least up to some extent.

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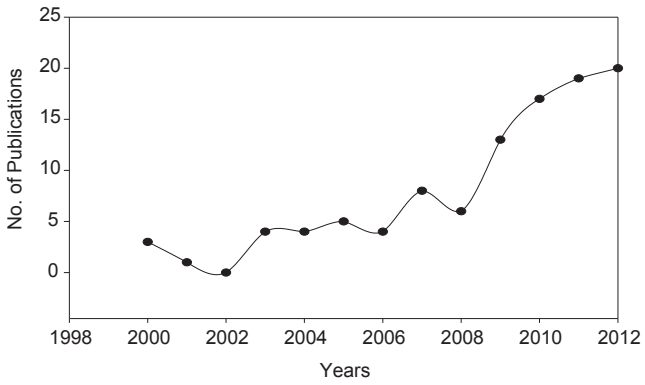

Figure 2: Research Papers archived in PUBMED, entitled with metabolic reconstruction.

an increasing appreciation of the reluctance of the biological organism at being engineered [1,4]. However, there is much less of an insight in how to the researcher may be able to deal with this reluctance. The recent the both the computational and experimental breakthroughs, in metabolic reconstruction engineering, empowers us the deal with the plasticity of the living cell factories and to turn the plasticity into the desire rather than the adverse direction. Generation of database is an important task but analyzing these data will facilitate the scientist to have directional approach. Developing more and more data on molecular interaction and networking will open lots of window in the field of metabolic engineering.

References

1. Kholodenko BN, Westerhoff HV (2004) Metabolic Engineering in The post genomic Era. Horizon Bioscience.
2. Morya VK (2012) Open access Biological Information: Deeds of Need. J Proteomics Bioinform 5.
3. Morya VK, Yadav S, Kim EK, Yadav D (2012) In Silico Characterization of Alkaline Proteases from Different Species of Aspergillus. Appl Biochem Biotechnol 166: 243-257.
4. Maudsley S, Chadwick W, Wang L, Zhou Y, Martin B, et al. (2011) Bioinformatic approaches to metabolic pathways analysis. Methods Mol Biol 756: 99-130.
5. Morya VK, Kumari S, Kim EK (2012) Virtual screening and evaluation of Ketol-Acid Reducto-Isomerase (KARI) as a putative drug target for Aspergillosis. Clin Proteomics 9.
6. Morya VK, Dewaker V, Kim EK (2012) In Silico Study and Validation of Phosphotransacetylase (PTA) as a Putative Drug Target for Staphylococcus aureus by Homology-Based Modelling and Virtual Screening. Appl Biochem Biotechnol.
7. Chen L, Huang T, Shi XH, Cai YD, Chou KC (2010) Analysis of protein pathway networks using hybrid properties. Molecules 15: 8177-8192.
8. Morya VK, Kumari S, Kim EK (2011) Imperative pathway analysis to identify the potential drug target for Aspergillus infection. International Journal of Latest Trends in Computing 2: 178-182.
9. Morya VK, Dewaker V, Mecarty SD, Singh R (2010) *In silico* Analysis of Metabolic Pathways for Identification of Putative Drug Targets for *Staphylococcus aureus*. J Comput Sci Syst Biol 3: 062-069.