

PREFACE

The almost complete sequencing of the genomes from numerous organisms paved the way for the development and application of new experimental and instrumental techniques which contribute to the understanding of complex biological pathways and networks by providing apparently endless opportunities to generate massive amounts of data. Cell machinery is currently envisaged as an inter-relationship of enzymes, proteins and chemical compounds. However, both a large number of metabolic pathways and enzymes even in well-described pathways still remain unknown. It is therefore necessary to develop further experimental and mathematical methods to reconstruct unknown parts of the networks, to identify genes for missing enzymes and to characterize the kinetic behaviour of those enzymes that have been identified.

The post-genomic era is also characterized by the concept of systems biology. This has gained significant momentum and metabolic research is now being conducted on an integrated and cross-disciplinary platform pulling together its resources from diverse fields such as mathematics, computational biology, bioinformatics, functional genomics and proteomics, and structural biology.

The enormous growth in the computation speed and data storage capability has fuelled new opportunities for both the accumulation of massive amounts of sequence, expression and functional data and the characterization, analysis and comparison of larger biological systems. However, as long as the data quality of the in-put and the resulting modelling data cannot be improved, the chances of success for this young discipline to escape from the verbally overused *-omics*-sciences are poor.

Systems level investigation of genomic and proteomic scale information requires incomparably higher demands for data quality than in previous decades. Truly integrated databases that deal with heterogeneous data need to be developed to be able to retrieve properties of genes, for kinetics of enzymes, for behaviour of complex networks and for the analysis and modelling of complex biological processes. One perspective of the output can be the investigation of cellular pathways involved in disease biology and targeted by newer molecular therapeutics. The understanding of these processes will assist the development of early diagnosis, prognosis and the prediction of response to individual therapies.

Despite the fast paced global efforts in biological systems research, the current analyses are limited by the lack of available systematic collections of comparable functional enzyme data. Besides its reliability, these data have to provide defined minimum experimental information, they must be available from the literature along with their accepted enzyme names, and must be as comprehensive as possible.

The STRENDA commission, founded on the 1st ESCEC meeting in 2003, has worked out a number of checklists which are intended to improve the quality of reporting enzyme data and thus to support the comparability of *inter alia* enzyme kinetics. The commission has also spent much time and effort in the creation of an electronic data submission system which allows authors to deposit their data and to provide an interaction record accession number that can be quoted in publications.

This 3rd ESCEC symposium, organized by the Beilstein-Institut together with the STRENDA commission, provided a platform to discuss the checklists (see also <http://www.strenda.org/documents>). Further suggestions regarding the checklists have been collected and discussed. Questions such as how to organize and store these massive data sets in standard and easily accessible forms have been asked and the first running draft of a data acquisition tool considering the STRENDA guidelines has been presented.

We would like to thank particularly the authors who provided us with written versions of the papers that they presented. Special thanks go to all those involved with the preparation and organization of the symposium, to the chairmen who piloted us successfully through the sessions and to the speakers and participants for their contribution in making this symposium a success.

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