Final report concerning the workshop

Physical and Chemical Foundations of Bioinformatics Methods (PCFBIM07)

Organizers:

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Bioinformatics is a relatively recent discipline that has been emerging in response to the need to the need of organizing and analysing the wealth of biological data generated by large scale programmes such as genome projects and structural genomics initiatives. Today, this discipline constitutes a very active area of research that provides efficient algorithms for a variety of applications, including sequence alignment, gene detection, and structure comparison. The idea of the workshop originated from the recognition that the physical and chemical foundations of the methodologies developed in Bioinformatics have not been, however, explored with the necessary depth. The goal of the meeting has been to bring together experts from Bioinformatics and Physics, since we believe that progress in understanding the structural properties of biological entities, including their physical and chemical interactions, can greatly help to improve existing bioinformatics methods, and ultimately suggesting new approaches.

The workshop provided an excellent opportunity to promote discussions among researchers from different scientific communities working within the following three main areas: (i) methodological developments in Bioinformatics, (ii) experimental and (iii) computational studies of the properties of biological macromolecules. Possible synergies between these experimental, theoretical, computational, and statistical analysis approaches are anticipated to take place on two main fronts. On the one hand, to improve our understanding of biological information storage and processing, and, on the other hand, to suggest new methods to extract this information from biological sequences. When achieved, such synergies will provide us with an integrated view of the subject. Our workshop has been fully successful in stimulating such an integration, by letting explore the connections between these different disciplines and providing a suitable framework for interaction. The workshop has been organized in several sessions, ‘Networks’ (D. Segrè and M. Schroeder), ‘Transcriptional Regulation’ (M. Lässig S. Bornholdt, and E. Domany), ‘Protein Structure and Function’ (A. Ortíz, C. Orengo, and R. Russell), ‘Protein Structure, Folding, and Complexes’ (H. Fraser, L. Holm, M. Sternberg, and A. Horovitz), ‘Bioinformatics’ (P. Baldi, S. Teichmann, and J. Meiler), ‘Protein Structure Space’ (S.-H. Kim, D. Frishman, A. Lee, and S. Pietrokovski), ‘DNA and RNA’ (R. Bundschuh, L. Mirny, and C. Kiel), ‘Genetics and Epigenetics’ (C. Ouzounis and E. Kussel), and ‘Systems Biology’ (H. Westerhoff). Besides the contributions of the invited speakers, the workshop has also benefited from the very high level contributions by non-invited participants, both in the form of short oral presentations as well as in the poster sessions. The friendly and communicative atmosphere that developed from the very beginning favored the discussions, which was also facilitated by the fact that most talks contained references to the work of other participants.

Participants' reactions to our efforts to integrate the so far separated disciplines into a single workshop, and possibly into a common scientific community, have been unanimously enthusiastic. We plan to publish a selection of peer-reviewed papers in special issues of the renowned journal 'Gene' edited by us.

The organizers wish to express their sincere gratitude to the MPIPKS for hosting and financing this workshop and for the very generous support.