ISCB and health / ISCB and drugs / for ISMB/ECCB 2013 in Berlin

Computational biology crucial for personalized health. Computational biology has contributed at different levels to the successful development of each new drug that reaches the market today. Modern biology increasingly relies on advanced research techniques such as high-throughput screening in particular biological systems or disease states. No single experiment can provide all the answers to a question; instead, partial answers are combined from multiple experiments to answer many questions. This high-throughput trend, which generates large volumes of data, requires computational biologists, while at the same time, challenges the community to quickly extract as much useful information from the data as possible. Novel drugs arrive on the market if and only if they undergo detailed analyses. Computational biology techniques further this analysis to make novel drugs a realization.

The relevance of computational biology and bioinformatics increased with the arrival of deep sequencing. Deep sequencing is a form of DNA sequencing that gives information on nucleotides present in an organism's tissue sample and can be used to get information on the extent to which these different regions of the genome are expressed under different conditions. Soon, it will cost significantly less than $1000 to sequence an entire genome (i.e., an organism's hereditary information) for an individual. Understanding variations in an individual's genome could possibly enable clinicians to make more concise medical recommendations for the patient. It is likely that there will come a point when hospitals and health insurance companies consider it valuable to pay for the sequencing of all their clients/patients.

Long before that point, analysis techniques developed by the community of computational biologists will have become crucial components to making personalized healthcare a reality. It can already be foreseen that the theoretical in-silico approach will in future lead and guide the design and planning of experiments and clinical trials based on the predictions and modeling of the various disciplines. The International Society for Computational Biology (ISCB) holds an annual meeting, Intelligent Systems for Molecular Biology (ISMB), where this research is presented and scientists from around the world come to learn. This year's meeting is in Berlin, Germany, and has six keynote presentations all who have contributed importantly to issues related to human healthcare.

David Eisenberg (UCLA, Los Angeles, USA) is the recipient of ISCB's Senior Scientist Award, recognizing a career of outstanding contributions to the field. Dr. Eisenberg is a structural biologist who has contributed many essential methods and results to the advancement of molecular biology. One particular recent focus has been on amyloid and prion diseases, such as Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), and the prion conditions (e.g. Creutzfeldt-Jakob disease, or BSE, i.e. Mad Cow disease).

Goncalo Abecasis (Univ. of Michigan, Ann Arbor, USA) is the recipient of ISCB's Overton Prize for an outstanding young scholar. Dr. Abecasis' research focuses on developing statistical tools that help in the study of human variation and disease.

Gary Stormo (Washington Univ., St. Louis, USA) has contributed some of the most essential tools for the study of the complexity of gene expression. Dr. Stormo's work is essential for many tasks related to the study of human health because understanding how the gene functions in the body helps researchers to determine correlations of those function to disease-causing alleles.

Gil Ast (Tel Aviv Univ., Israel) has also contributed importantly to the understanding of regulation and transcription. Dr. Ast's mostly experimental work touches upon the issue of epigenetic markers and control, i.e., the molecular biology of imprints upon how our bodies function that we acquire during our life. The work of the Ast lab also includes particular studies relevant for neurodegenerative brain disorders, such as Familial Dysautonomia and the link between splicing and cancer.

Lior Pachter (Univ. of California, Berkeley, USA) is a computational biologist who has contributed toward the ENCODE project (Encyclopedia of DNA Elements) – a research collaboration charged to find all functioning elements within the human genome.

Carole Goble (Manchester Univ., England) is one of the early builders of the Semantic Web, and one of the first behind pushing those concepts into biology. Dr. Goble is currently working on several initiatives related to human healthcare, for instance, PsyGrid, which provides resources to clinicians, researchers, and others interested in psychosis. However, her talk will focus on more general questions related to science and society.

About ISCB. The International Society for Computational Biology (ISCB) - www.iscb.org - has been the first and continues to be the only society representing computational biology and bioinformatics on a worldwide scale. ISCB serves a global community of nearly 3,000 scientists dedicated to advancing the scientific understanding of living systems through computation. It convenes the world's experts and future leaders in top conferences and partners with publications that promote discovery and expand access to computational biology and bioinformatics. It delivers valuable information about training, education, employment, and relevant news. ISCB also provides an influential voice on government and scientific policies that are important to its members and benefit the public.

The ISCB hosts annual meetings, including ISMB (Intelligent Systems for Molecular Biology), the world's longest running and largest conference in computational biology and bioinformatics. ISMB alternates between North America and Europe where it is held jointly with the European Conference on Computational Biology (ECCB) every odd-numbered year.   The ISCB also affiliates with many other significant meetings, associations, and groups in our field; it has two official journals of the highest impact factors in the Mathematical & Computational Biology category, and has affiliations in place with several other publications for the benefit of our members.

Over the course of the last 7 years, ISCB has recognized the increased need to bring together researchers to collaborate and learn and has addressed this by organizing a greater number of meetings. Outside of the ISMB, the meetings include ISCB-Africa (since 2009), ISCB-Latin America (since 2010), and ISCB-Asia (since 2011), as well as focused meetings (now running under the title of ISCB-focus meeting): CSHALS (since

2007), RECOMB/ISCB Regulatory and Systems Genomics (since 2012), and ISCB-NGS (since 2013). Another activity is US regional meetings: Rocky (since 2003), and GLBIO (since 2011).

The ISCB is incorporated in the United States as a 501(c) (3) non-profit corporation, and registered in the state of California as a Charitable Trust. For more information about ISCB and its initiatives and programs, please visit www.iscb.org.

About ISMB. The annual ISMB (Intelligent Systems for Molecular Biology) conference began 1993 and was the driving force behind the founding of the International Society for Computational Biology in 1997. ISMB has become the largest conference on computational biology worldwide. ISCB continues to see ISMB as its major flagship annual event.

A considerable fraction of all the major scholars in computational biology frequently participate in ISMB. Consistent with this leading role in representation, ISMB has become a major outlet for increasing the visibility of this extremely dynamic new discipline, and for maintaining and elevating its scientific standards. It has become the vehicle for the education of scholars at all stages of their career. ISMB has also become a forum for reviewing the state-of-the-art advances in the many fields of this growing discipline, for introducing new directions, and for announcing technological breakthroughs. ISMB and ISCB continue to contribute to the advancement of biology, and build the bridges necessary to support research developments by dedicated and passionate groups of scholars from an unusual variety of backgrounds.

The ISMB conference aims at attracting the top research contributions in all areas of computational molecular biology. Typical, but not exclusively, the topics of interest are: sequence analysis, evolution and phylogeny, comparative genomics, protein structure, molecular and supramolecular dynamics, molecular evolution, gene regulation and transcriptomics, proteomics, systems biology, ontologies, data bases and data integration, text mining and information extraction, and human health. A greater understanding of these topics enables researchers to make better predictions on how the human responds to disease, illness, and treatment.