

Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2011 Special Issue

OVER THE PAST 10 YEARS, the study of cell regulatory processes and their integration within complex “systems-level” models of cell physiology and cell pathology has flourished, with geometric increase in scientific publications and impact on biology. Within the broad spectrum of molecular biology disciplines, systems biology and regulatory genomics are perhaps the ones that have been most characterized by the seamless and unique integration of computational and experimental sciences, allowing the rapid transformation of high-throughput data into complex computational models, of models into testable hypotheses, and finally of hypotheses into knowledge via experimental validation. Today, these disciplines are achieving maturity, as also demonstrated by the creation of several university departments, centers, and institutes dedicated to their study and by the popularity and growth of meeting such as the RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges. This event, which is currently in its fourth edition as a joint meeting, is particularly relevant as it combines unique computational and experimental perspectives, while also establishing a unique frame of reference, via the DREAM challenges, to objectively gauge the progress of our ability to dissect regulatory networks and to model biological processes.

The 4th edition of the Joint RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges was held in Barcelona, Spain on October 14–19, 2011. The conference brought together computational and experimental scientists to discuss current research directions and latest findings, and to establish new collaborations towards a systems-level understanding of gene regulation and modeling of biological systems. The conference included oral presentations from accepted full-length manuscripts and from a few high-quality abstracts, as well as invited presentations from thought leaders in the field. Accepted full-length manuscripts that constitute significant theoretical advances to the fields of systems biology and regulatory genomics have been combined in a collection that is presented in the current issue of the *Journal of Computational Biology*.

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