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*RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges 2010 Special Issue, Preface*

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**Citation:** Kellis, Manolis, Andrea Califano, and Ziv Bar-Joseph. "RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges 2010 Special Issue, Preface." *Journal of Computational Biology* 18.2 (2011) : 131-131. ©2011 Mary Ann Liebert, Inc.

**As Published:** <http://dx.doi.org/10.1089/cmb.2010.005p>

**Publisher:** Mary Ann Liebert, Inc.

**Persistent URL:** <http://hdl.handle.net/1721.1/65588>

**Version:** Final published version: final published article, as it appeared in a journal, conference proceedings, or other formally published context

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## Preface: RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges 2010 Special Issue

MANOLIS KELLIS, ANDREA CALIFANO, and ZIV BAR-JOSEPH

OVER THE PAST TEN 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 increases 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 seamless and unique integration of computational and experimental sciences, allowing 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 demonstrated by the creation of several university departments, centers, and institutes dedicated to their study and by the popularity and growth of meetings such as the RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges. This event, which is currently in its third 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.

After two highly successful previous meetings at the Broad Institute, the 3rd edition of the Joint RECOMB Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges was held at Columbia University, November 16–20, 2010. The conference brought together computational and experimental scientists to discuss current research directions, latest findings, and 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 high-quality abstracts, as well as 14 invited presentations from 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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