Preface

Research in the field of gene regulation is evolving rapidly in an ever-changing scientific environment. Microarray techniques and comparative genomics have enabled more comprehensive studies of regulatory genomics and are proving to be powerful tools of discovery. The application of chromatin immunoprecipitation and microarrays (chIP-on-chip) to directly study the genomic binding locations of transcription factors has enabled more comprehensive modeling of regulatory networks. In addition, complete genome sequences and the comparison of numerous related species has demonstrated that conservation in non-coding DNA sequences often provides evidence for cis-regulatory binding sites. That said, much is still to be learned about the regulatory networks of these sequenced genomes.

Systematic methods to decipher the regulatory mechanism are also crucial for corroborating these regulatory networks. The core of these methods are the motif discovery algorithms that can help predict cis-regulatory elements. These DNA-motif discovery programs are becoming more sophisticated and are beginning to leverage evidence from comparative genomics (phylogenetic footprinting) and chIP-on-chip studies. How to use these new sources of evidence is an active area of research.

The first RECOMB Regulatory Genomics workshop exceeded the organizers' expectations. More than 130 attendees enjoyed many excellent talks from leading researchers in the field. Ideas were shared during active discussion time between talks and hopefully many collaborations were born. This preceedings contains ten original manuscripts presented by the authors during the workshop. The organizers for the first annual Regulatory Genomics workshop would like to thank all the speakers and participants for their interest and participation in this meeting. The 1st Annual RECOMB Satellite Workshop on Regulatory Genomics would not have been possible without the generous support of UC Discovery and Cal-IT^2.

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Industry-University Cooperative Research Program, The UC Discovery Grant
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