

"This is a comprehensive introduction to a powerful and important new technique that is transforming our understanding of gene regulation. This volume contains everything you need to know to become an expert in CAGE, from library construction to bioinformatic analysis of the voluminous data sets."

Gene E. Robinson
University of Illinois

The output of eukaryotic genomes is much more complex than expected. Genes produce different variants of RNAs from multiple promoters. One of the ultimate targets of biological analysis is to establish a relationship between the messenger RNAs that are transcribed from the genome and the genomic regions that control their expression — the promoters — in order to decipher the networks that regulate gene expression and the transcription factors that act as master regulators of transcriptional control.

Novel technologies have recently appeared that allow deciphering of transcriptional network, based on the identification of the starting site of gene transcription, with the simultaneous measurement of expression level and identification of the promoter elements. These tagging technologies (including cap-analysis gene expression — CAGE — and others) are further boosted from the development of the novel generation of sequencing instruments, which allow transcriptional profiling by sequencing at the cost of microarray experiments.

This book is a guide for users of new technologies, as it includes accurately proven protocols, allowing readers to prepare their samples for experiments. Additionally, it provides a guide for the bioinformatics tools that are available for the analysis of the obtained tags, including the design of the software, the sources and web information where they can be downloaded. Finally, the book provides examples of the application of these technologies to identify promoters, annotate genomes, identify new RNAs and reconstruct models of transcriptional control. Although examples mainly regard mammals, the discussion expands to other groups of eukaryotes, where these approaches are complementing genome sequencing.



Piero Carninci

Born and Educated in Italy he obtained his doctoral degree at the University of Trieste. He moved to Japan in 1995 at RIKEN, Tsukuba Life Science center where he became tenure researcher in 1997. From 2008 he is Tem and Unit Leader and Deputy Project Director at the RIKEN Omics Science Center in Yokohama. He has developed technologies to analyze the part of the genome transcribed in RNAs (transcriptome), such as the cap-trapper and the CAGE technologies. These technologies have been broadly used in the RIKEN Fantom projects and allowed to find that non-coding RNAs are the major output of the mammalian genome. Additionally, these have provided the most comprehensive maps of the mammalian transcripts and promoters. From the application of these technologies, he has published more than 150 publications and book chapters.



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