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| I got my B.S. in Mech. Eng. from USTC and joined the first CUSPEA (initiated by T.D. Lee) group studying physics in USA in 1981. After getting Statistical Physics PhD from Rutgers University in 1987, I became a postdoc at the Courant Institute of Mathematics at NYU until I became a Genome Research fellow at CSHL in 1991. I started my Computational Genomics Lab there in 1996 and became full professor in 2002. I became 1000-Talent guest professor of Tsinghua University in 2009 and moved to The University of Texas at Dallas as the Cecil H. and Ida Green Distinguished endowed chair Professor in 2010. I am currently the director of Center for Systems Biology at UT Dallas and the co-director of Center for Synthetic and Systems Biology at Tsinghua U. | |
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| **Computational Biology of Genome Regulation from 1D to 3D**  **Michael Q. Zhang**  **The University of Texas at Dallas & Tsinghua University** | |
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Cell fate determination and transformation is intimately related to chromatin interaction and 3D genome structure. Many 1D cancer or other developmental regulatory disease markers, such as GWAS SNPs/CNVs, heritable or somatic mutations, gene fusions, viral insertion hotspots, epi-mutations, etc., are often linked to dis-regulation of *cis*-regulatory elements to their target genes through altered 3D DNA loops. I will review the history of computational genome regulation and then introduce some new biochemical (BL-Hi-C), biophysical (Super-resolution imaging) and Bioinformatics (MICC, 3CPET, FIND) technology developments that may be used for studying 3D genomes and disease markers in the near future.