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Powering cross-species and whole-genome lncRNA/DNA binding analysis using lncRNA database and high-performance computing

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LncRNAs are key epigenomic regulators and abundant lncRNAs have been identified not only in humans and mice but also in other mammals. By binding DNA sequences to form DNA:RNA triplexes, many lncRNAs recruit histone and DNA modifying enzymes to specific genomic sites to epigenetically regulate gene expression during embryonic and post-natal development, under physiological conditions and in cancer cells. The abundant lncRNAs in diverse species and lncRNA binding sites in the whole genomes call for integrative platforms containing lncRNA sequences and analytic tools and such platforms should be effectively powered by high performance computing. Here, we introduce a platform that integrates our mammalian lncRNA database LongMan and the lncRNA/DNA binding prediction program LongTarget for cross-species and whole-genome lncRNA/DNA binding analysis. The database currently contains the GENCODE-annotated 13,562 human lncRNAs and 10,481 mouse lncRNAs, 133,646 orthologues of the human lncRNAs in 16 mammals and whole-genome sequences of 17 mammals. We demonstrate that cross-species and whole-genome lncRNA/DNA binding analysis, together with the publicly available data including the ENCODE histone modification, ENCODE DNA methylation and GTEx in the UCSC Genome Browser, can generate rich, novel and valuable findings, clues and insights for diverse studies.

Biography

Hao Zhu has obtained his MS degree in Computer Science from National University of Defense Technology, China and PhD in Pathophysiology from Southern Medical University, China. He has pursued his Postdoctoral studies in Singapore Bioinformatics Institute and School of Mathematical Sciences, University of Nottingham. He is a Professor of Bioinfoamtics at School of Basic Medical Sciences at Southern Medical University.

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