

Drosophila Epigenomics

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Understanding how genomic information is translated into cellular functions constitutes a main challenge in Biology. The eukaryotic genome exists as chromatin, a nucleoprotein complex composed by DNA, regulatory RNAs and a variety of histone and non-histone proteins that are often modified and regulate expression of the genetic information contained in DNA. Chromatin contains both genetic information encoded in the DNA sequence and epigenetic instructions that, residing in DNA-associated factors and modifications, regulate its expression. Full understanding of the functional content of the genome requires description of the epigenetic information contained in chromatin or, in other words, the epigenome.

In recent years, after sequencing the genomes of several model organisms, large amounts of data have been gathered regarding different aspects of genome functioning, from gene expression and non-coding RNAs to the genomic distribution of epigenetic factors, namely DNA methylation, histone modifications and chromatin associated proteins. There are also numerous databases describing gene functions and interactions. Tools to analyze, visualize and integrate genomic data at a functional level are available. However, integrating experimental results and databases on epigenetic factors and genetic elements remains a challenge. In this regard we developed chroGPS, a global chromatin positioning system to integrate and visualize the associations between epigenetic factors and their relation to functional genetic elements in low dimensional maps. Here, we will describe chroGPS using data from the modENCODE project in *Drosophila*, which constitutes the most comprehensive dataset on epigenetic factors available to date, and its use to study new epigenetic factors and mechanisms in *Drosophila*.