Genome packing: the complicated complexity!

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Key words: Genome, nucleosome, PWS, ChromSTEM, heterochromatin, euchromatin.

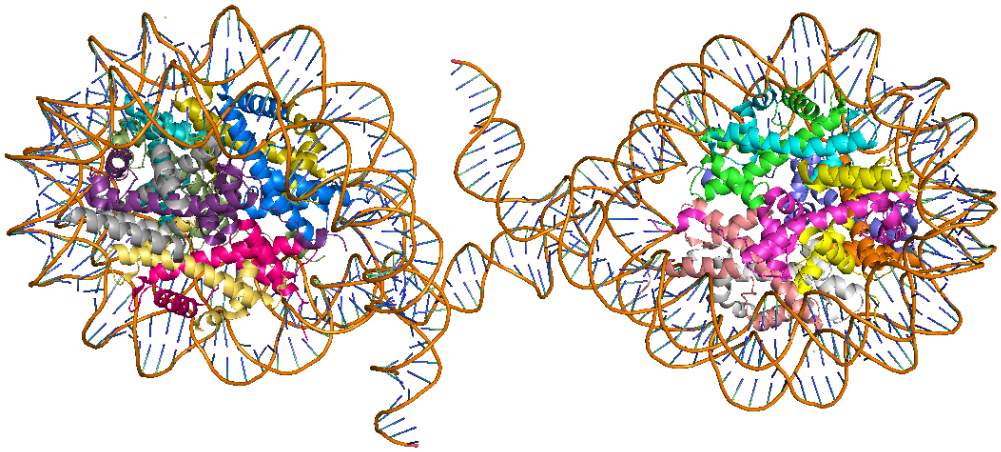

Figure 1. Structure of a di-nucleosome (PDB ID: 6M44) downloaded from the protein data bank. DNA double helix is wrapped around the complex of histones in each nucleosome.

Human genome is packed into 23 pairs of chromosomes that are contained inside the tiny nucleus of the human cell. Typically high school students learn the highly simplified structure of DNA double helix from textbooks with two strands running in parallel to each other with complementary sequences, A-T and G-C base pairs. However, in college, suddenly they are expected to understand the structure of nucleosomes (Figure 1). If one thinks that is hard, imagine the quasi-structure of nucleosomes which is of even higher order of genome packing! It is known that the genome is packed into chromatin where certain parts are silent with no activity (heterochromatin) while others are transcriptionally active (euchromatin). This commentary is about a recent article published in Science Advances by Huang *et al*. that describes the 3D model of chromatin packing. Huang *et al.* used live-cell partial wave spectroscopy (PWS) to image cells after 1 hour of heat shock at 42 °C to understand the chromatin response to a stress perturbation. This technique enabled them to image the live changes in the chromatin packing (heterochromatin vs. euchromatin). They used a self-returning random walk (SRRW) as a mathematical model to describe the quasi-structure of chromatin as tree-like domains connected with open backbone. With the help of chromatin scanning transmission electron microscopy (ChromSTEM) and PWS, they were able to show that the chromatin is minimally entangled due to higher-order folding principles and it varies from cell to cell as an added advantage to the humans. However, there is still a significant amount of randomness in packing!

References

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How to cite this article?
Ravikiran S. Yedidi. (2020). *TCABSE-J* Spl. issue 1:7-8. Epub: Oct25th, 2020.

Acknowledgements: The author thanks all staff members and volunteers that were an integral part of launching this special inaugural edition of TCABSE-J.

Funding: The author thanks TCABS-E, Rajahmundry, India and TyiDE-Toronto, Canada for financial support.

Conflict of interest: The author declares no conflict of interest.