There are approximately 40 trillion cells in human body. These cells are highly specialized as neurons, lipocytes, and muscle or blood cells, etc., to form tissues and execute essential processes for life. Strikingly, despite the diversity in their functionality, almost all cells in our body have the exact same copy of our genetic code, namely DNA. Therefore, cellular variety is not a consequence of genetic variances between cell types but it is rather due to epigenetic differences among our cells. That is, even though each cell bears the same genes, the way that those genes are activated in each cell type is different. One important component of epigenetics is three dimensional (3d) organization of genome inside the small, micrometer-size cell nucleus. While DNA molecules are essentially long, meter-size polymer chains, they can fit inside the micron-size nucleus and further take almost unique folding configuration for different cell types. Thus, the same DNA can organize differently in each cell type. This may be analogous to folding of the same type of A4 paper into different *Origami* shapes. Inevitably, abnormalities in the 3d organization of genome can impair the biological functions of a healthy cell since genetic regulation and genome organization are coupled. Interestingly, 3d genome organization also affects the shape of nucleus that it resides in. Nucleus is an elastic shell and thus can change shape under relatively weak forces caused by distortions in the normal DNA organization of a cell. Research has shown that anomalies in the nuclear shape and impaired nuclear organization of chromatin appear together in many cancer types and genetic diseases, including premature aging in children (Hutchinson-Gilford syndrome). Further, a gradual disruption of nuclear chromatin organization and shape is a hallmark of aging. Interestingly, malignant cancer cells seem to change the mechanical properties of their nucleus in a way that they can spread more efficiently to other tissues. Taken together, all these evidence suggests that there is a strong relationship between the 3d architecture of the genome, shape of the cell nucleus, and genetic function. A thorough understanding of such correlations at any level could generate groundbreaking information in a broad range of scientific and biotechnological fields. Our results will allow to connect hierarchical organization of the genome and shape and mechanics of cell nucleus . This project proposes to study this relationship in a computational-theoretical framework by combining the expertise and skills of two researchers. Overall, this research will contribute to the high-quality research environment of Poland by focusing on a highly inter-disciplinary, difficult, and novel research problem.