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Research area: Computational algorithms to investigate DNA packing and chromatin dynamics.

Main carriers of a hereditary information DNA molecules interact with histone proteins and form nucleosomes. Self-organized nucleosomes form a 30 nanometer fiber which coils into a very compact spatial structure called chromatin that forms chromosomes in the nuclei of the cells of the organisms. Patterns of nucleotide arrangement in DNA sequences influence chromatin formation. Our research topic is development and application of computational algorithms that can detect regularities of nucleotide arrangements in DNA sequences facilitating formation of a very compact chromatin structures.

Main publications

Pranckeviciene, E., Hosid, S., Liang, N., & Ioshikhes, I. (2020). Nucleosome positioning sequence patterns as packing or regulatory. *PLoS Computational Biology*, *16*(1), e1007365.

Pranckeviciene, E., Hosid, S., Maziukas, I., & Ioshikhes, I. (2022). Galaxy Dnpatterntools for Computational Analysis of Nucleosome Positioning Sequence Patterns. *International journal of molecular sciences*, *23*(9), 4869.