

Relating Epigenetic Information to the Structure of DNA Using Deep Learning

DNA is packaged around histone proteins as part of a structure called chromatin. In chromatin, histones make up spools which allow DNA to wind and unwind depending on which genomic regions need to be accessed. The structure of chromatin is dynamic: different pieces of DNA may be unwound or unwound depending on the cell's environment. Some changes in structure are normal, for instance exposure of clock genes at different stages of the circadian cycle, while others indicate disease such as cancer.

Small chemical tags called epigenetic tags can attach to the histone spools. They do not change the DNA itself, but influence how tightly the DNA is wrapped around the histones, and thus which genes are accessible. Epigenetic tags are sometimes inherited and their presence or absence can be influenced by factors such as diet and exercise. Epigenetic tags near a gene could indicate disease.

The goal of our research is to relate the structure of chromatin to epigenetic tags. We are building deep neural networks to predict the result of structural assays from epigenetic assays and vice versa. Since assays require costly materials and the time of an expert to conduct, the ability to predict the result of one assay from another could accelerate the pace of biological discovery. Additionally, an interpretability analysis of our system may explain how epigenetic tags affect the structure of chromatin.

LA-UR-21-27856