Bioinformatics Seminar Series

July 8th, 2022

14:00-15:30 at CB207

Contact: Hiroyuki Ogata (ogata@kuicr.kyoto-u.ac.jp)

A structural classification for plant transcription factors

Romain Blanc-Mathieu
Laboratoire Physiologie Cellulaire et Végétale, Université Grenoble Alpes, CNRS, CEA

Transcription factors (TF) recognize and bind specific DNA sequences in promoter regions of their target genes to regulate their expression. The binding occurs between the DNA binding domain (DBD) of the protein and its cognate DNA sequence called TF binding site (TFBS). The 3D structure of the DBD and the nature of amino acid lateral chains that establish contacts with the DNA define the protein binding specificity. On this basis, a structural hierarchical classification of mammalian transcription factors has been established (Wingender et al 2018). We reviewed experimental and predicted DBD structures available for transcription factor families in plant to integrate them into the mammalian classification and proposed new classes for plant-specific DBD folds. This classification clarifies evolutionary relationships between plant TF families and is currently used to arrange plant TFBS models in the JASPAR database. In the second part of the talk, I will introduce the bioinformatics tools we developed to characterize TFBS from genome-wide DNA binding data. I will illustrate the use of these tools by presenting a study where we tested the sensitivity of LFY, a master regulator of floral development, to DNA methylation and its ability to access closed chromatin and nucleosome-occupied regions.