Master 2 research internship in Integrated Structural & Cell Biology in Grenoble

Supervisor(s):
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Host laboratory:
LPCV, https://www.lpcv.fr/en

Host group/team:
 Flo_Re: Floral Regulators - Function, structure and evolution

Title of the M2 research internship:
Meta-analysis of Arabidopsis transcription factors DNA binding sites properties integrated in a structural classification

Project summary:
Transcription factors (TF) have a major role in the regulation of gene expression. They control the vast majority of biological processes ranging from the response to environmental stimuli to developmental programs such as flower formation in plants. To fulfil their function, TF specifically bind to DNA sequences (called transcription factor binding sites - TFBSs) or cis-regulatory elements to induce or repress gene expression. Our work on model TF such as LEAFY, ARF or MADS TF in the Flo_Re team (1–3) shows that the capacity to confront genome-wide in vivo and in vitro binding data is a key pre-requisite to future integrated functional analyses.

In this project, the applicant will process dozens of TF genome-wide DNA binding data (DAP-seq and ChIP-seq), using a bioinformatics pipeline developed in our laboratory, to characterize their binding properties. The applicant can build upon the existing pipeline to improve or add new tools. For example, he can contribute to ongoing efforts to identity DNA motifs that are specific to genomics regions bound by the TF in complex with an unknown partner. The applicant will synthesize the obtained knowledge to represent differences and similarities in binding properties between TF belonging to different groups (classes, families) organized based on the 3D structure of their DNA binding domain. The applicant will take advantage of this novel framework to interpret his results.

Keywords:
plant transcription factors, DNA binding sites, bioinformatics

Relevant publications of the team:
Lai X, Blanc-Mathieu R, GrandVuillemin L, Huang Y, Stigliani A, Lucas J, Thévenon E, Loue-Manifel J, Turchi L, Daher H, Brun-Hernandez E, Vachon G, Latrasse D, Benhamed M, Dumas R, Zubieta C, Parcy F. 2021. The LEAFY floral regulator displays pioneer transcription factor properties. Molecular Plant 14:829–837.

Lai X, Vega-Léon R, Hugouvieux V, Blanc-Mathieu R, Wal F van der, Lucas J, Silva C, Jourdain A, Muino J, Nanao M, Immink R, Kaufmann K, Parcy F, Smaczniak C, Zubieta C. 2021. The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors. Nature Communications 12.

Castro-Mondragon JA, Riudavets-Puig R, Rauluseviciute I, Berhanu Lemma R, Turchi L, Blanc-Mathieu R, Lucas J, Boddie P, Khan A, Manosalva Pérez N, Fornes O, Leung TY, Aguirre A, Hammal F, Schmelter D, Baranasic D, Ballester B, Sandelin A, Lenhard B, Vandepoele K, Wasserman WW, Parcy F, Mathelier A. 2022. JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Research 50:D165–D173.

Blanc-Mathieu R, Dumas R, Turchi L, Lucas J, Parcy F. 2022. Plant-TFClass: a structural classification for plant transcription factors. bioRxiv https://doi.org/10.1101/2022.11.22.517060.