



Grenoble Alliance for Integrated  
Structural & Cell Biology

## GRAL MSc RESEARCH SCHOLARSHIP 2020-2021 RESEARCH INTERNSHIP PROPOSAL

### Institute / Group

IRIG / PCV – Floral\_Regulators

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### Research Project Title

Prediction of gene regulatory network from genome sequence

### Description of the project

The regulation of gene expression is central to all biological processes. It involves a class of proteins called transcription factors (TF) that recognize short DNA sequences in the genome, and assemble into complexes to modulate gene expression. There are many experimental methods available to identify regulations, organism by organism and cell type by cell type, but this is a tedious task. Since a large part of the instructions governing these regulations are encoded in the genomic sequence, it should be possible to identify and deduce the structure of regulatory networks from the mere examination of multiple genome sequences. The availability of an increasing number of genomic sequences is a unique asset for detecting transcription factor binding sites (TFBS) and studying their conservation throughout multiple genomes as a criterion for a functional role.

The originality of the project is to combine several types of conservations: conservation of the binding sites, deep conservation of variable nucleotides in the vicinity of the binding sites (<https://doi.org/10.1105/tpc.19.00129>) and conservation of binding sites arrangements (spacing and orientation). This method will be first set up on a few transcription factors for which we have a good knowledge of transcriptional targets. The identification of conserved TFBS module will serve as a basis for the analyses of the protein/DNA complexes they form using biochemical and structural methods.

Background in programming (Python, R, Bash, statistical methods and data representation) highly recommended.

### Keywords

Computational biology, Transcription Factors, Complex formation, Flower development

### Relevant publications of the team

Khan, A., Fornes, O., Stigliani, A., Gheorghe, M., Castro-Mondragon, J. A., Van Der Lee, R., Bessy, A., Chèneby, J., Kulkarni, S. R., Tan, G., et al. (2018). JASPAR 2018: Update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 46.

Sayou, C., Monniaux, M., Nanao, M. H., Moyroud, E., Brockington, S. F., Thévenon, E., Chahtane, H., Warthmann, N., Melkonian, M., Zhang, Y., et al. (2014). A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. *Science* 343:645–8.

Stigliani, A., Martin-Arevalillo, R., Lucas, J., Bessy, A., Vinos-Poyo, T., Mironova, V., Vernoux, T., Dumas, R., and Parcy, F. (2019). Capturing Auxin Response Factors Syntax Using DNA Binding Models. *Mol. Plant* 12:822–832.

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