## Introduction

Previous research analyzing inter-species functional-genomics has mostly been focused on compare same assay matched experiments. These works have been crucial for in-depth study of molecular machinery, but missed the power of diverse datasets for conservation inference. In contrast to this narrow but deep knowledge bottleneck, we adopted a broad but shallow approach using heterogeneous functional-genomics to directly search simple large-scale answers that we would never have contemplated asking based on our understanding of single-assay/species information (cita). In the current Earth Biogenome era there are more and more genomes and functional tracks becoming available (cita), thus, highlighting the urge of using integrative tools that consider the vast diversity of biological strategies and enable broad genomic elements prediction. In the present study, taking into account the abovementioned knowledge trade-off, we introduced PlantFUN(ctional)CO(nservation) database constituted by several tools and two main resources, inter-species chromatin states and functional genomics conservation scores, for the well-known plant models *Arabidopsis thaliana*, *Oryza sativa* and *Zea mays*. Overall, both resources can elucidate evolutionary information in terms of cross-species functional agreement, therefore PlantFUNCO can complement other comparative-genomics sources to asses conservation and diversity. To illustrate how results derived from the resources generated could be functionally relevant, we developed an application of the database and found that chromatin state information improved paralogous degree of functional divergence predictions. Lastly, we validated the redundancy predictions based on phenotypic effects of AOX genes knockout mutants under several stres conditions.