PLAZA workshop

Functional annotation + rationale GO projection

September 14-15, 2017

# Topics Covered

In this series of exercises you will learn how to search the PLAZA platform for specific gene functions using keyword searches, Gene Ontology and InterPro. You will compare the results of different search functions and use gene family information to study gene function across different green plants and algae.

# Exercises

## Part 1: Searching the PLAZA 4.0 Dicots platform for a specific gene function

1. Perform a keyword search to identify **histone H4** genes. For *Arabidopsis thaliana*, *Zea mays* and *Amborella trichopoda* write down the number of genes found. [Search bar - Gene - do NOT filter for species of interest]
2. Repeat by searching for an InterPro term. How many genes do you recover for these 3 species? [Search bar – GO/InterPro/MapMan description]
3. Starting from the InterPro Histone H4 page, can you identify how many gene families in PLAZA4.0 contain histone H4 genes? [View the associated gene families]
4. Based on the phylogenetic profile of this histone H4 gene family, which species has the largest number of genes?
5. Again for this histone H4 gene family, generate a genome mapping view to determine how many of these genes are located in tandem duplicates. [Gene family page – View the genome wide organization of this gene family – Select species of interest]

## Part 2: Explore the GO annotations and evidences for a specific gene

1. Starting from the *Arabidopsis thaliana* gene PISTILLATA, which Biological Process GO annotations have been Inferred from Mutant Phenotype [Search bar - Gene - filter for species of interest – Explore GeneOntology tab]
2. For this GO term, how many species contain genes with this GO term based on Primary data?
3. Look for orthologs of PISTILLATA in *Brassica rapa* and check their GO annotations: based on what evidence are these genes annotated with floral organ identity? [Gene page – Explore the orthologs using the Integrative Orthology Viewer]