

docker: rocesv/plantina-chiplike

Epigenetic files processing

Preprocess - *trim_galore*

Mapping - *bowtie2*

Filter - *samtools/picard*

Calling - *macs2*

Format - *bedtools*

SRA+PCSD

10 marks

A.thaliana: 130

O.sativa: 63

Z.mays: 96

Table S1

Peaks and signal tracks

Correlations - *deepTools*

Figure S2

Inter-species CS: hiHMM

Annotation - *ChromHMM*

Figure 1

Overlap enrich. - *LOLA*

Figure 2

F. enrich. - *clusterProfiler*

Figure 3; S3

Application: Paralog modelling

Replicate two published models in *A.thaliana* including new CS-metrics

**Figure 4
Table S3**

Ezoe *et al.*, 2021

LR RImpt., Wilcox

LR Evaluation
(ROC,PR)

Filters and Prediction*

Cusack *et al.*, 2021

RF FImpt. Top Variables

SVM Evaluation
(ROC, PR)

Experimental Validation*; **Figure 6**

Whole Genome Alignments

WGA - *lastz CNEr***

Format - *lavToPsl, maf-cover***

Chaining - *axtChain, chainMergeSort***

Improve - *RepeatFiller, chainCleaner*

Netting - *chainNet, netSyntenic, netToAxt***

Bidirectional WGA using Kent+Hiller tools to improve sensitivity

CNEs
.netAxt files

WGA LiftOver
pipeline**

docker: rocesv/compcnes

Format - *deepTools*

Mapping - *STAR*

Preprocess - *trim_galore*

EBI-ATLAS

A.thaliana: 118

O.sativa: 43

Z.mays: 411

Table S2

RNA-seq files processing

LECIF Functional Conservation

Preprocess input - *LECIF*

Split data - *LECIF*

Training/tuning - *LECIF*

Score prediction - *LECIF*

Conservation - CNEs,
PhastCons-PlantRegMap

CS similarity- *R, philentropy*

Genetic variability- *LOLA*

Bidirectional
LECIF functional
conservation
score

At vs Os
At vs Zm
Os vs At
Os vs Zm
Zm vs At
Zm vs Os

**Figure 5
Table S4**

Resource: Database

Search

Genome Browser

LOLA enrichments

Public DB
tracks available
for future
applications

