

High-throughput data

Transcriptome arrays

ChIP-seq / DNase1 accessibility

1. Clustering of co-expressed genes

Transition profile discretization*

Discrete transcriptional signatures

Reported clusters

Co-expressed gene groups

2. Sequence retrieval

retrieve-ensemble-seq

upstream TSS | first intron | 5'UTR | 3'UTR

4. GO enrichment

compare-classes

Enriched GO classes

3. Motif discovery

dyad-analysis

oligo-analysis

peak-motifs

Discovered motifs

peaks

Read density

ZGA cluster

5. Motif enrichment

CisTargetX

Enriched motifs

6. Scanning for sites and CRERs

matrix-scan

Predicted sites and CRMs

RedFly

7. Enrichment of ChIP-seq reads

region ranking according to read densities*

Association CRM / chromatin marks

Putative CRMs involved in ZGA