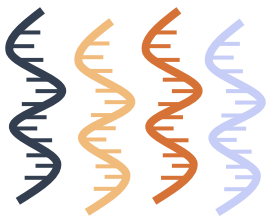
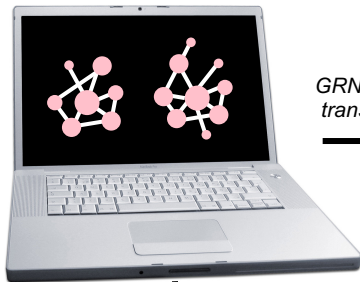


Transcriptome:
microarray, RNA-seq

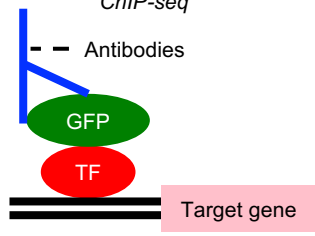


Coexpression network modeling

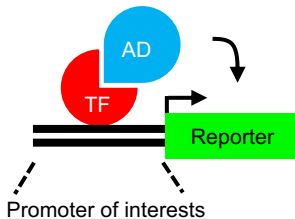


GRN inference from
transcriptome data

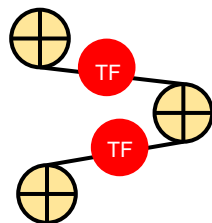
TF-DNA interactome
(Protein-centered approach):
ChIP-seq



TF-DNA interactome
(Gene-centered approach):
Y1H



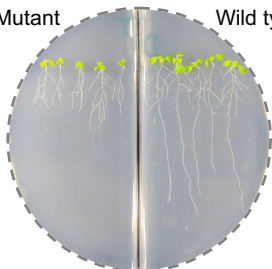
TF footprints:
Mnase-seq, DNase-seq,
ATAC-seq



Cistrome database
(DAP-seq and PBM)

Evaluation of biological functions of networks

Mutant Wild type



Integration into GRNs

CAAT

