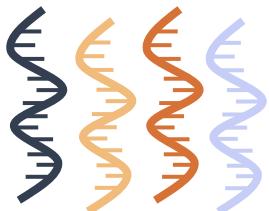
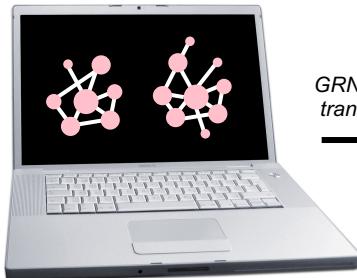


*Transcriptome:*  
microarray, RNA-seq



*Coexpression network modeling*



*GRN inference from transcriptome data*

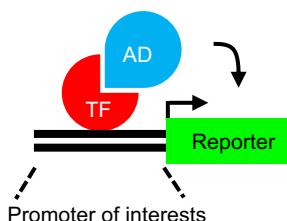
*TF-DNA interactome*  
(Protein-centered approach):  
ChIP-seq

— Antibodies

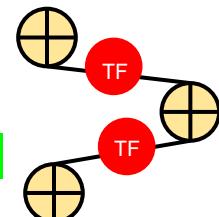


Target gene

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



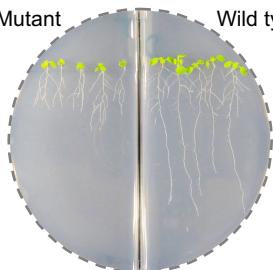
*TF footprints:*  
Mnase-seq, DNase-seq,  
ATAC-seq



Cistrome database  
(DAP-seq and PBM)

*Evaluation of biological functions of networks*

Mutant      Wild type



*Integration into GRNs*

