

- DHS-sites
- ATAC-seq peaks
- NOMe peaks
- TF-footprints
- ChromHMM segments
- Custom areas
- ...

Position specific energy  
matrices (PSEM)

Annotation of  
candidate sites

*(Thresholded) TF affinities  
computed per TF*

- Parameters for annotation
- Gene annotation

Gene scores

- *(Thresholded) TF- gene scores*
- *Region-based features*

INVOKE

Log2 fold changes of gene  
expression between samples

DYNAMITE

Gene-expression measured  
across several time points

EPIC-DREM

*Infer regulators related to  
measured static gene expression*

*Infer regulators related to gene  
expression changes*

*Key regulators in time series data*