

# Systematically validated inference of quantitative regulatory networks and condition-specific TF activity

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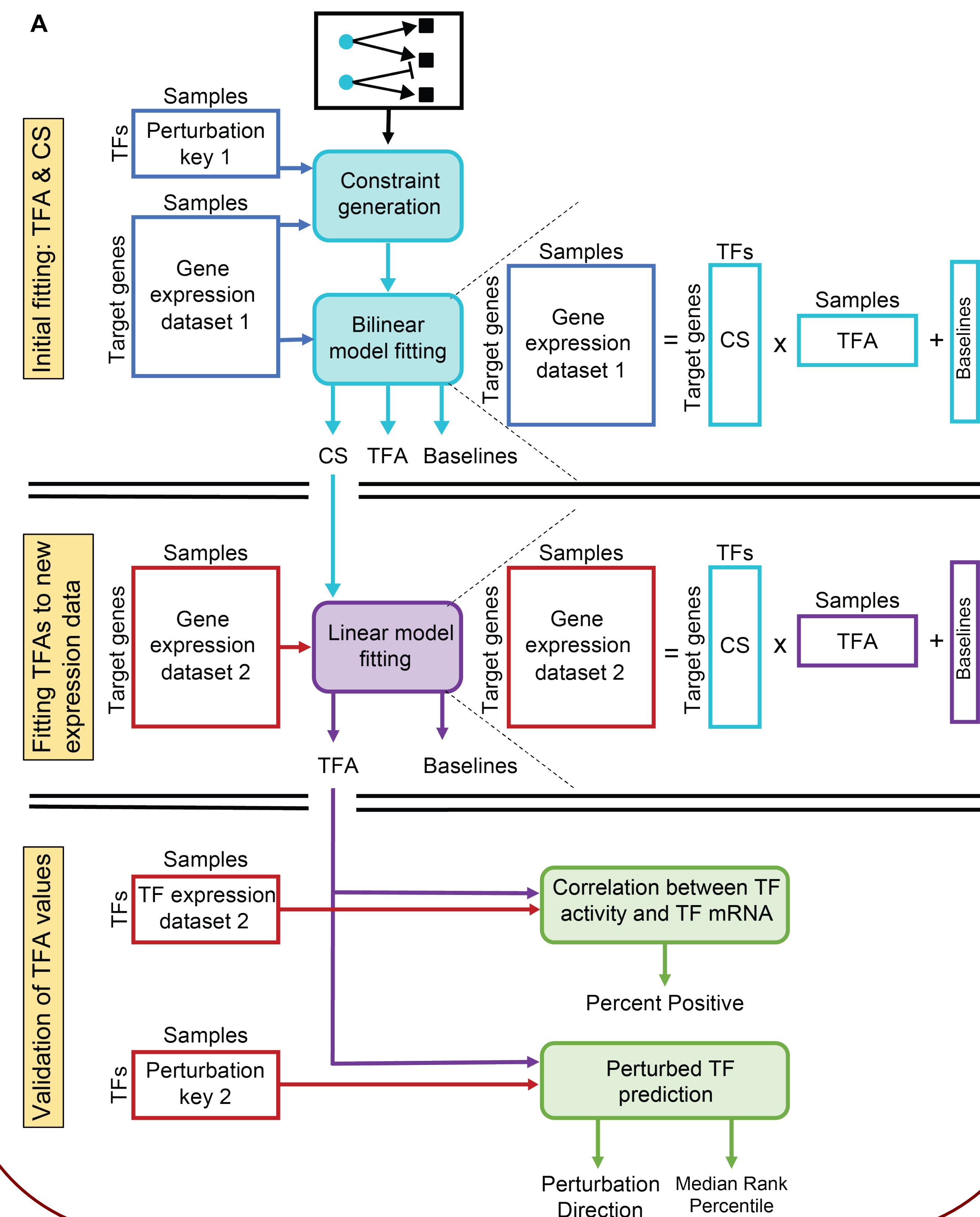
## Transcription factor activity inference

- Quantitative regulatory networks indicate the regulatory potential of TFs on their target genes
- Transcription factor activity (TFA) is the extent to which a TF is exerting its regulatory potential
- Many signals in biological systems are ultimately transduced by TFs, thus they are key to modeling gene regulation and predicting gene expression
- How might we quantitatively evaluate inferred regulatory networks and TFA?

## Signed binary starting networks

- 50 TF networks built with top ranked edges from ChIP, differential expression (DE) or log fold-change (LFC) after TF perturbation, or PWM
- TF-target edges defined repressing or activating using correlation of expression (CC) or expression after TF perturbation (PC)

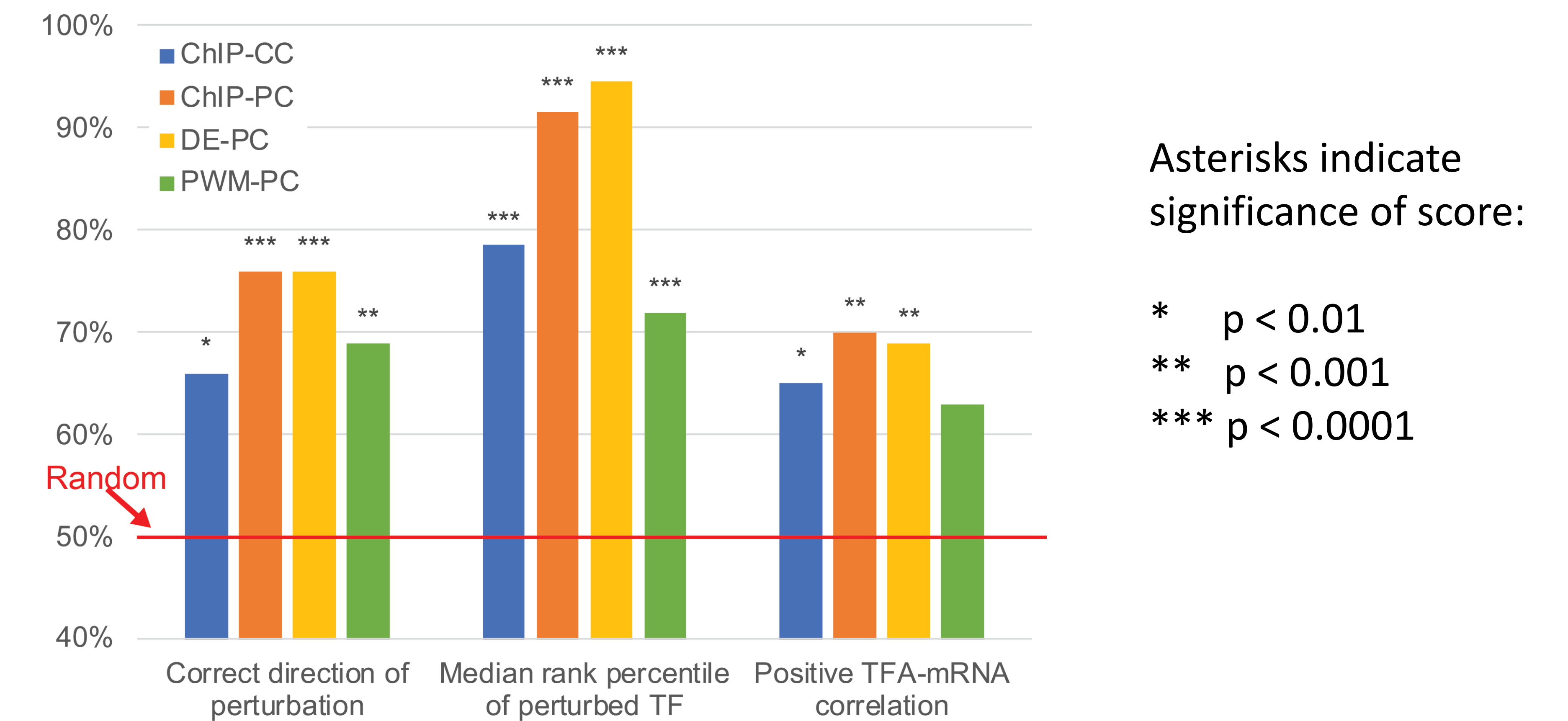
## Evaluation framework



## Performance metrics

- Correct direction of perturbation:** In samples where TFs are deleted/induced, percent correctly inferred activity values as less/greater than in the WT sample
- Median rank percentile of perturbed TF:** In samples where TFs are deleted/induced, median rank of inferred activity levels compared to unperturbed TFs. Rank 1 = 100%
- Positive TFA-mRNA correlation:** Percent of TFs whose inferred activity positively correlates with mRNA levels of their encoding genes

## Performance of inferred TFA



## Impact of optimizing a quantitative network

