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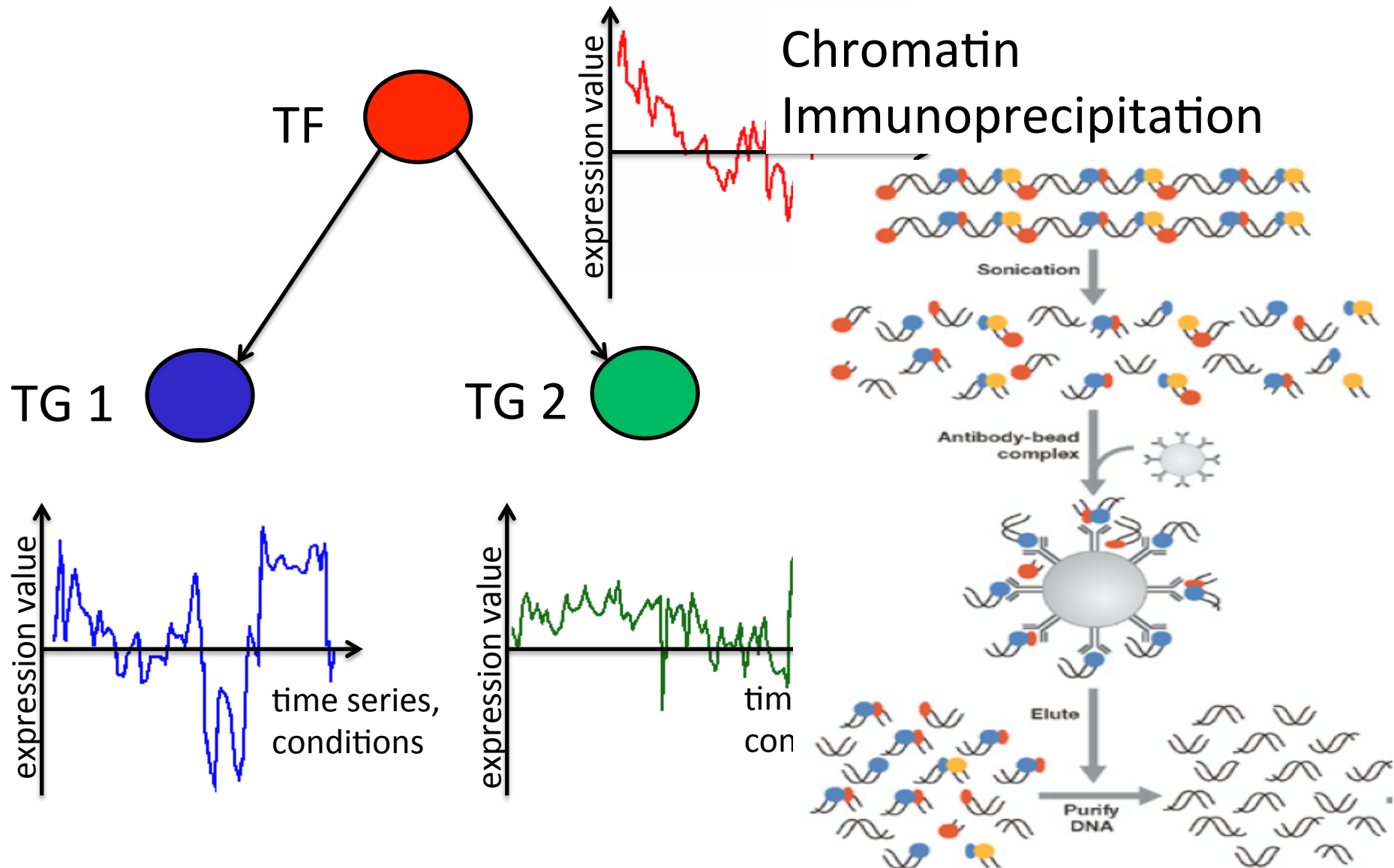
Extending partially known networks from SGS data

[STATSEQ meeting on Gene Network Inference
with Systems genetic data and beyond.](#)

28-29th March 2013, Paris, France
AgroParisTech - ENGREF 19 avenue du Maine

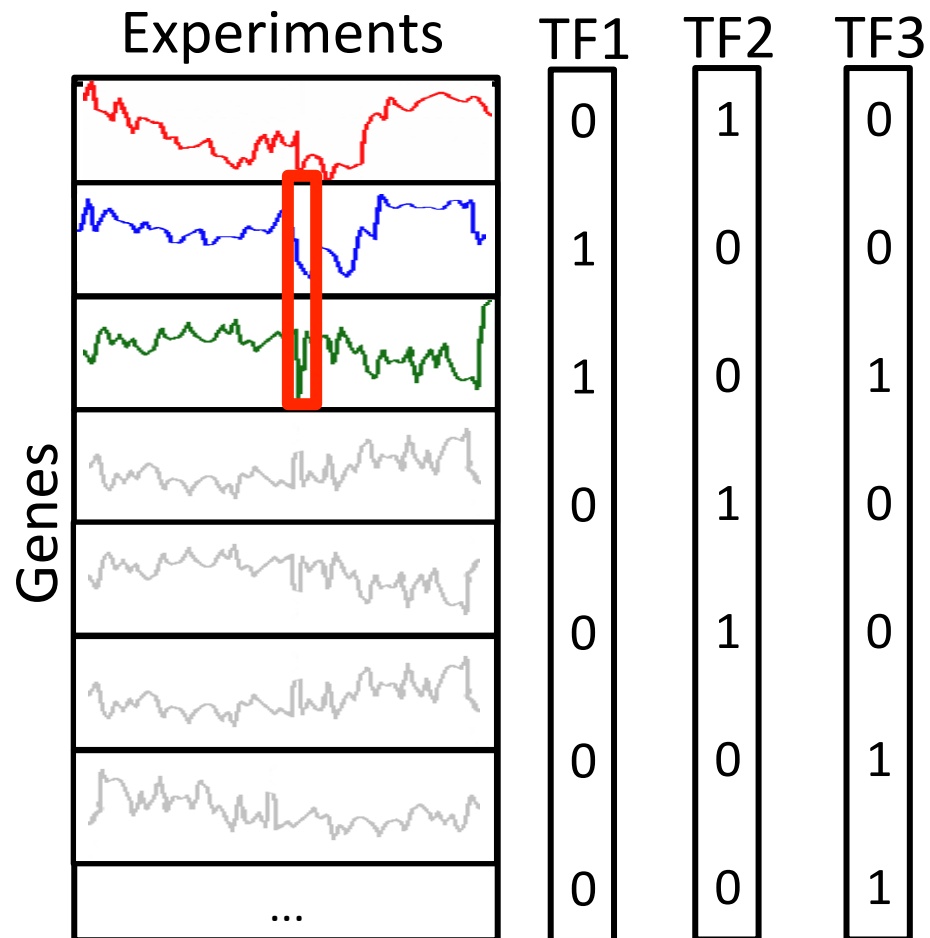


Intro: Gene Regulatory Networks

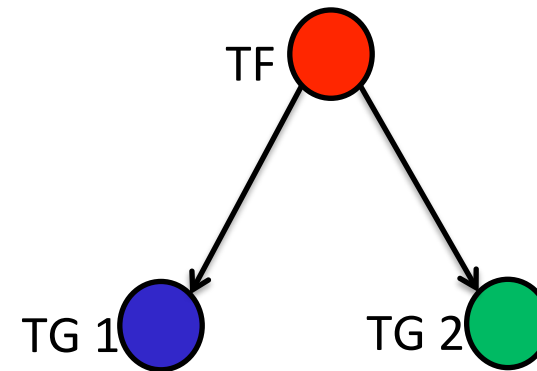


Methods: Unsupervised vs. Supervised

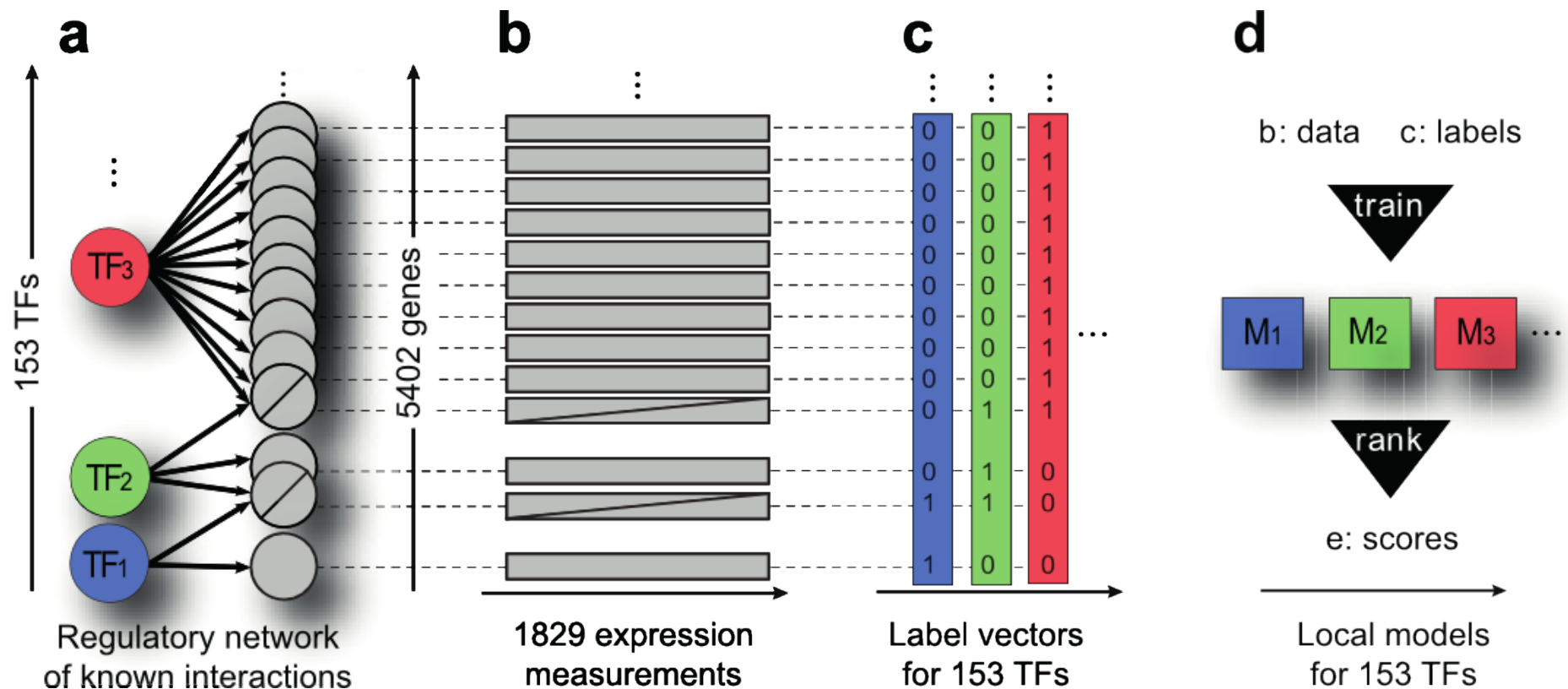
Unsupervised



Supervised

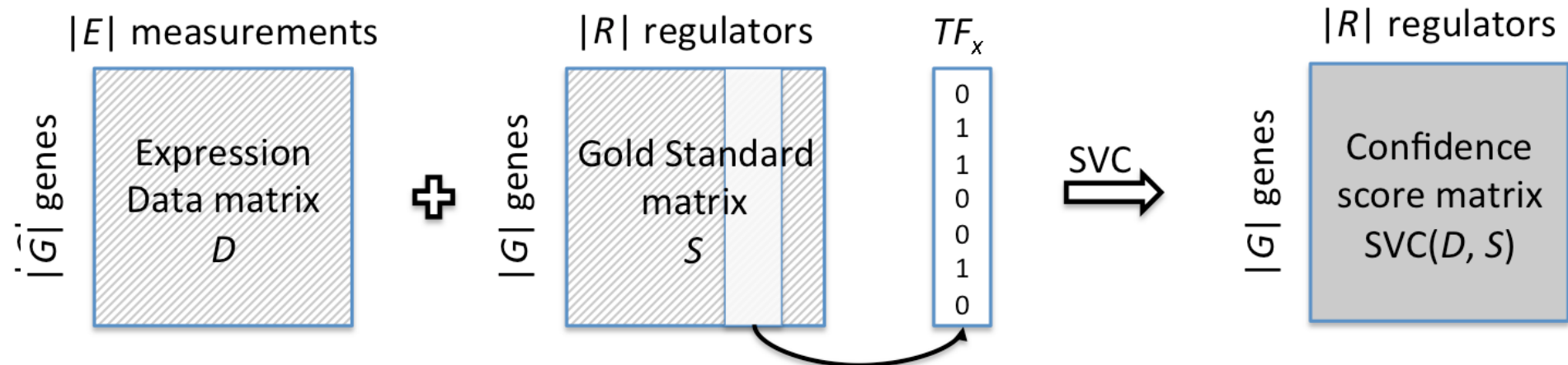


Methods: Supervised inference

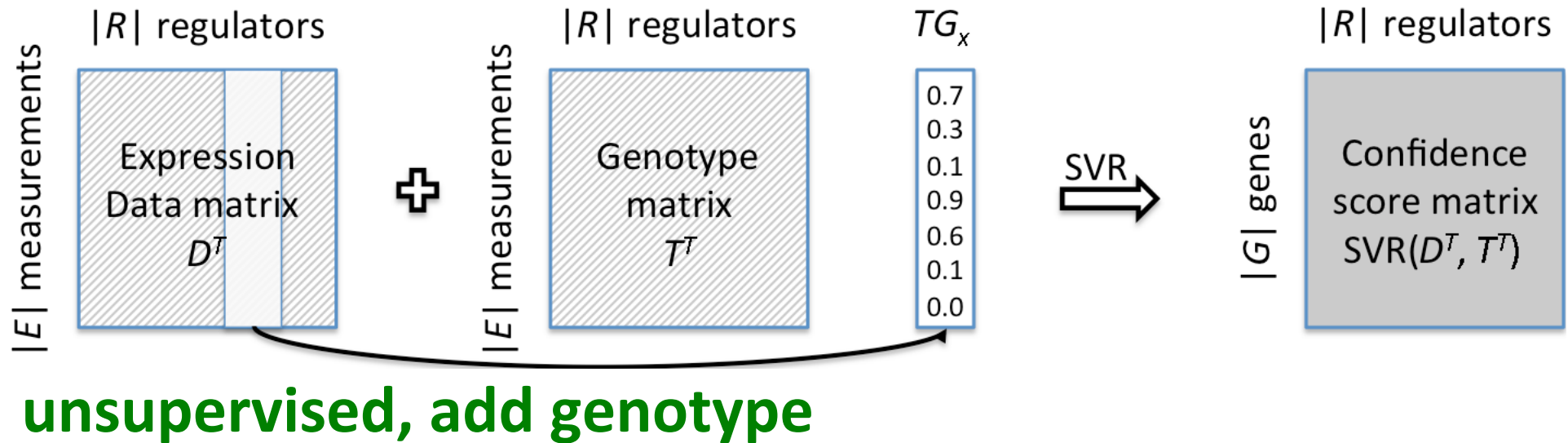


Methods: Variant 1

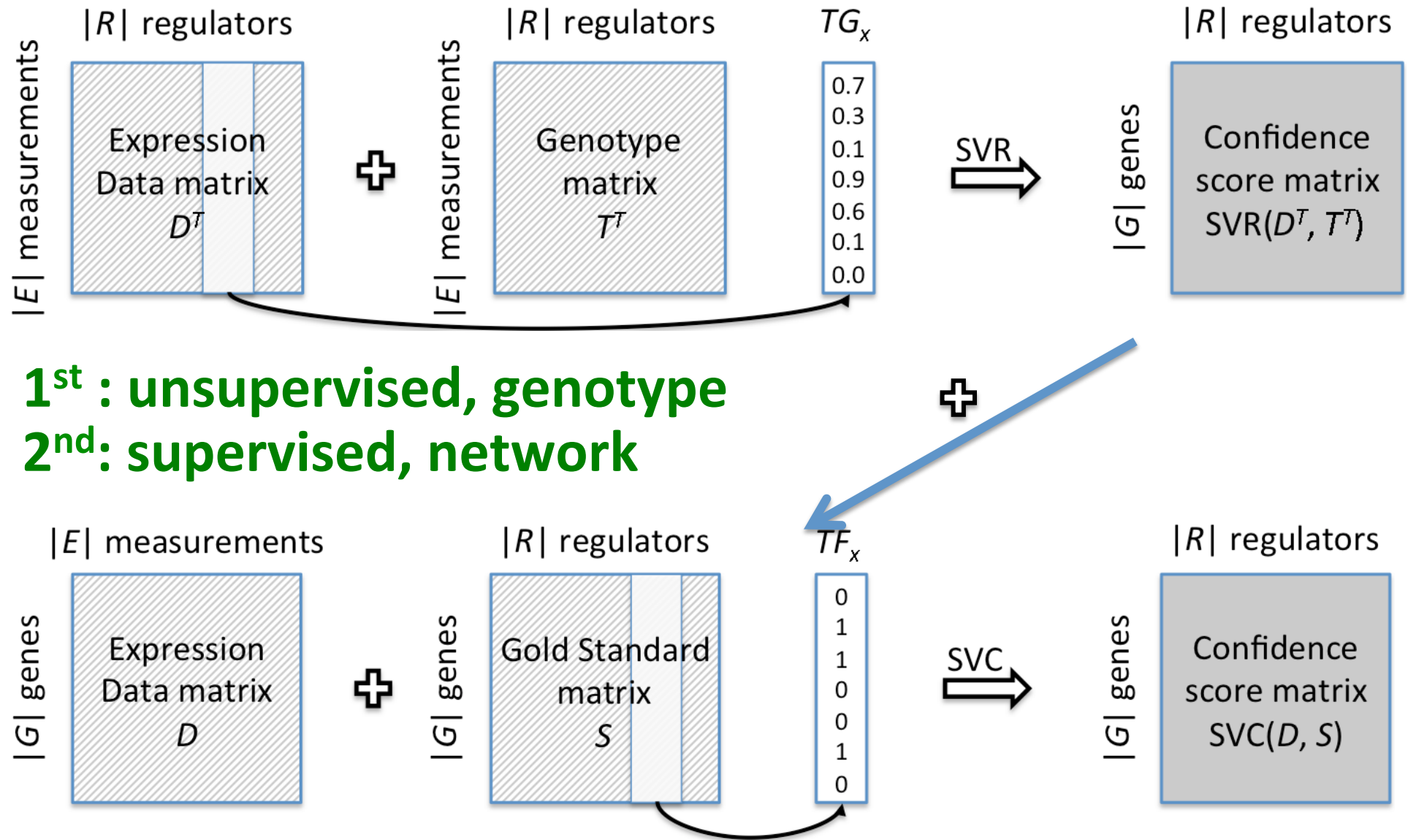
supervised, add network



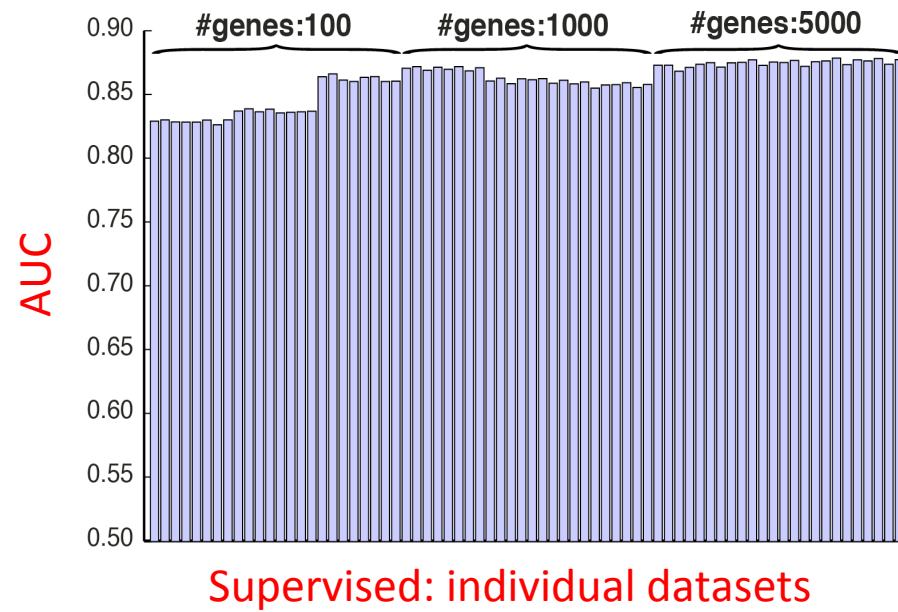
Methods: Variant 2



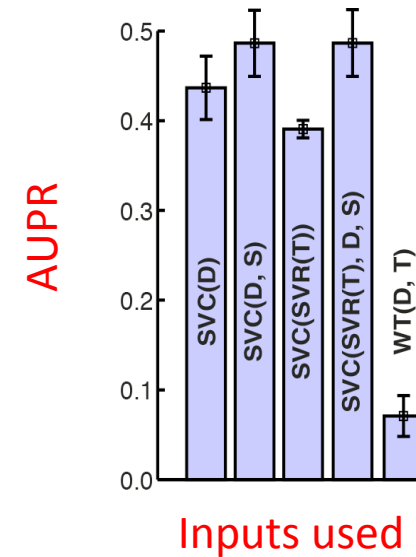
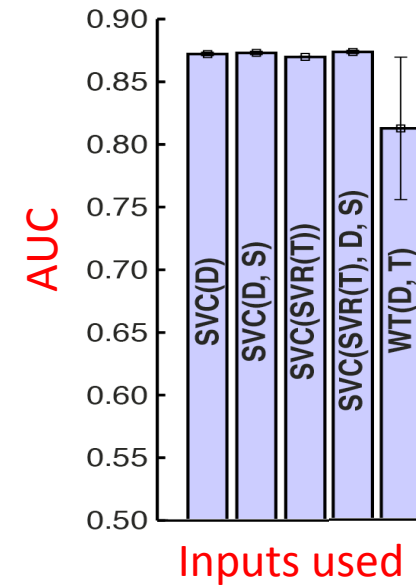
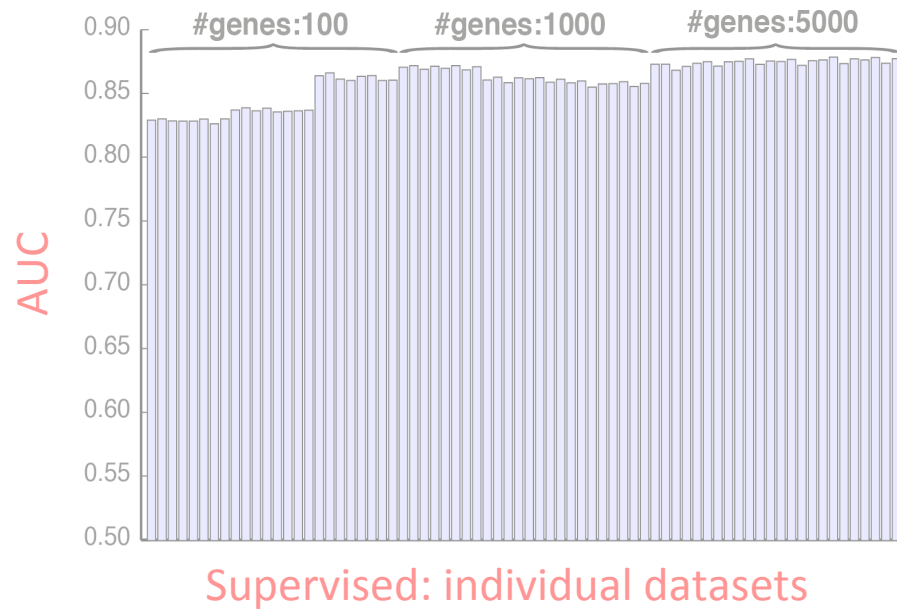
Methods: Both Genotype+Network



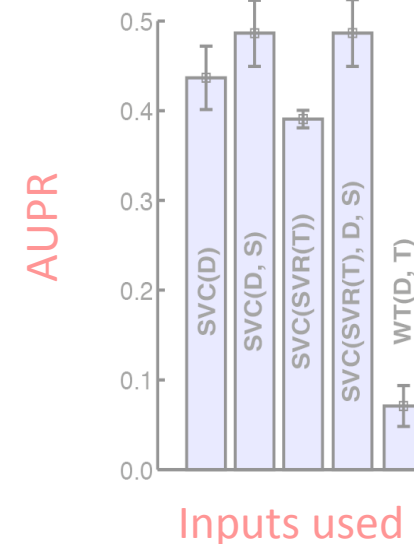
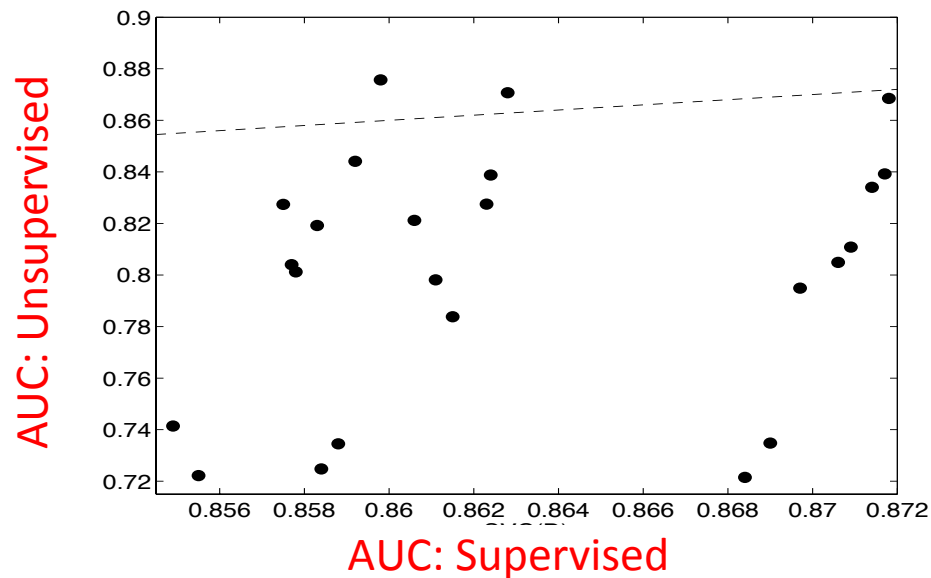
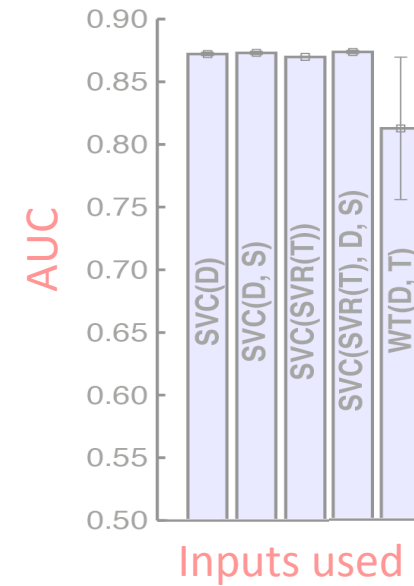
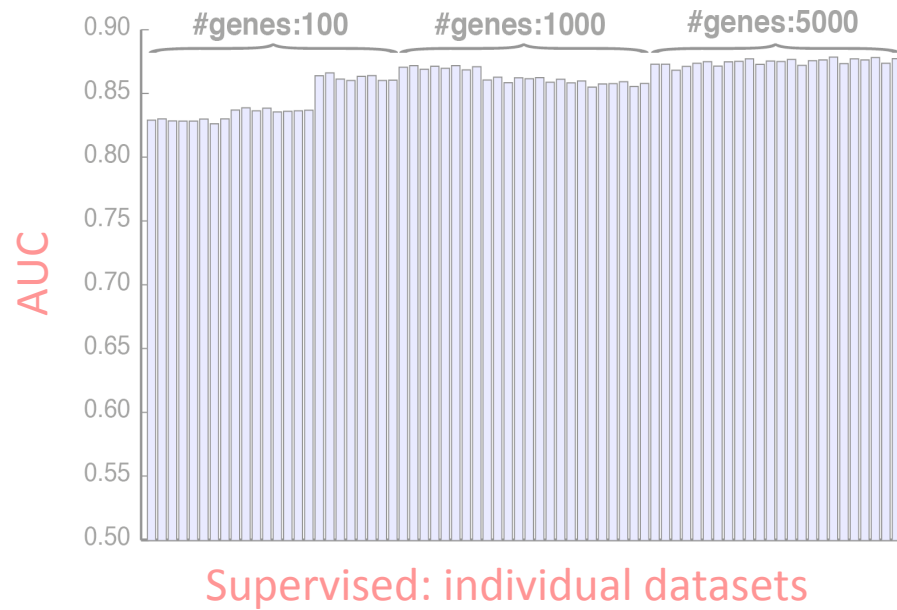
Results: Performance



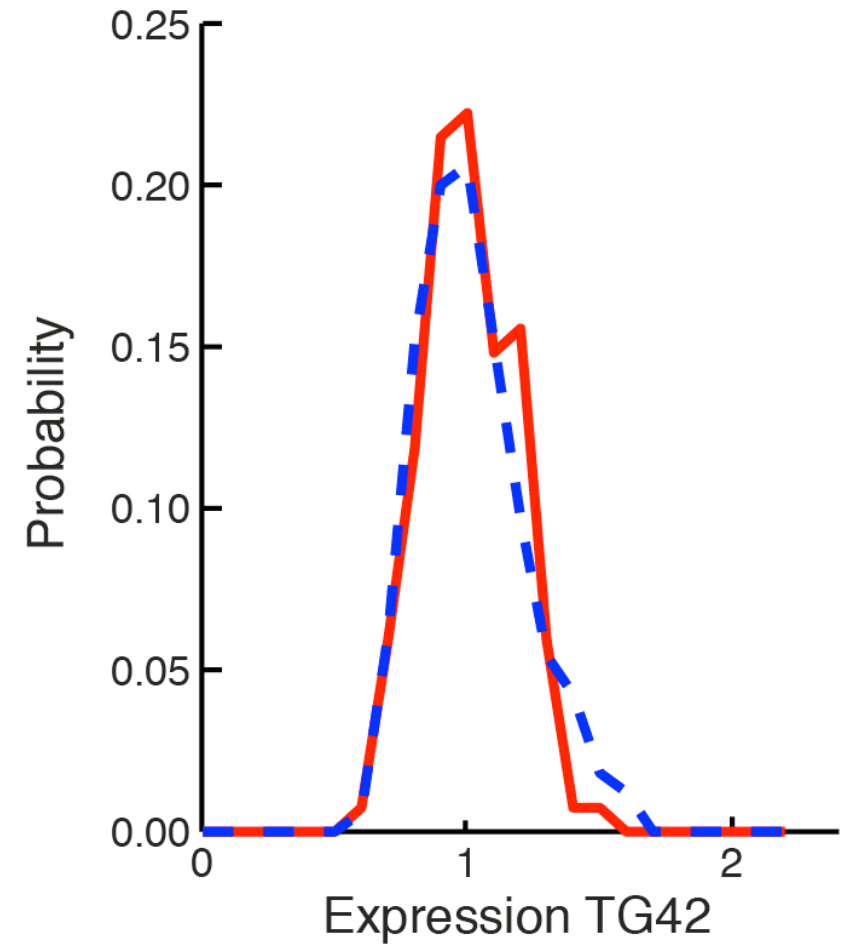
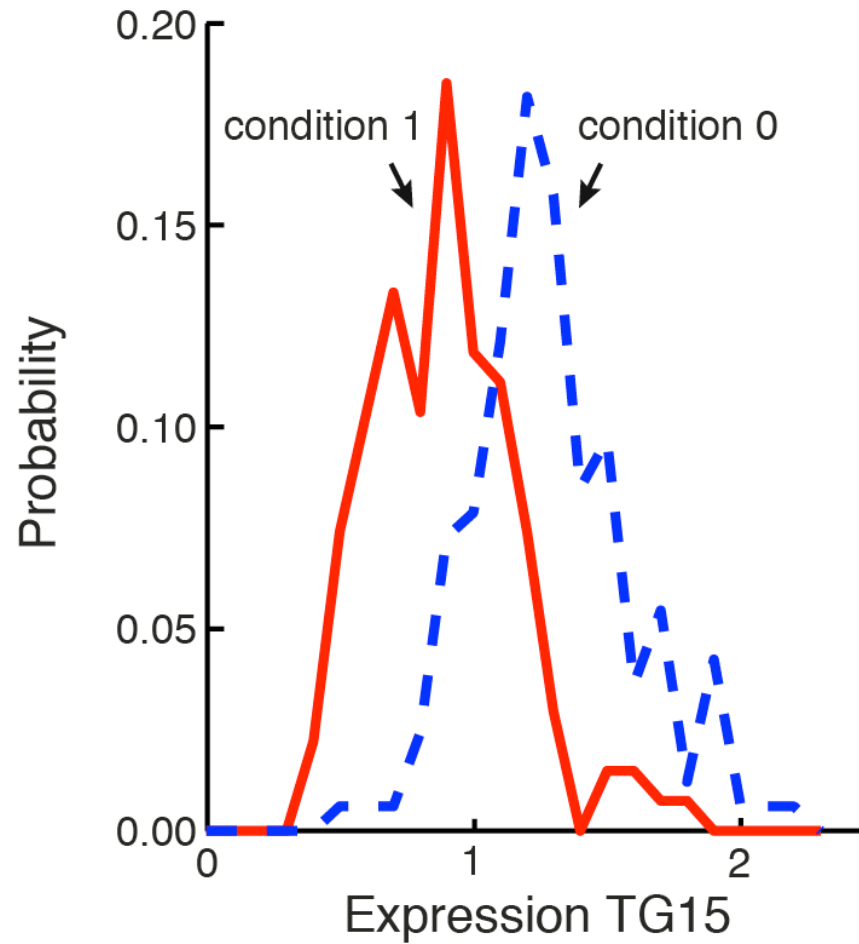
Results: Performance



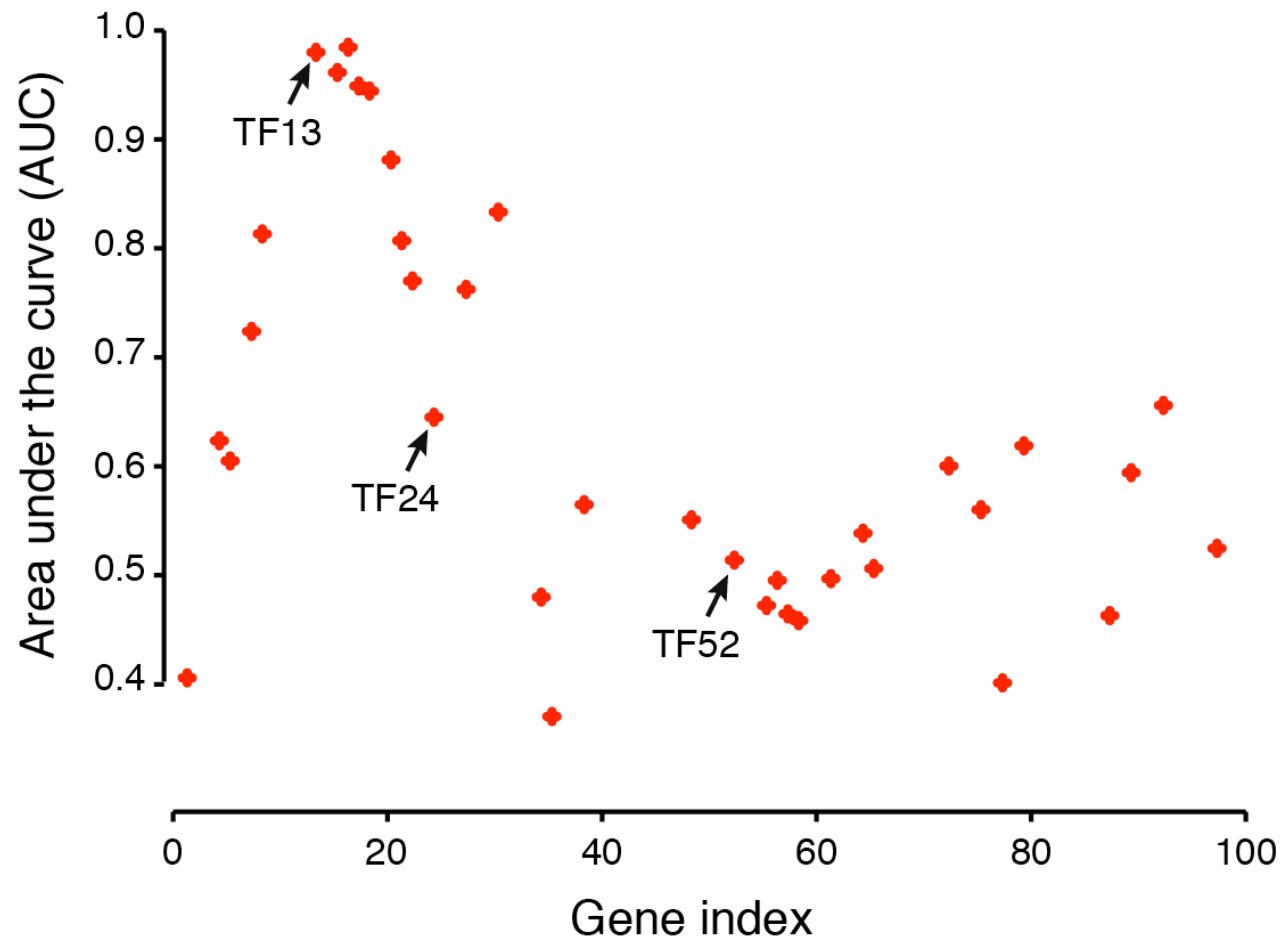
Results: Performance



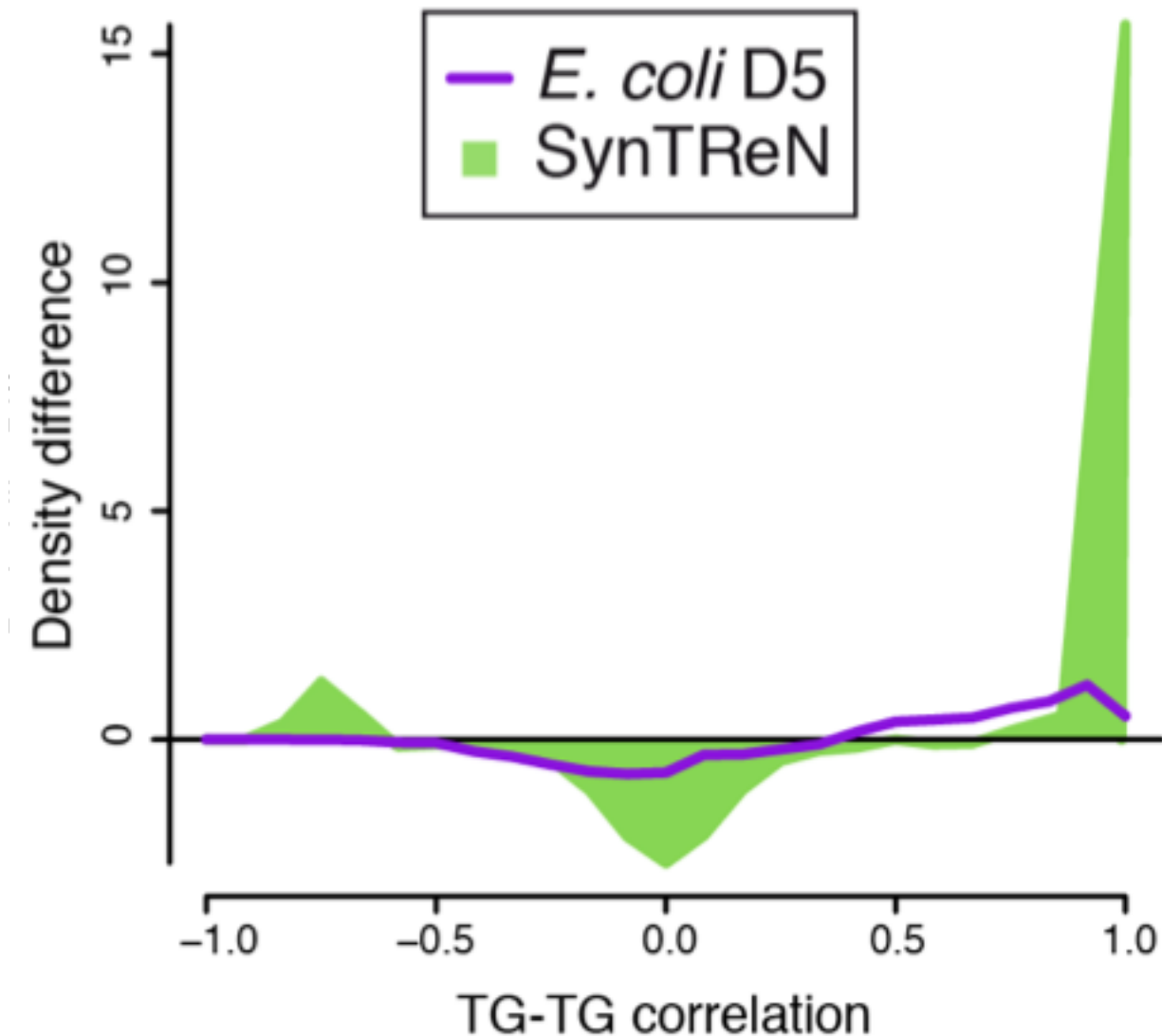
Results: Effect of Regulator Genotype



Results: Chromosomal Proximity



Results: Correlation vs Co-Regulation



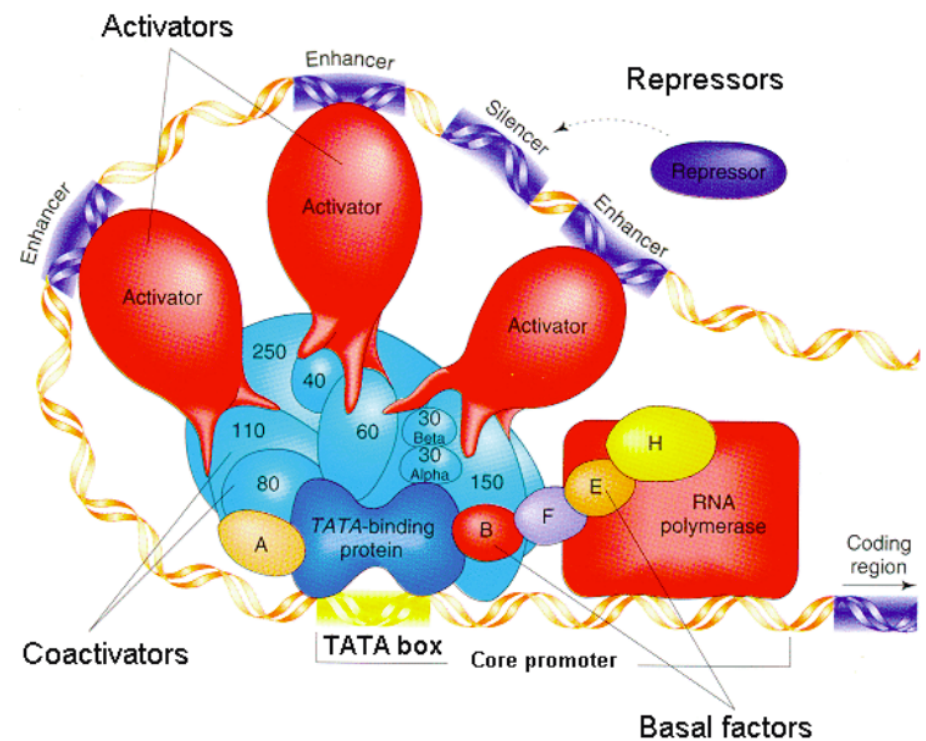
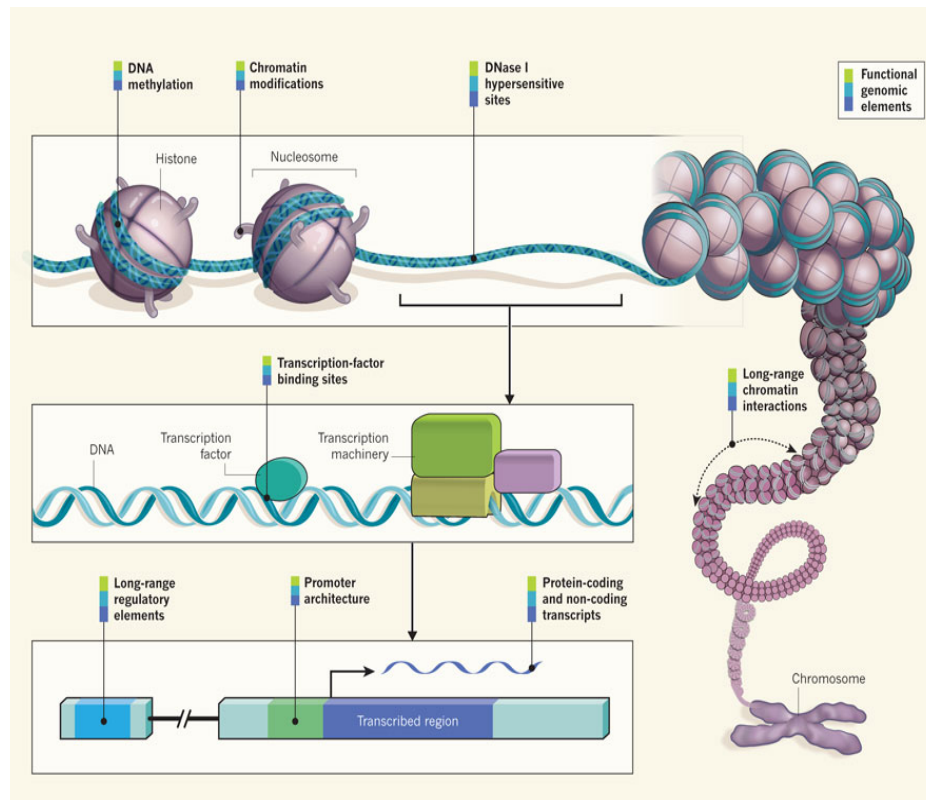
Discussion: Performance

- Supervision increases performance on SGS
- Robust against preprocessing, parameters
- Expression data most informative
 - Genotype information did not help
 - Less information for close TFs?
 - Deducible from expression in supervised setup?
 - Network context hardly helps

Discussion: Real vs SGS

- Network context hardly helps
 - functionally related TGs regulated by same TFs
 - functionally related TFs regulate similar TGs
 - TG overlaps $\Leftrightarrow$ correlated expression of TFs
- TGs regulated by same TF show extreme correlation in SGS
 - in comparison to bacteria
 - no correlation in eucaryotes!

Discussion: Complexity of Transcription



Discussion: Potential improvements

- Realistic network topologies?
- Careful parametrization of models?
- Complex genotypes & effects?
- Alternative splicing, protein networks?
- What else affects expression?
 - Methylation?
 - 3D DNA-DNA contacts
 - ...

Acknowledgements



- Robert Küffner
- Pegah Tavakkolkhah
- Tobias Petri
- Ludwig Geistlinger
- Ralf Zimmer

