

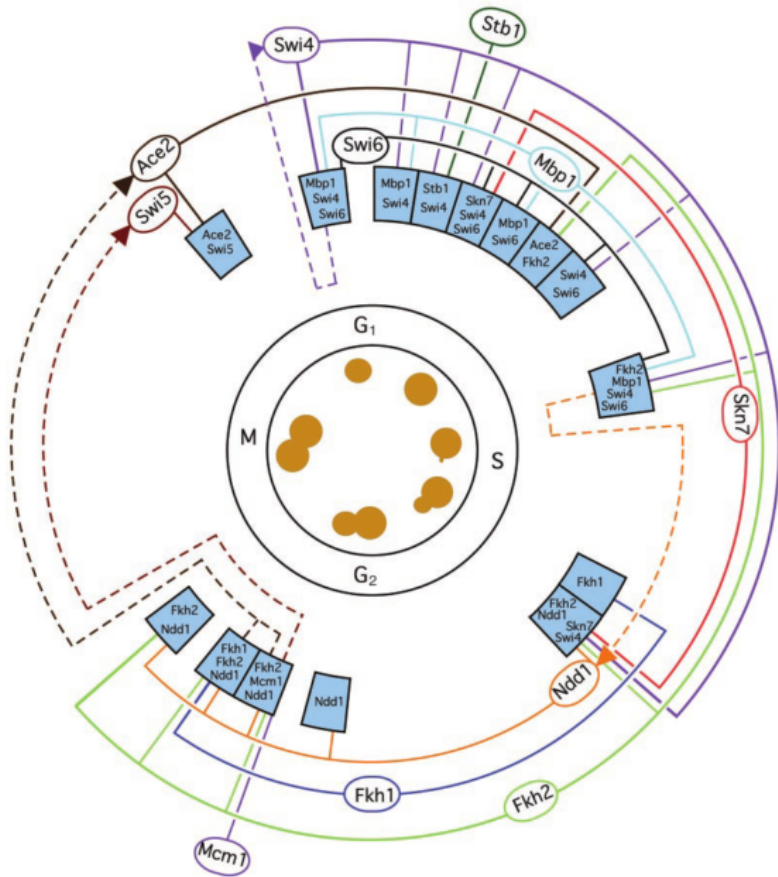
Multiomic regulatory network analysis via txRegQuery (formerly mongoDrillConductor)

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- Brief scientific overview
- Sketch of attack for one tissue, one TF

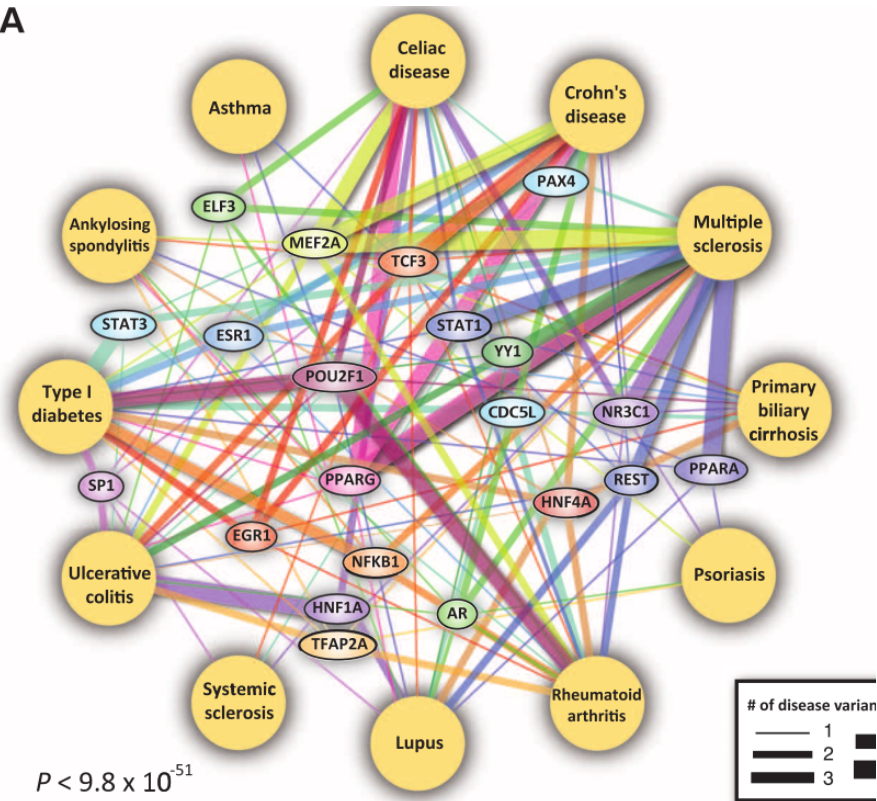
Lee, Rinaldi et al. *Science* 2002: TxRegNet for *S. cerevisiae*



- Condition/phenotype: stage G_1 , S , G_2 , M , budding
- Blue boxes: upregulated genes
- Ovals/Arcs: transcription factors and their periods of influence

Maurano, Humbert et al. *Science* 2012: “Common (human) disease network”

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- Disease:DNA – GWAS SNPs in FIMO-identified binding sites
- Sequence for motif finding: hg19-alt – all SNP sites coded as alternate allele , with GWAS SNPs that disrupt FIMO-identified binding sites (BSgenome has a method for SNP-injection)
- *New challenge:* from sequence-derived TFBS, epigenomically defined regulatory regions (tissue-specific), tissue-specific (GTEx) eQTL, derive regulatory networks to help interpret local COPD GWAS

FoxP1 Demo - FoxP1

Fox P1, eQTL, DNase I FP Data Demo

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