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Networks in the yeast genome

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We are far from understanding the how complex **transcriptional programs** are generated from genomic information. In the October 25 *Science*, Lee *et al.* report how they constructed a map of transcriptional regulatory networks in *Saccharomyces cerevisiae* by identifying all the sites bound by a large number of transcriptional regulators (*Science* 2002, **298**:799-804). They performed genome-wide **location analysis** to find binding sites for all 141 transcription factors listed in the Yeast Proteome Database. They then introduced a myc epitope tag into the genomic sequences encoding each factor. Using immunoprecipitation and microarray analysis, almost 4,000 regulator-DNA interactions could be defined. More than a third of all yeast genes were bound by one or more of the regulators and many were bound by multiple factors. The average number of gene promoters bound by an individual factor was 38. These data were used to construct **regulatory network** that are made up of different motifs - autoregulation, multicomponent loops, feedforward loops, and so on. Lee *et al.* studied cell-cycle-regulated genes to illustrate how an automated approach combining genome-wide location and expression data can be used to generate complex regulatory network models.

References

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