IN BRIEF

SYNTHETIC BIOLOGY

A fast, robust and tunable synthetic gene oscillator.

Stricker, J. *et al. Nature* 29 Oct 2008 (doi:10.1038/nature07389)

Synthetic biologists aim to engineer biological circuits that have predictable functions. The authors have constructed a genetic oscillator in *Escherichia coli* that is based on linking positive and negative transcriptional feedback loops. The oscillator is fast (with periods as short as 13 minutes), robust (oscillations are detected in almost every cell) and persistent, and the oscillatory period can be tuned by varying environmental conditions. A computational model that incorporates processes such as protein translation was used to develop an oscillator that was even more robust.

TECHNOLOGY

Nested patch PCR enables highly multiplexed mutation discovery in candidate genes.

Varley, K. E. & Mitra, R. D. *Genome Res.* 10 Oct 2008 (doi:0.1101/gr.078204.108)

One application of next-generation sequencing technologies will be to resequence candidate genes across many samples. The authors report a quick, sensitive and low-cost way of achieving this: nested patch PCR amplifies targeted regions of the genome for sequencing, and DNA barcoding allows samples to be pooled, thus reducing the number of sequencing runs. In a pilot study that used this method to compare colon cancer tissue and normal tissue, 90 out of 94 targeted exons were amplified from across the genome, and SNPs and one mutation previously associated with this type of cancer were reliably identified.

EPIGENOMICS

ChromaSig: a probabilistic approach to finding common chromatin signatures in the human genome.

Hon, G. *et al. PLoS Comp. Biol.* **4**, e1000201 (2008)

Few tools exist for identifying functional genomic elements from epigenetic information. This study describes a novel, unbiased computational method to address this challenge, called ChromaSig. The method identifies, from tiling microarray and sequencing data, commonly occurring combinations of histone modifications (chromatin signatures) that are associated with known regulatory elements. The authors recover previously known and novel chromatin patterns at known enhancers and promoters, and use these signatures to predict new elements of both types.

GENE REGULATION

Transcriptome-wide analysis of uncapped mRNAs in *Arabidopsis* reveals regulation of mRNA degradation.

Yuling, J. *et al. Plant Cell* 24 Oct 2008 (doi:10.1105/tpc.108.062786)

This study shows that mRNA uncapping is an important, previously unappreciated level of gene regulation. Uncapped transcripts are a key intermediate in mRNA decay, but they have not been studied on a large scale. The authors describe a new method for transcriptome-wide profiling of uncapped mRNAs that can be applied to any eukaryotic system. Using this approach in *Arabidopsis thaliana*, they showed that uncapped transcripts are highly regulated. The extent of uncapping varied among transcripts and correlated with the function of the encoded proteins.