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Studies of the transcriptome rarely take into account the structural context within a living cell. In the August 2 Science, Levsky *et al.* describe a sophisticated approach that monitors mRNA synthesis of multiple genes within single cells (*Science* 2002, **297:**836-840). They prepared oligomer DNA probes each tagged with a distinct fluorophore and combined them to create gene-specific spectral barcodes. They used these probes to follow the transcription of 11 genes in starved and serum-stimulated cells by FISH (fluorescence *in situ* hybridisation). They were able to measure expression in terms of signal intensity and the number of transcribed alleles. Some genes showed strong co-regulation, implying similar regulatory mechanisms. Comparison with microarray data ('FISH and Chips') highlighted the differences between single-cell recordings and global measurements of entire cell populations, and differences between the rate of transcription and the abundance of mRNA.

References

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2. The Singer lab, [http://www.singerlab.org]