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A cell of few modes

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In the July 18 [Proceedings of the National Academy of Sciences](#) Holter *et al.* subject existing microarray gene expression data to a kind of spectral analysis (*Proc. Natl. Acad. Sci. USA* 2000, **97**:8409-8414). This process of singular value decomposition (SVD) yields a set of "characteristic modes" that, when summed, reconstitute the entire expression pattern. But Holter *et al.* find that just two or three of the modes are sufficient to describe the vast majority of the expression data. This shows that expression patterns are simple, usually undergoing a single "on to off" or "off to on" transition in response to a perturbation. Analysis of [cell cycle data](#) suggests that generally genes are not activated or repressed in large, discrete groups, as previously thought, but that cell cycle progression is a smooth function with roughly equal numbers of expression changes per unit time.

References

1. Proceedings of the National Academy of Sciences, [<http://www.pnas.org/>]
2. Comprehensive identification of cell cycle-regulated genes of the yeast *Saccharomyces cerevisiae* by microarray hybridization.