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The Transcription Consortium of the [EUROFAN network](#) set itself the task of generating a large set of gene expression data in yeast using classical northern analysis. In the June 15 [EMBO Journal](#), Brown *et al.* present the results of analysing over 1,000 genes in yeast under eight different physiological conditions (*EMBO J* 2001, **20**:3177-3186). These include mid-exponential phase growth, and various physiological stress conditions. The five member laboratories of the [Consortium](#) paid especial attention to the standardizing of their RNA and hybridization protocols. They used [algorithms](#) to 'mine' the data and perform cluster analysis. This analysis enabled them to assign potential functions to clusters of ORFs. They compared the northern blot [data](#) for 1,008 ORFs with that generated by [microarray analysis](#). Brown *et al.* claim that this is probably the 'largest set of transcription data that has ever been collected using this classical technique... and it is unlikely to be surpassed.' The authors urge the yeast research community to adopt standardized strains, growth conditions and data normalization procedures, in an attempt to generate reproducible and comparable transcriptome data.

References

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