



“ potential of this approach to map gene regulatory programmes in great detail ”

Two studies published in *Science* report the comprehensive transcriptional profiling of multicellular organisms using single-cell sequencing.

Cao *et al.* present a newly developed technique termed single-cell combinatorial indexing RNA sequencing (sci-RNA-seq), which they use to obtain 42,035 transcriptome profiles of single cells from the nematode *Caenorhabditis elegans* at the L2 larval stage. The team defined consensus expression profiles for 27 cell types from the transcriptomic data. In addition to the mapping of 18 non-neuronal cell types, the authors identified many neuronal cell types, including some known to correspond to merely one or two cells in the larval worm, highlighting the potential of this approach to map gene regulatory programmes in great detail. Integration of the sci-RNA-seq profiles with whole-animal chromatin immunoprecipitation followed by sequencing (ChIP-seq) data enabled the team to elucidate cell type-specific effects of individual transcription factors.

Karaiskos *et al.* focused on mapping gene expression in the *Drosophila melanogaster* embryo at single-cell resolution using massively parallel droplet-based single-cell sequencing (Drop-seq). The authors devised a computational mapping strategy called DistMap, with which they were able to predict spatial gene expression at near single-cell resolution. They used DistMap to virtually reconstruct the fly embryo, with each single-cell transcriptome (~8,000 expressed genes per cell) mapped to its specific location within the embryo, and built the *Drosophila* Virtual Expression eXplorer (DVEX). DVEX enables the prediction of spatial expression for thousands of genes, the computation of expression gradients, and the generation of virtual *in situ* hybridizations for single genes and gene combinations. The team showcased the potential of DVEX by applying it to uncover patterned expression of transcription factors, long non-coding RNAs and signalling pathway components.

To allow further exploration of the transcriptomes by the community, both teams have made their data available online.

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ORIGINAL ARTICLES Cao, J. *et al.* Comprehensive single-cell transcriptional profiling of a multicellular organism. *Science* 357, 661–667 (2017) | Karaiskos, N. *et al.* The *Drosophila* embryo at single-cell transcriptome resolution. *Science* <http://dx.doi.org/10.1126/science.aan3235> (2017)

WEB SITES

Cell Atlas of Worm: <http://atlas.gs.washington.edu> | DVEX: www.dvex.org