

TRANSCRIPTOMICS



Bulk sequencing

Yields averaged gene expression across entire tissue sample



Single-cell mRNA seq

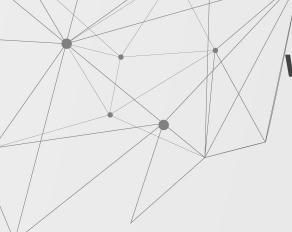
Dissociate cells from tissue to discern cell types on the basis of gene expression



Spatially resolved

Get transcriptomic data and know the positional context of those cells in a tissue

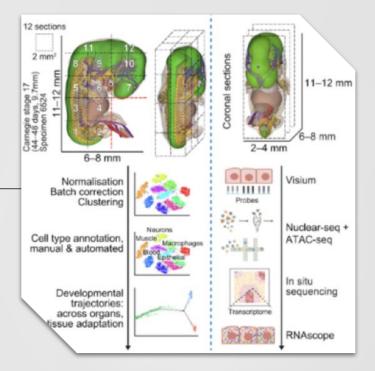




WHOLE EMBRYO PROJECT

HUMAN CELL ATLAS

Profile single cells from dissociated tissues and within intact tissue sections, to reconstruct a three dimensional atlas of the whole human embryo.





WEB PORTAL PROJECT TEAMS



DAVE HORSFALLResearch Software
Engineer, Newcastle

University



OMER BAYRAKTAR
Group leader in Cellular
Genetics, Wellcome Sanger
Institute



Professor of Dermatology and Immunology, Newcastle University & Wellcome Sanger Institute

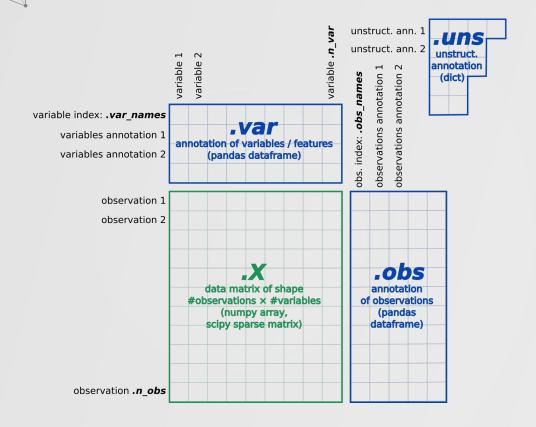


JASON SWEDLOW

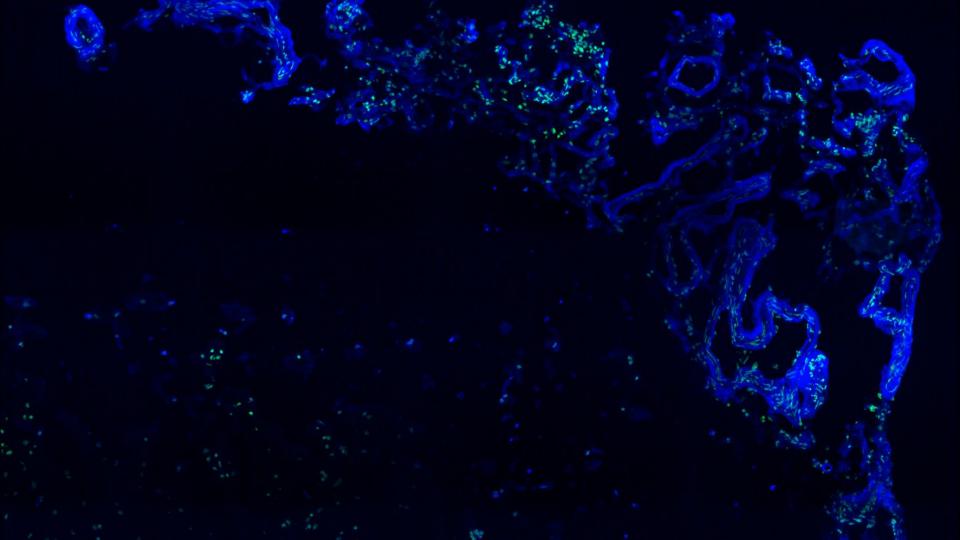
Professor of Quantitative Cell Biology, Open Microscopy Environment, University of Dundee

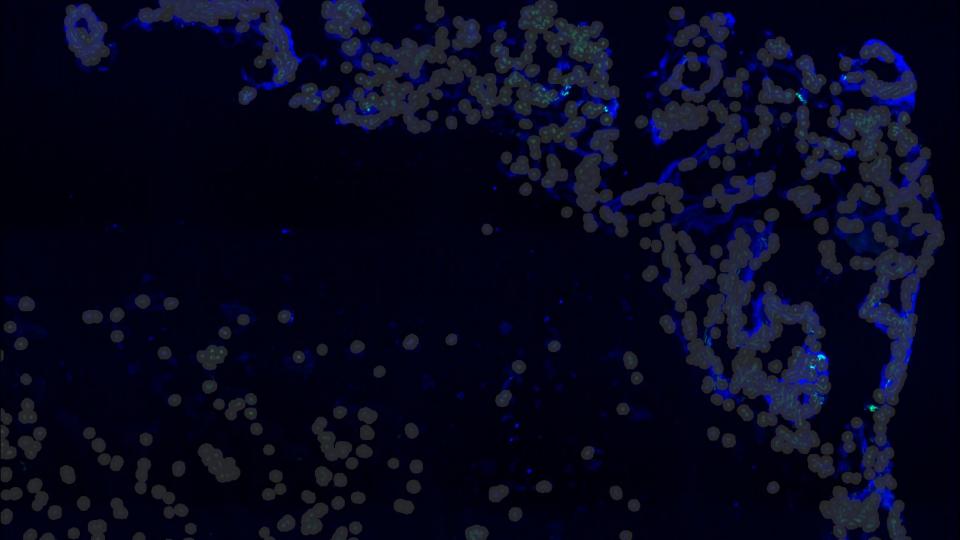


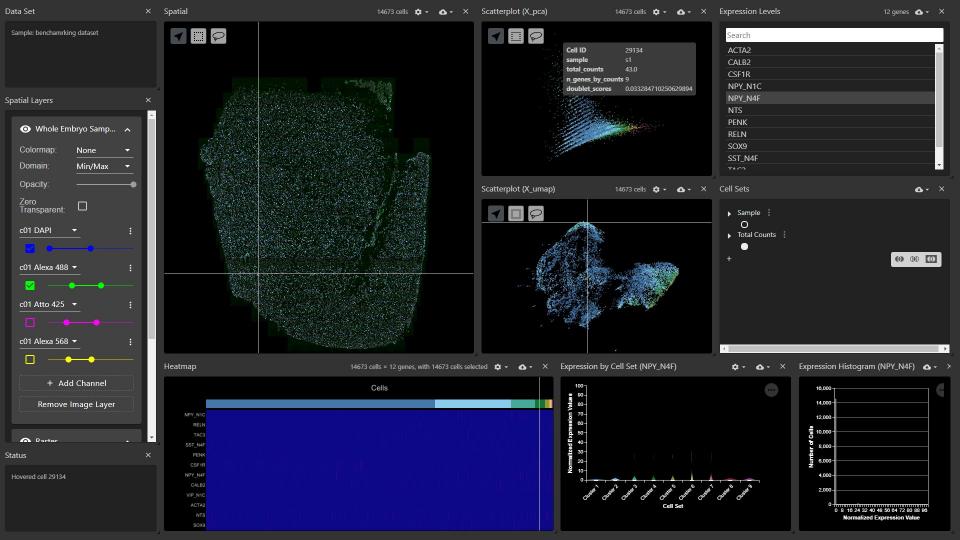
ANNDATA MODEL





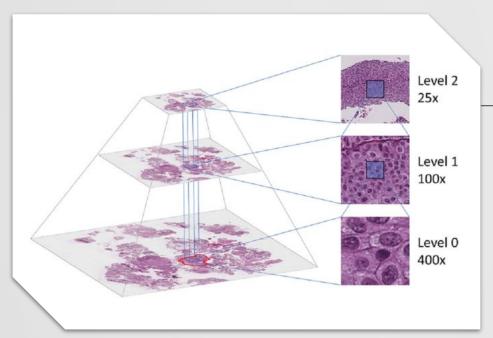








PYRAMIDAL IMAGE FORMATS



A Multiscale Approach for Whole-Slide Image Segmentation of five Tissue Classes in Urothelial Carcinoma Slides

DOWNSAMPLE

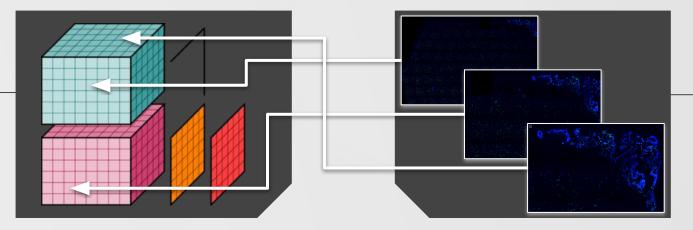
Pyramids are used to improve performance. They are a downsampled version of the original raster dataset, and are designed to support efficient zooming to different spatial resolutions.



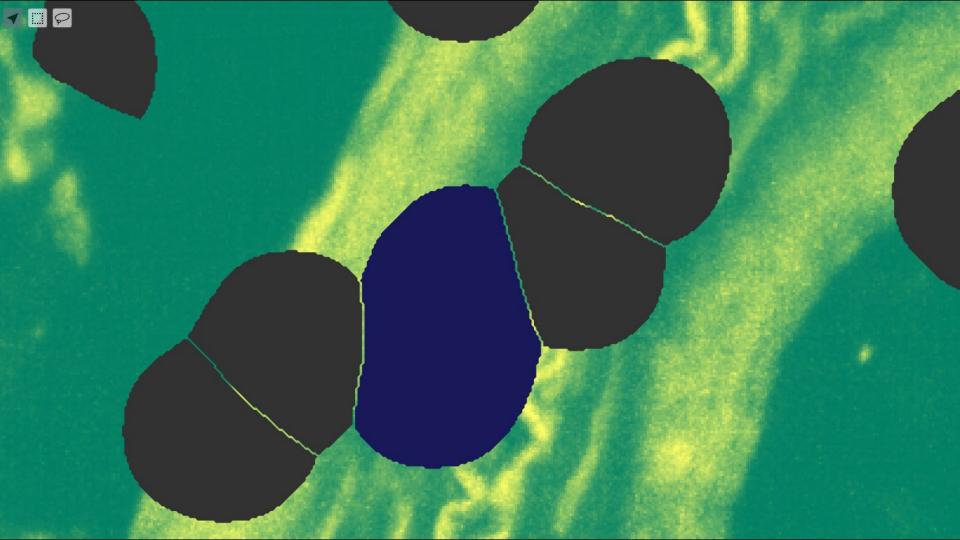
Zarr is a format for the storage of chunked, compressed, N-dimensional arrays.

CLOUD HOSTED ZARR STORE

VISUALISATION APP













City of Melbourne 3D Point Cloud 2018, visualised in experimental Tile3DLayer of DeckGL

CELL BOUNDARIES AS RASTER BITMASKS

