

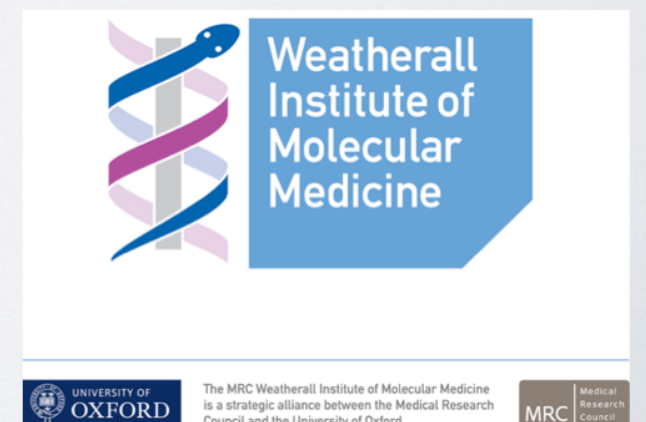


Nanoscscopy Oxford

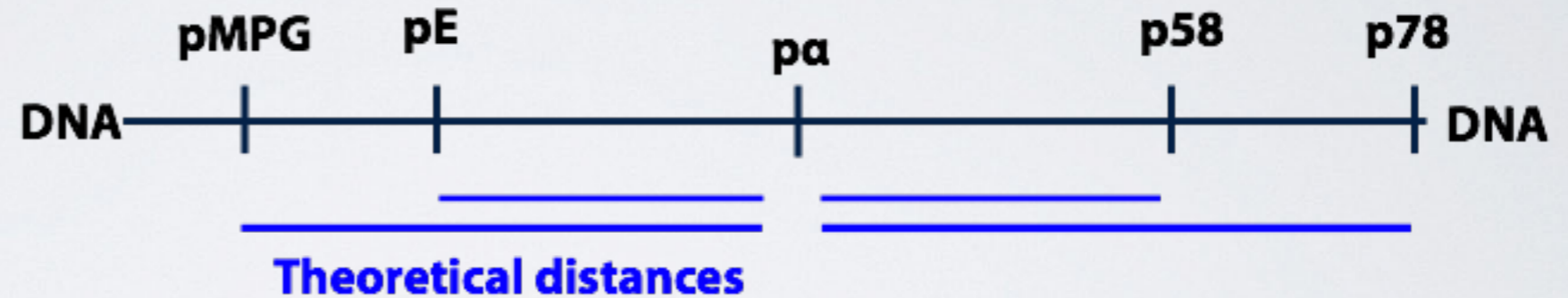
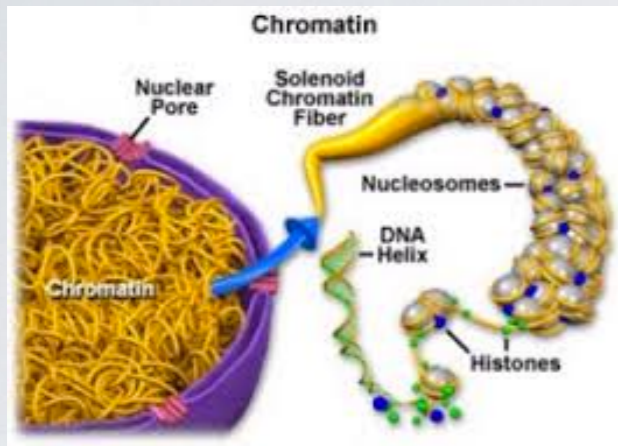


High-throughput FISH image analysis pipeline using OMERO.

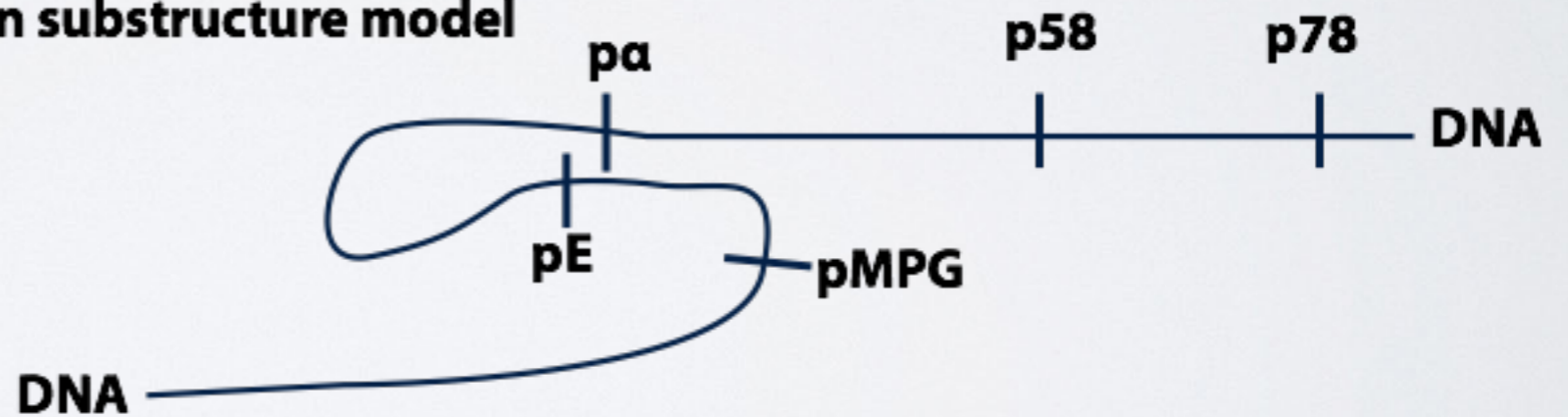
by Dominic Waithe



CHROMATIN STRUCTURE



Chromatin substructure model

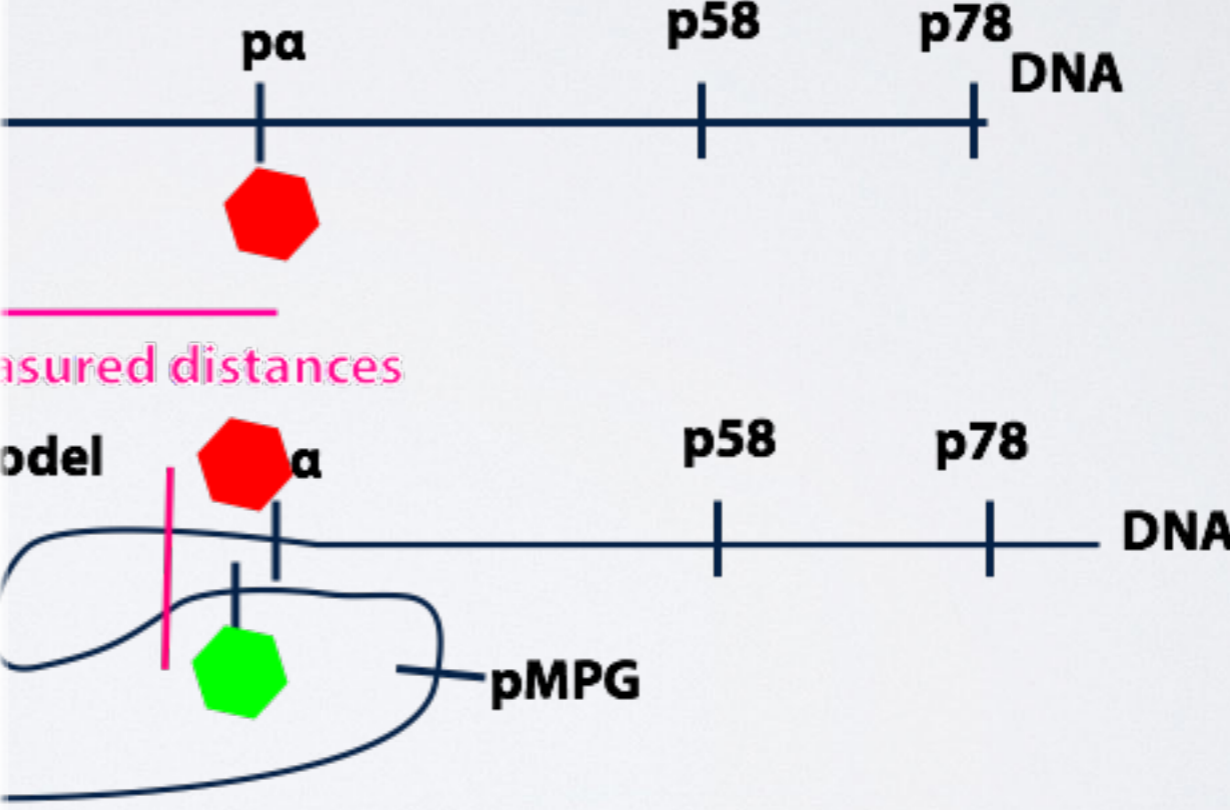
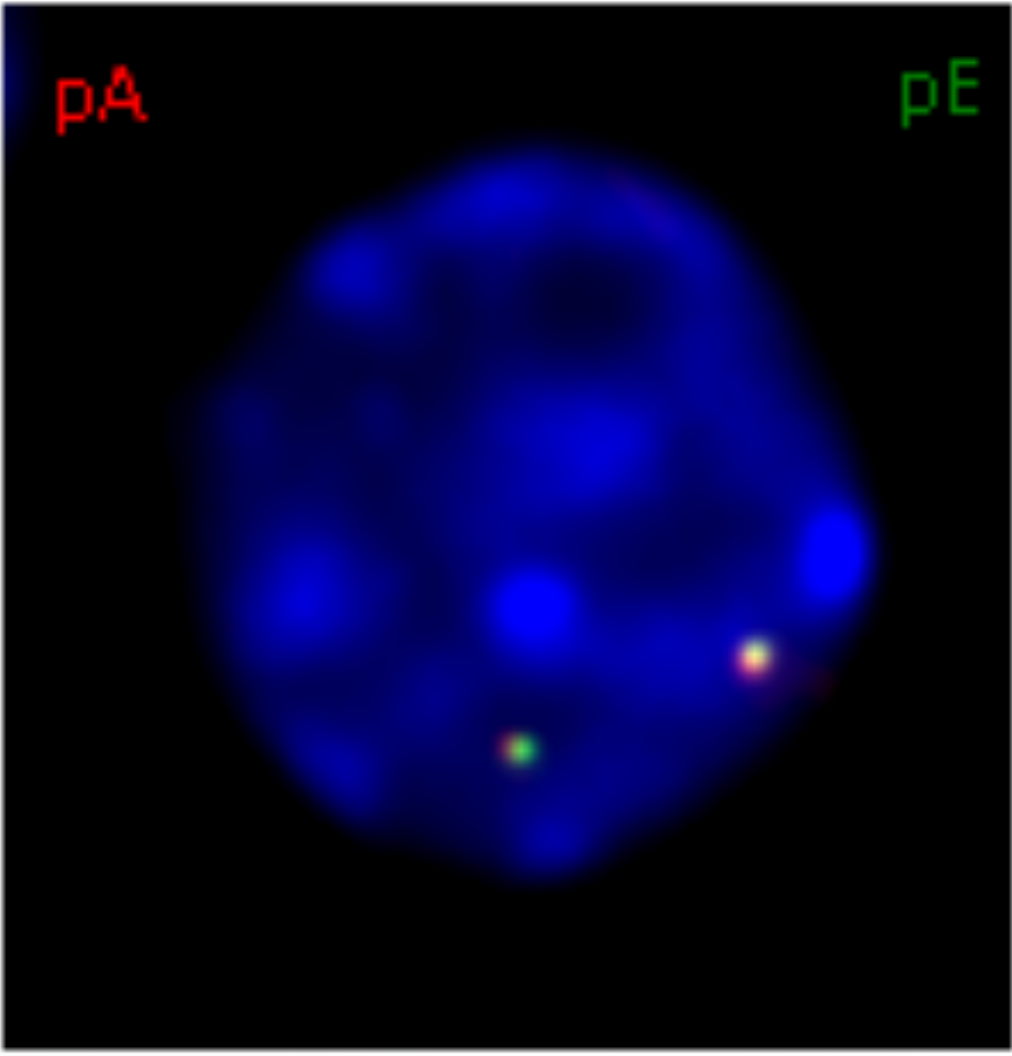


The alpha-globin gene is an important gene in the maturation of erythroblasts

FLUORESCENCE IN-SITU HYBRIDISATION LABELLING

FISH labelling

Chromatin linear model

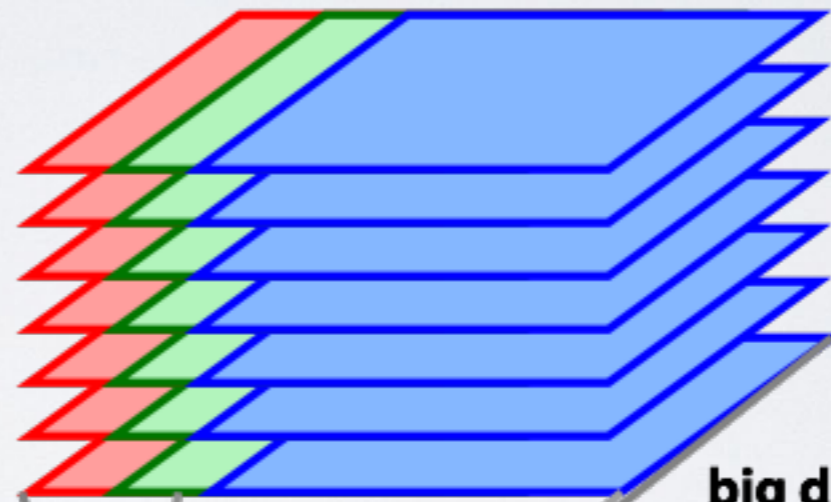


ACQUISITION



DELTAVISION

MULTI-CHANNEL STACK ACQUISITION



**big data
400 MB/stack**

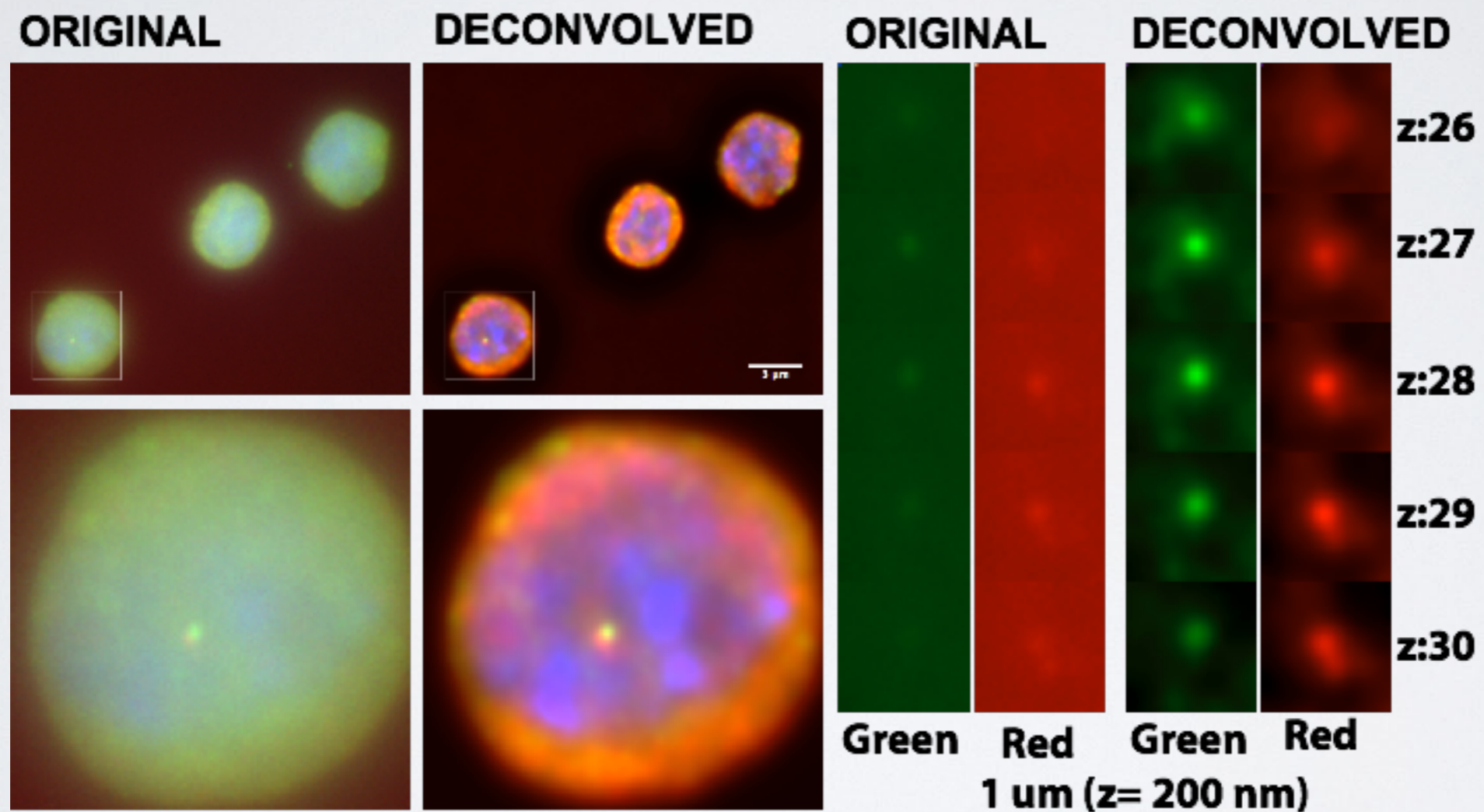


MULTIPLE POSITIONS ON SLIDE

Thousands of stacks

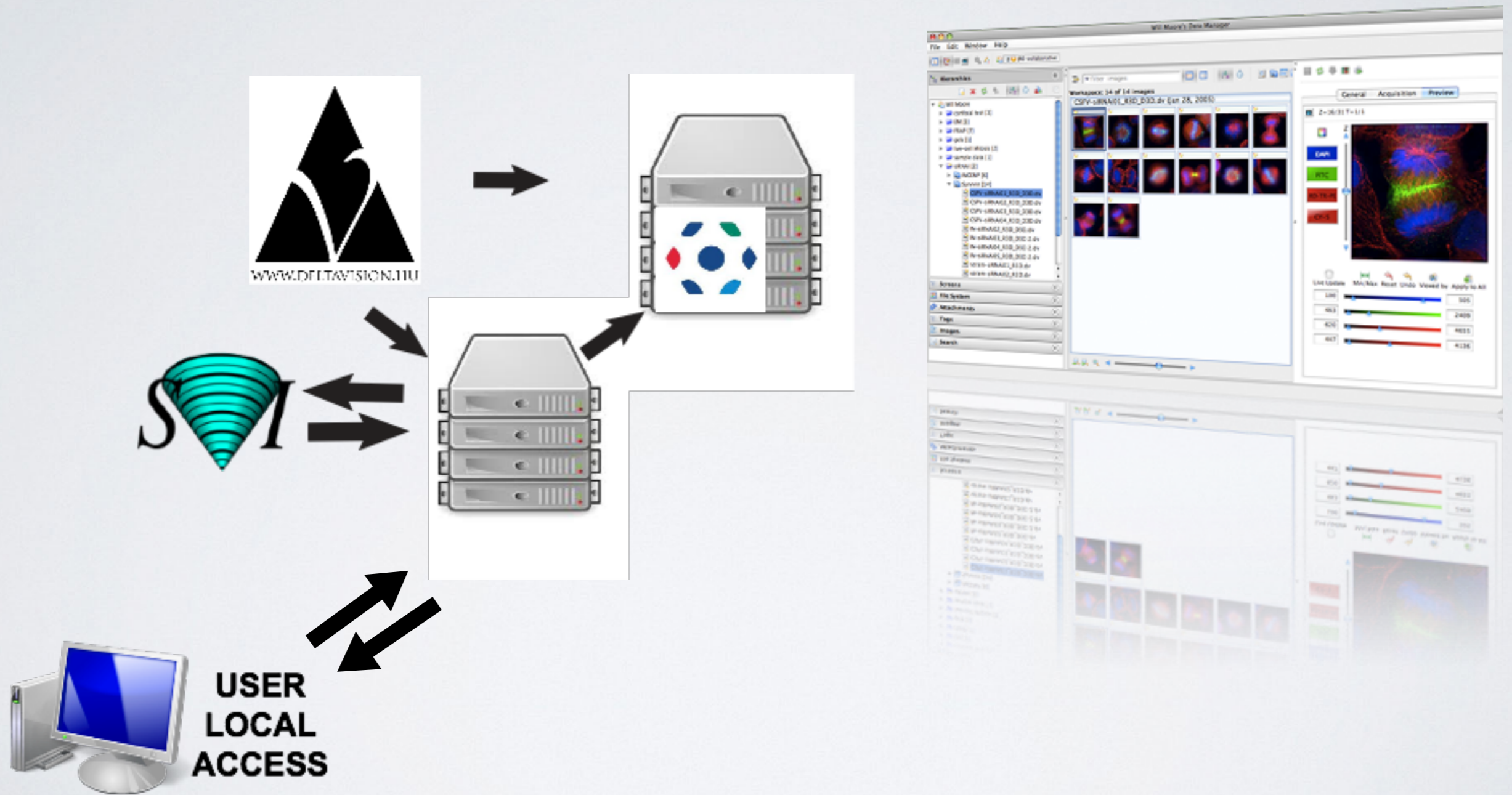
Soon we move on to super-resolution imaging

DECONVOLUTION WITH HUYGENS

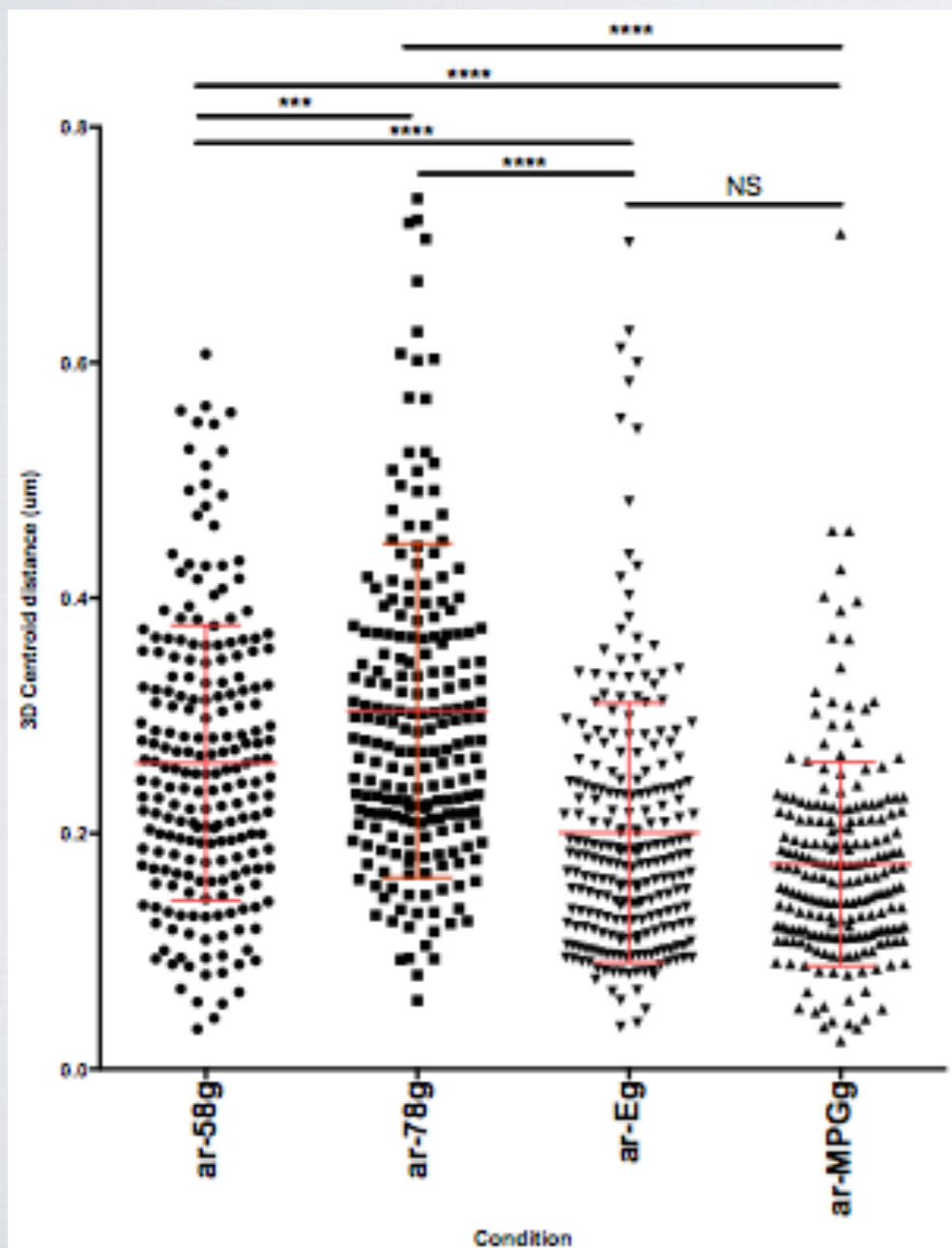


Run in batch-mode, worth doing for this application

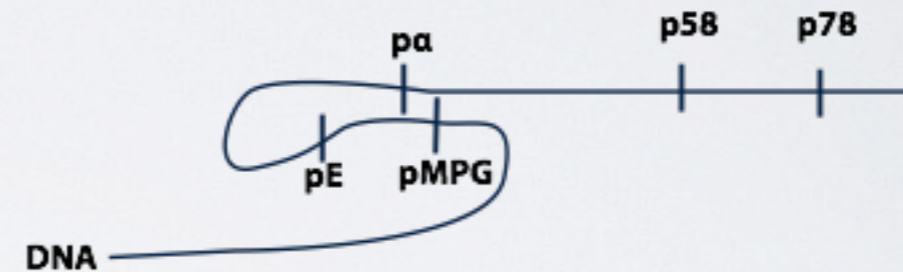
DATA PROCESSING AND ARCHIVING



EXAMPLE DATA



DNA secondary structure model



- Brackley, Chris A., Jill M. Brown, Dominic Waithe, Christian Babbs, James Davies, Jim R. Hughes, Veronica J. Buckle, and Davide Marenduzzo. "Predicting the three-dimensional folding of cis-regulatory regions in mammalian genomes using bioinformatic data and polymer models." *Genome Biology*:1601.02822 (2016).

REANALYSIS

- ACCESS DATA DIRECTLY IN OMERO

The screenshot shows the Oracle VM VirtualBox Manager interface. On the left, a list of virtual machines is shown, including 'Ubuntu_virtual', 'mavericks_virtual', 'Win_virtual', 'OMERO.vm-5.1.2-b45', 'Win10_virtual', and 'Ubuntu test'. The 'Ubuntu_virtual' VM is selected and shown as 'Powered Off'. The main window displays the configuration for the 'Ubuntu_virtual' VM, including system, display, and storage settings.

Overlaid on the VM window is an IPython Notebook interface. The notebook title is 'IP[y]: Notebook Untitled0 (autosaved)'. The code in the notebook is:

```
In [ ]: from omero import BlitzGateway
```

```
In [ ]:
```

The notebook interface includes a menu bar (File, Edit, View, Insert, Cell, Kernel, Help) and a toolbar with various icons for file operations and execution.

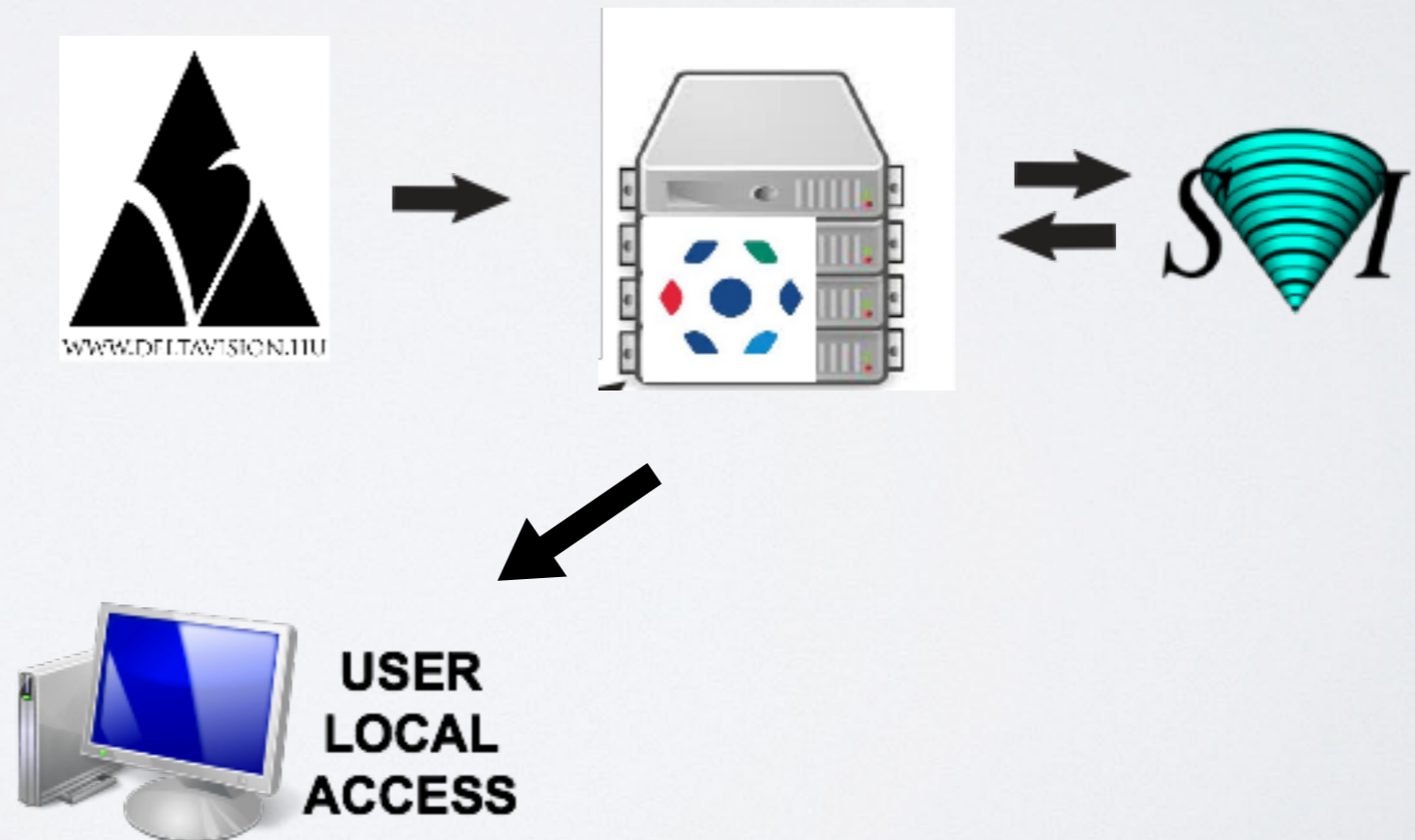
To the right of the notebook is a scatter plot titled 'COMPARISON OF FOCI CENTER DETECTION METHODS'. The y-axis is labeled 'Inter foci distance (µm)' and ranges from 0.0 to 0.8. The x-axis has two categories: 'Threshold and centroid' and '3D Gaussian fit'. The 'Threshold and centroid' category shows a distribution of blue dots with a mean around 0.25 µm. The '3D Gaussian fit' category shows a distribution of purple dots with a mean around 0.25 µm. Both distributions have vertical error bars indicating the mean and standard deviation.

Access data using python through virtual machine or through Fiji

WHAT NEXT

Thorough comparison of all available automated detection and localisation methods for foci.

Better integration with OMERO

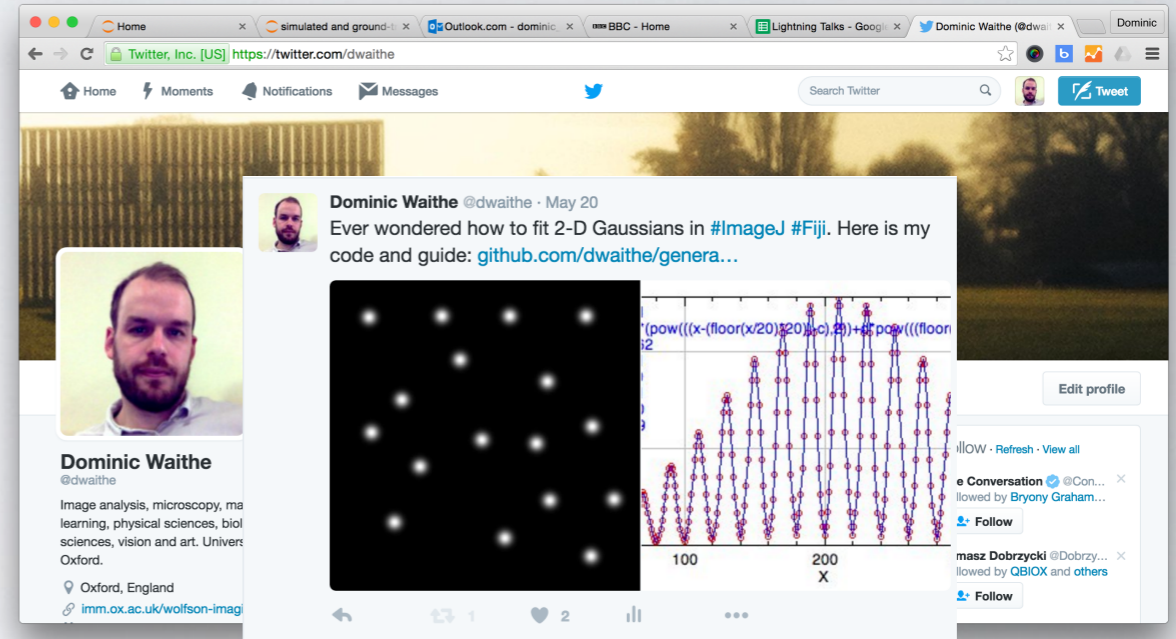




Nanoscopy Oxford



- Thanks to:
- Molecular Heamatology group:
Veronica Buckle, Jill Brown
- Wolfson Imaging Group:
Christian Eggeling, Chris Lagerholm, Esther Garcia
- Members of CBRG
- Members of Micron



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