




Visium HD tutorial

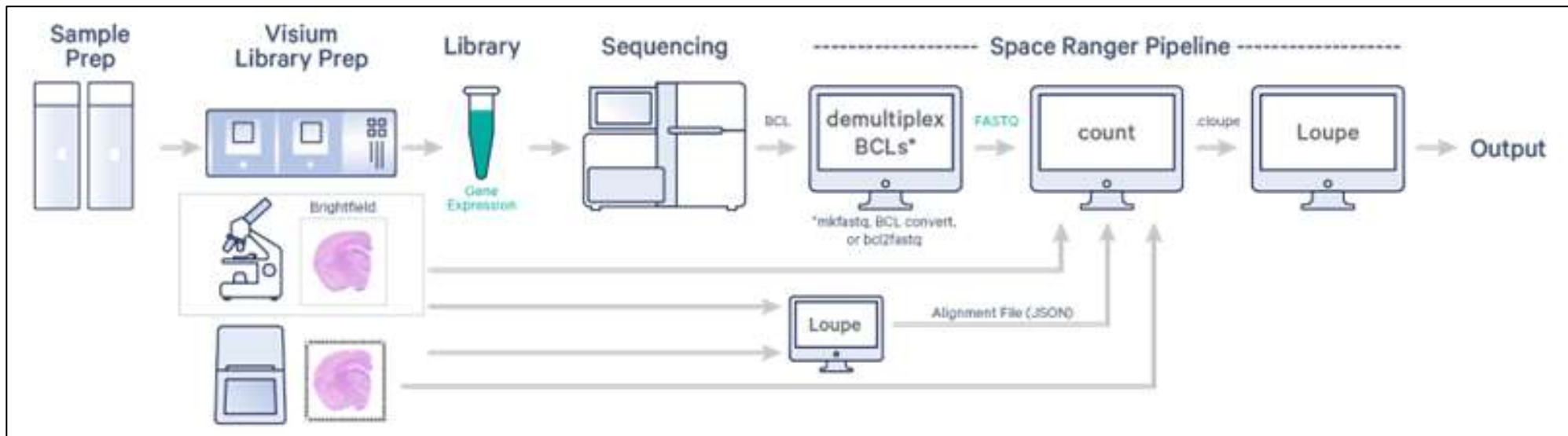
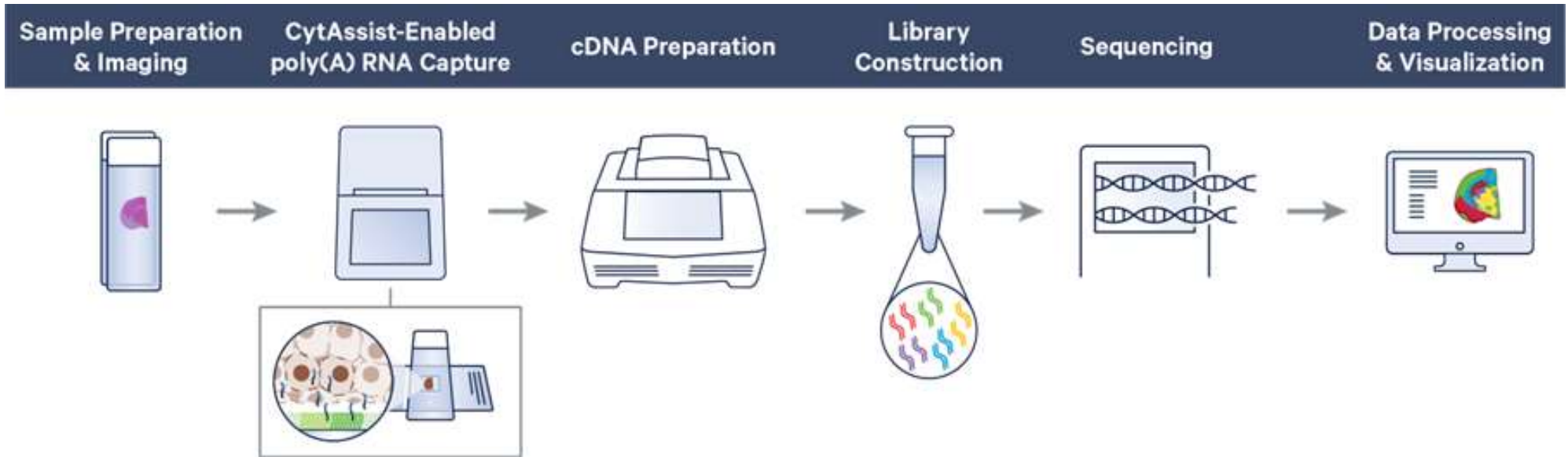
8th Dec 2025

EMBL PhD Workshop

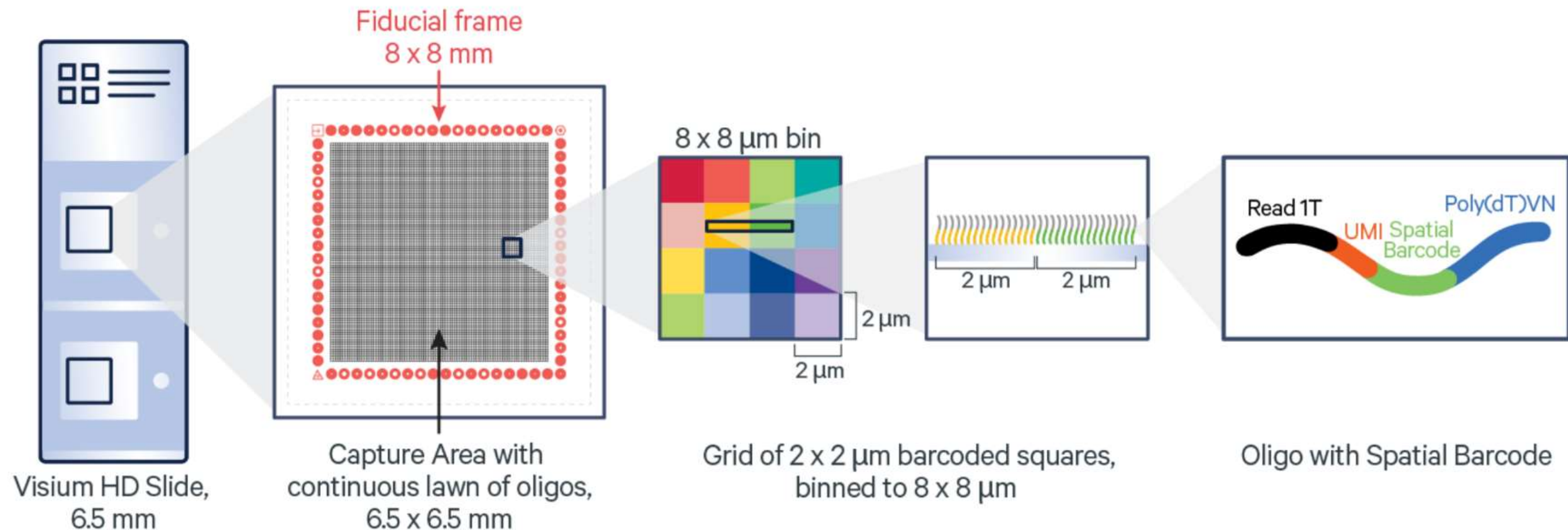
Sarah Shah, John Salomon, Cathal King

Platform	Chromium Single Cell 	Visium Spatial 	Xenium Spatial 
When to use	Comprehensive single cell data. For characterization of cell populations and states.	High-resolution spatial gene expression. Understand complex tissues, neighborhoods, and cell to cell interactions. Integration with other spatial-omics, histology, and morphology.	
Why to use	Unbiased single cell discovery. High per-gene sensitivity	Unbiased spatial discovery	Targeted spatial exploration. High per-gene sensitivity
Applications	Whole transcriptome gene expression. Protein. TCR, BCR. CRISPR. ATAC	Whole transcriptome gene expression	Targeted gene expression (up to 5,000 genes)
Resolution	Single cell	Transcripts assigned to 2-µm areas	Single cell
Data readout	NGS-based	NGS-based	Imaging-based
Sample compatibility	Single cell or nuclei suspensions from fresh, frozen, or FFPE samples	FFPE, Fresh frozen, Fixed frozen	Fresh frozen, FFPE

Visium HD workflow



Visium HD barcoding



Today's agenda

1. On Pawsey: run Space Ranger on Mouse Embryo example set
2. On your local computer: explore outputs from Space Ranger on Loupe Browser, and run differential expression gene (DEG) analysis
3. On Pawsey: run an R script via Singularity to perform Gene Set Enrichment Analysis (GSEA)

Downsides of using Loupe Browser

- Cannot set seed for UMAP
- Cannot choose custom colours, scales, legend for exporting plots.

That's why some researchers prefer to use third-party R libraries and write their own code 😊

Links to more info

[Inside-Visium-Spatial-Capture-Technology.pdf](#)

[Your introduction to Visium HD: Spatial biology in high definition | 10x Genomics](#)