Research

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Group Photo of JPT lab

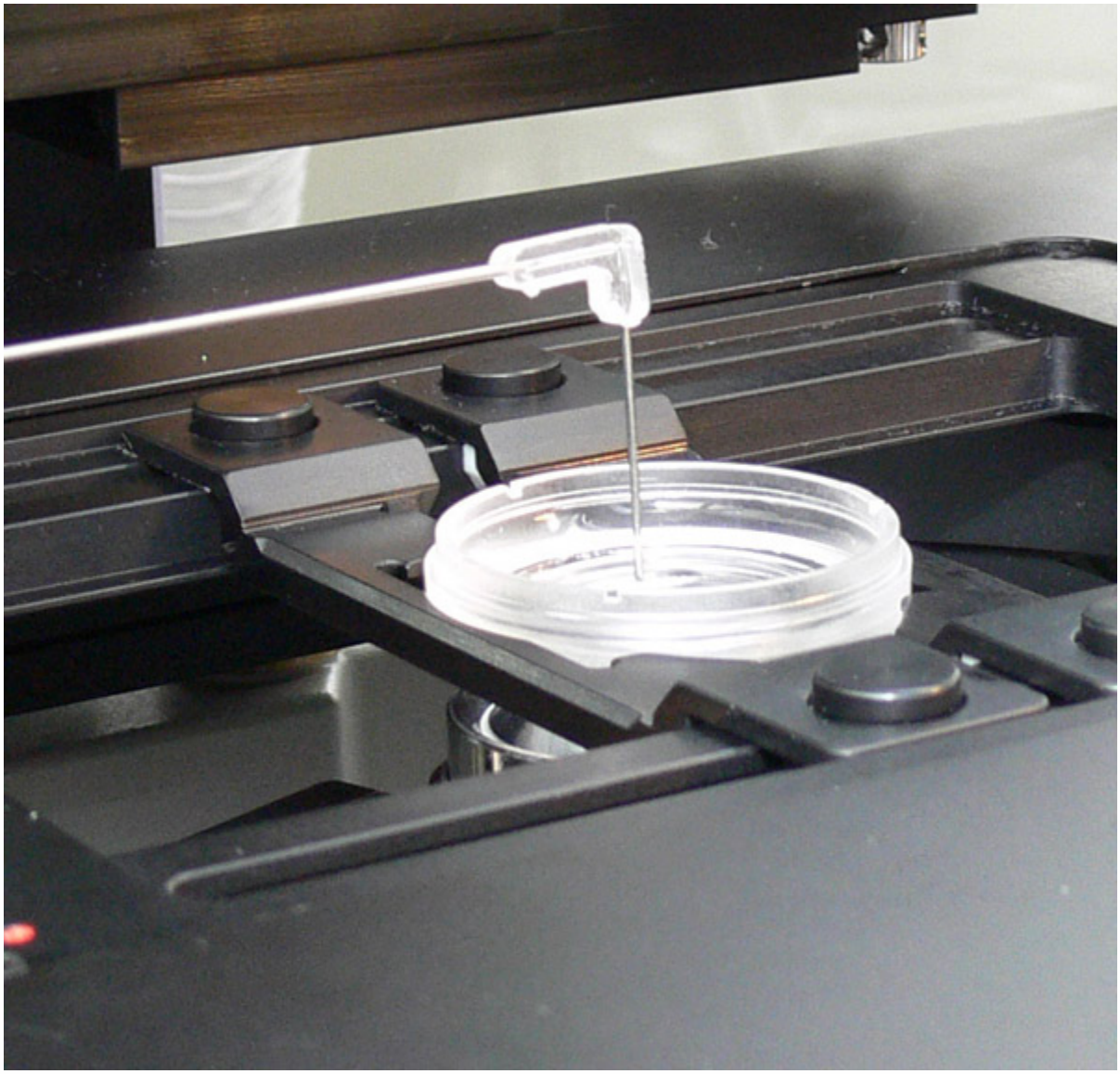
Optics and bioinformatics

Optics and bioinformatics
State-of-the-art optical, image analysis, and bioinformatics approaches are being used to quantitatively describe biological processes involved in cell adhesion, epithelial-mesenchymal transition, tissue morphogenesis and tumour progression. These approaches utilise instrumentation development , image analysis, high throughput screening and bioinformatics techniques.

Real time imaging
We are using the most advanced optical microscopy techniques to study real-time dynamics of major cellular processes including intracellular trafficking, adhesion, motility and generalised cell behaviour. Our multi-modality microscope system combines the following functions:

- Nikon wide-field inverted video-microscope
- Piezo-driven 3D-imaging software with point spread function based deconvolution facility
- Rapid FRAP (fluorescent recovery after photo-bleaching) and PA (photo-activation) system for induced photo-bleaching or photo-activation of appropriately tagged proteins at precise cellular locations or on specific organelles
- TIRF (total internal reflection fluorescence) to study real-time membrane dynamics
- Dual View system to separate the signal of two simultaneously emitting fluorophores

Contacts: Yeh-Shiu Chu, Eva Tomaskovic-Crook, Victor Racine
Mechanochemistry of cell adhesion
Micropipette force probes for studies of cell-cell and cell-substrate adhesion (pipette assay)



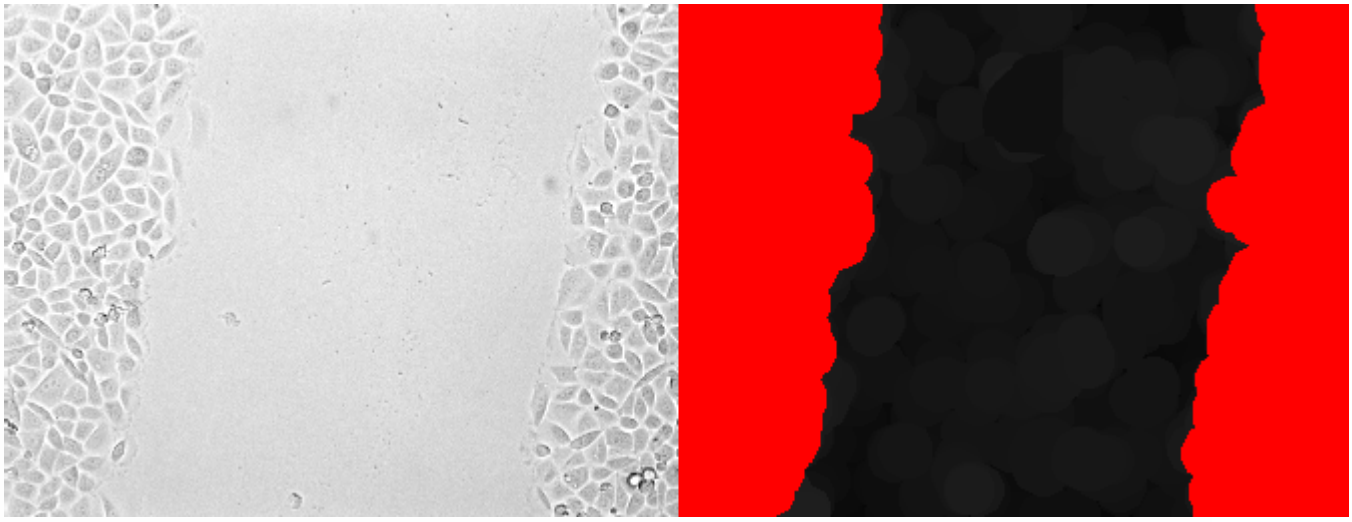
- Development of substrate patterning by micro-contact printing technologies to investigate contact adhesion

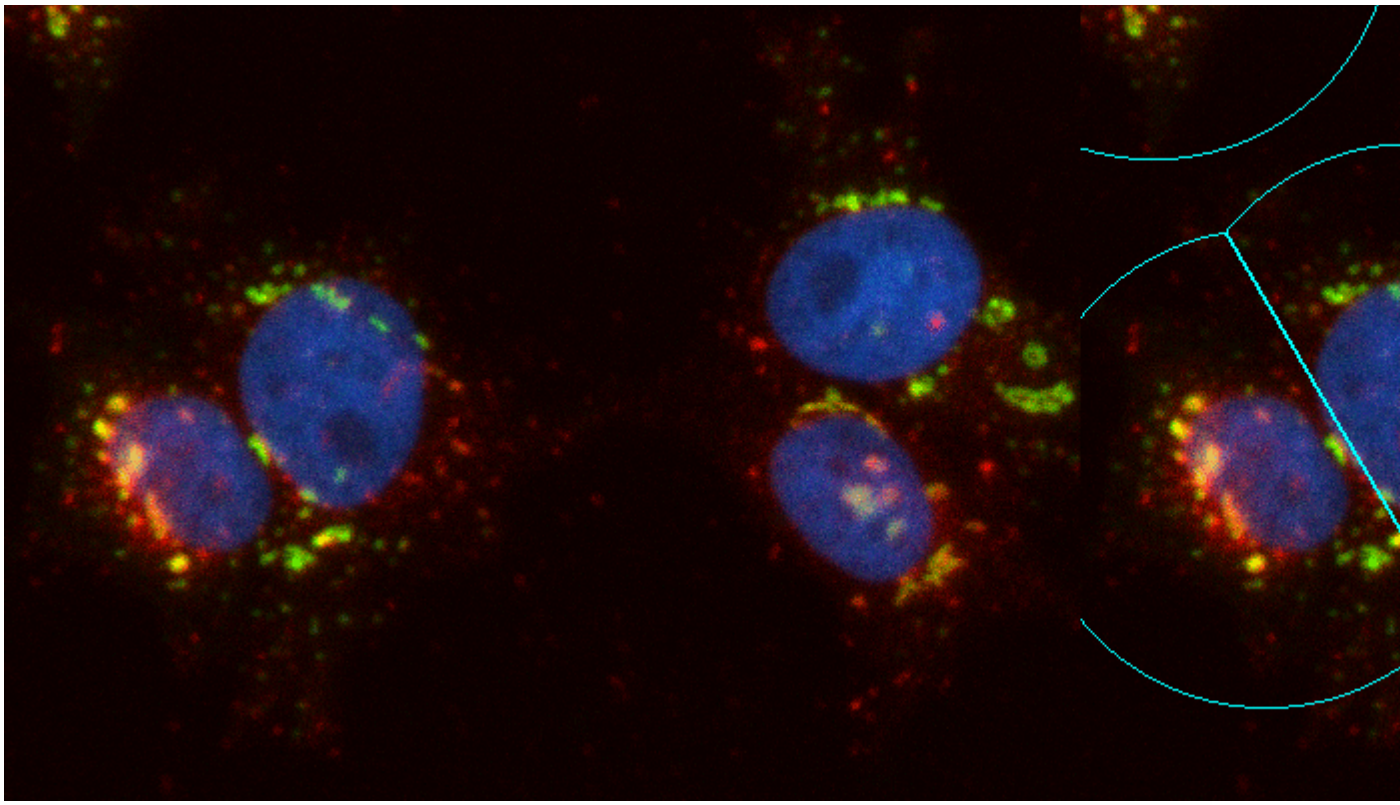
Contacts: Yeh-Shiu Chu, Kelvin Kian Ngiap Chua

Image analysis

Image analysis aims to extract quantitative information to describe fluorescence distribution, cell morphology and dynamics. Analyses must be reproducible, user-independent and can perform large scale sampling without tedious work. Our main analyses include:

- FRAP recovery quantification
- Would healing measurement
- Fluorescence colocalization analysis
- Fluorescence and phase contrast segmentation
- Cell morphometry
- Cell / object tracking
- High content image analysis





In collaboration with Frederic Bard Group

Contact: Victor Racine

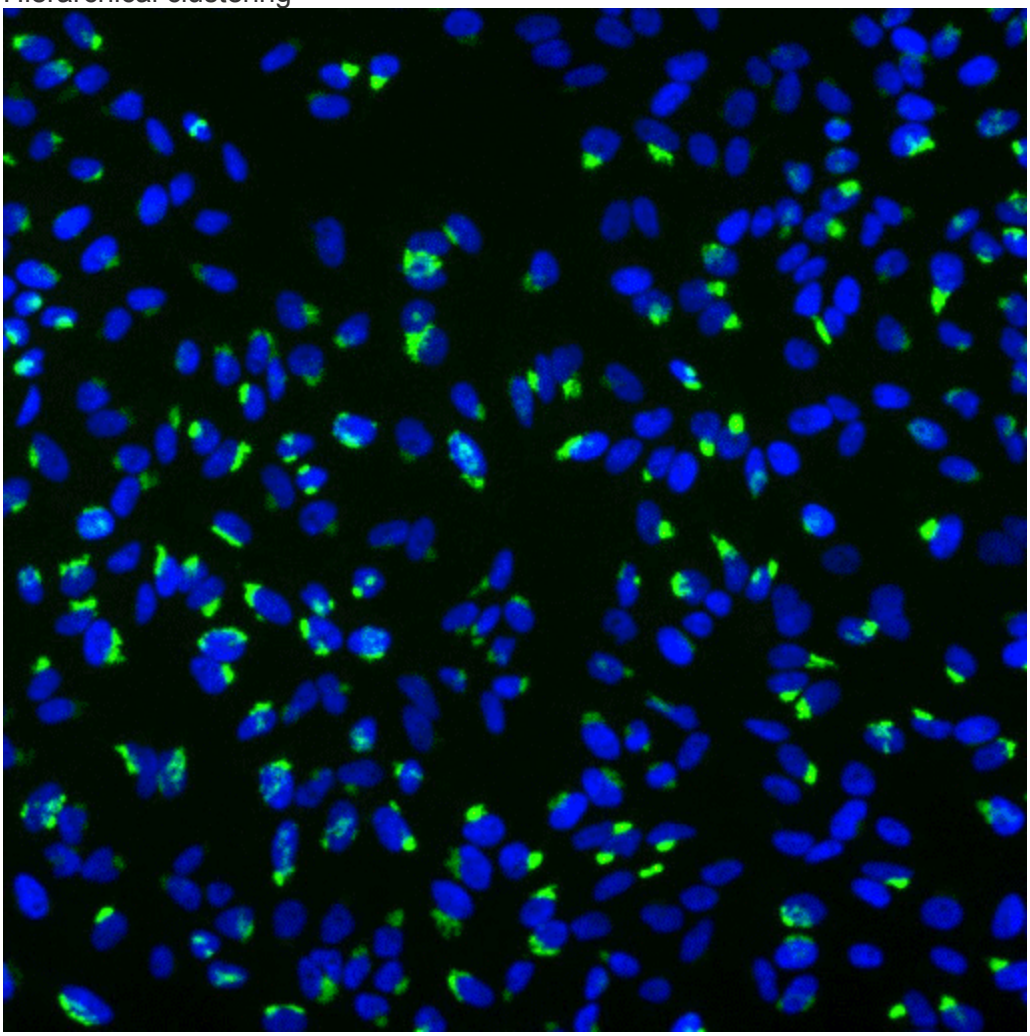
Bioinformatics

Our current work focuses on gene expression data of breast cancer samples and cell lines. A principal aim of this approach is to discover relevant pathways in the basal phenotype. In collaboration with Prof Alan Porter we are using computer-aided drug discovery programs to discover new therapeutic molecules to target breast cancer.

We are also in collaboration with Frederic Bard Group to support bioinformatic aspects of high content screening experiments such as:

- Cell segmentation

- Morphometric cell features extraction
- Feature normalization
- Feature selection
- SVM classification
- Hierarchical clustering



Contact: Agnes Tan, Victor Racine