CARDIFF UNIVERSITY
PRIFYSGOL CAERDYDD

Biological insights into 3D organoids using a modular, scalable and data efficient image analysis pipeline

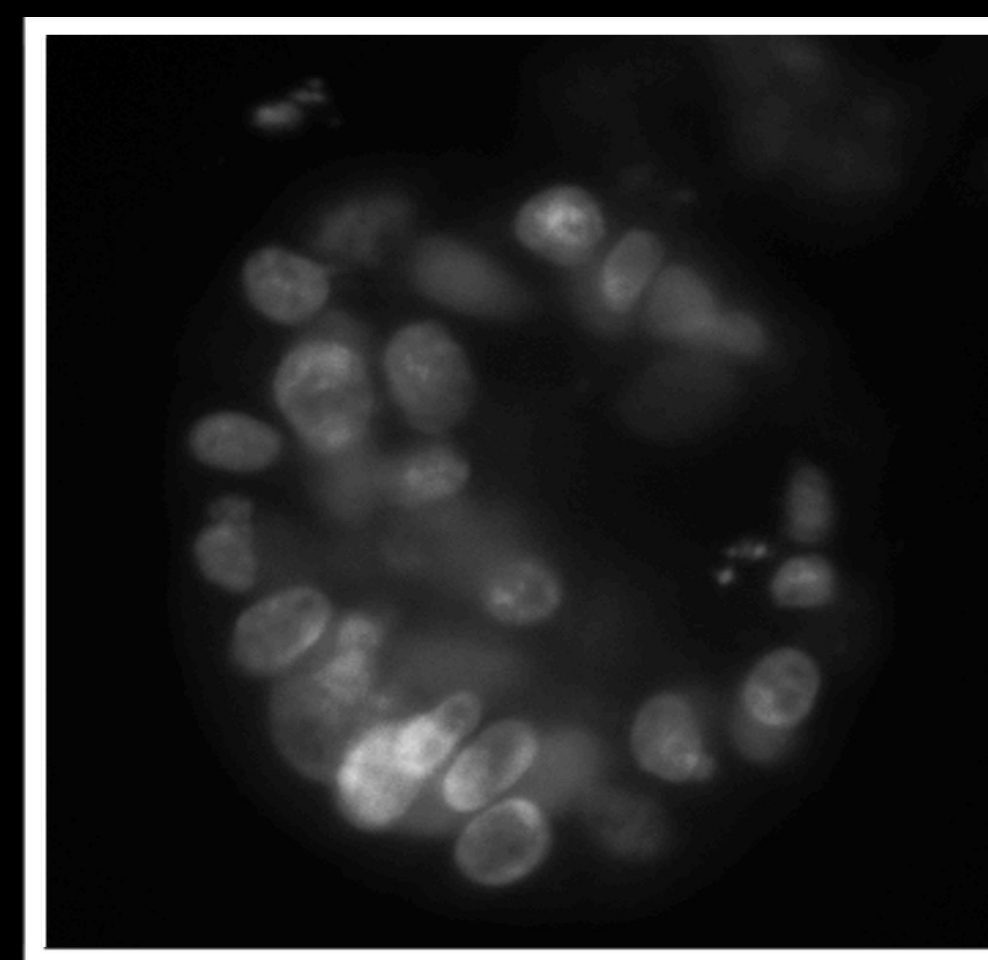J. Bleddyn Williams, Verônica A. Grieneisen, Athanasius F. M. Marée

What are we trying to achieve?

A framework for a reproducible, cross platform image analysis pipeline which can incorporate elements from multiple programming languages and is scalable for use on workstations, High Performance Clusters and on the cloud. This pipeline will be developed to extract key morphometric features from 3D images of screened organoids in drug trials to classify organoid response for the assessment of therapeutic efficacy for application in the pharmaceutical industry.
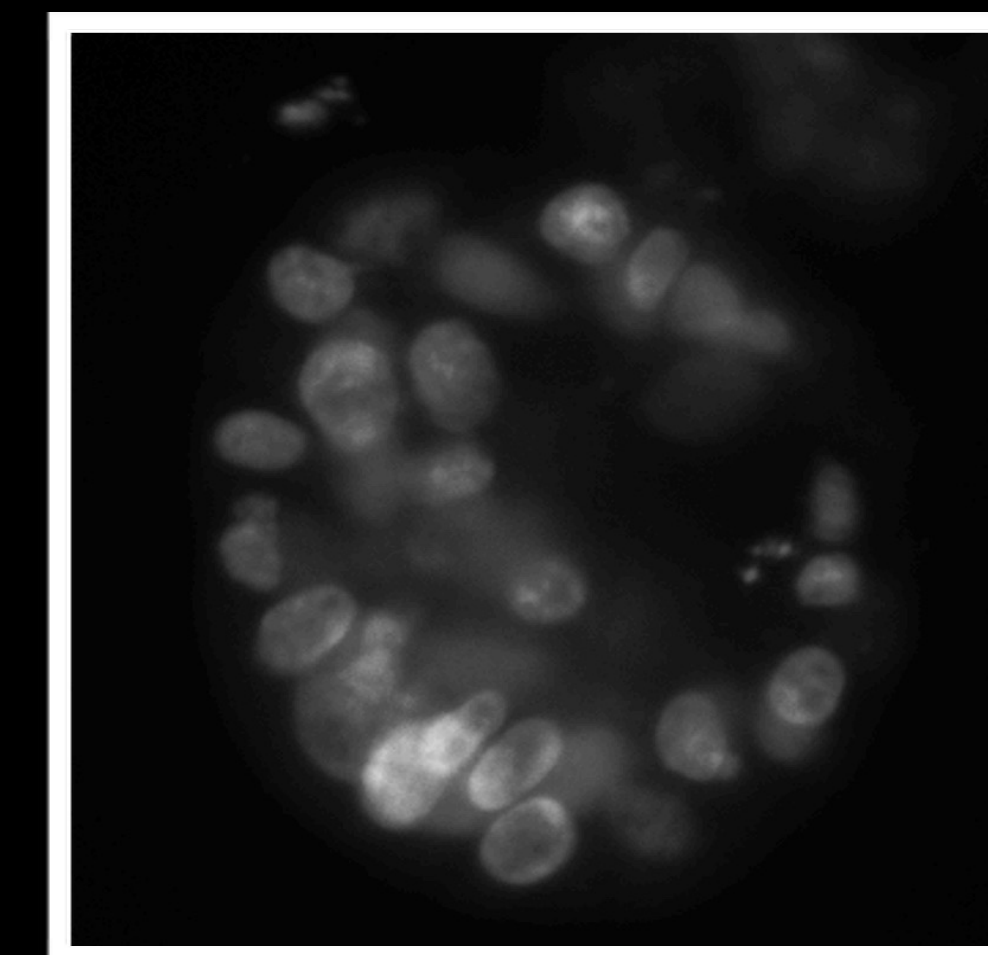
How are we building this?

We are developing a Standardised Data Interchange file format in order to efficiently encapsulate the morphometric features of cells and tissues. To populate this file format, we will use a modular image analysis pipeline which will be accessible to users without a programming background. To avoid installation issues and allow cross platform usage (Windows macOS and Linux), the image analysis pipeline will be containerised. The image analysis pipeline will be flexible so that 3rd party modules can be incorporated and won't be limited to the analysis of organoids.
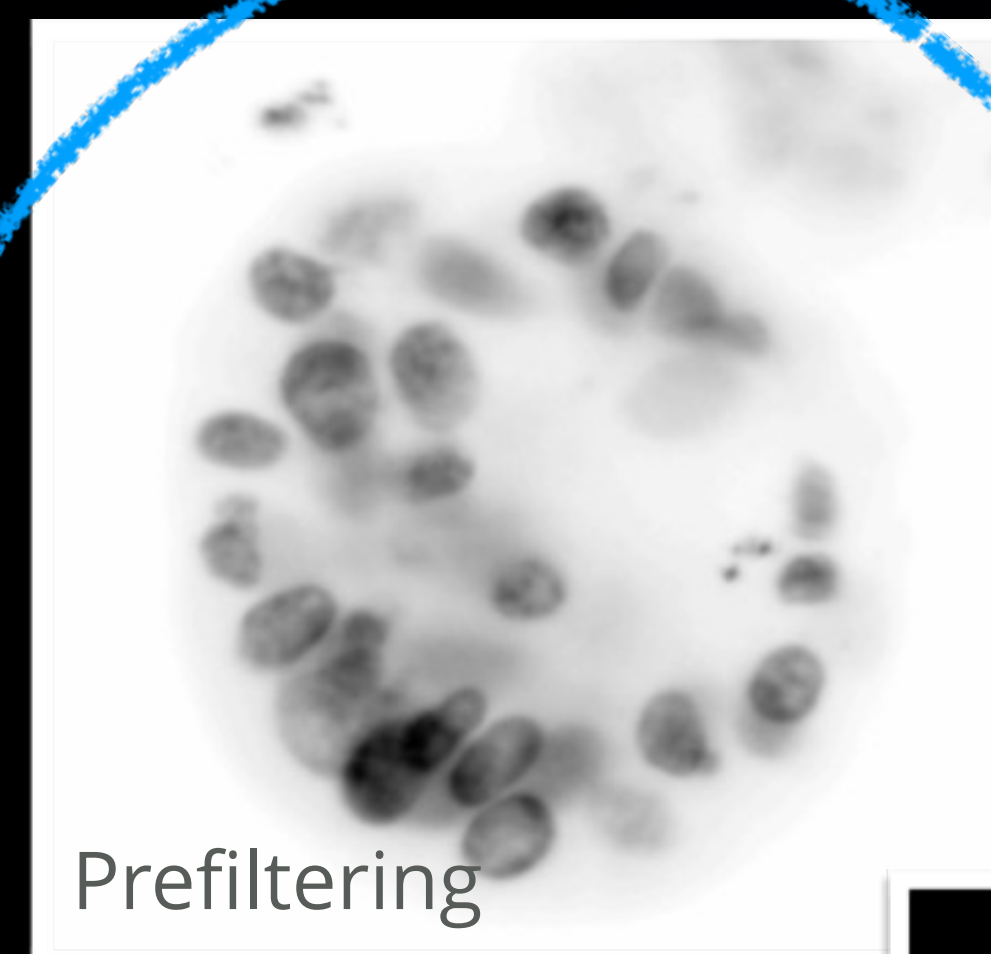
Snakefile:
Sequentially running scripts
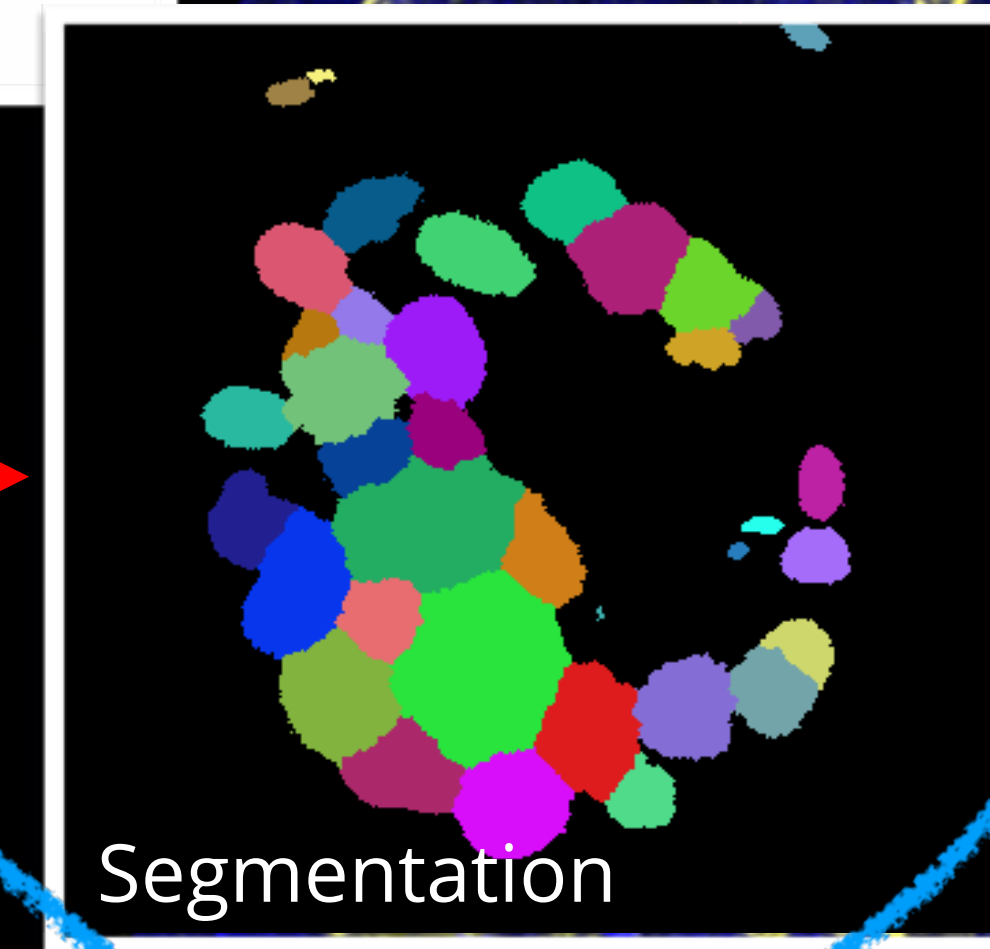
microscopy2ome.py

ome2json.py

Prefiltering

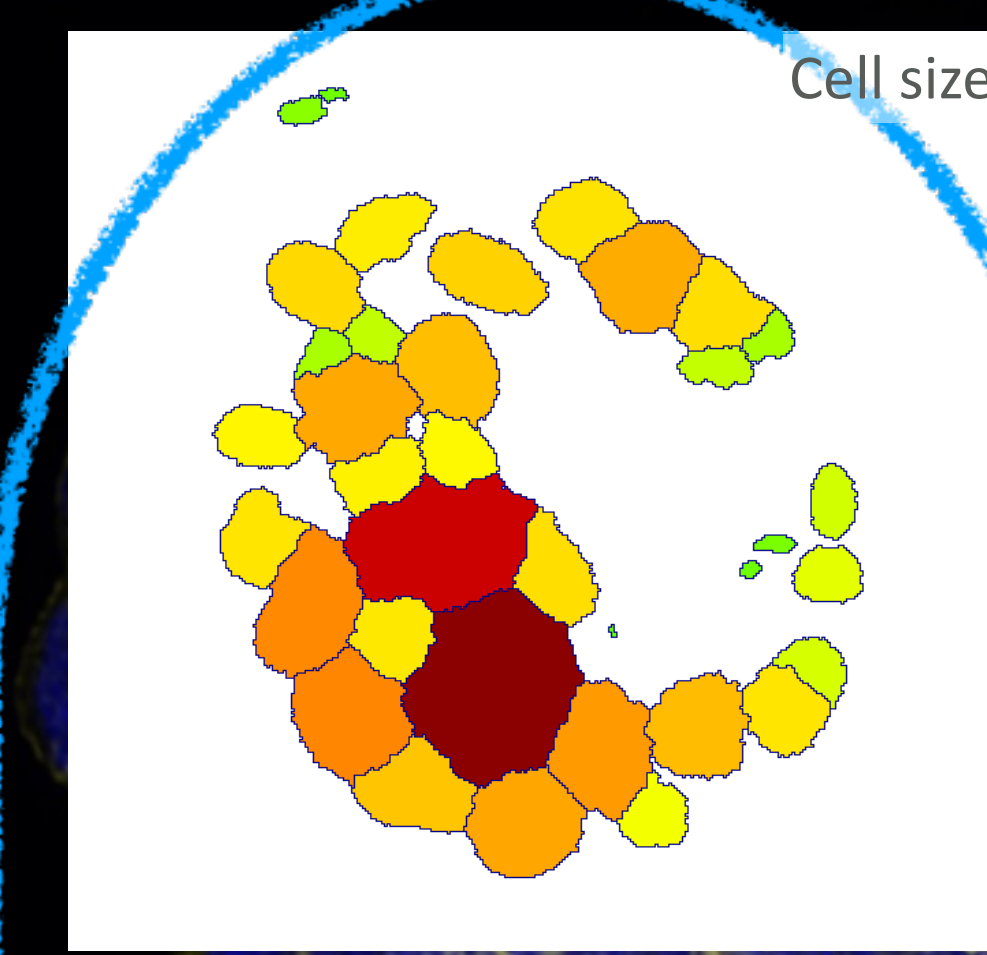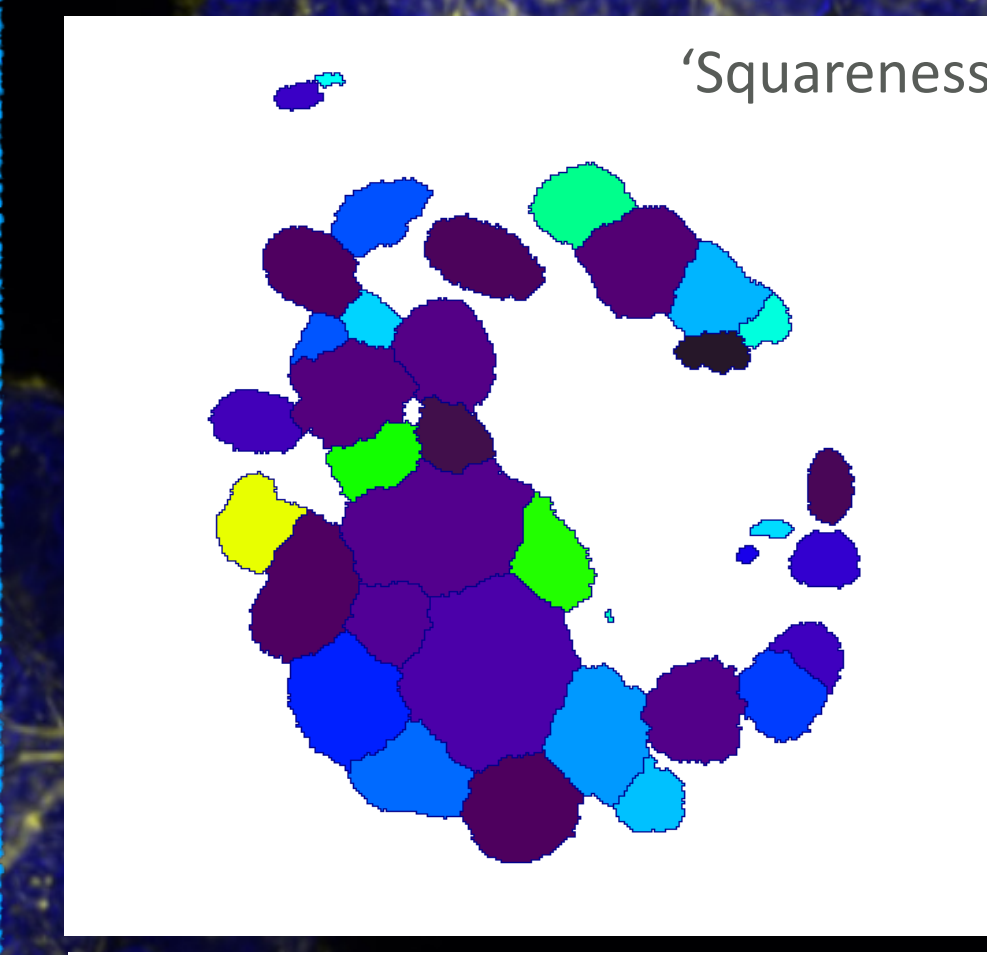SPM.py

Segmentation

JSON output to track and record it all:
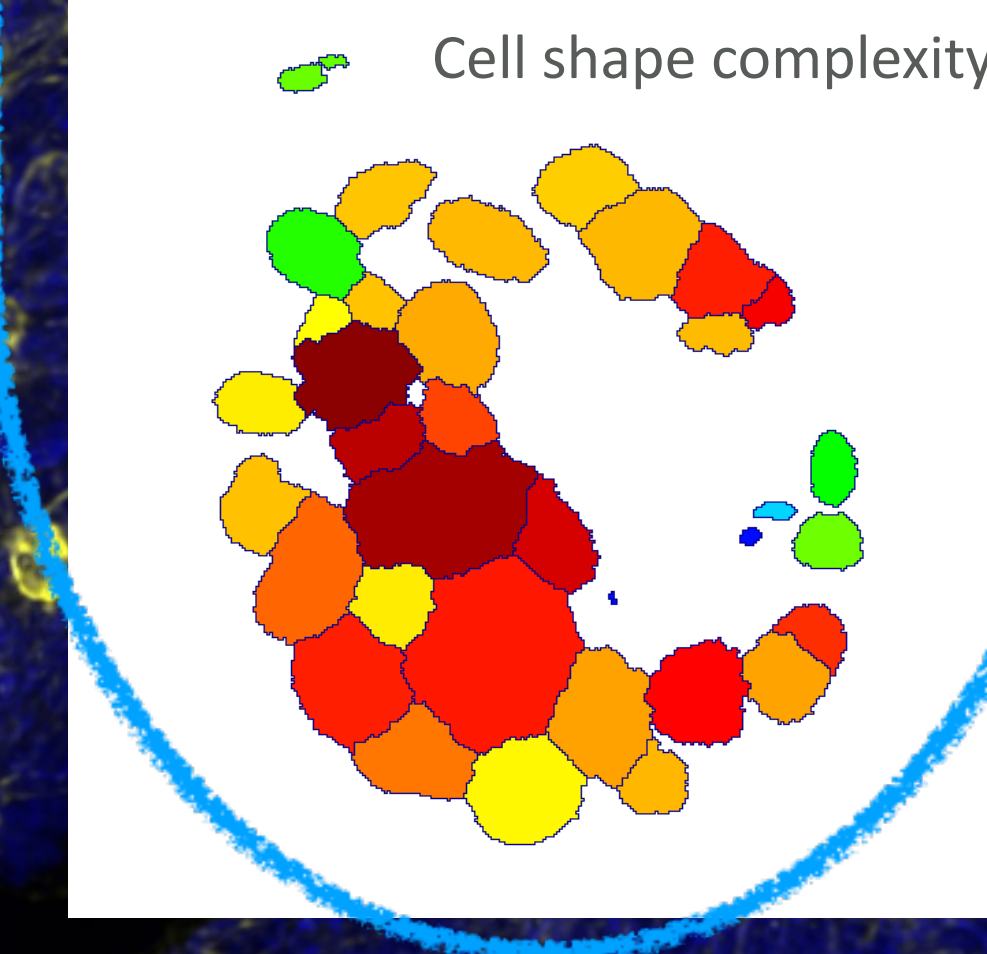
```
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            "Version": {
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                "ome2json.py": 0.1
            }
        }
    },
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            "@Creator": "OME Bio-Formats 6.9.0",
            "@UUID": "urn:uuid:a95521ec-e22f-42e2-9549-43f5
            "@xsi:schemaLocation": "http://www.openmicrosco
```

LOCOEFA.R

Cell size

'Squareness'

Cell shape complexity

What's currently out there?

Data efficiency is becoming increasingly important in high throughput screening. Currently morphometric outputs from data analysis pipelines often contain a large amount of redundant data. Vast amounts of redundant data can quickly mount causing storage issues and will often lead to slower post processing. Here we present a pipeline which produces a minimal morphometric descriptor set which encapsulates morphometric data with low redundancy in a data efficient manner.

Who will benefit?

The Standardised Data Interchange format, basic Snakemake workflow management scripts and related tools such as containers will be made available for use for novel analysis applications. Previously published morphometric extraction modules such as LOCOEFA and to be published methods such as Segmentation Potts model will be incorporated into a publicly available pipeline. A proprietary layer will be built using this framework for Cellesce Limited, to assess the morphometric response of organoids in the context of compound screening.

PDOs are superior in vitro models

Multicellular, 3D models of major tissue types
✓ Models cell interactions
✓ Wide range of tissues; broad range of therapeutic targets

Faithful & predictive
✓ Can be used in therapeutics and across life sciences

Genetically diverse
✓ Can model by disease subtype
✓ Single-donor approach

Can add other cell types
✓ Can model complex cell interactions

Cellesce technology enables industry adoption of PDOs

Scalable Bioprocess
✓ Large batches enable large screening campaigns including high-throughput screening

Quality Assured
✓ QA/QC processes to ensure products meet industry requirements

Dedicated Manufacturing
✓ PDO expertise
✓ Dedicated facility

Off-the-shelf Product
✓ Convenient and rapidly deployed

UKRI

Innovate UK KTN

Cellesce®