

# **The SciLifeLab Data Repository from a user perspective**

Jonne Rietdijk

Dataset accompanying manuscript:

## “A phenomics approach for in vitro antiviral drug discovery”



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bioRxiv is receiving many new papers on coronavirus SARS-CoV-2. A reminder: these are preliminary reports that have not been peer-reviewed and should not be used to guide practice/health-related behavior, or be reported in news media as established information.

New Results

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### A phenomics approach for *in vitro* antiviral drug discovery

Jonne Rietdijk, Marianna Tampere, Aleksandra Pettke, Polina Georgieva, Maris Lapins, Ulrika Warpman Berglund,  Ola Spjuth, Marjo-Riitta Puimalainen,  Jordi Carreras-Puigvert

doi: <https://doi.org/10.1101/2021.01.13.423947>

This article is a preprint and has not been certified by peer review [what does this mean?].

Abstract

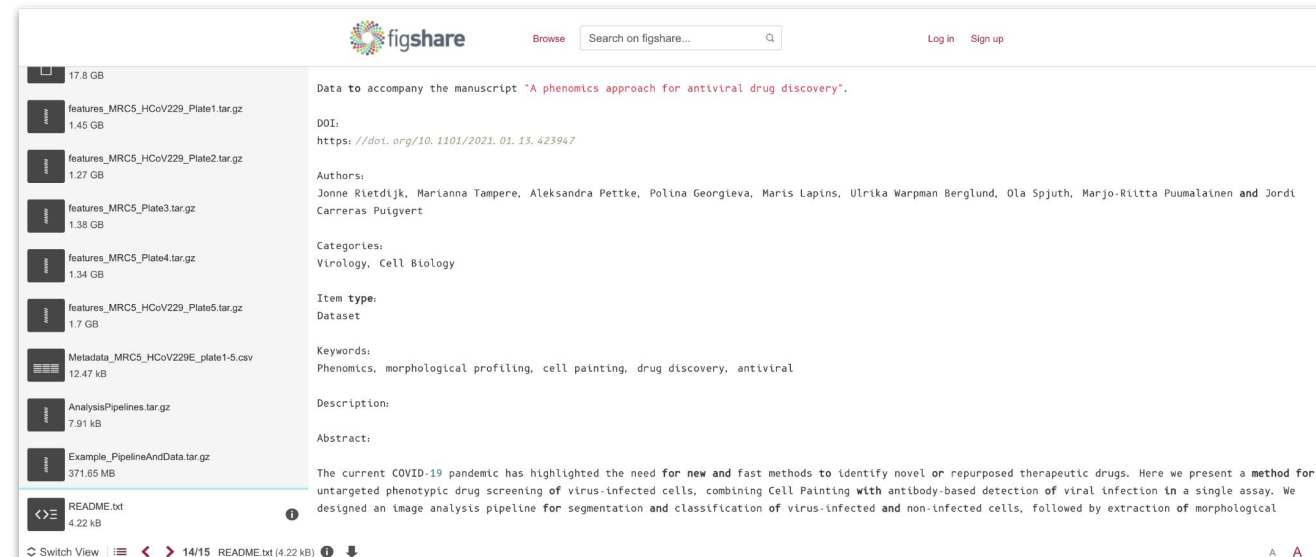
Full Text

Info/History

Metrics

 Preview PDF

## Images, analysis pipelines and feature data



Figshare dataset page for "A phenomics approach for in vitro antiviral drug discovery".

**Data to accompany the manuscript "A phenomics approach for antiviral drug discovery".**

DOI: <https://doi.org/10.1101/2021.01.13.423947>

**Authors:** Jonne Rietdijk, Marianna Tampere, Aleksandra Pettke, Polina Georgieva, Maris Lapins, Ulrika Warpman Berglund, Ola Spjuth, Marjo-Riitta Puimalainen and Jordi Carreras Puigvert

**Categories:** Virology, Cell Biology

**Item type:** Dataset

**Keywords:** Phenomics, morphological profiling, cell painting, drug discovery, antiviral

**Description:**

**Abstract:**

The current COVID-19 pandemic has highlighted the need for new and fast methods to identify novel or repurposed therapeutic drugs. Here we present a method for untargeted phenotypic drug screening of virus-infected cells, combining Cell Painting with antibody-based detection of viral infection in a single assay. We designed an image analysis pipeline for segmentation and classification of virus-infected and non-infected cells, followed by extraction of morphological

**Files:**

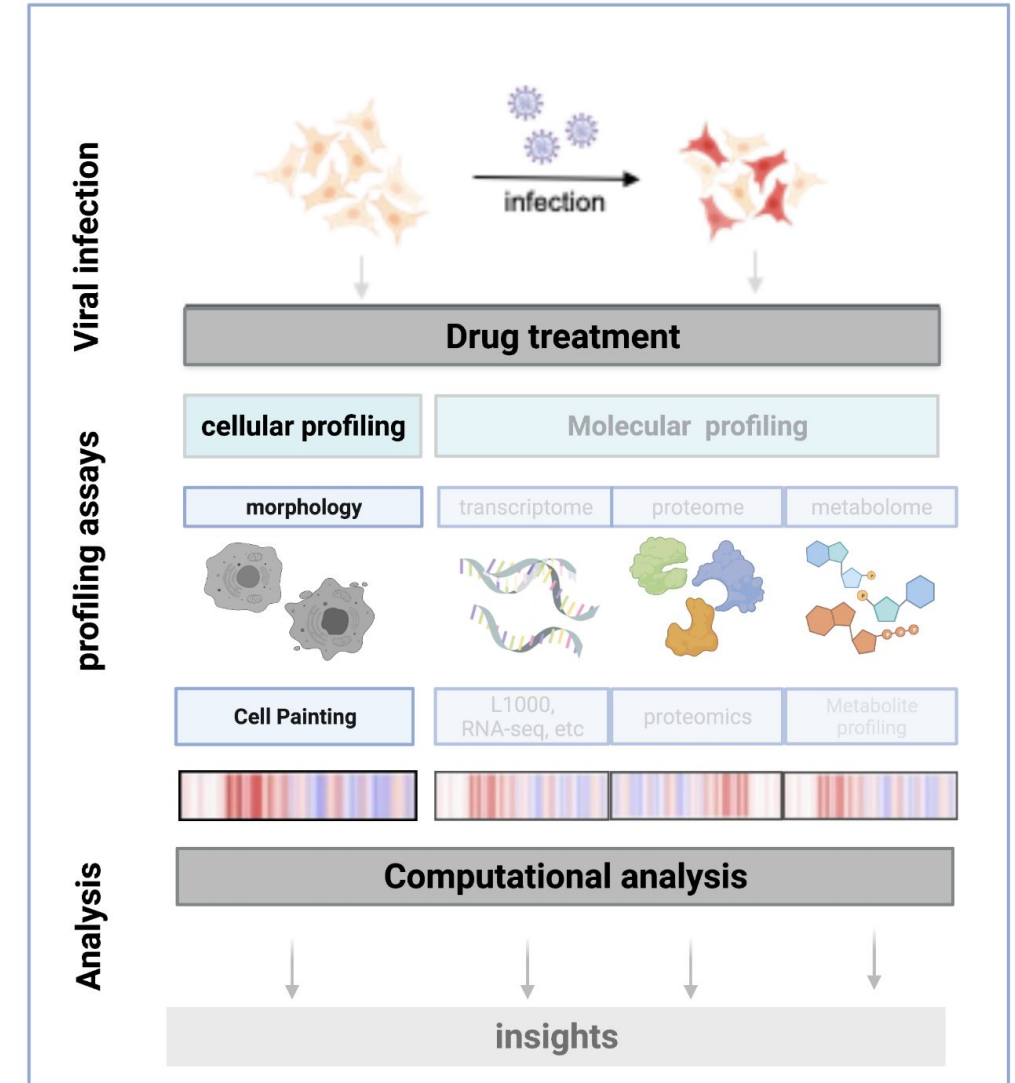
- 17.8 GB
- features\_MRC5\_HCoV229\_Plate1.tar.gz 1.45 GB
- features\_MRC5\_HCoV229\_Plate2.tar.gz 1.27 GB
- features\_MRC5\_Plate3.tar.gz 1.38 GB
- features\_MRC5\_Plate4.tar.gz 1.34 GB
- features\_MRC5\_HCoV229\_Plate5.tar.gz 1.7 GB
- Metadata\_MRC5\_HCoV229E\_plate1-5.csv 12.47 kB
- AnalysisPipelines.tar.gz 7.91 kB
- Example\_PipelineAndData.tar.gz 371.65 MB
- README.txt 4.22 kB

Switch View | 14/15 | README.txt (4.22 kB)

# phenomics



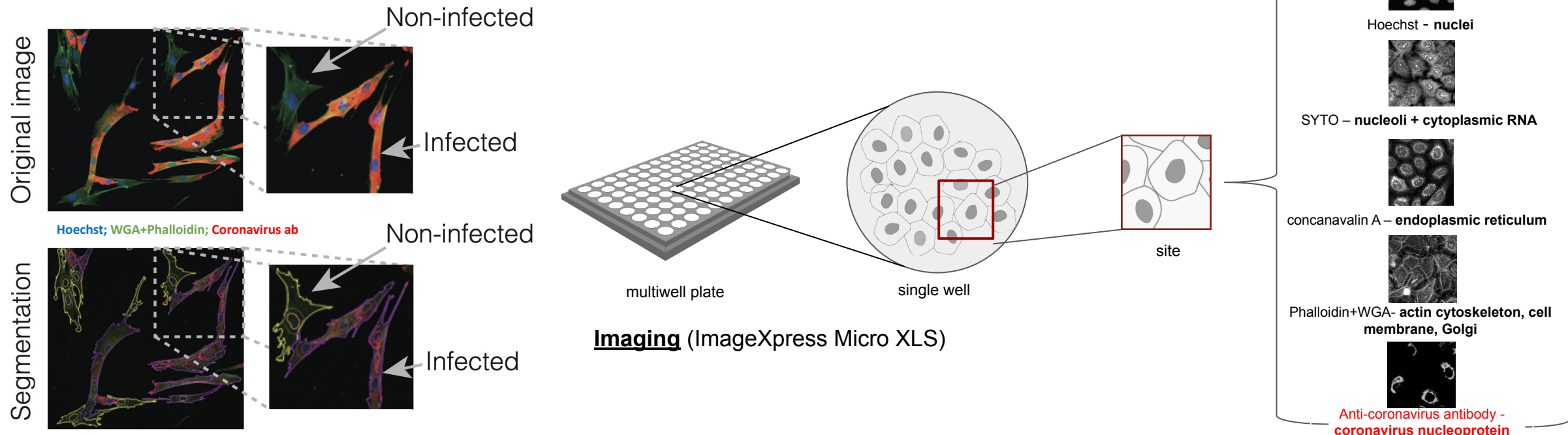
- Study changes in cellular morphology
- Image-based morphological profiling of cells using multiplexed fluorescent dyes
- Cell Painting protocol (Bray et al. 2016)



# Morphological profiling of infected cells

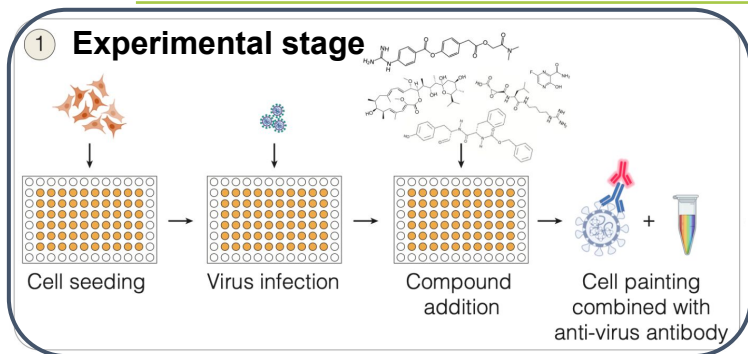


- human lung fibroblasts (MRC-5) cells infected with human coronavirus 229E
- stained for 7 important cell components + virus nucleoprotein
- treated with 9 antiviral drugs

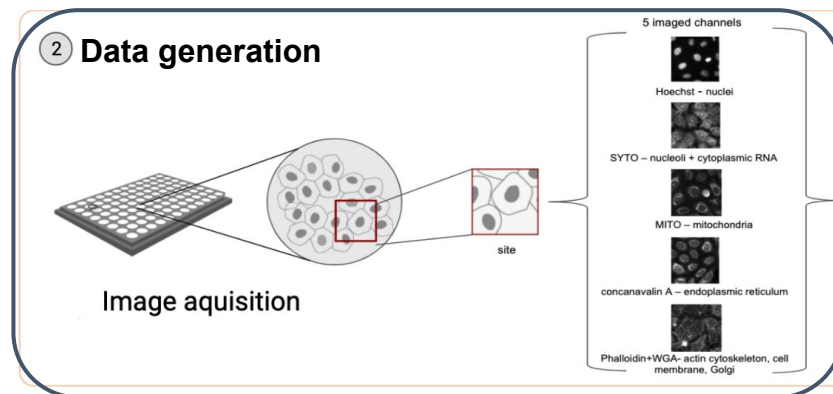




# Images, pipelines and features



Method for combining Cell Painting and antibody-based viral detection described in manuscript



>13000 raw microscopy images of infected, non-infected and antiviral treated cells published in Figshare

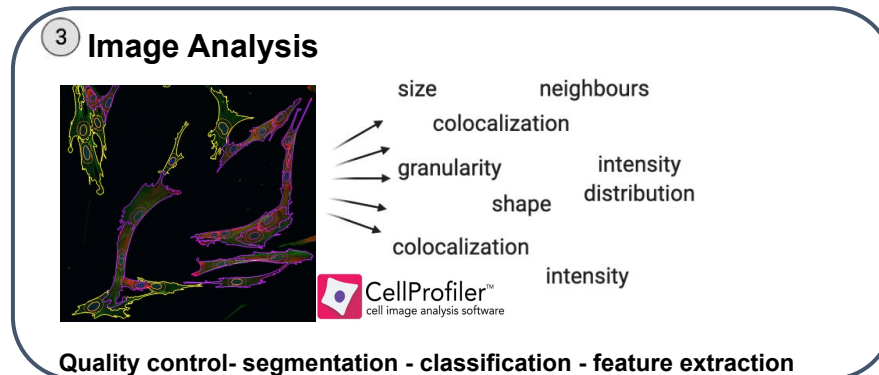


Image analysis pipelines and extracted features published in Figshare

# Why we use the repository



- FAIR
- High-content data
  - multiple questions can be asked
  - Different analysis methods can give new insights
- Flexibility to upload big files and different types of files

## FAIR DATA PRINCIPLES



# Uploading big data

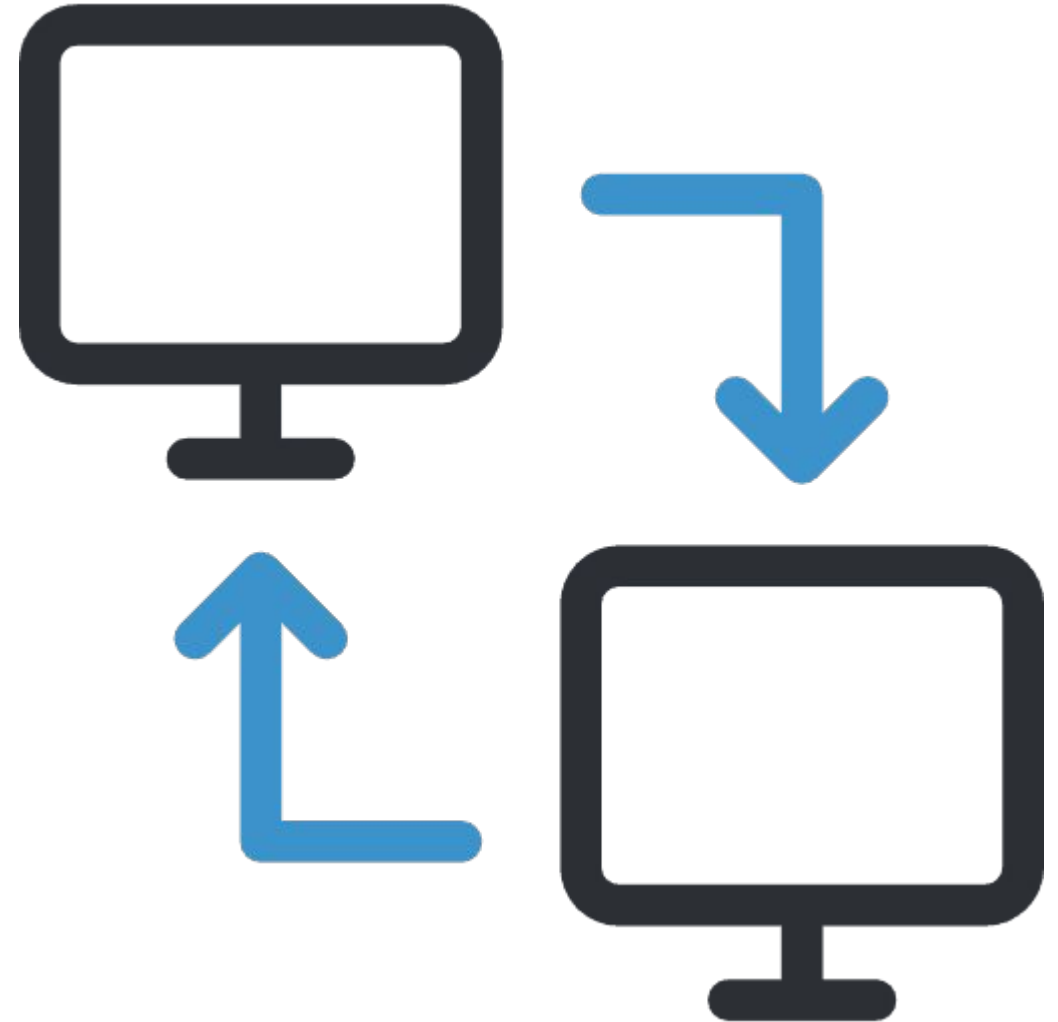


- Good documentation on how to upload big datasets

<https://www.scilifelab.se/data/repository/submission/>

<https://github.com/ScilifelabDataCentre/SciLifeLab-Data-Repository-API-examples>

- Easy to do streaming uploads using a FTP uploader, Python API or bash scripts. Also it is possible to upload from S3 storage backends



- {}pharmb.io

[illegible]