This readme file was modified on 2024-03-06 by Lucia Maddalena

GENERAL INFORMATION

Title of Dataset: ALFI

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Date of data collection: 2012 - 2022

Geographic location of data collection: Roma, Italy

Information about funding sources that supported the collection of the data:

This work has been partially funded by the BiBiNet project (H35F21000430002) within POR-Lazio FESR 2014-2020.

It was carried out also within the activities of the authors as members of the INdAM Research group GNCS and the ICAR-CNR INdAM Research Unit.

The work of M.R.G. was conducted within the framework of the Basic Research Program at the National Research University Higher School of Economics (HSE).

The microscopy experiments were performed at the IBPM Nikon Reference Centre and have been partially supported by POR-Lazio FESR 2014-2020 (N. A0375-2020-36597 to F.D. and G.G.) and by AIRC (IG-2021 ID:25648 to G.G.).

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SHARING/ACCESS INFORMATION

Licenses/restrictions placed on the data: CC-BY

Links to publications that cite or use the data: https://doi.org/10.1038/s41597-023-02540-1

L. Antonelli, F. Polverino, A. Albu, A. Hada, I.A. Asteriti, F. Degrassi, G. Guarguaglini, L. Maddalena, M.R. Guarracino, ALFI: Cell cycle phenotype annotations of label-free time-lapse imaging data from cultured human cells, Scientific Data, accepted August 2023

Data was not derived from other sources.

Recommended citation for this dataset https://doi.org/10.6084/m9.figshare.c.6436958.v1: see https://doi.org/10.1038/s41597-023-02540-1.

DATA & FILE OVERVIEW

Data is divided into three folders:

1) Folder "Data&Annotations" includes images and annotations for all the sequences.

1.1) For sequences MI01 through MI08 (including annotations for both Task 1 and Task 2), the content is, e.g.,

─ Data&Annotations ├── MI01



For each j, I_MI01_j.png is the j-th image of video MI01 and M_MI01_j.png is the corresponding ground truth segmentation mask.

The MI01_DTLTruth.csv file includes annotation information consisting of a) Number of sequence image (ImNo), b) Cell ID (ID), c) Cell class (Class, either Interphase or Mitosis), d) Bounding box, specified by its upper left corner (xmin, ymin) and its dimensions (width, height), and e) Parent cell ID (Parent). The MI01_PhenoTruth.csv file includes annotation information consisting of a) Number of sequence image (ImNo), b) Cell ID (ID), c) Cell class (Class, including EarlyMitosis, LateMitosis, CellDeath, and Multipolar), and d) Bounding box, specified by its upper left corner (xmin, ymin) and its dimensions (width, height). 1.2) For sequences CD01 through CD09 and TP01 through TP12 (including only annotations for Task 2), the content is similar, but there is no "Masks" subdirectory nor "*PhenoTruth.csv" file. 2) Folder "UseExamples" includes two usage examples and two directories including their output, in the form of Matlab/Python scripts. UseExamples UseExample1 m UseExample1.py UseExample1.py.readme.txt UseExample10ut **TP06BBannots** — TP06_py_WithBB_0001.png – TP06_py_WithBB_0016.png — TP06 WithBB 0001 png └── TP06_WithBB_0016 png UseExample2.m UseExample20ut MI01Lineage png MI01LineageCrops.png MI02Lineage png MI02LineageCrops.png MI03Lineage.png MI03LineageCrops.png MI04Lineage.png MI04LineageCrops.png MI05Lineage.png MI05LineageCrops.png MI06Lineage.png MI06LineageCrops.png MI07Lineage png MI07Lineage(Mitoses).png MI07LineageCrops.png MI08Lineage.png MI08Lineage(Mitoses).png MI08LineageCrops.png

2.1) UseExample1.m is a Matlab script for plotting the bounding box annotations over the original sequence images; the output is included in folder UseExample1Out/TP06BBannots, that contains images TP06_WithBB_0001.png, ..., TP06_WithBB_0016.png. UseExample1.py is the analogous examples written in Python and UseExample1.py.readme.txt is the related readme file; the output is included in folder UseExample1Out/TP06BBannots, that contains images TP06_py_WithBB_0001.png, ..., TP06_py_WithBB_0016.png.

2.2) UseExample2.m is a Matlab script for plotting the cells lineage for one of the sequences MI01–MI08; the output of this example is the lineage representation and image crops of mitotic cells given in the PNG images included in folder UseExample2Out.

For the user convenience, we provide the output images for all MI* sequences, without need to run it. Please, observe that, for the very crowded sequences MI07 and MI08, we also also provide the lineage representation reduced only to Mitoses (e.g., MI07Lineage(Mitoses).png), obtained setting the parameter OnlyMitoses = 1; (line 49 of the script).

3) Folder "Videos" includes the 29 videos stored in ND2 format. └── Videos └── CD01.nd2

└___ TP10.nd2

METHODOLOGICAL INFORMATION

Description of methods used for collection/generation of data: see https://doi.org/10.1038/ s41597-023-02540-1.

Methods for processing the data: see https://doi.org/10.1038/s41597-023-02540-1.

Instrument- or software-specific information needed to interpret the data: The Use Example scripts were created using Matlab R2020a and Python.