1. ABOUT THE DATASET

Title: Images supporting 'Fully automated platelet Differential Interference Contrast image analysis via deep learning'

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Organisation(s):

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Publication Year: 2022

Description:

This dataset supports the publication 'Fully automated platelet Differential Interference Contrast image analysis via deep learning' submitted to the journal of Scientific Reports[1]. All data was gathered or generated at The University of Reading from 2020 to 2021.

This dataset consists of i) 120 training images used to train a convolutional neural network (CNN) to automate platelet analyses, ii) 12 test images independent from the training images to test the CNN performance, and iii) a total of 225 8-bit images (representative of 3 independent experiments, with five fields of view captured per condition) of platelets spread over three different substrates (CRP-XL, fibrinogen, and vWF) and in the presence or absence of inhibitors (dasatinib, ibrutinib and PRT-060318) or an agonist (thrombin). These inhibitors and agonist are known to impact platelet morphology, and were used to assess the CNN's performance on morphological extremes.

NB: The original 16-bit images with dimensions 2424x2424 were rescaled and converted to 970x970 8-bit images to reduce the file size using ImageJ. All images within this dataset are the 8-bit images.

Cite as:

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2. TERMS OF USE

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3. PROJECT AND FUNDING INFORMATION

Title: Fusogenic liposomes, the innovative delivery of cargo into platelets

Dates: October 2019 – October 2022

Funding organisation: British Heart Foundation (BHF) and National Centre for the Replacement, Refinement and Reduction of Animals in Research (NC3Rs).

Grant no.: NC/S001441/1

4. CONTENTS

Folder listing

- train
    - folders 'training1 – training120' each contain one 8-bit TIF image file. All images were manually annotated to identify the perimeter of each platelet in each image to provide a supervised guide for training the neural network.

- test
    - folders '01 – 12' each contain one 8-bit TIF image file used to assess the performance of the CNN on a new data set. These 12 images were also manually annotated by a trainer and 5 independent platelet annotators which identified variability between users.

- inhibitor – 25 8-bit TIF image files per substrate were acquired to assess if the CNN could detect extremes in platelet shape in the presence or absence of inhibitor or agonist (see key below) for three independent experiments. Folder structure:
    - experiment1
        - crp-xl - folders '01 – 25' each contain one 8-bit TIF image file.
        - fibrinogen - folders '01 – 25' each contain one 8-bit TIF image file.
        - vwf - folders '01 – 25' each contain one 8-bit TIF image file.
    - experiment2

        - crp-xl - folders '01 – 25' each contain one 8-bit TIF image file.
        - fibrinogen - folders '01 – 25' each contain one 8-bit TIF image file.
        - vwf - folders '01 – 25' each contain one 8-bit TIF image file.
    - experiment3
        - crp-xl - folders '01 – 25' each contain one 8-bit TIF image file.
        - fibrinogen - folders '01 – 25' each contain one 8-bit TIF image file.
        - vwf - folders '01 – 25' each contain one 8-bit TIF image file.

Key for inhibitor/agonist pre-treatment:

Pre-treatment	**Image N°**
Dasatinib	1-5
Ibrutinib	6-10
PRT-060318	11-15
Thrombin	16-20
N/A – control, washed platelets	21-25

All images were captured by Köhler illuminated Nomarski differential interference contrast (DIC) optics using a Nikon eclipse Ti2 inverted microscope, equipped with a Nikon DS-Qi2 camera, and visualised using a 100x oil immersion objective lens. NIS Elements software was used for image capture and each image was acquired as .ND2 image files. All original images were rescaled and resized to 8-bit TIF image files prior to processing using Fiji ImageJ [2].

Training images were manually annotated and labelled images generated by using the LOCI plugin for Fiji ImageJ as per instructions detailed for the Usiigaci pipeline [3].

5. METHODS

Imaging:

Full experimental methods are available within the manuscript titled 'Fully automated platelet Differential Interference Contrast image analysis via deep learning' published by Scientific Reports.

CNN:

All scripts and model weights used for this experimental set up can be accessed via the following open-source GitHub repository: https://github.com/george-butler/Automated_DIC_platelet_analysis

Software installations required can be accessed here.

For a detailed method of how to curate the training material using the LOCI plugin, and to pre-process the training material follow the instructions here.

The GitHub repository includes:

- Python script to pre-process the training material.
- Python script to train the CNN.
- The three model weights are available to download - the model weights relate to the three independent networks which were trained using the 120 training images and used in an ensemble analysis approach.
- Python script to segment each image.
- Python script for quality control of each segmented image.
- Finally, a detailed method for using the quality control panel and generating quantitative outputs for each image.

REFERENCES

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1 Kempster, C. *et al.* Fully automated platelet differential interference contrast image analysis via deep learning. *Scientific Reports* **12**, 4614, doi:10.1038/s41598-022-08613-2 (2022).

2 Schindelin, J. *et al.* Fiji: an open-source platform for biological-image analysis. *Nat Methods* **9**, 676-682, doi:10.1038/nmeth.2019 (2012).

3 Tsai, H.-F., Gajda, J., Sloan, T. F. W., Rares, A. & Shen, A. Q. Usiigaci: Instance-aware cell tracking in stain-free phase contrast microscopy enabled by machine learning. *SoftwareX* **9**, 230-237, doi:https://doi.org/10.1016/j.softx.2019.02.007 (2019).