Deep Learning for Structured Illumination Microscopy Image Processing

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Project Report

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28th June 2024

Acknowledgements

Firstly I would like to thank my supervisor, Dr Edward Ward, for all of his support over the course of this project. The project involved a lot of concepts from microscopy and image processing that were very new to me, but Dr Ward made it clear from early on in the project that this would not be a problem, and was quick to provide reading materials to help me get to grips with the subject. Having been trained in Mathematics during my time as an undergraduate, the chance to go into the laboratory and capture real microscope images that were later used in the work was incredibly exciting. Dr Ward was eager to provide this opportunity and welcomed me to the Chemical Engineering and Biotechnology (CEB) Department and his research group.

I also had the opportunity to attend some of the Laser Analytics Group (LAG) lab meetings, where I had the privilege of learning about some of the world-leading research being undertaken by the group. Later, I shared details about my own project in two presentations to the group. I would like to thank all of the members of the LAG for welcoming me, listening to my presentations and providing great feedback. In particular I wish to thank Professor Clemens Kaminski for his helpful suggestions and words of encouragement.

I would also like to thank Jeremy Wilkinson, Esther Gray, and Emilio Luz-Ricca. I had very insightful conversations about the project with all of them that helped me see the work in a new light.

Lastly, I would like to thank my parents for being a continual source of support and strength throughout my education, in particular for encouraging me to make the most of every opportunity that comes my way.

Contents

1 Introduction

Structured Illumination Microscopy (SIM) is a technique that combines a specialised microscope set-up, alongside computational processing of the acquired images, in order to achieve a greater spatial resolution than can typically be expected from equivalent widefield microscopy imagery. The theoretical foundations of the technique were first established in 2008 [1].

Guarantees of SIM (Abbe‘s limit, doubled resolution, axial resolution, number of beams, fourier space, missing cone)

Importantly, whilst other techniques can be used (e.g. confocal) to achieve greater resolution imagery, SIM has its own specific practical advantages. Photo-bleaching, confocal loses important signal.

Deep-learning approaches (e.g. ML-OS-SIM)

Nat Biotech paper [2]

Objectives

2 Methods

2.1 Data

In silico noising

2D real data (specifications of the Microscope, cells)

3D vh data

2.2 RCAN

Use elsewhere

Diagram

2.3 Reconstruction process

preprocessing

fairSIM and parameters.

2.4 Pipeline

Describe building from scratch (pytorch vs tflow)

Diagram

Software
Using CSD3, hardware, parallel -¿ serial

3 Results

3.1 2D Data

Parameter estimation
Generalizability
Tables of results, metrics
Images

3.2 3D Data

Axial resolution
Tables of results, metrics
Images

4 Discussion

Results/conclusions Further work What I learned How I could have improved - Pt about training second step denoising. Maybe you should have train,test,val,train2,test2,val2. Otherwise, the step 2 is trained to map denoised images (that step1 has seen and so does better on) to GT, but then evaluated on how it maps unseen step 1 denoised images to GT. Also the testing set gets seen too much (Mike's last image analysis lecture about overexposure to hold out test set)

5 References

[1] G. Mats G.L. *et al.*, "Three-dimensional resolution doubling in wide-field fluorescence microscopy by structured illumination," *Biophysical Journal*, vol. 94, no. 12, pp. 4957–4970, 2008. [Online]. Available: https://doi.org/10.1529/biophysj.107.120345

[2] X. Li *et al.*, "Three-dimensional structured illumination microscopy with enhanced axial resolution," *Nature Biotechnology*, vol. 41, pp. 1307–1319, 2023. [Online]. Available: https://doi.org/10.1038/s41587-022-01651-1

A Statement on the use of auto-generation tools

B High-Performance Computing Resources

This work was performed using resources provided by the Cambridge Service for Data Driven Discovery (CSD3) operated by the University of Cambridge Research Computing Service (www.csd3.cam.ac.uk), provided by Dell EMC and Intel using Tier-2 funding from the Engineering and Physical Sciences Research Council (capital grant EP/T022159/1), and DiRAC funding from the Science and Technology Facilities Council (www.dirac.ac.uk).