Lecture 20: Microscopy

Course: Biomedical Data Science

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Outline

- Overview
- Simple tasks such as cell counting
- More complicated tasks
- Code

Credit

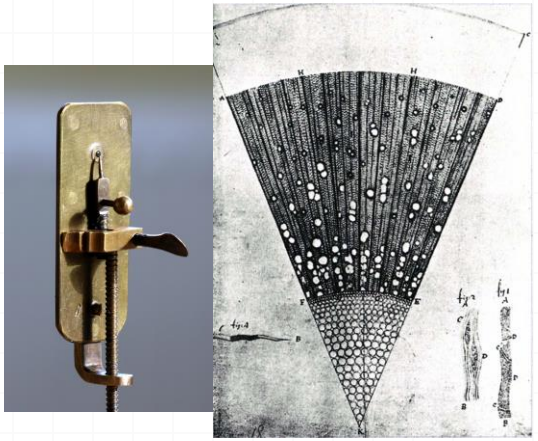
Slides are partially based on the material in Ramsundar, Bharath; Eastman, Peter; Walters, Patrick; Pande, Vijay. Deep Learning for the Life Sciences, Chapter 7.

Background

- A vital tool in life sciences.
- Until recently, humans manually inspected the images.
- More recently, tools such as CellProfiler have made possible to automatically handle microscopy data.
  - No programming experience is needed.
  - However, complex vision tasks cannot be performed by existing pipelines.
- Lots of interest in deep microscopy in recent years.

Microscopy Overview

- It has been in use since 17th century.
  - Antonie van Leeuwenhoek
- Optical microscopes have a theoretical limit on resolution (*Optical diffraction limit*)
- How to bypass the limit:
  - Electron Microscopy
  - Atomic Force Microscopy
  - Super-resolution microscopy



A replica of a microscope by van Leeuwenhoek [1], and a microscopic section of a one-year-old ash tree [2].

[1] By Jeroen Rouwkema, CC BY-SA 3.0, https://commons.wikimedia.org/w/index.php?curid=3657142

[2] By Antoni van Leeuwenhoek - T. Cremer, Von der Zellenlehre zur Chromosomentheorie, Springer Verlag Berlin Heidelberg New York Tokyo, 1985, ISBN 3-540-13987-7. Online Version. Source given in there: The collected letters from Antoni van Leeuwenhoek, Vol. II, Amsterdam, Sweets and Zeitlinger LTD (1941), Public Domain, https://commons.wikimedia.org/w/index.php?curid=3652421

Deep Learning and Diffraction Limit

- A few early papers have shown that deep learning techniques can be used to speed up super-resolution microscopy imaging.
- Deep learning can effectively perform tasks such as deblurring.
  - No compelling tools yet in the super-resolution microscopy domain

ARTICLES

nature biotechnology

Deep learning massively accelerates super-resolution localization microscopy

Wei Ouyang[1–3], Andrey Aristov[1–3], Mickaël Lelek[1–3], Xian Hao[1–3] & Christophe Zimmer[1–3]

The speed of super-resolution microscopy methods based on single-molecule localization, for example, PALM and STORM, is limited by the need to record many thousands of frames with a small number of observed molecules in each. Here, we present ANNA-PALM, a computational strategy that uses artificial neural networks to reconstruct super-resolution views from sparse, rapidly acquired localization images and/or widefield images. Simulations and experimental imaging of microtubules, nuclear pores, and mitochondria show that high-quality, super-resolution images can be reconstructed from up to two orders of magnitude fewer frames than usually needed, without compromising spatial resolution. Super-resolution reconstructions are even possible from widefield images alone, though adding localization data improves image quality. We demonstrate super-resolution imaging of >1,000 fields of view containing >1,000 cells in ~3 h, yielding an image spanning spatial scales from ~20 nm to ~2 mm. The drastic reduction in acquisition time and sample irradiation afforded by ANNA-PALM enables faster and gentler high-throughput and live-cell super-resolution imaging.

Scale-recurrent Network for Deep Image Deblurring

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Abstract

In single image deblurring, the "coarse-to-fine" scheme, i.e. gradually restoring the sharp image on different resolutions in a pyramid, is very successful in both traditional optimization-based methods and recent neural-network-based approaches. In this paper, we investigate this strategy and propose a Scale-recurrent Network (SRN-DeblurNet) for this deblurring task. Compared with the many recent learning-based approaches in [25], it has a simpler network structure, a smaller number of parameters and is easier to train. We evaluate our method on large-scale deblurring datasets with complex motion. Results show that our method can produce better quality results than state-of-the-arts, both quantitatively and qualitatively.

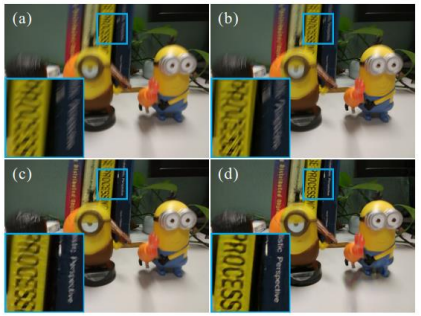

Figure 1. **One real example.** (a) Input blurred image. (b) Result of Sun *et al.* [34]. (c) Result of Nah *et al.* [25]. (d) Our result.

1. Introduction

Image deblurring has long been an important task in

al [25] have achieved state-of-the-art results using a multi-

Example 1: Cell Counting

Experiment

- Cell counting is important, e.g. to track the number of cells that survive after a given intervention.
- We will use the Broad Bioimage Benchmark Collection (BBBC).
  - A collection of freely downloadable microscopy images.
  - Each set includes a description of the biological application and some type of "ground truth".

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Notebook

- See cell counting notebook for the code

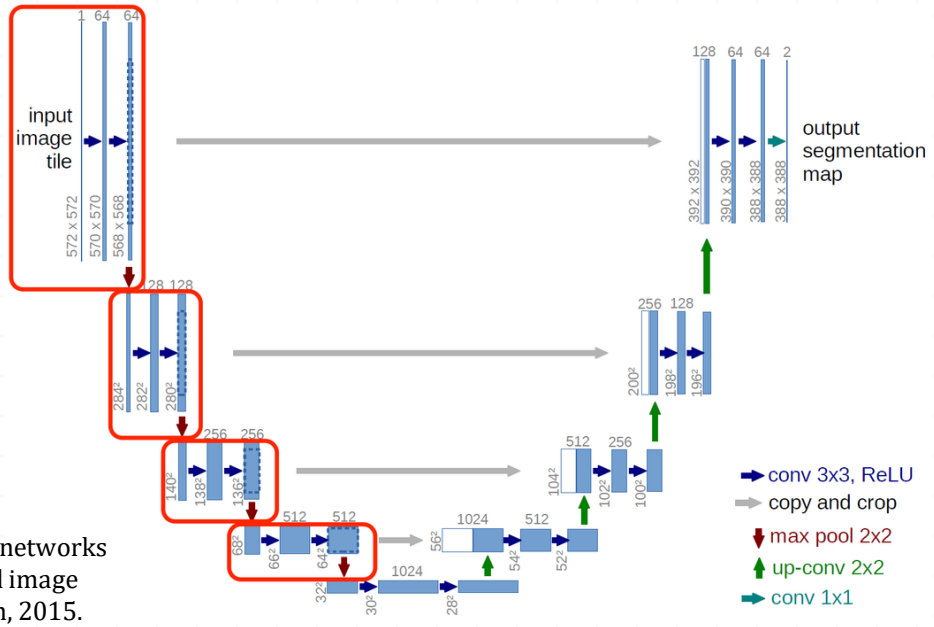
Example 2: Cell Segmentation

Experiment

- Cell segmentation involves annotating where the cells appear and where background appears.
- We will use the same dataset as before: BBBC005.
- In a segmentation task, each label is an image itself.

Architecture

- We will use the U-Net architecture.
- It progressively down-samples and then up-samples the source images.



Ronneberger, Olaf, Philipp Fischer, and Thomas Brox. "U-net: Convolutional networks for biomedical image segmentation." In International Conference on Medical image computing and computer-assisted intervention, pp. 234-241. Springer, Cham, 2015.

Notebook

- See cell segmentation notebook for the code