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3D reconstruction of complex biological structures from noisy microscopy images

Living organisms have evolved over millions of years into intricate functional systems that are structured at multiple scales: DNA and other molecules at the nanometer scale, cells at the microscopic, and organs at the macroscopic scale. Over the past few decades, microscopy techniques have been developed to 3D scan these structures at the sub-cellular level, including laser confocal scanning microscopy, electron microscopy, and X-ray microtomography (micro-CT). However, this type of equipment requires an initial investment of several hundred thousand dollars and therefore remains inaccessible to most laboratories around the world. Surprisingly, it is also possible to obtain 3D microscopic data with technology has been around since the 18th century using a device called the microtome. This 3D microscopy scan can be achieved by cutting consecutive micrometer-thin slices of the sample using a sharp knife. One of the biggest challenges is that most of the data acquisition is performed manually, meaning that information about original 3D conformation is blurred by several independent sources of noise. On the other hand, microtomes are able to produce a vast amount of structural data at relatively low-cost. During this lecture, I will present an overview of current microscopy techniques and their limitations, our current attempts to solve this multi-scale problem by machine learning, comparing results to existing algorithms, and will discuss the usage of some applied mathematical analyses such as particle image velocimetry (PIV).

Brief C.V.

2006 Bachelor of Science (Life Sciences) – Université Paris 5, France
2008 Master of Science (Cellular Biology) – Université Paris 5, France
2013 Ph. D. (Molecular Biology) – The University of Tokyo
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