"Zero-Shot" Enhancement of SARS-CoV-2 Images

Denoising and Structure Enhancement of Medical Images With Current Emphasis on Electron Microscopy Data of SARS-CoV-2

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In Short

- Latest available machine learning approaches can be used for image denoising in scenarios where only a single noisy image is available.

- The project aims to apply such "zero-shot" learning approaches to enhance noisy microscopic images with current focus on images of SARS-CoV-2 viruses.

- The execution of the used probabilistic generative networks on desired scales requires large parallel computers.

Electron microscopy (EM) images such as recent recordings of SARS-CoV-2 viruses are often produced at the limit of the possible resolution and they are often contaminated by strong noise. For SARS-CoV-2, also the amount of available recordings is limited. Machine Learning algorithms have greatly advanced the field of image denoising within the last two decades, their application to EM data is associated with particular challenges though. While for macroscopic images, typically large data sets with clean images are available which can be exploited to train the algorithms, denoising methods for EM images need to be trainable on noisy data. If only a few or even a single noisy image is available for training, algorithms require "few-shot" or respectively "zero-shot" learning abilities. For "zero-shot" learning, algorithms use only the information of the single available noisy image. Previous work (see, e.g., [1,2]) has shown that probabilistic generative model algorithms can achieve state-of-the-art denoising performance in "zero-shot" settings. Such approaches, in a first step, learn a generative representation from the noisy data and they, in a second step, exploit the learned representation to perform denoising.

This project aims to apply probabilistic generative model algorithms to enhance medical image data with current focus on EM images of SARS-CoV-2. Visualizing image details showing the virus and its interaction with cells and cell structures hidden in the noise can significantly contribute to understanding the infection process. First examples of enhanced EM images have been obtained in preliminary experiments; they are shown in Figures 1 and 2. In these experiments, EM recordings of SARS-CoV-1 viruses were used.

For the project, simulations with large-scale models and large numbers of test runs are planned; for these purposes large parallel computers are very valuable as they can be well exploited by the parallelized implementations of the used algorithms.

WWW

`www.uol.de/ml`

More Information

[1] A.-S. Sheikh, J. A. Shelton, J. Lücke. A Truncated EM Approach for Spike-and-Slab Sparse Coding. *JMLR*, 2014. `doi: 10.5555/2627435.2697052`

[2] E. Guiraud, J. Drefs, J. Lücke. Evolutionary Expectation Maximization. In *Genetic and Evolutionary Computation Conference (GECCO)*, 2018. `doi:10.1145/3205455.3205588`

[3] H. R. Gelderblom, A. Schnartendorff, F. Kaulbars. Robert Koch Institut. `http://www.rki.de/DE/Content/Infekt/NRZ/EM/Aufnahmen/EM_Tab_SARS.html`
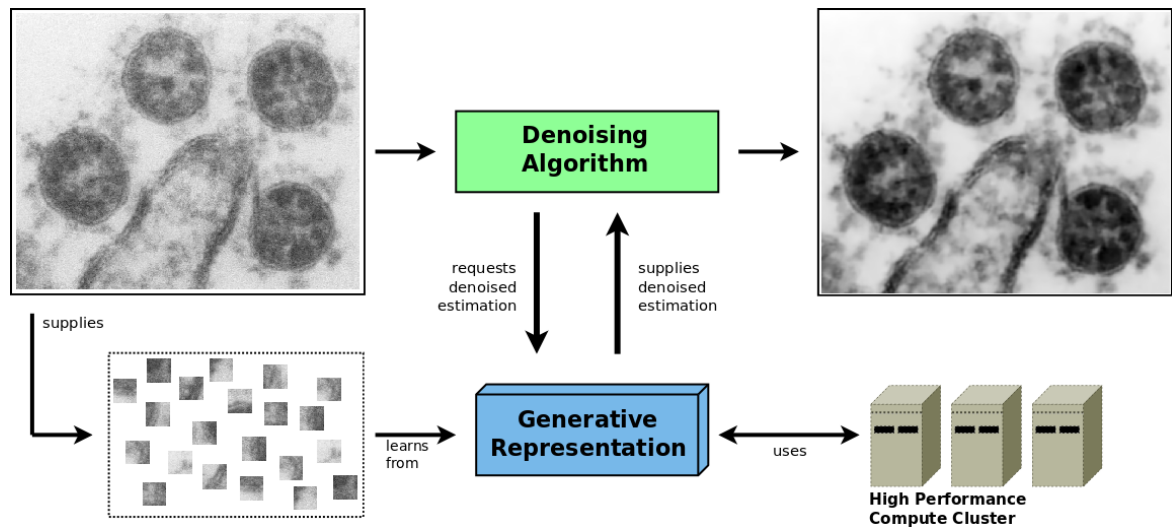
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Figure 1: *Schematic representation of a method for denoising electron microscopic (EM) images. On the left is an example of a noisy EM image of a SARS-CoV-1 virus (source: RKI [3]). The approach followed here uses the noisy image itself as the only input ("zero-shot" setting). The learning algorithm used first builds up a statistical/generative representation of the local image structures. These structures are then used by a denoising algorithm, which estimates the non-noisy pixel values by statistical averaging. The picture above right shows a test run demonstrating the feasibility and first denoising results on SARS-CoV-1 (based on [1,2]).*
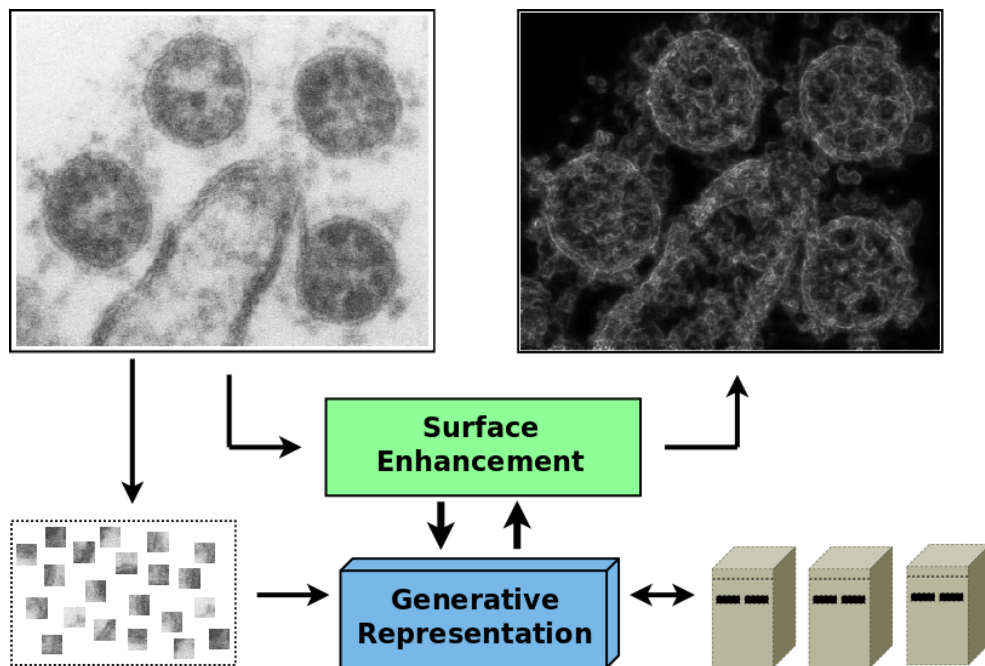

Figure 2: *Example of detail extraction of EM images using higher order image statistics. On the left, the same image of SARS-CoV-1 viruses is shown as in Figure 1. Also the use of the probabilistic algorithm to learn a statistical representation is analogous to Figure 1. In contrast to the denoising algorithm (which uses the first statistical moment), this is an approach that uses higher order statistics to sharpen details and display surfaces and edges. From the planar-looking original image, an image that creates a three-dimensional impression can be calculated. The spherical structure of the viruses thus becomes visible, and the assignment of virus and cell structures can be made easier. The images were calculated as trial runs based on the work of [2] and follow-up work.*