

DISCOVERING CELL PHENOTYPES WITH DL

Context

In drug discovery research, large quantities of cells exposed to various treatments and dosages are imaged with microscopes. Deep learning techniques can be applied to these images, which are superior at tasks like distinguishing healthy from dead cells compared to traditional techniques. The downside is that a deep learning model is typically a black box. Particularly, this makes it difficult to discover relevant and novel phenotypes that cells exhibit.

Generative models (such as variational auto-encoders and generative adversarial networks) can be used to convert input data to a much smaller latent dimension (see figure). When the network architecture and loss functions are chosen appropriately, these latent features can correspond to relevant biological phenotypes that a biologist would like to discover. Because generative models can generate images from latent space representations, they provide a unique possibility to visualize and interpret these phenotypes.

Internship overview

- Master Student
- Internship / Graduation
- Mathware
- Location: Eindhoven

Technologies

- Deep learning
- Generative models
- Dimensionality reduction
- Image analysis



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Assignment

Create and train a state-of-the-art generative model for dimensionality reduction of microscope images of cells. With dimensionality reduction, we mean that the model should be able to reduce a given cell image to a small number of features that contain all the essential information that was in the image. We do not simply want any features that result from efficient data compression, but we want features that each have an individual biological meaning: in other words it should be a disentangled representation.

The generative model can subsequently be used to generate sharp and realistic cell images corresponding to various values of these disentangled features. This focus on disentanglement and visualization should lead to a model of which the output is interpretable and understandable for an end user, thereby helping to discover new cellular phenotypes!

Activities

- Literature research on state-of-the-art deep learning methods and techniques regarding creating disentangled representations, visualization, and interpretability.
- Implement the most promising model(s) and evaluate them for our use case.
- Apply you model to our customers dataset and share your findings with the Mathware team!

Why choose Sioux?

- Working on innovative technology
- Challenging, dynamic and varied work
- A comfortable and personal work environment
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- Great carreer opportunities
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Get in touch!

Would you like to know more about this student assignment?

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