

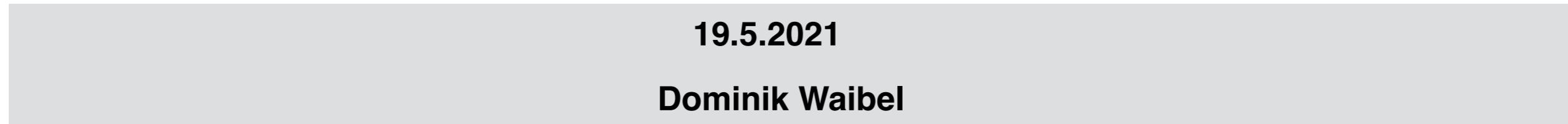


Software | [Open Access](#) | Published: 02 March 2021

InstantDL: an easy-to-use deep learning pipeline for image segmentation and classification

[Dominik Jens Elias Waibel](#), [Sayedali Shetab Boushehri](#) & [Carsten Marr](#)✉

BMC Bioinformatics **22**, Article number: 103 (2021) | [Cite this article](#)

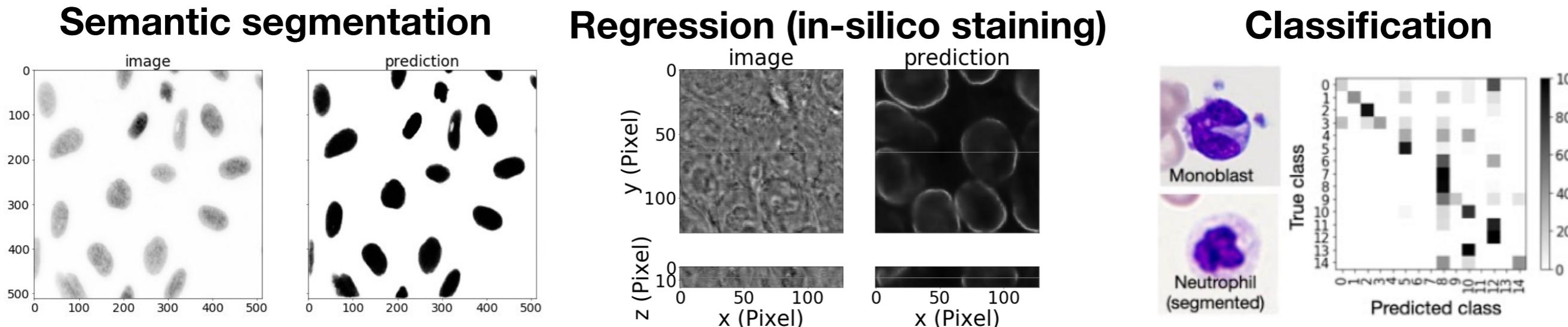


Problems:

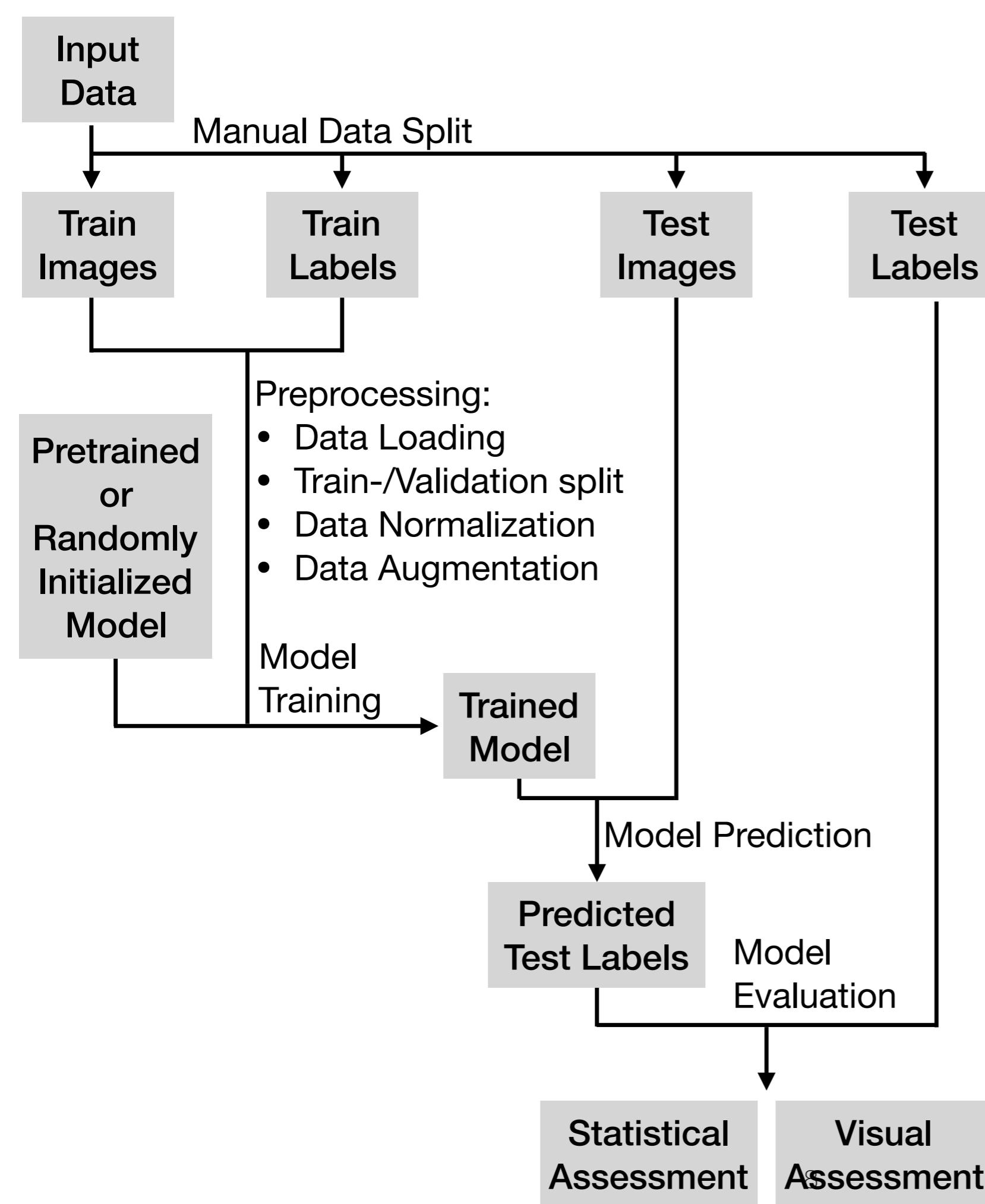
- Developed to solve a single specific problem
- Only applicable by experts

Solution:

- One Pipeline for:

**Goals:**

- Debugged and benchmarked
- Easily and convenient application
- Automated data pre-processing and augmentation
- Pre-trained models for efficient transfer learning
- Standardized data post-processing and performance evaluation
- Competitive results



<https://github.com/marrlab/InstantDL>

InstandDL Documentation

build passing

This is the documentation section for InstantDL. InstantDL enables experts and non-experts to use state-of-the art deep learning methods on biomedical image data. InstantDL offers the four most common tasks in medical image processing: Semantic segmentation, instance segmentation, pixel-wise regression and classification. For more in depth discussion on the methods, as well as comparing the results and benchmarks using this package, please refer to our preprint on bioRxiv [here](#)



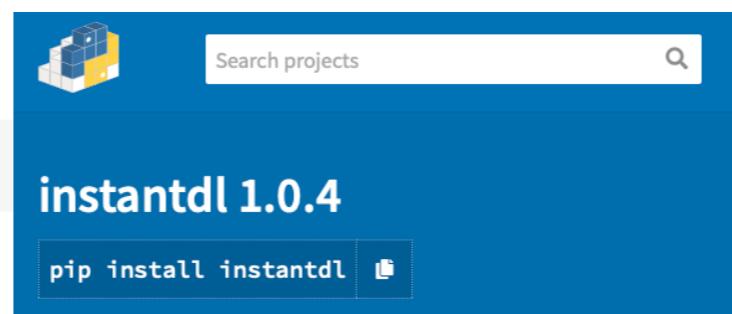
Installation

For installing the package, you should download the repository and run

```
python setup.py install
```

or install it via PyPI using:

```
pip install instantdl
```



How to use the code

There are three ways to use the code which are explained here:

1. With installation

In case you have installed the package, you can run the code by calling the pipeline by:

```
from instantdl import GetPipeLine
```

The you should pass the parameters to the pipeline

```
configs = { "use_algorithm" : str, # mandatory field
            "path" : str, # mandatory field
            "pretrained_weights" : str or None,
            "batchsize" : int,
            "iterations_over_dataset" : int,
            "data_gen_args" : dict,
            "loss_function" : str,
            "num_classes" : int,
            "image_size" : int,
            "calculate_uncertainty" : bool,
            "evaluation" : bool}

pipeline = GetPipeLine(configs)
pipeline.run()
```

This simply runs the Deep Learning pipeline.

InstantDL - Settings

```
from instantdl import GetPipeLine

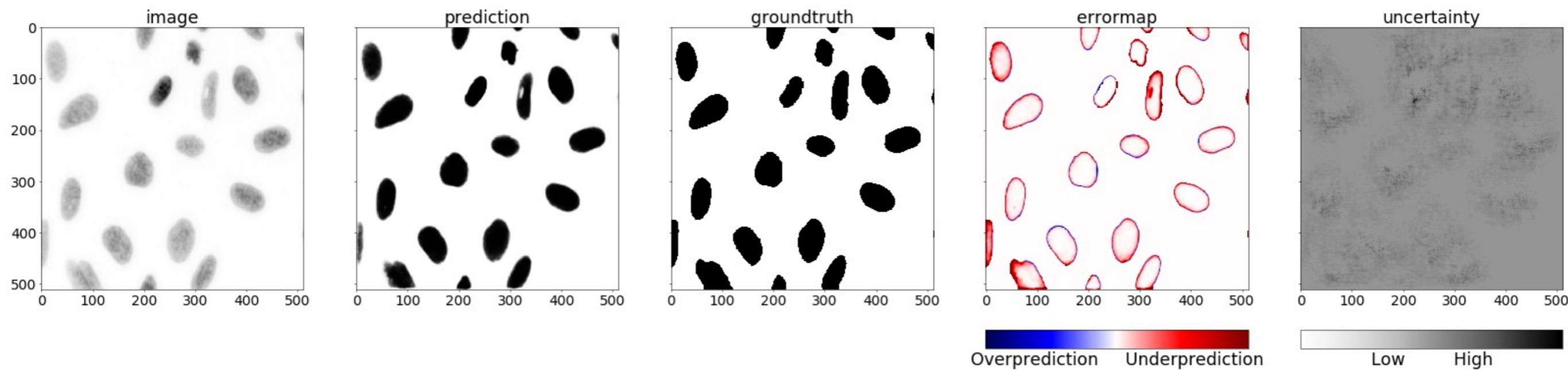
configs = {
    "use_algorithm": "Classification",
    "path": "examples/Classification",
    "pretrained_weights": "examples/data/Classification/logs/pretrained_weights_Classification.hdf5",
    "batchsize": 2,
    "iterations_over_dataset": 0,
    "data_gen_args": {
        "save_augmented_images": False,
        "resample_images": False,
        "std_normalization": False,
        "feature_scaling": False,
        "horizontal_flip": False,
        "vertical_flip": False,
        "poission_noise": 1,
        "rotation_range": 20,
        "zoom_range": False,
        "contrast_range": 1,
        "brightness_range": 1,
        "gamma_shift": 0,
        "threshold_background_image": False,
        "threshold_background_groundtruth": False,
        "binarize_mask": False
    },
    "loss_function": "binary_crossentropy",
    "num_classes": 2,
    "image_size": [128,128,3],
    "calculate_uncertainty": False,
    "evaluation": True }

pipeline = GetPipeLine(configs)

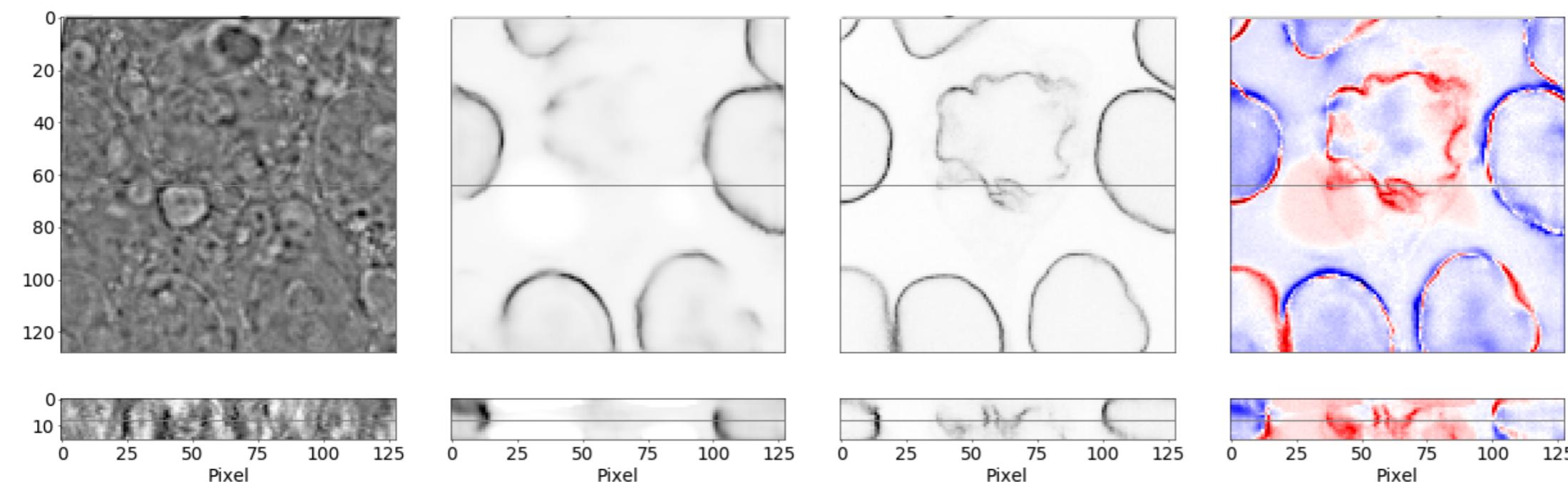
pipeline.run()
```

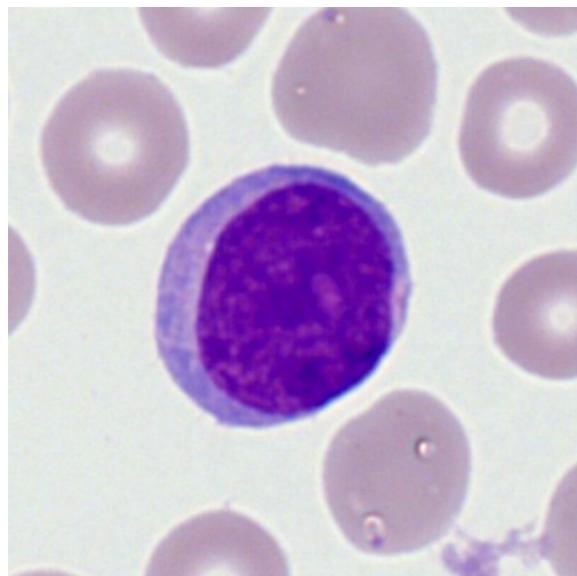
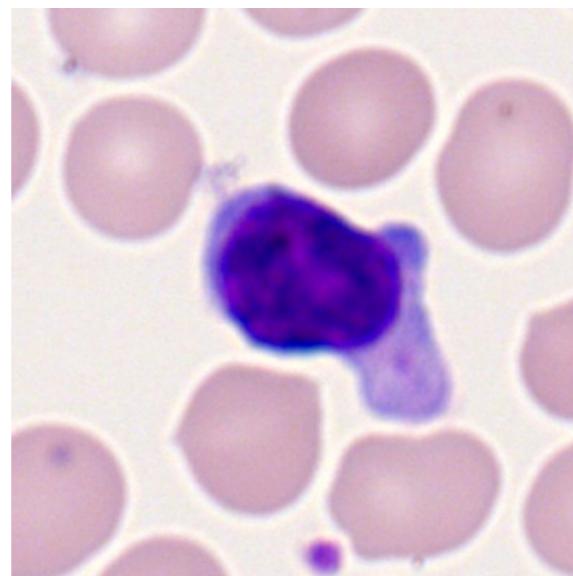
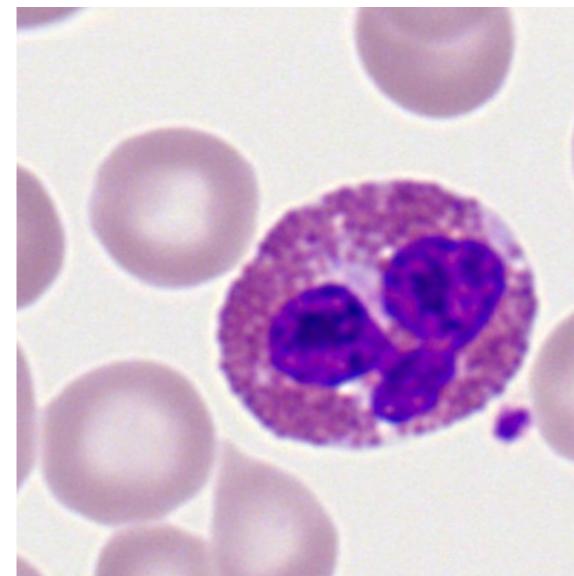
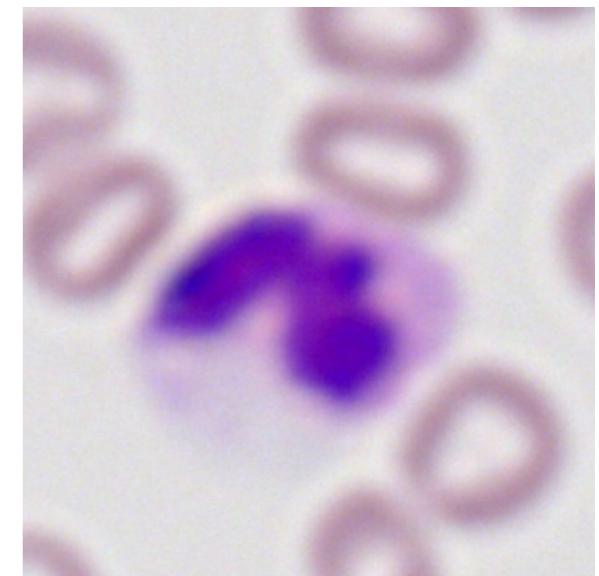
InstantDL - Segmentation and Regression

2D



3D



Myeloblast**Lymphocyte****Eosinophil****Neutrophil**

nature
machine intelligence

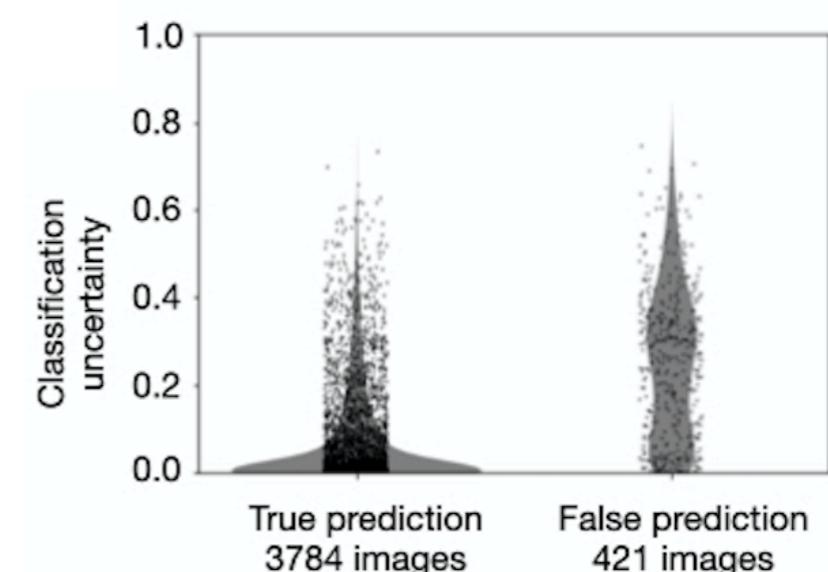
Article | Published: 12 November 2019

Human-level recognition of blast cells in acute myeloid leukaemia with convolutional neural networks

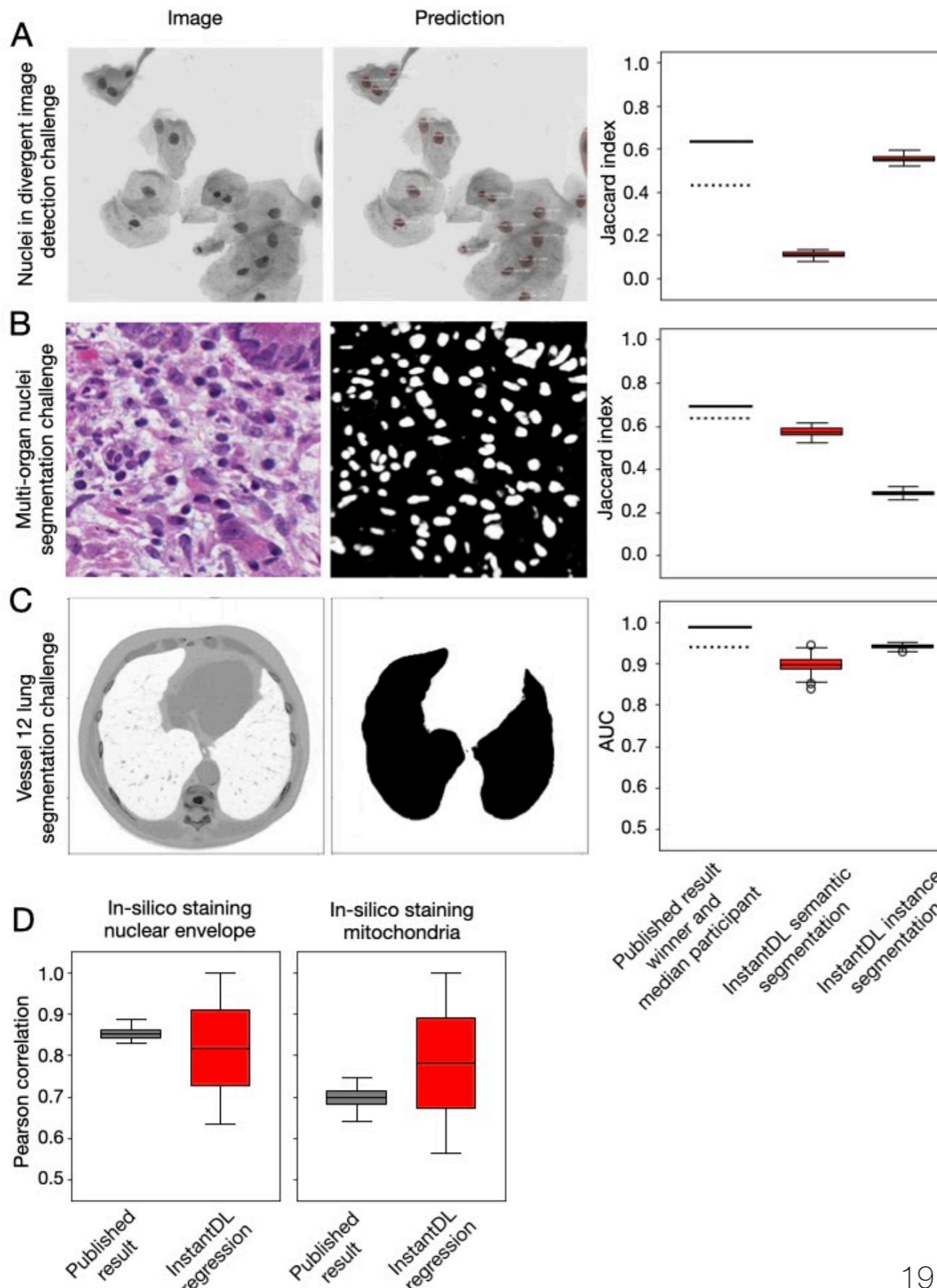
Christian Matek, Simone Schwarz, Karsten Spiekermann & Carsten Marr

Nature Machine Intelligence 1, 538–544(2019) | Cite this article

True class	Predicted class	Classification uncertainty
Monoblast	Monoblast	0.15
Myeloblast	Myeloblast	0.11
Neutrophil (segmented)	Myelocyte	0.89



InstantDL - Benchmarking



Nucleus segmentation across imaging experiments: the 2018 Data Science Bowl

Juan C. Caicedo, Allen Goodman, Kyle W. Karhohs, Beth A. Cimini, Jeanelle Ackerman, Marzieh Haghghi, CherKeng Heng, Tim Becker, Minh Doan, Claire McQuin, Mohammad Rohban, Shantanu Singh & Anne E. Carpenter [✉](#)

Nature Methods 16, 1247–1253(2019) | Cite this article

1550 IEEE TRANSACTIONS ON MEDICAL IMAGING, VOL. 36, NO. 7, JULY 2017 EMB IEEE NPSS Signal Processing Society UFFC

A Dataset and a Technique for Generalized Nuclear Segmentation for Computational Pathology

Neeraj Kumar,* Ruchika Verma, Sanuj Sharma, Surabhi Bhargava, Abhishek Vahadane, and Amit Sethi



Comparing algorithms for automated vessel segmentation in computed tomography scans of the lung: the VESSEL12 study

Rina D. Rudyanto ^a Sjoerd Kerkstra ^b, Eva M. van Rikxoort ^b, Catalin Fetita ^c, Pierre-Yves Brillet ^c, Christophe Lefevre ^c, Wenzhe Xue ^d, Xiangjun Zhu ^d, Jianming Liang ^d, İlker Öksüz ^e, Devrim Ünay ^e, Kamuran Kadıpaşaoglu ^e, Raúl San José Estépar ^f, James C. Ross ^f, George R. Washko ^f, Juan-Carlos Prieto ^f, Marcela Hernández Hoyos ^h, Maciej Orkisz ^g ... Bram van Ginneken ^b

nature methods

Brief Communication | Published: 17 September 2018

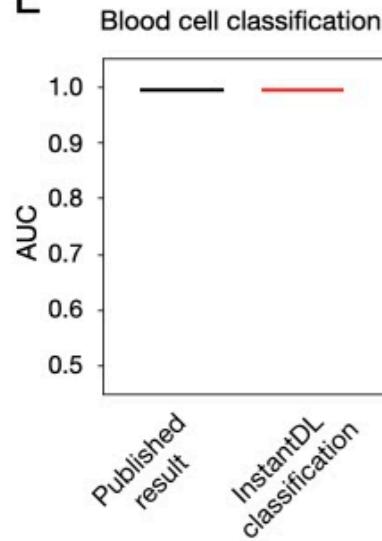
Label-free prediction of three-dimensional fluorescence images from transmitted-light microscopy

Chawin Ounkomol, Sharmishta Seshamani, Mary M. Malekar, Forrest Collman & Gregory R. Johnson [✉](#)

Nature Methods 15, 917–920(2018) | Cite this article

InstantDL - Benchmarking

E



nature
machine intelligence

Article | Published: 12 November 2019

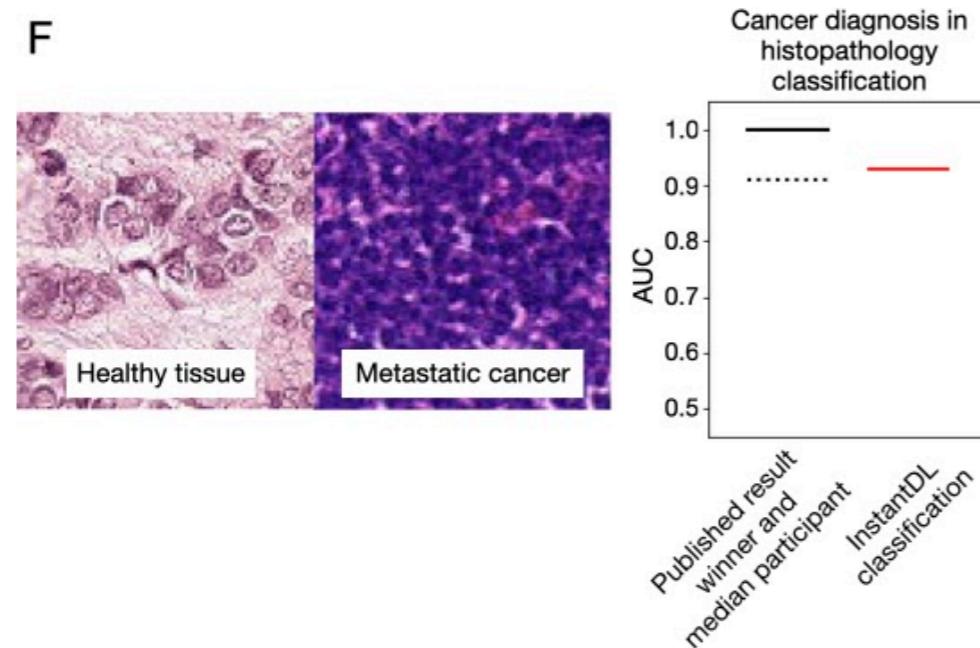
Human-level recognition of blast cells in acute myeloid leukaemia with convolutional neural networks

Christian Matek, Simone Schwarz, Karsten Spiekermann & Carsten Marr

Nature Machine Intelligence 1, 538–544(2019) | Cite this article

Comparative Study > JAMA. 2017 Dec 12;318(22):2199–2210. doi: 10.1001/jama.2017.14585.

F



Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer

Babak Ehteshami Bejnordi ¹, Mitko Veta ², Paul Johannes van Diest ³, Bram van Ginneken ¹, Nico Karssemeijer ¹, Geert Litjens ⁴, Jeroen A W M van der Laak ⁴, the CAMELYON16 Consortium; Meyke HermSEN ⁴, Quirine F Manson ³, Maschenka Balkenhol ⁴, Oscar Geessink ⁴ ⁵, Nikolaos Stathnikos ³, Marcory Crf van Dijk ⁶, Peter Bult ⁴, Francisco Beca ⁷, Andrew H Beck ⁷ ⁸, Dayong Wang ⁷ ⁸, Aditya Khosla ⁸ ⁹, Rishab Gargya ¹⁰, Humayun Irshad ⁷, Aoxiao Zhong ¹¹, Qi Dou ¹¹ ¹², Quanzheng Li ¹¹, Hao Chen ¹², Huang-Jing Lin ¹², Pheng-Ann Heng ¹², Christian Haß ¹³, Elia Bruni ¹³, Quincy Wong ¹⁴, Ugur Halici ¹⁵ ¹⁶, Mustafa Ümit Öner ¹⁵, Rengul Cetin-Atalay ¹⁷, Matt Berseth ¹⁸, Vitali Khvatkov ¹⁹, Alexei Vylegzhanin ¹⁹, Oren Kraus ²⁰, Muhammad Shaban ²¹, Nasir Rajpoot ²¹ ²², Ruqayya Awan ²³, Korsuk Sirinukunwattana ²¹, Talha Qaiser ²¹, Yee-Wah Tsang ²², David Tellez ⁴, Jonas Annuscheit ²⁴, Peter Hufnagl ²⁴, Mira Valkonen ²⁵, Kimmo Kartasalo ²⁴ ²⁶, Leena Latonen ²⁷, Pekka Ruusuvuori ²⁴ ²⁸, Kaisa Liimatainen ²⁴, Shadi Albarqouni ²⁹, Bharti Mungal ²⁹, Ami George ²⁹, Stefanie Demirci ²⁹, Nassir Navab ²⁹, Seiryo Watanabe ³⁰, Shigeto Seno ³⁰, Yoichi Takenaka ³⁰, Hideo Matsuda ³⁰, Hady Ahmady Phouladhy ³¹, Vassili Kovalev ³², Alexander Kalinovsky ³², Vitali Liachuk ³², Gloria Bueno ³³, M Milagro Fernandez-Carrobles ³³, Ismael Serrano ³³, Oscar Deniz ³³, Daniel Racoceanu ³⁴ ³⁵, Rui Venâncio ³⁶



Demands to the user:

Know the basics of:

- Machine Learning
 - Task
 - Train-/Test-split
 - Loss functions
 - Training time and overfitting
 - Sparse data limits
- Statistics
 - Error metrics

A screenshot of a Google Colab notebook titled "GoogleCollabConfig.ipynb". The interface shows a menu bar with File, Edit, View, Insert, Runtime, Tools, Help, and "All changes saved". Below the menu is a toolbar with "+ Code" and "+ Text". A code cell is visible with the following Python code:

```
[1] from google.colab import drive  
drive.mount('/content/drive')
```

<https://github.com/marrlab/InstantDL>