A Workflow for efficient creation of high quality cell classification data sets

Henning Höfener[1], Martina Pontones[2], Farina Kock[1], Tabita Ghete[2], Max Westphal[1], Markus Metzler[2]

1) Fraunhofer MEVIS, Institute for Digital Medicine, Germany
2) Department of Pediatrics and Adolescent Medicine, University Hospital Erlangen, Germany

Introduction

Large, high quality datasets are essential for training and evaluating supervised cell classification algorithms. To reduce efforts for generating such datasets, each sample is usually labeled by only a single observer. However, as inter-observer variability in medical images is often high, this results in suboptimal datasets.

Material and methods

We propose a workflow for rapid labeling of samples by multiple observers. The workflow requires each sample to be labeled by at least two observers and that there is an absolute majority for a label value. The second observer is shown the value of the first label (validation). In case of disagreement, however, further observers cannot see the previous labels. We implemented the workflow as a web-based labeling tool, designed to require minimal interaction to facilitate rapid labeling. Our goal was to label cell images from bone marrow smears. The dataset contains more than 26,000 samples to be assigned to 53 different classes. Using this workflow we can additionally measure agreement between observers.

Results

In our dataset, labels of different observers did not match in 17.03% of the cells. Cell labeling takes a median of 3.62s in normal mode and 2.08s in validation mode. Considering the number of labels needed, this results in 6.52s (IQR: 4.31s - 11.90s) of labeling time per cell.

Conclusion

The high level of disagreement between observers demonstrates the need for multiple observers combined with a strategy for dealing with conflicting labels in order to produce high quality datasets. Our streamlined workflow facilitates rapid labeling to obtain such datasets in a reasonable amount of time.

Keywords: Image Labeling, Cell Classification, Dataset Generation, Inter-Observer Variability, Bone Marrow Smear,

Notes:

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