MULTI-TASK PRE-TRAINING OF DEEP NEURAL NETWORKS FOR DIGITAL PATHOLOGY

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In recent years, deep learning has been applied with great success in many domains where images are prevalent. Digital pathology, a domain that focuses on the analysis of large digitized glass slides images containing tissue and cell samples, is no exception. Even if deep learning has shown promising results, several difficulties have so far prevented advances similar to those in other communities, one of which is data scarcity. Indeed, deep learning algorithms are data-hungry and the number and scale of datasets is usually much lower in digital-pathology than in the natural image community. In this context, a common approach which has been adopted to overcome data scarcity is transfer learning which consists in pre-training a model on a large dataset (source task), and then somehow transfer the learned knowledge to facilitate training on the second dataset (target task). The source task must be large and the most common choice is using ImageNet as a source, a classification dataset containing more than 1 million natural images and 1000 classes. Although ImageNet transfer has proven to boost performance compared to direct training in digital pathology, it is expected that pre-training should provide an even better improvement if both the source and target are digital pathology tasks.

Whereas there is no digital pathology dataset that compares to ImageNet in terms of the scale and versatility, the community has made available many small and medium size datasets through challenges and publications over the years. This setting is actually ideal for multi-task learning, a subfield of supervised learning which focuses on methods that solve several tasks simultaneously. Therefore, in [1], we investigate multi-task learning as a way of pre-training neural networks for digital pathology.

1. MATERIALS, METHODS AND RESULTS

We have collected, assembled and transformed several digital pathology datasets into a large versatile pool of classification datasets featuring 22 tasks, 81 classes and almost 900k images. Then, we have developed a multi-task architecture

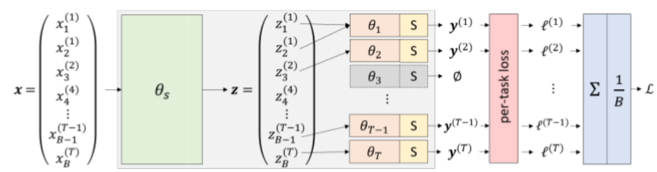

Fig. 1. Multi-task architecture. $\mathcal{L}$ is the multi-task loss and S is a softmax layer. $x_j^{(i)}$ and $z_j^{(i)}$ designate respectively the j^{th} sample of the batch $\mathbf{x}$ and its corresponding features produced by θ_s. This sample belongs to task t_i. Features produced for samples of a given task t_i are routed to this task head θ_i.

(see Fig. 1) and training scheme for creating a transferable model using popular architectures as backbone (*i.e.* ResNet, DenseNet). We show that our pre-trained models offer a credible alternative to ImageNet transfer as, depending on the target task, they either improve significantly over the former pre-training approach or provide comparable performance. More specifically, our pre-trained models used as feature extractors outperform ImageNet pre-trained models especially on more complex target tasks. Fine-tuning our models yields comparable transfer performance compared to fine-tuning ImageNet models.

Our pre-trained models and code are available on GitHub (`github.com/waliens/multitask-dipath`). We also plan to make our algorithms available as workflows in the Cytomine [2] (`cytomine.org`) and BIAFLOWS [3] (`biaflows.neubias.org`) open-source web platforms.

The authors have no conflict of interests to report. This research study was conducted retrospectively using human and animal subject data made available in open access by different sources (see [1] for all references). Ethical approval was not required as confirmed by the license attached with the open access data.

2. REFERENCES

[1] Romain Mormont, Pierre Geurts, and Raphaël Marée, "Multi-task pre-training of deep neural networks for digital pathology," *IEEE Journal of Biomedical and Health Informatics*, 2020.

[2] Raphaël Marée et al., "Collaborative analysis of multi-gigapixel imaging data using cytomine," *Bioinformatics*, vol. 32, no. 9, pp. 1395–1401, 2016.

[3] Ulysse Rubens et al., "Biaflows: A collaborative framework to reproducibly deploy and benchmark bioimage analysis workflows," *Patterns*, p. 100040, 2020.