Project Proposal: Benchmarking SOT Feature Transforms for Biomedical Few-Shot Learning Tasks

Jonas-Mika Senghaas, Adam Barla and Ludek Cizinsky École Polytechnique Fédérale de Lausanne (EPFL), Switzerland

I. INTRODUCTION

Few-shot classification has gained prominence for its ability to accurately assign class membership with limited examples per class, which is particularly relevant in the biomedical field where data scarcity is common. Traditional machine learning techniques often fall short in such scenarios, as they need a large number of training samples and iterations to perform well.

The primary strategies for few-shot classification can be categorised into two approaches. The first involves training a classifier from scratch or adapting pre-trained models through fine-tuning. This approach is exemplified by Model-Agnostic Meta-Learning (MAML) [1], which extends beyond basic fine-tuning by integrating a meta-training phase. This phase is designed to optimise weight initialisation, such that the model can generalise well to any downstream few-shot classification task..

The second category encompasses metric-based methods, which focus on learning discriminative embeddings through meta-learning. Unlike the first approach, these methods do not directly map features to targets. Instead, they use the learned embeddings to classify new instances based on simple distance-based heuristics. Notable methods in this category include Matching Networks [2] and Prototypical Networks (ProtoNet) [3].

II. PROJECT PROPOSAL

All of the above approaches rely on meaningful embeddings of features. However, a notable challenge arises due to the potential discrepancy in data distributions between the meta-training and testing phases. This discrepancy can result in embeddings that are not fully transferable, leading to suboptimal performance in downstream tasks. To address this issue, Self-Optimal-Transport (SOT) [4] has been proposed. SOT is a parameter-less feature transform module, grounded in probabilistic interpretations, and has shown promising results in improving performance across various few-shot learning benchmarks [4].

The primary objective of this project is to explore the effectiveness of the SOT feature transform in the context of few-shot learning tasks within the biomedical domain. Our approach involves establishing a comprehensive benchmarking suite to compare a range of few-shot learning algorithms, including [5], [1], [2], [3], both with and without

the integration of the SOT feature transform module. This comparison will be conducted using two distinct biomedical datasets. The aim is to assess whether the SOT method can consistently enhance the performance of few-shot learning models in scenarios where data is limited and highly specialised, a common challenge in biomedical applications.

III. DATASET

This project will utilise two distinct datasets, each offering unique insights into few-shot learning applications in the biomedical field. The first dataset, Tabula Muris [6], comprises a comprehensive mouse single-cell RNA sequencing collection. It serves as a molecular atlas, including various cell types across multiple organs. Within this study, the objective with this dataset is to predict cell types based on the gene expression profiles of cells of various tissue types. The dataset can be phrased as a few-shot classification task by only using a distinct set of tissue types for training, validation and testing splits and controlling for the number of samples seen during each episodic training iteration.

The second dataset, Swiss-Prot [7], represents a curated repository of protein sequences. This dataset is known for its high-quality, manually annotated protein sequences, which are enriched with detailed information about their functions, structures, and biological significance. The goal in utilising Swiss-Prot is to predict gene ontology labels from protein sequences.

IV. PROPOSED EXPERIMENTS

We hypothesise that the improvements in few-shot learning performance as observed by the authors in the original paper on common vision few-shot benchmarks[8] translate to the biomedical domain.

To evaluate this hypothesis, we plan to assess the performance of all combinations of datasets and few-shot learning methods, each with and without the SOT model and ablate the performance gains seen in various few-shot learning settings.

To this end, we aim to test the SOT model in the general N-way-K-shot framework by varying the number of classes to distinguish ($N=\{2,5,10,20\}$) and the number of samples available in each class ($K=\{1,5,10,50\}$). Each experiment will evaluated on multiple times to increase the statistical robustness of the reported findings.

REFERENCES

- C. Finn, P. Abbeel, and S. Levine, "Model-agnostic metalearning for fast adaptation of deep networks," *CoRR*, vol. abs/1703.03400, 2017. [Online]. Available: http://arxiv.org/ abs/1703.03400
- [2] O. Vinyals, C. Blundell, T. P. Lillicrap, K. Kavukcuoglu, and D. Wierstra, "Matching networks for one shot learning," *CoRR*, vol. abs/1606.04080, 2016. [Online]. Available: http://arxiv.org/abs/1606.04080
- [3] J. Snell, K. Swersky, and R. S. Zemel, "Prototypical networks for few-shot learning," *CoRR*, vol. abs/1703.05175, 2017. [Online]. Available: http://arxiv.org/abs/1703.05175
- [4] D. Shalam and S. Korman, "The self-optimal-transport feature transform," *arXiv preprint arXiv:2204.03065*, 2022.
- [5] W. Chen, Y. Liu, Z. Kira, Y. F. Wang, and J. Huang, "A closer look at few-shot classification," *CoRR*, vol. abs/1904.04232, 2019. [Online]. Available: http://arxiv.org/abs/1904.04232
- [6] N. Schaum, J. Karkanias, N. F. Neff, A. P. May, S. R. Quake, T. Wyss-Coray, S. Darmanis, J. Batson, A. Botvinnik, M. Chen et al., "Tabula muris: single-cell transcriptomics of 20 mouse organs," *Genome Biology*, vol. 20, no. 1, pp. 1–16, 2019.
- [7] T. U. Consortium, "Uniprot: a worldwide hub of protein knowledge," *Nucleic Acids Research*, vol. 47, no. D1, pp. D506–D515, 2019. [Online]. Available: https://doi.org/10. 1093/nar/gky1049
- [8] G. S. Dhillon, P. Chaudhari, A. Ravichandran, and S. Soatto, "A baseline for few-shot image classification," 2020.