

Professor Dr Sara Zandomeneghi  
Editor-in-Chief  
*BMC Bioinformatics*

25-Nov-2025

Dear Editor-in-Chief:

We are submitting our manuscript entitled “Toward reliable false discovery rate control in classification problems under distribution shift” for consideration for publication in *BMC Bioinformatics*.

**Affiliations:**

1. The corresponding author is: Prof. Attila Kertesz-Farkas, [akerteszfarkas@hse.ru](mailto:akerteszfarkas@hse.ru),
2. Co-author, first author: Andrey Borevskiy.

We are both part of the same laboratory: Laboratory on AI for Computational Biology, Faculty of Computer Science, HSE University, Moscow Russian Federation

We note that our institution is not under sanctions and we are not involved in any research related to the Russian military, etc.

**An explanation of why your manuscript should be published in BMC Bioinformatics:**

We present our study on controlling false discovery rates (FDR) under data distribution shift in classification problems in the biomedical domain. In this study, we draw attention to a very important but often neglected problem; namely, the performance of deep-learning based classifiers is assumed to be the same in application. However, it often can be much worse than thought due to data distribution shift (a.k.a. covariate shift), data label distribution shift, batch effects caused by some confounding factors, and overfitting. This performance drop of a machine learning system often remains undetected, resulting in risk for people in health care and clinical applications.

In this manuscript, we present a simple, fast and robust method to adjust the test prediction scores so that the latent test null distribution will be more similar to the train null distribution. This will result in more accurate FDR control.

Our method operates in the 1-dimensional prediction score space. Therefore, it is not hindered by high-dimensional space, data sparsity (i.e. curse-of-dimensionality), and correlated features. In addition, our method does not rely on data clustering or graphical causal models.

We tested our method with four public benchmark datasets commonly used in biomedical image analysis: PatchCamelyon (PCam), Chest x-ray (CheXpert), TissueNet, and Breast Cancer Semantic Segmentation (BCSS). With our method, we obtained much more accurate FDR control under data distribution shifts in the test data compared to a recent algorithm, called Learn-then-test, developed by Michael Jordan’s lab from Stanford University.

**A declaration of any potential competing interests:**

None.

**Confirmation that all authors have approved the manuscript for submission:**

This manuscript has been approved by both authors.

**Confirmation that the content of the manuscript has not been published:**

This manuscript has never been submitted to any other journals. The manuscript will be properly formatted for the journal if it is needed for the reviewing stage or once it is accepted. We did not use AI chat bots in manuscript preparation or in this study in general.

**Suggested reviewers:**

1. Nikita Moshkov, PhD, Institute of Biochemistry, Biological Research Center. Szeged, Hungary, Deep Learning specialist in biological image analysis, cell segmentation, etc. [nikita.moshkov@brc.hu](mailto:nikita.moshkov@brc.hu)
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We hope that this manuscript provides a useful and interesting study for the readers of *BMC Bioinformatics*.

Best regards,

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