



Computer Methods and
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Mahalul Azam <mahalul.azam@mail.unnes.ac.id>

Invitation to review for Computer Methods and Programs in Biomedicine Update

1 message

Usman Iqbal <em@editorialmanager.com>
Reply-To: Usman Iqbal <usmaniqbal@tmu.edu.tw>
To: Mahalul Azam <mahalul.azam@mail.unnes.ac.id>

Wed, Nov 25, 2020 at 4:24 PM

Manuscript Number: CMPBUP-D-20-00003
Data quality-aware genomic data integration
Anna Bernasconi, M.D.

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Usman Iqbal
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Computer Methods and Programs in Biomedicine Update

Abstract.

Genomic data are growing at unprecedented pace, along with new protocols, update policies, formats and guidelines, terminologies and ontologies, which are made available every day by data providers. In this continuously evolving universe, enforcing quality on data and metadata is increasingly critical. While many aspects of data quality are addressed at each individual source, we focus on the need for a systematic approach when data from several sources are integrated, as such integration is an essential aspect for modern genomic data analysis. Data quality must be assessed from many perspectives, including accessibility, currency, representational consistency, specificity, and reliability.

In this article we review relevant literature and, based on the analysis of many datasets and platforms, we report on methods used for guaranteeing data quality while integrating heterogeneous data sources. We explore several real-world cases that are exemplary of more general underlying data quality problems and we illustrate how they can be

resolved with a structured method, sensibly applicable also to other biomedical domains. The overviewed methods are implemented in a large framework for the integration of processed genomic data, which is made available to the research community for supporting tertiary data analysis over Next Generation Sequencing datasets, continuously loaded from many open data sources, bringing considerable added value to biological knowledge discovery.

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Computer Methods and Programs in Biomedicine Update <em@editorialmanager.com> Sun, Dec 6, 2020 at 9:16 PM
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To: Mahalul Azam <mahalul.azam@mail.unnes.ac.id>

Manuscript Number: CMPBUP-D-20-00003
Data quality-aware genomic data integration
Anna Bernasconi, M.D.

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Usman Iqbal <em@editorialmanager.com>

Mon, Dec 21, 2020 at 10:11 AM

Reply-To: Usman Iqbal <usmaniqbal@tmu.edu.tw>

To: Mahalul Azam <mahalul.azam@mail.unnes.ac.id>

Manuscript Number: CMPBUP-D-20-00060

Impact of stain normalization and patch selection on the performance of convolutional neural networks in histological breast and prostate cancer classification

Massimo Salvi; Filippo Molinari; Rajendra U Acharya; Kristen M Meiburger

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Usman Iqbal
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Computer Methods and Programs in Biomedicine Update

Abstract:

Background: Recently, deep learning has rapidly become the methodology of choice in digital pathology image

analysis. However, due to the current challenges of digital pathology (color stain variability, large images, etc.), specific pre-processing steps are required to train a reliable deep learning model.

Method: In this work, there are two main goals: i) present a fully automated pre-processing algorithm for a smart patch selection within histopathological images, and ii) evaluate the impact of the proposed strategy within a deep learning framework for the detection of prostate and breast cancer. The proposed algorithm is specifically designed to extract patches only on informative regions (i.e., high density of nuclei), most likely representative of where cancer can be detected.

Results: Our strategy was developed and tested on 1000 hematoxylin and eosin (H&E) stained images of prostate and breast tissue. By combining a stain normalization step and a segmentation-driven patch extraction, the proposed approach is capable of increasing the performance of a CAD system for the detection of prostate cancer (18.61% accuracy improvement) and breast cancer (17.92% accuracy improvement).

Conclusion: We strongly believe that the integration of the proposed pre-processing steps within deep learning frameworks will allow the achievement of robust and reliable CAD systems. Being based on nuclei detection, this strategy can be easily extended to other glandular tissues (e.g., colon, thyroid, pancreas, etc.) or staining methods (e.g., PAS).

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