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Introducing the research article reporting checklist for bioinformatic and data re-analysis studies

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“The checklist is intended as a novel, helpful tool to enable authors to inform reviewers and readers of their methods and findings clearly, completely and transparently.”

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Against all the odds, skepticism and critique that epigenetics research faced in its early years, the field has continued to grow exponentially. Milestone projects such as the Human Epigenome Project and The Cancer Genome Atlas have allowed investigation of the epigenome in large-scale, multi-level, interdisciplinary science projects, enabling substantial developments in our knowledge and understanding of genomics and epigenetics.

In recent years, *Epigenomics* has responded to the expansion of the field by extending the research focus from solely DNA methylation and cancer to non-coding RNAs, bioinformatics, neuroepigenetics and immunoepigenetics. *Epigenomics* has also been publishing work on *in utero* environment/pre- and peri-natal environment, environmental stressors, behavioral epigenetics and much more as epigenetics continues to permeate all areas of biomedical science.

As the era of big data dawns upon us, the growing availability of information and data provides many opportunities for epigenomic research to progress. However, the ability to re-use and re-analyze data gives rise to new challenges concerning the repetition of research and the novelty of studies solely utilizing publicly available bioinformatic data. The scientific and publishing communities have a duty to uphold the integrity of research and *Epigenomics* aims to support authors in publishing innovative work employing a bioinformatic and/or data re-analysis approach, *Epigenomics* has therefore introduced the 'Research Article Reporting Checklist for Bioinformatic and Data Re-analysis Studies' to ensure that the journal commits to this mission [1].

So, what is the new reporting checklist?

The checklist is a carefully elaborated list of six criteria against which authors submitting research articles reporting on bioinformatic and data re-analysis studies will check their manuscripts prior to submission. The criteria include a range of qualities deemed important for confirming the novelty of the research as well as scientific rigor in processing, integrating and analyzing datasets, ensuring the accurateness and reproducibility of the analyses. They include:

- If and how new data were generated within the presented study;
- How differences between data types/datasets have been adjusted for and how the data have been processed to allow for accurate comparison;
- Description of how the suitable tool for data analysis was identified or developed;
- A detailed comparison of the new findings in the present study against those in the original study;
- A detailed explanation of the impact of the research in the wider field;
- A demonstration that the study has implemented findable, accessible, interoperable and reusable (FAIR) principles on data management [2].

The checklist is intended as a novel, helpful tool to enable authors to inform reviewers and readers of their methods and findings clearly, completely and transparently. Moving forward, the checklist will be adapted to accommodate new advances in the field to ensure that *Epigenomics* publishes research of the highest standard.

Epigenomics hopes that the reporting checklist will bring clarity to future publications of this nature and its introduction list will be welcomed by the epigenomics research community. *Epigenomics* appreciates feedback and suggestions for its improvement to best serve the community.

Supplementary data

To view the supplementary data that accompany this paper please visit the journal website at: www.futuremedicine.com/doi/suppl/10.2217/epi-2022-0083

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