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Bioinformatics in Action

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Cover picture: Dahlia (*Dahlia pinnata*), The Linnaean Gardens of Uppsala, Sweden, 2022, © Erik Bongcam-Rudloff

Editorial

We are thrilled to present the latest issue of the EMBnet.journal, volume 28, featuring a collection of articles that cover a broad range of topics in bioinformatics and computational biology.

One of the highlights of this issue is the paper that provides a proof-of-concept example demonstrating the limitations of differential expression analysis with non-linear machine learning models. The article suggests that this issue could be overcome by the adoption of the innovative paradigm of eXplainable Artificial Intelligence, which consists in building an additional explainer to get a trustworthy interpretation of the model outputs and building a reliable set of genes characterising each group, also preserving non-linear relations, to be used for downstream analysis and validation.

Another noteworthy contribution is the description of a bioinformatics pipeline for variant discovery from Targeted Next Generation Sequencing of the human mitochondrial genome.

In this issue, our readers can also explore other interesting articles, including enlightening "protein spotlight" pieces that delve into specific proteins or protein families informally and engagingly. These articles aim to comprehensively understand the chosen protein(s) and their significance.

We sincerely appreciate all the authors, reviewers, and editorial team members who have contributed invaluable to this issue. Their unwavering dedication and hard work have been instrumental in ensuring the success of this volume. We sincerely hope our readers will find the articles on this issue informative and inspiring.

Lastly, we invite all bioinformatics and computational biology researchers to submit their valuable work to the EMBnet.journal. We wholeheartedly welcome original research articles, reviews, and perspectives encompassing every field facet.

Join our esteemed community of researchers and showcase your contributions to bioinformatics and computational biology.

Thank you for your continued support of EMBnet.journal, and we look forward to bringing you more exciting research in the future.

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