First Person – Baharak Ahmaderaghi

How would you explain the main findings of your paper to non-scientific family and friends?
Molecular Subtyping Resource (MouSR) is a freely available, click-of-the-button platform for analysing data derived from human tumours and mouse models of disease, where significant volumes of data can be analysed using multiple methodologies on a single app. This platform is easy to use, and no computational expertise is required. It provides publication-ready plots with customised option for the users.

“Our app provides a user-friendly graphical interface for biological characterisation and interrogation of transcriptional datasets.”

What are the potential implications of these results for your field of research?
Our app provides a user-friendly graphical interface for biological characterisation and interrogation of transcriptional datasets. Approaches such as ours help remove a bottleneck in biological discovery for users with limited programming skills, enabling them to perform statistically controlled bioinformatics analyses to make valid biologically informed conclusions more precisely.

What has surprised you the most while conducting your research?
As a computer scientist, it was particularly impressive to observe how biological findings could be complex to analyse.

What are the main advantages and drawbacks of the model system you have used as it relates to the disease you are investigating?
MouSR provides a unique opportunity for non-specialist users to analyse their data using customised easy-to-use bioinformatic tools, while also having dual functionality embedded within the app to investigate disease-specific models and algorithms that offer deeper insights to facilitate simultaneous classification between human and mouse-derived data. The user can choose to deploy all the features within our intuitive transcriptional analysis pipeline for comprehensive work-up, or in other instances the user might decide to utilise only a selection of the available options within MouSR for their bespoke analysis requirements.

However, the tool only controls data from the point of input into the application, leaving the user responsible for the source of the data and the pre-processing steps performed.

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A schematic description of the MouSR implementation structure. Starting from importing two sets of data obtained from the data preparation section through RNA extraction and profiling, these data will then be sent for in-depth analysis using different methods. Finally, the results presented as tables and plots will be accessible via web browsers.

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What changes do you think could improve the professional lives of early-career scientists?
Finding a mentor and collaboration are the key factors. They will help researchers to enhance their skills, learn from experts and start building their own network.

What’s next for you?
An increased focus on biomarker development and target-drug discovery for personalised medicine requires results generated by gene expression profiling to be interrogated using high-performance computing and potentially with advanced AI or machine-learning algorithms, again requiring the use of complex bioinformatics tools. For the non-computational biologist, applications such as ours with its intuitive structure and user-friendly navigation while providing rapid point-and-click publication-ready analysis of highly complex information is necessary, and my focus will be on building a Smart application using AI.

Reference