One Biosciences' Single Cell Data Mining Algorithm "MAYA" Featured in *Nature Communications*

- MAYA is a transformative computational algorithm which enables the automatic detection and scoring of the diverse modes of activation of biological pathways across cell populations.

- For cancer patients, MAYA is a generational shift in precision medicine enabling the detection of shared therapeutic vulnerabilities across patients

Paris, France – April 6, 2023 – One Biosciences, a biotech leveraging the power of single-cell analysis and AI to unlock a new wave of targets and precision medicines for a broad range of difficult-to-treat conditions, today announced that its single-cell data mining algorithm named "MAYA" article was published in the March edition of *Nature Communications* journal.

For the complete article titled, Multi-modal quantification of pathway activity with MAYA," which was published on March 25, 2023, please visit: https://rdcu.be/c8rGx

In summary, the publication reveals one of the many components of One Biosciences' discovery engine - MAYA. MAYA is an algorithm for ultra-efficient data mining of large single-cell datasets. MAYA deciphers the complexity of the biological pathways at stake in complex human diseases. In contrast to existing algorithms, MAYA dissects biological crosstalks at single-cell resolution.

Celine Vallot, co-founder and chair of One Biosciences' Scientific Advisory Board noted, *"We are pleased with the momentum and development progress of One Biosciences' single-cell discovery engine. MAYA is one example of One Biosciences' capacity to develop cutting-edge data mining algorithms. Based on the findings presented in Nature Communications, we are confident in One Biosciences' ability to discover shared therapeutic vulnerabilities in cancer patients and beyond."*

As background, signaling pathways can be activated through various cascades of genes depending on cell identity and biological context. Single-cell atlases now provide the

opportunity to inspect such complexity in health and disease. MAYA's computational method enables the automatic detection and scoring of the diverse modes of activation of biological pathways across cell populations. It significantly improves the granularity of pathway analysis by detecting subgroups of genes within reference pathways, each characteristic of a cell population and how it activates a pathway. Using multiple single-cell datasets, One Biosciences demonstrates the biological relevance of identified modes of activation, the robustness of MAYA to noisy pathway lists and batch effect. MAYA can also predict cell types starting from lists of reference markers in a cluster-free manner. Finally, MAYA reveals common modes of pathway activation in tumor cells across patients, opening the perspective to discover shared therapeutic vulnerabilities.

More about One Biosciences' discovery engine which includes three differentiating components that it leverages across its current and forthcoming discovery programs:

1. Protocols and know how to generate high quality single-cell and single-nuclei RNAseq datasets for in depth analyses from various human tissues, including small frozen biopsies from solid tissues

2. A proprietary application ('OneApp') for the visualization and the collaborative analysis to interpret sc/snRNAseq data.

3. A proprietary database and architecture that is fully GDPR compliant to operate with required authentication processes and secured access rights and to store and process large patient-derived data sets.

About One Biosciences:

One Biosciences leverages the power of single-cell analysis and AI to unlock a new wave of targets and precision medicines for a broad range of difficult-to-treat conditions. One Biosciences is an integrated discovery engine combining a multi-disciplinary team with in-house computational capabilities. One Biosciences is backed by Institut Curie and Home Biosciences. For more information, visit: www.onebiosciences.fr

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