**SimpliFi: democratizing the analysis and accessibility of multiomics data**

**Other**

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Our ability to generate omics data in many cases outstrips our ability to explore, share, understand and ultimately make decisions from our results; the complexity added via multiomics worsens the problem. Consequentially, the widespread adaptation of omics is especially difficult for non-omics experts whose domain specific expertise is often essential. To enable everyone understand and use omics, we created SimpliFi, the world's first cloud-based, GPU-driven, streamlined and browser-accessible data-to-meaning engine for integrated omics analysis of all kinds: proteomics, lipidomics, metabolomics, transcriptomics, glycomics and genomics. Results are easily shared, explored or published simply by sending a URL.

After upload of untransformed quantified value tables (counts or reads, Uniprot or ChEBI accessions), SimpliFi obligates QC including batch and run order effects. Sample replicates are then used to nonparametrically model biology: the distributions of living systems are frequently non-Gaussian making the results of T-tests and ANOVA invalid. Indeed T-test p-values often differ by several orders of magnitude compared to non-parametric approaches, and T-tests produce both false positives (when variability is oversampled, e.g. when an outlier is present) and false negatives (when replicates are by chance close in value, undersampling variability).

p-values and fold-changes are calculated as a function of biological variation, number of samples and observations, and measurement error, taking into account any increased data variance at low or high intensities. All results are presented with corresponding confidence intervals to inform end-user decisions of the potential risks of the next experimental choices. SimpliFi's user interface, accessible via browser, is intuitive and user-friendly even for new-to-omics users. Analyses of either mono- or integrated multiomics data are simplified into clean interactive displays of pathways, states of tissues, disease, cells and molecular-level classifications.

To our knowledge, SimpliFi is the first platform to combine unbiased statistics, GPU computation and an interactive and intuitive user interface.