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Flimma: a federated and privacy-aware tool for differential gene expression analysis

Aggregating transcriptomics data across hospitals can increase sensitivity and robustness of differential expression analyses, yielding deeper clinical insights. As data exchange is often restricted by privacy legislation, meta-analyses are frequently employed to pool local results. However, the accuracy might drop if class labels are inhomogeneously distributed among cohorts. Flimma (https://featurecloud.ai/app/flimma) addresses this issue by implementing the state-of-the-art workflow limma voom in a federated manner, i.e., patient data never leaves its source site. Flimma results are identical to those generated by limma voom on aggregated datasets even in imbalanced scenarios where meta-analysis approaches fail.

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