Docket #: S15-051

GateFinder: Automated Identification of Simple FACS Signatures from High Dimensional Mass Cytometry

GateFinder is a flexible, automated, objective algorithm that quickly analyzes complex mass cytometry datasets to identify simple signatures (“gates”) for FACS (fluorescent automated cell sorting) purification. Mass cytometry is a powerful tool for identifying novel cell populations with up to 42 markers (parameters) per cell. However, mass cytometry instruments are expensive, the analysis destroys cells, and the resulting high-parameter data is time consuming for humans to interpret. GateFinder provides a bioinformatics tool to interpret mass cytometry data and construct simple phenotypic signatures for target cell populations. These signatures can then be used to guide development of either high-throughput screens or gating strategies for enriching live cells using FACS in a variety of research, clinical or diagnostic applications.

Stage of Research
The inventors have demonstrated the utility of the algorithm on several real-world use cases and will make an R package available for non-commercial users when the work is published.

Enlarge thumbnail figure in the **Media** section below to see an overview of how the algorithm works and a sample use case on 31-parameter mass cytometry.

Applications

- **Research** - develop sorting strategies to isolate live cells from complex and rare cell types, with end-user applications such as functional studies or high-throughput exploratory studies

- **Clinical** - develop sorting strategies to purify cells with end user applications such as bone marrow transplants or cancer immunotherapy
- **Diagnostic** - develop sorting strategies to validate diagnostic tests based on complex mass cytometry assays or perform analysis when complex high-dimensional instruments are not available

Advantages

- **Automated** - algorithm provides objective analysis of data in much less time than possible by a human expert
- **Live cell assays** - FACS assays using surrogate signatures identified by GateFinder do not destroy the cells (as would be the case with high parameter mass cytometry), allowing downstream analysis and use of sorted cells

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