Introducing REM-I

A benchtop single-cell imaging and sorting instrument for high-dimensional morphology analysis

 Highlights

• Obtain high-dimensional single-cell morphology analysis with the REM-I instrument
• A fast workflow to go from sample to publishable figure in a few hours
• Part of the REM-I platform, which also includes Deepcell’s Human Foundation Model (HFM) and Axon data suite

Cell morphology can be highly indicative of a cell’s phenotype and function, but it is also highly dynamic and complex, and analyzing morphology by eye can only tell us so much.

A more quantitative, high-dimensional, unbiased approach to assessing cell morphology would magnify the insights into a cell’s phenotype and function. Methodologies to assess and characterize cell morphology have been limited to either imaging or sorting with labels—until now.

Deepcell’s REM-I instrument takes the best of these worlds and builds upon them to provide imaging of single cells and label-free sorting in one platform (Figure 1A). REM-I directly takes real, high-resolution brightfield images of each individual cell. REM-I also has the ability to sort cells 6 ways based on their morphology without the need for any labels. Furthermore, you can collect these viable, minimally perturbed cells for downstream analysis such as single-cell RNA sequencing (scRNAseq).

The REM-I instrument is part of the REM-I platform, which also consists of Deepcell’s Human Foundation Model (HFM) for high-dimensional morphological feature analysis and Axon data suite, where you can store, visualize, and analyze images and high-dimensional data (Figure 1B).
Figure 1. The REM-I platform. (A) The REM-I instrument is a benchtop microfluidics instrument that captures high-resolution brightfield images of single cells and can sort cells 6 ways in a label-free manner. (B) The REM-I instrument is part of a fully integrated platform, compatible with Deepcell’s Human Foundation Model (HFM) and Axon data suite.

Key Features

- Imaging: High-resolution brightfield imaging of single cells
- Sorting: 6-way, label-free sorting
- Single Cell: Real-time analysis of single-cell morphology
- High-Dimensional: Powered by Deepcell’s Human Foundation Model
- End-to-End: Comes with Axon, Deepcell’s data suite
Figure 2. How the REM-I instrument works. The REM-I instrument uses a set of reagents and chips provided by Deepcell. Reagents are placed in the reagent drawer (A) and chips are loaded onto the stage. (B) The REM-I instrument is controlled by the REM-I controller software while the REM-I on-instrument display (C) shows real-time run status. (D) The workflow is simple and streamlined, starting with dissociation of cells into a single-cell suspension, followed by loading of the suspension onto the instrument. The cells are imaged and characterized in real-time with the Deepcell HFM as they flow through the microfluidic chip. Axon, Deepcell's data suite, pairs with the REM-I instrument for in-depth data analysis, including the ability to select cell populations of interest to sort on the REM-I instrument. Sorted cells can be used for further downstream analyses such as scRNAseq.

How it works

The REM-I instrument uses high-throughput imaging to characterize, classify, and sort cells based on morphological analyses (Figure 2).

The benchtop instrument uses a microfluidic chip, which allows for the input and flow of cells in suspension. The high-speed system collects brightfield images of cells (up to 1,000 events per second) as they flow through a microfluidic chip. High-resolution images capture subcellular and subnuclear features of the cells in high contrast. The HFM classifies cells, allowing them to be sorted in up to 6 collection wells. A laser-based system tracks cells in real-time to assist with imaging and sorting, and to report on the purity and yield of the run.

The REM-I workflow is simple and streamlined, starting with preparation of a single-cell suspension, followed by loading of the cells onto the instrument. The cells are imaged and features are extracted in real-time and sorted using the HFM. Axon, Deepcell's data suite, pairs with the REM-I instrument for in-depth data analysis, including the ability to select cell populations of interest to sort on the REM-I instrument. Sorted cells can be recovered in up to 6 wells and used for further downstream analyses such as scRNAseq.

Prepare and load cells onto the REM-I instrument

Image, extract features in real time, and sort using the Deepcell Human Foundational Model

Explore high-dimensional morphology in the Axon data suite

Recover sorted cells in up to 6 wells for downstream analyses
**Key research areas**

- Cancer Research
- Developmental Biology
- Cell & Gene Therapy
- Drug & Functional Screening

**Applications**

- Discovery
  - Morphology as a novel biomarker
  - Drug and CRISPR perturbation screening
- Sample-Level Profiling
  - Heterogeneous sample evaluation and characterization
  - Disease detection and enrichment
  - Sample clean up
- Cell-Level Phenotyping
  - Cell health status
  - Cell state characterization
  - Multi-omic integration

**Table 1. REM-I Instrument Key Parameters and Specifications**

<table>
<thead>
<tr>
<th>Category</th>
<th>Parameter</th>
<th>Specification</th>
</tr>
</thead>
</table>
| **Facilities**    | Instrument dimensions         | H: 29.5 in / 75 cm  
W: 35.5 in / 90 cm  
D: 29.5 in / 75 cm |
|                   | Included ancillary equipment  | Computer tower  
Monitor  
Keyboard  
Mouse |
|                   | Electrical                    | 3x 100-240 V surge-protected outlets               |
|                   | Network connection            | 1 Gbps ethernet with >150 Mbps upload bandwidth    |
|                   | Clean dry air connection      | 0.55–0.72 MPa / 80–105 psi                        |
|                   | Temperature operation ranges  | 59–86 °F / 15–30 °C                                |
|                   | Operating relative humidity (%)| 15–70, non-condensing                             |
| **Instrument**    | Input cell size (µm)          | 6 – 25                                             |
|                   | Output cell viability (% of input viability) | ≥95*                                                |
|                   | Output collection             | 6x positive outlet wells  
1x negative outlet tube  
1x waste bottle       |
Table 1. (Continued from previous page)

<table>
<thead>
<tr>
<th>Instrument</th>
<th>Positive outlet capacity (cells/well)</th>
<th>Up to 3,000</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Recommended run time (min)</td>
<td></td>
</tr>
<tr>
<td>Live cells:</td>
<td>Up to 180</td>
<td></td>
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<tr>
<td>Fixed cells:</td>
<td>Up to 600</td>
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</tr>
<tr>
<td>Image resolution (µm/pixel)</td>
<td>0.16</td>
<td></td>
</tr>
<tr>
<td>Image size (pixels)</td>
<td>256 x 256</td>
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</tr>
<tr>
<td>Imaging throughput (events/s)</td>
<td>Up to 1,000</td>
<td></td>
</tr>
<tr>
<td>Sorting throughput (cells/s)</td>
<td>Up to 30</td>
<td></td>
</tr>
</tbody>
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Table 2. REM-I Platform Components

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>REM–I Instrument</td>
<td>Microfluidic instrument</td>
</tr>
<tr>
<td>REM–I Imaging Kit</td>
<td>Reagents and consumables for imaging workflow</td>
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<tr>
<td>REM–I Sorting Kit</td>
<td>Reagents and consumables for imaging plus sorting workflow</td>
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<tr>
<td>Human Foundation Model (HFM)</td>
<td>Deepcell's AI model for high-dimensional single-cell morphology analysis</td>
</tr>
<tr>
<td>Axon data suite</td>
<td>Deepcell's data suite for visualizing, analyzing, and storing data</td>
</tr>
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References


Resources

→ REM-I Platform Brochure
→ Human Foundation Model Panel Sheet
→ Public Datasets and Axon Demo
→ Oncology Application Note
→ Other Resources