

# The power of morphology *magnified by AI*



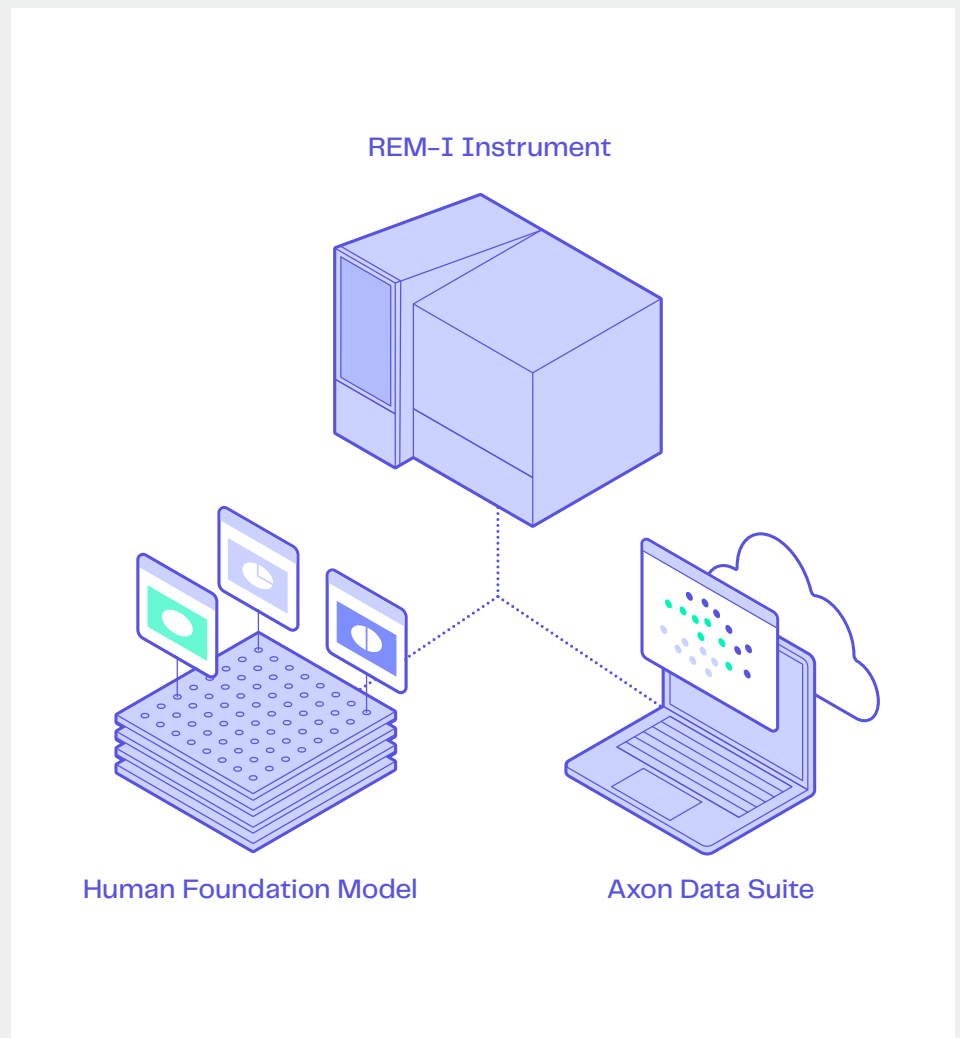
# The cell is central to pan-omic understanding of biology

Similar to molecular analytes, cell morphology is a rich source of biological information that is indicative of phenotype and function.

However, it is also highly dynamic, complex, and subjective and therefore hard to interpret.

To unlock the insights embedded in cell morphology, multi-dimensional morphological traits must be turned into a quantitative, high-dimensional “-ome”.

**Our approach:**  
high-resolution single-cell imaging, cutting-edge AI, and label-free sorting for high-dimensional morphology analysis



# REM-I: Microfluidic and imaging instrument

REM-I is an AI-powered benchtop instrument for high-dimensional morphology analysis.



## What makes REM-I innovative

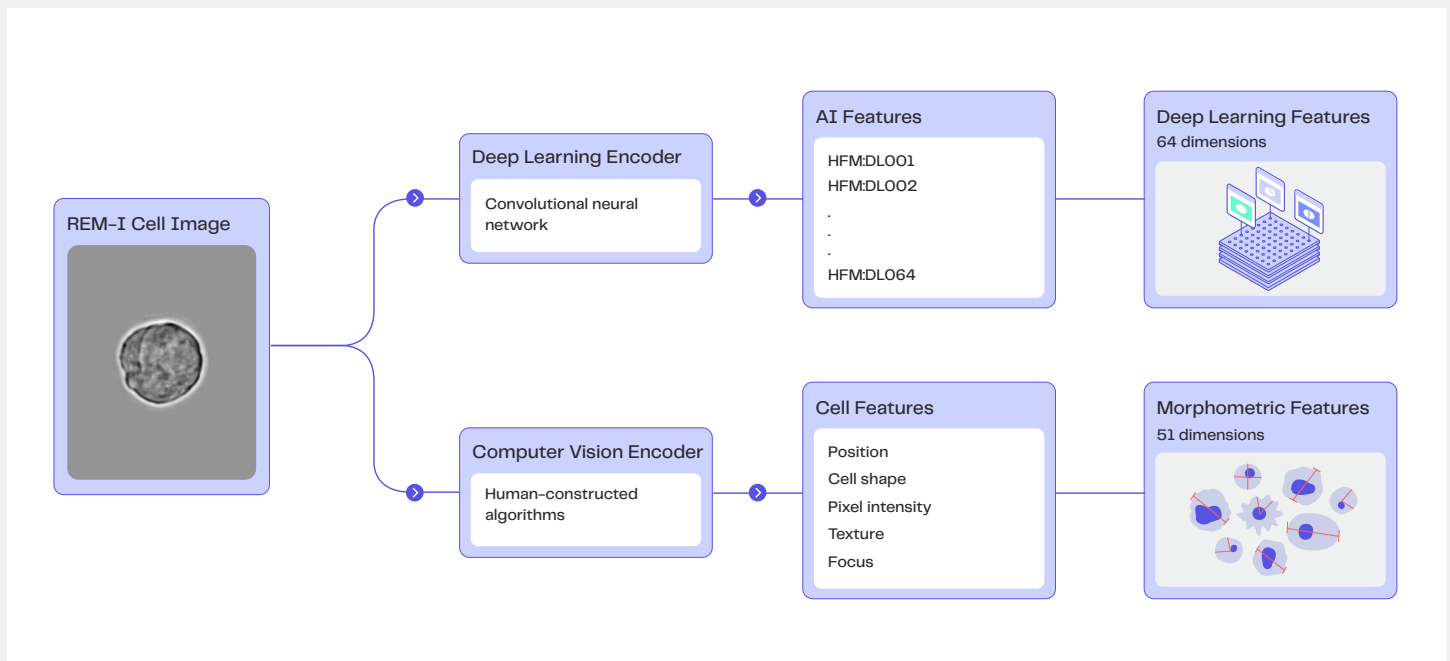
- High-resolution images of single cells captured at high speed
- Completely label-free workflow
- 6-way sorting of uncompromised cells of interest for downstream analysis
- AI characterization of captured cell images in real-time
- Flexible experimental designs for imaging or imaging + sorting

# Human Foundation Model: Leading-edge AI

The Deepcell Human Foundation Model (HFM) extracts features from diverse cell images without prior knowledge of specific cell types, cell preparation, or other application-specific markers for an unbounded approach to hypothesis generation and testing.

## What makes Deepcell HFM truly unique

- Trained completely label-free
- Assesses 115 dimensions of cell morphology
- Broadly applicable across human applications/cell types
- Ready to use on day 1 with no additional training needed



# Axon: Deepcell's data suite

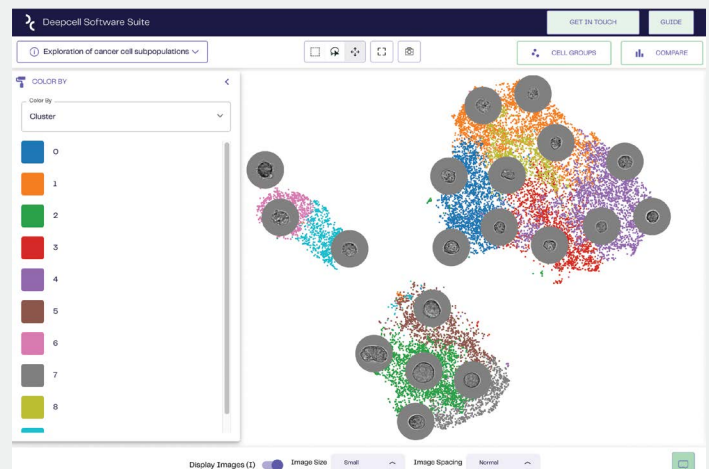
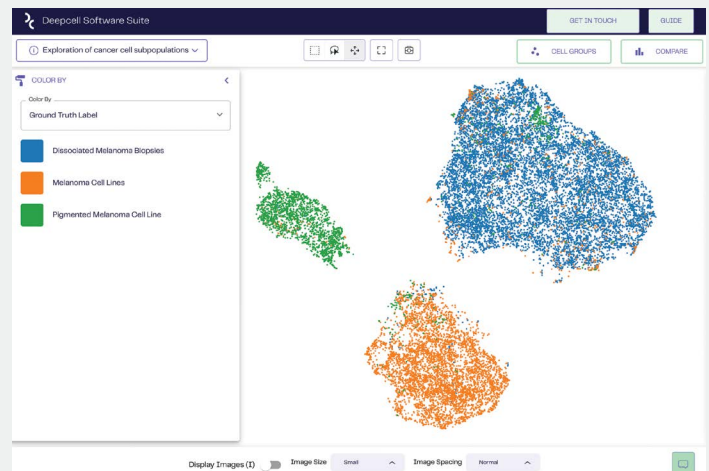
Axon, our powerful data suite, enables real-time exploration of data from the REM-I instrument.

## What makes the Axon data suite powerful

- Store, review, and organize runs
- Visualize AI embeddings as morphology UMAPs
- View and/or overlay cell images directly on the morphology UMAP
- Explore AI embeddings interactively through comparative analytics graphs
- Train custom classification models
- Define cell populations of interest for collection in up to 6 wells

See the power of the REM-I platform for yourself with our public datasets and interactive software demo at:

[exploredata.deepcell.com](https://exploredata.deepcell.com)

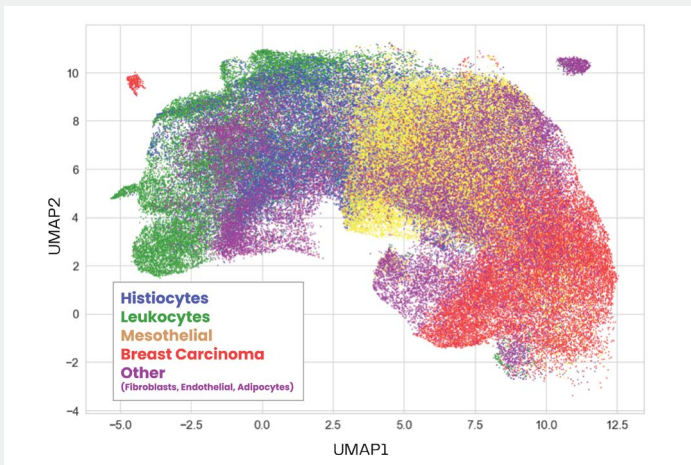


Screenshots of the Axon data demo demonstrating the ability to color UMAPs based on ground truth labels (left), morphologically distinct clusters (right). Individual cell images can also be overlaid directly on the UMAP (right).

# Application and research areas

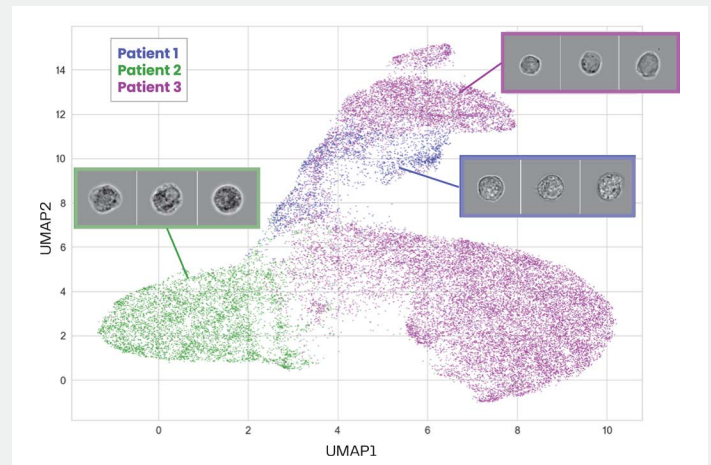
## Complex Tissues

Morphological heterogeneity in complex tissues



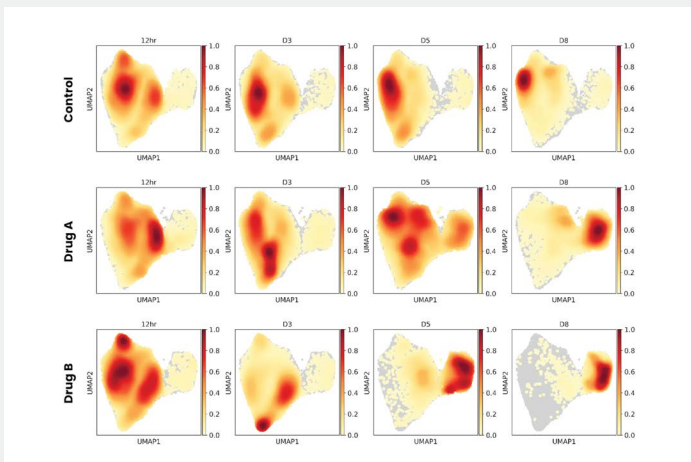
## Cancer Biology

Cancer cell heterogeneity within and across patients



## Perturbations

Effects on morphology in response to treatments



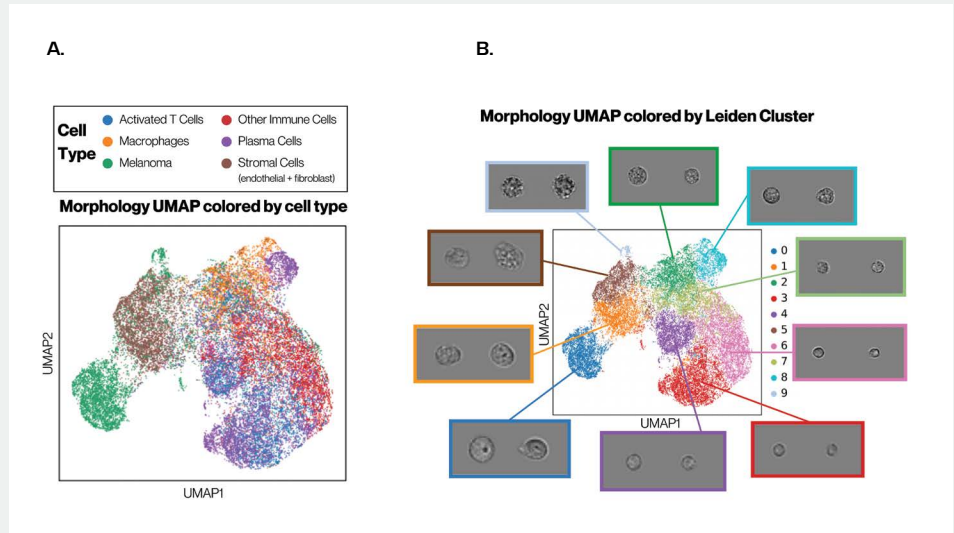
Valuable morphology information to drive discoveries in:

- Cancer research
- Developmental biology
- Cell therapy
- Drug & functional screening and more

# Deepcell in action

## Characterization of the tumor microenvironment by morphology

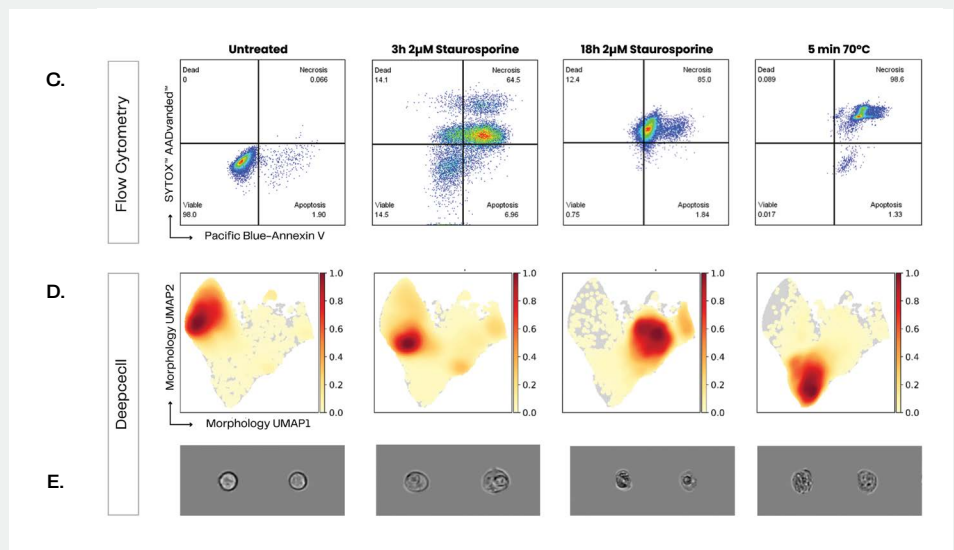
A mixture of human melanoma cell lines and primary tumor samples analyzed on the REM-I platform to identify tumor, immune, and stromal cell populations. Of note, melanoma cells are morphologically distinct and cluster separately from non-tumor cells, while immune cells have subtle but separable morphologies.



(A) Embeddings UMAP colored by cell type and clustered by morphological features. (B) Embeddings UMAP colored by cluster (Leiden algorithm), with representative images from each cluster shown.

## Cell health states correspond to distinct morphological profiles

Cell death was induced in Jurkat T lymphocytes with either staurosporine or heat shock. Cells occupying the same flow cytometry gate segregate in distinct clusters based on morphological traits determined by the REM-I platform, indicating the ability of multi-dimensional morphology to detect and/or monitor subtle changes in sample health status and assess sample quality.



(C) Flow cytometry profiles. (D) Embeddings UMAP generated from the REM-I platform imaging and colored by population density. (E) Representative images from the REM-I platform of each condition.

## Related references

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3. Wu, P., et al. (2020). Single-cell morphology encodes metastatic potential. *Science Advances*, 6(4). <https://www.science.org/doi/full/10.1126/sciadv.aaw6938>
4. Kusumoto, D., et al. (2021). Anti-senescent drug screening by deep learning-based morphology senescence scoring. *Nature Communications*, 12, Article 257. <https://www.nature.com/articles/s41467-020-20213-0>
5. Pratapa, A., et al. (2021). Image-based cell phenotyping with deep learning. *Current Opinion in Chemical Biology*, 65, 9–17. <https://www.sciencedirect.com/science/article/abs/pii/S1367593121000478?via%3Dihub>

## Contact us

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