Cell Geometry

A web application for Cell Shape Analysis

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Mathematical Methods for Exploring and Analyzing Morphological Shapes across Biological Scales

GOALS OF THIS TALK

Introduce CellGeometry

Discuss 3D Cell Segmentation

Discuss Computing Cell and Nuclear Shape Modes

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Discuss 3D Cell Segmentation

Discuss Computing Cell and Nuclear Shape Modes

And we are doing this

AT SCALE!


CELLGEOMETRY

Project Goal

The goal of this project was to build a web app that makes shape analysis techniques implemented in geomstats and similar projects accessible to non-technical users

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```python
def exhaustive_align(curve, base_curve):
    """Align curve to base_curve to minimize the L² distance.

    Returns
    -------
    aligned_curve : discrete curve
    """
    nb_sampling = len(curve)
    distances = gs.zeros(nb_sampling)
    base_curve = gs.array(base_curve)
    for shift in range(nb_sampling):
        reparametrized = [curve[(i + shift) % nb_sampling] for i in range(nb_sampling)]
        aligned = PRESHAPE_SPACE.fiber_bundle.align(
            point=gs.array(reparametrized), base_point=base_curve
        )
        distances[shift] = PRESHAPE_SPACE.embedding_space.metric.norm(
            gs.array(aligned) - gs.array(base_curve)
        )
    shift_min = gs.argmin(distances)
    reparametrized_min = [
        curve[(i + shift_min) % nb_sampling] for i in range(nb_sampling)
    ]
    aligned_curve = PRESHAPE_SPACE.fiber_bundle.align(
        point=gs.array(reparametrized_min), base_point=base_curve
    )
    return aligned_curve


def preprocess(
    cells,
    labels_a,
    labels_b,
    n_cells,
    n_sampling_points,
    quotient=["scaling", "rotation"],
):
    """Preprocess a dataset of cells.

    if n_cells > 0:
        print(f"... Selecting only a random subset of {n_cells} / {len(cells)} cells.")
        indices = sorted(
            np.random.choice(gs.arange(0, len(cells), 1), size=n_cells, replace=False)
        )
        cells = [cells[idx] for idx in indices]
        labels_a = [labels_a[idx] for idx in indices]
        labels_b = [labels_b[idx] for idx in indices]

    if n_sampling_points > 0:
        print(
            "... Interpolating: "
            f"Cell boundaries have {n_sampling_points} samplings points."
        )
        interpolated_cells = gs.zeros((n_cells, n_sampling_points, 2))
        for i_cell, cell in enumerate(cells):
            interpolated_cells[i_cell] = _interpolate(cell, n_sampling_points)

        cells = interpolated_cells

    print("... Removing potential duplicate sampling points on cell boundaries.")
    for i_cell, cell in enumerate(cells):
        cells[i_cell] = _remove_consecutive_duplicates(cell)

    print("\n- Cells: quotienting translation.")
    cells = cells - gs.mean(cells, axis=-2)[..., None, :]

    cell_shapes = gs.zeros_like(cells)
    if "scaling" in quotient:
        print("- Cell shapes: quotienting scaling (length).")
        for i_cell, cell in enumerate(cells):
            cell_shapes[i_cell] = cell / basic.perimeter(cell)

    if "rotation" in quotient:
        print("- Cell shapes: quotienting rotation.")
        if "scaling" not in quotient:
            for i_cell, cell_shape in enumerate(cells):
                cell_shapes[i_cell] = _exhaustive_align(cell_shape, cells[0])
        else:
```

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Data Structure

- Load Data
  - Accepted Filetypes:
    - TXT/CSV
    - Zipped ROI Files from FIJI/ ImageJ
- Visualize Loaded Data
  - Interactive Visualization for Sanity Check

Cell 1

X	Y
548	-744
544	-740
544	-739
541	-736
540	-736
538	-734
536	-734
535	-733

Cell 2

613	-666
612	-667
610	-667
610	-668
609	-669
606	-669
605	-670
603	-670
602	-671

PAGE 1

Let’s Load some data!

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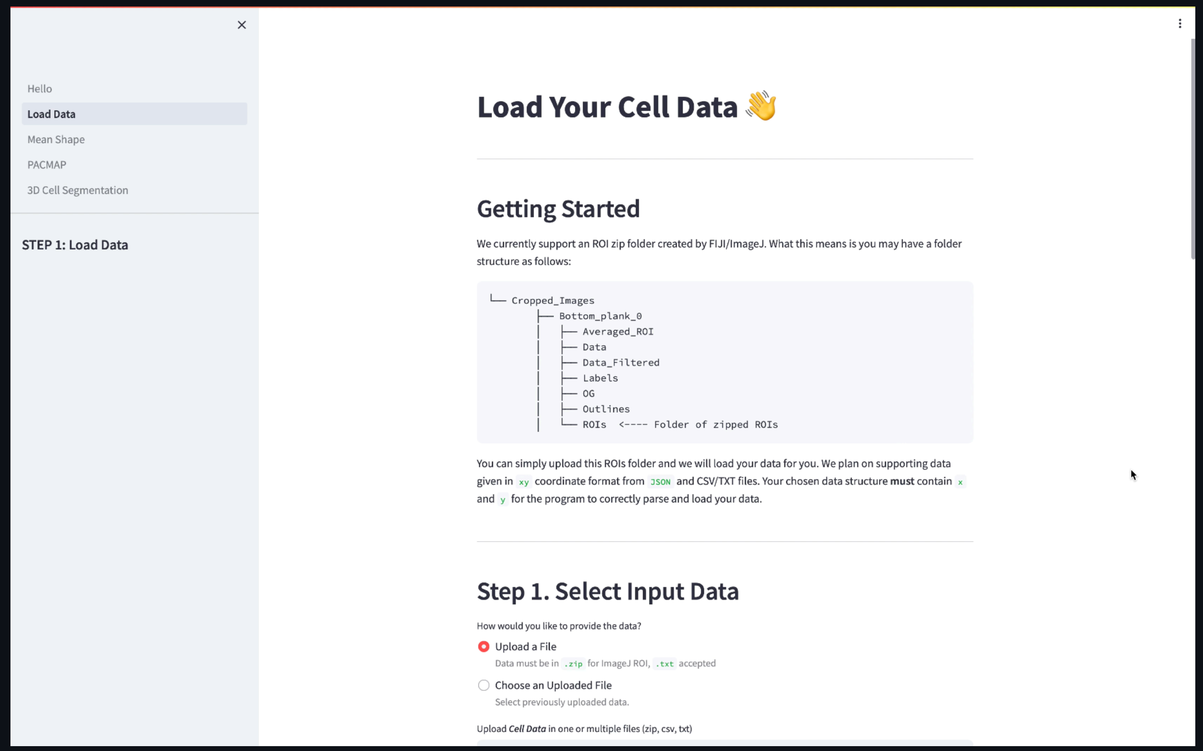
CELL GEOMETRY

Amil Khan, Samuel Feinstein, Adele Myers, Wanxin Li, Ashok Prasad, Khanh Dao Duc, Nina Miolane



PAGE 2

Preprocessing Input Data

- Interpolation
  - Need discrete curves with the same number of sampled points to compute pairwise distances
- Remove Duplicates
  - During interpolation some of the discrete curves in the dataset are downsampled from higher number of discrete data points to lower number of data points

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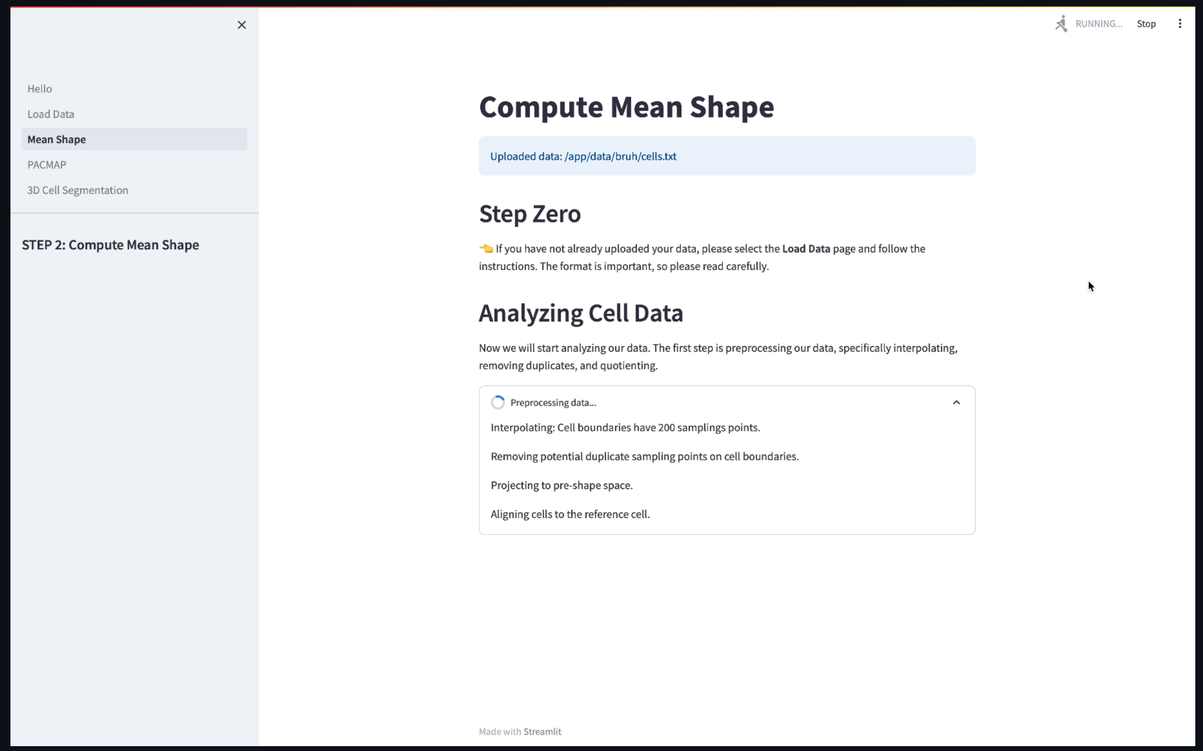

PAGE 2

Preprocessing

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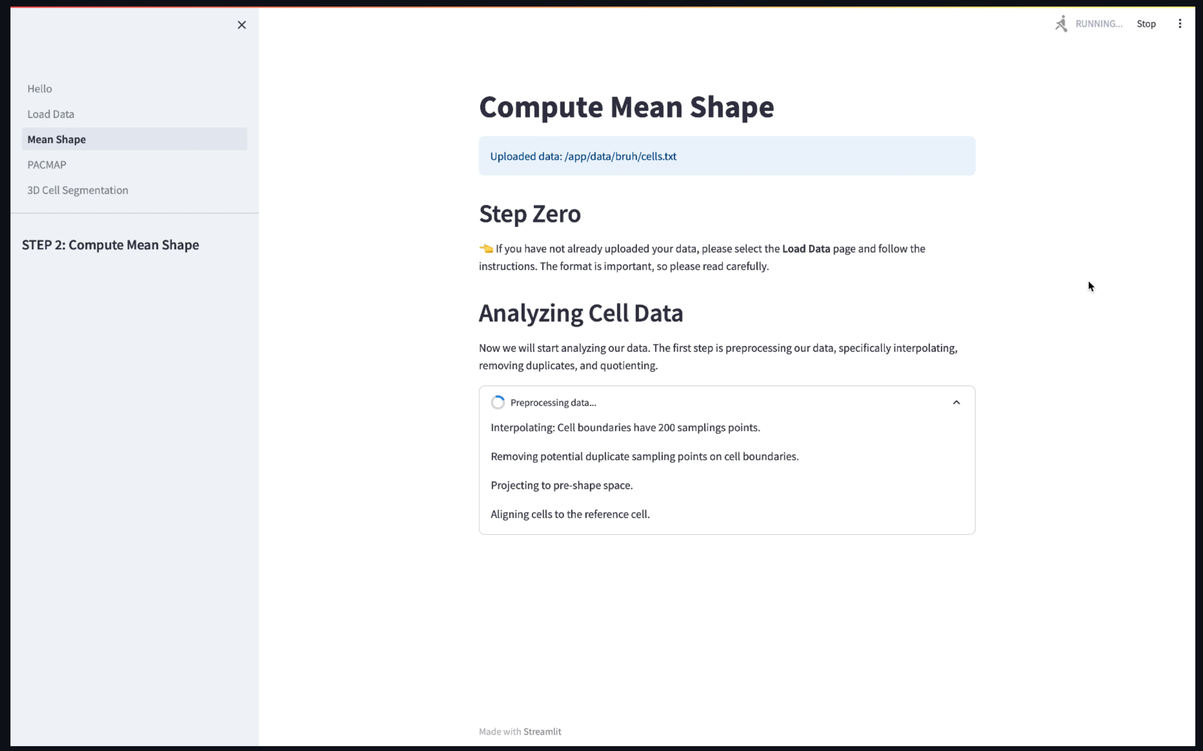
- Projection to Pre-shape Space
  - We center (subtract the barycenter), rescale (divide by the Frobenius norm) and then align (find the rotation minimizing the L2 distance) two sets of landmarks.
  - These operations are performed by leveraging the geometry of the Kendall preshape spaces



PAGE 2

Preprocessing

- Alignment
  - Since we are working with closed curves, the starting point associated with the parametrization of the discrete curves is also arbitrary.
  - We conduct an exhaustive search to find which parametrization produces the best alignment according to the above procedure (i.e. the distance to the base curve is the smallest)

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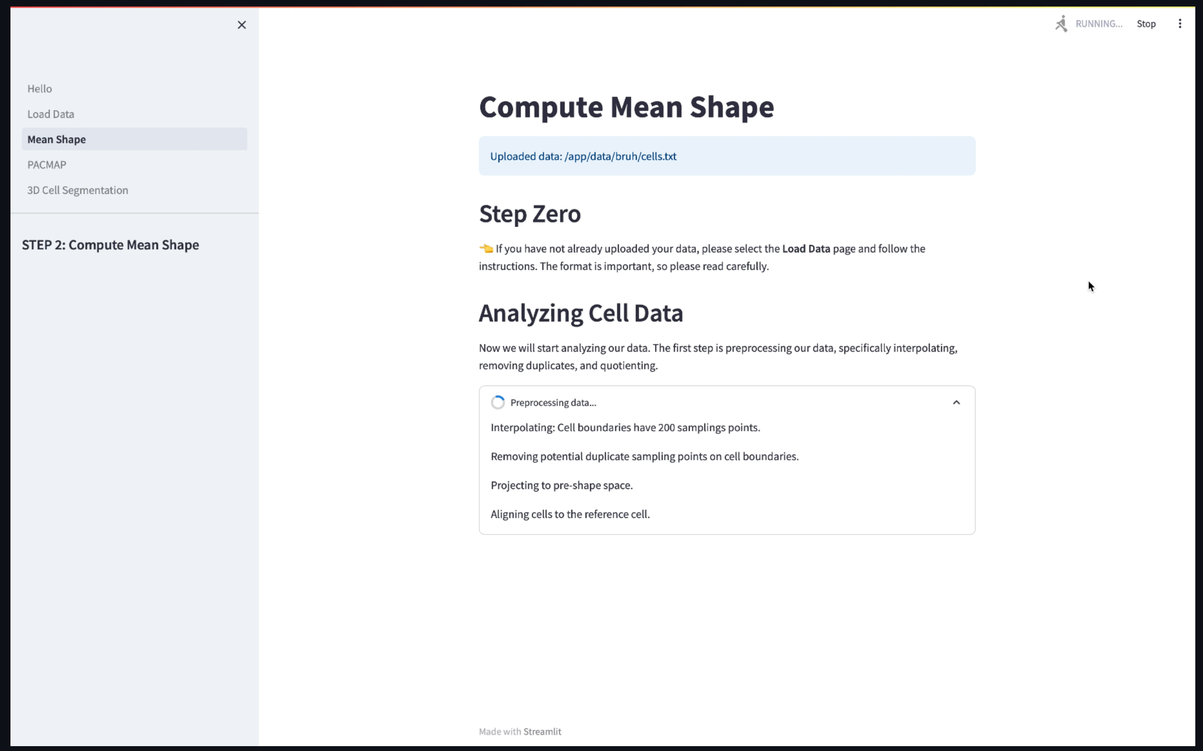

PAGE 2

Geodesic Trajectory

- Elastic Metric
  - Compute geodesics between discrete curves with respect to the elastic metric
  - These geodesics represent trajectories between cell boundaries that minimize an elastic energy, and the length of the geodesic defines a distance between curves

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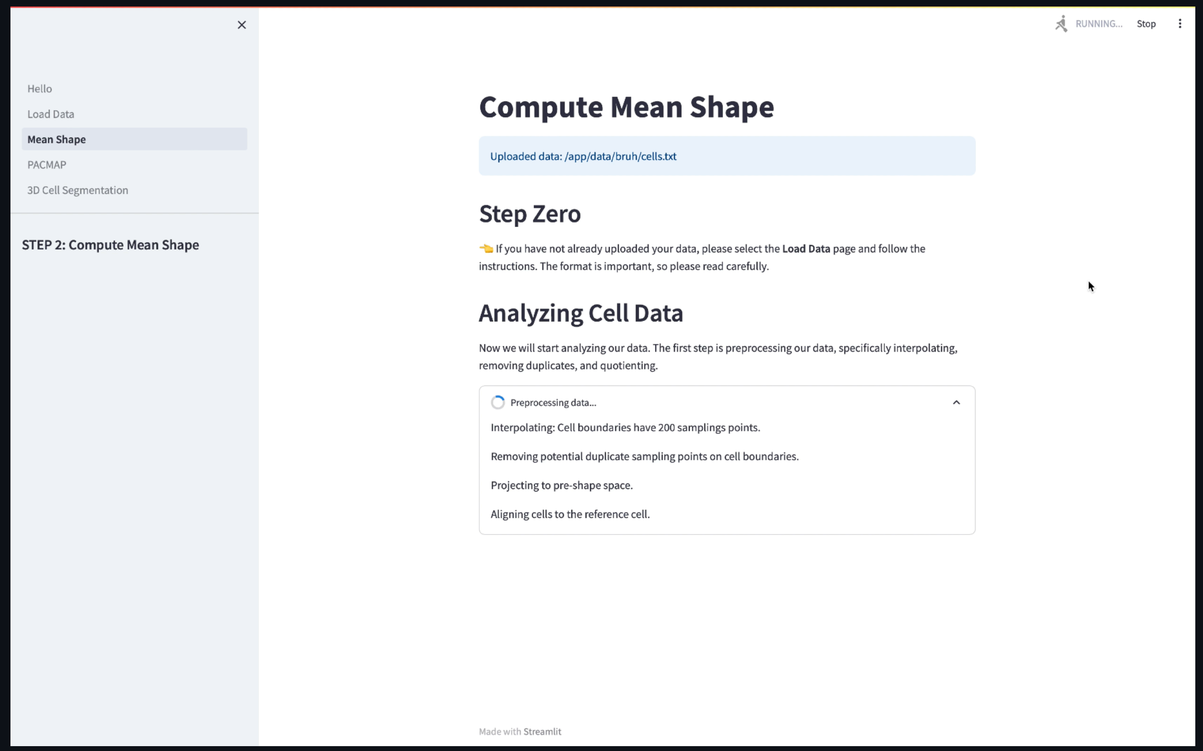

PAGE 3

Pairwise Controlled Manifold Approximation

- PACMAP
  - After computing the mean shape, click on **PACMAP** on the sidebar
- Visualization of PACMAP
  - We visualize the first 3 components, plot is automatically updated when params are changed

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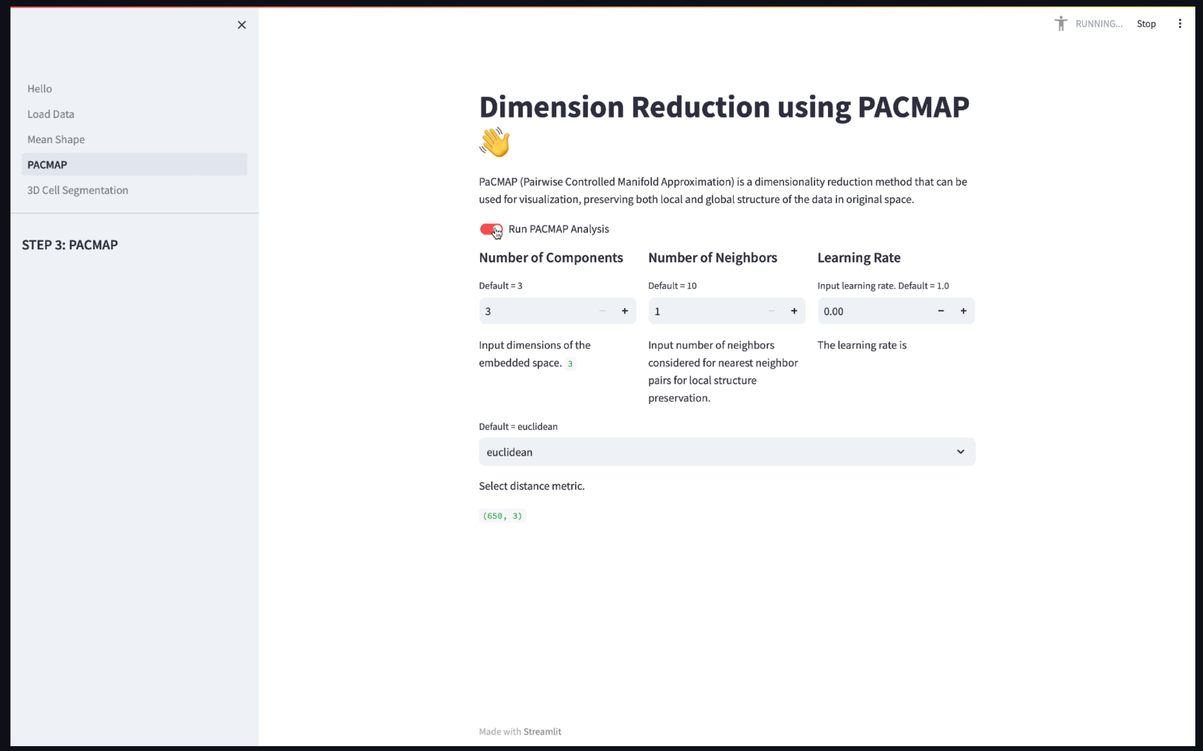
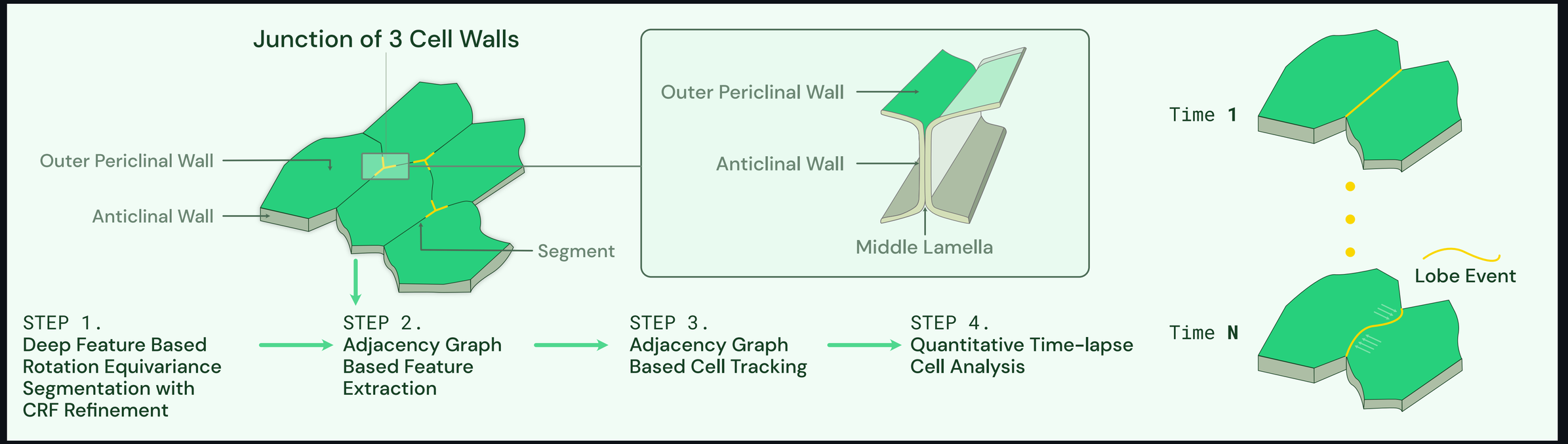


CELLECT 2.0

3D Cell Segmentation

Segmentation, tracking, and sub-cellular feature extraction in 3D time-lapse images



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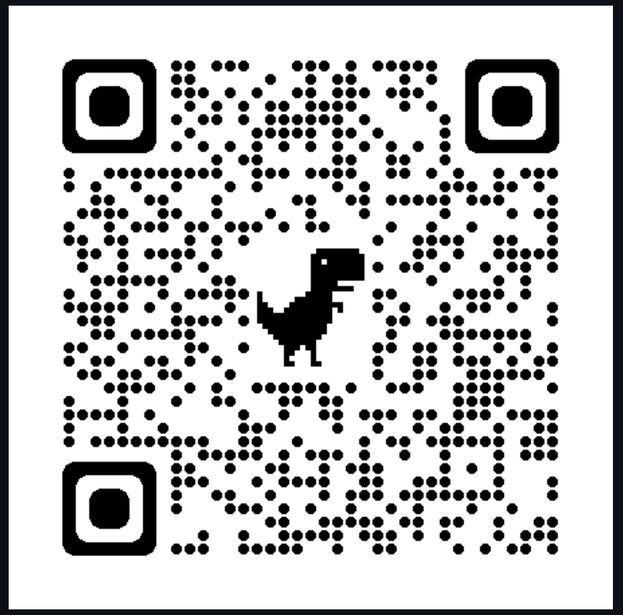
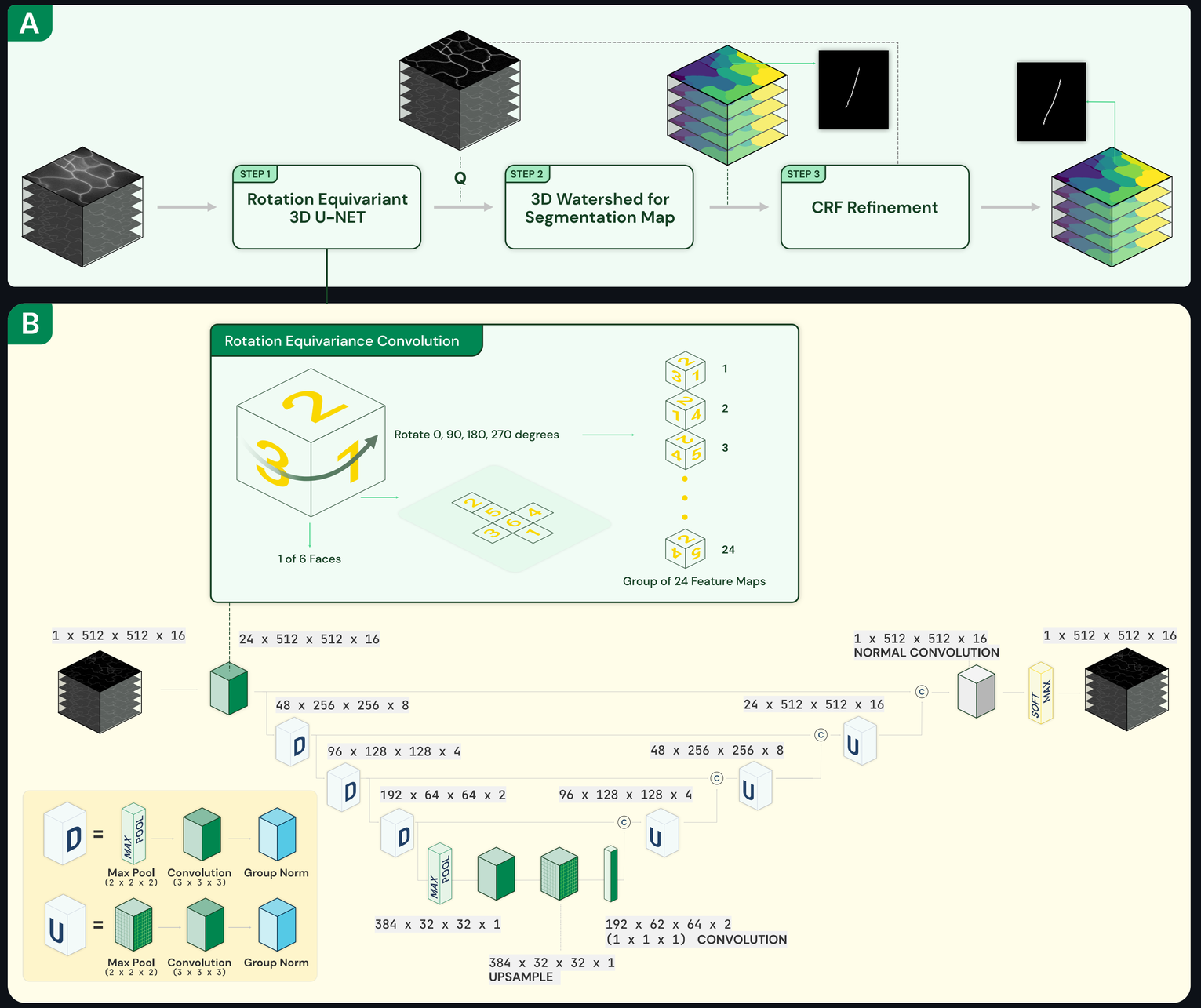
Read the Paper





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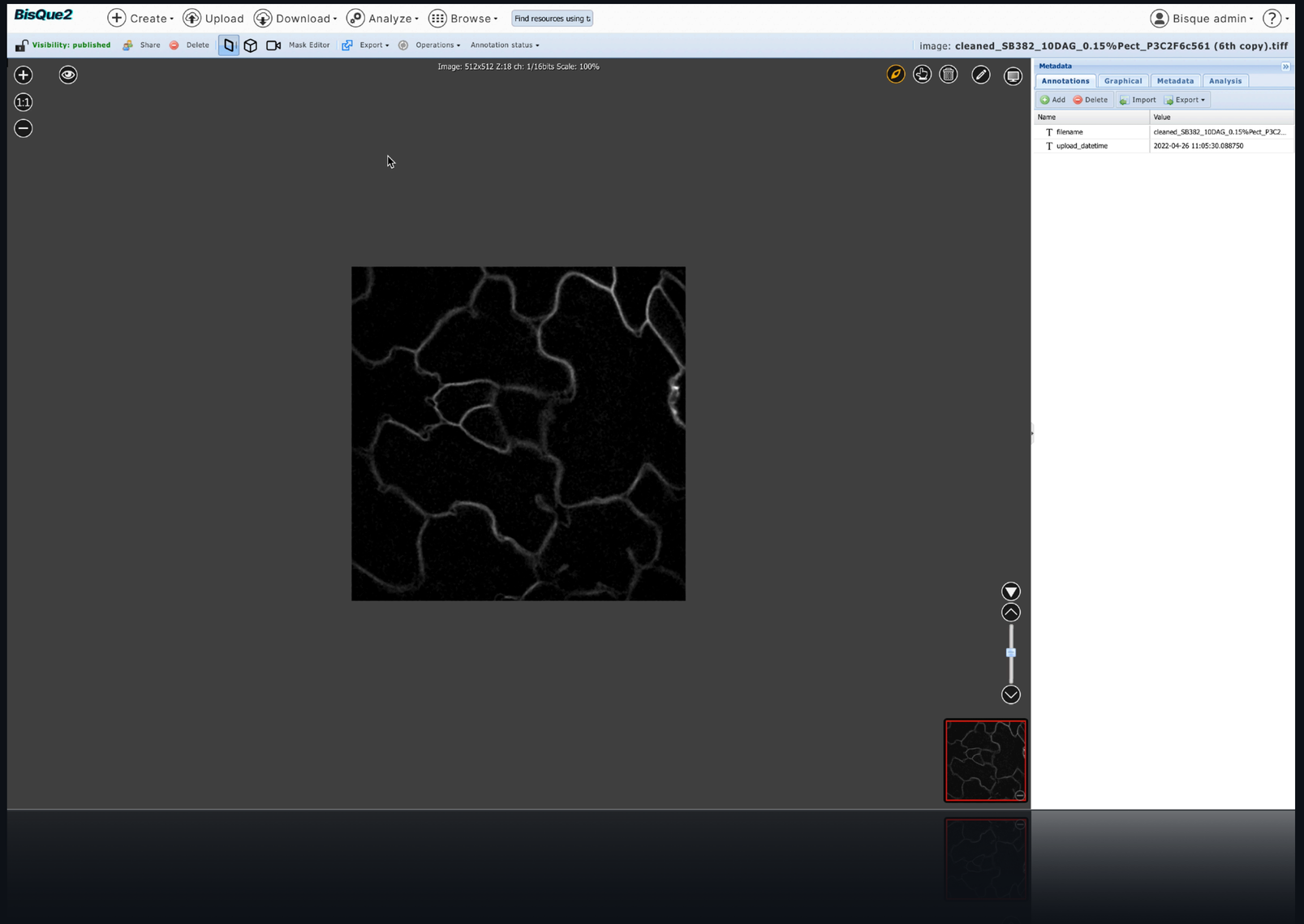
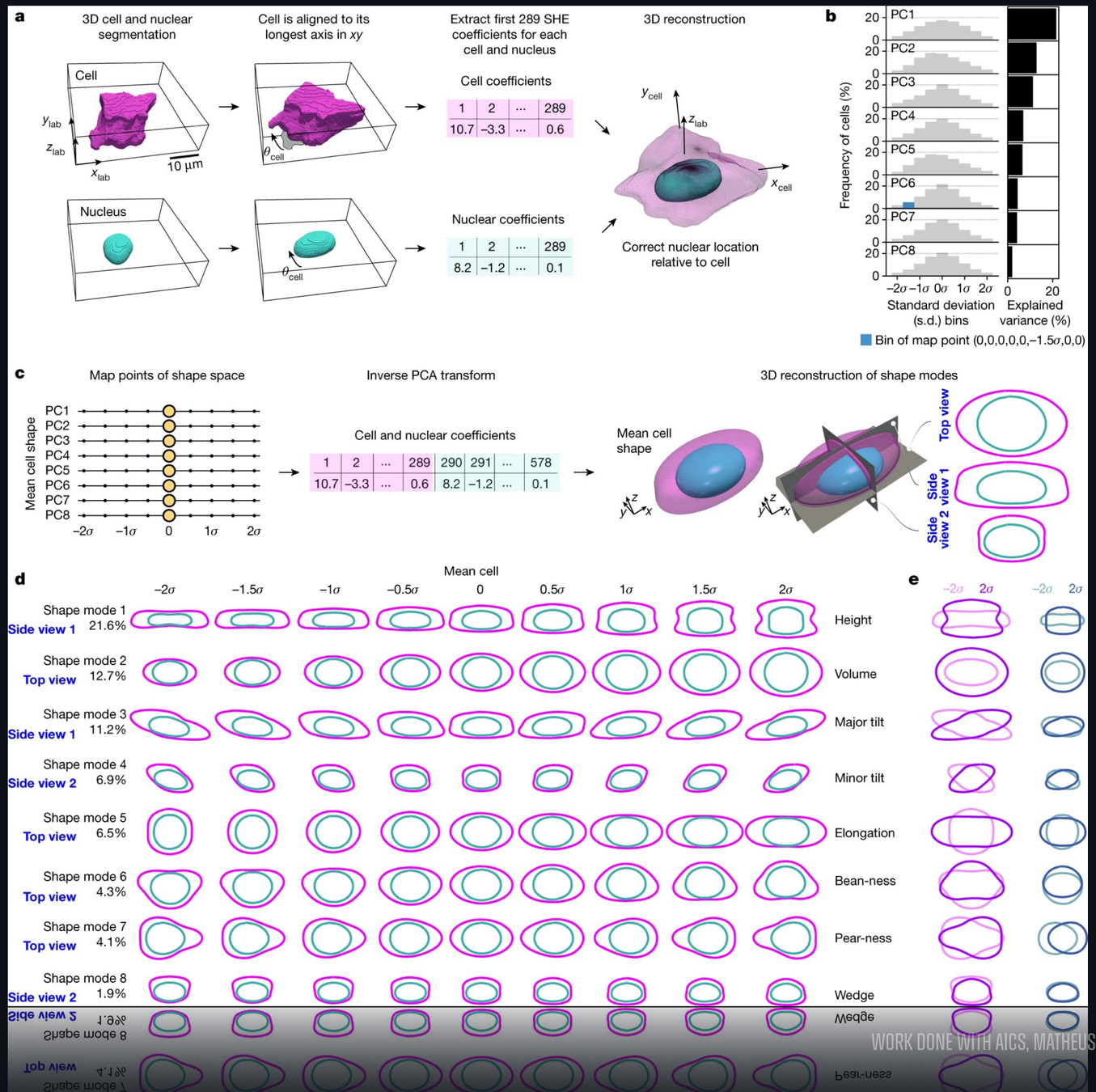


ALLEN INSTITUTE CELL SCIENCE

CVAPIPE

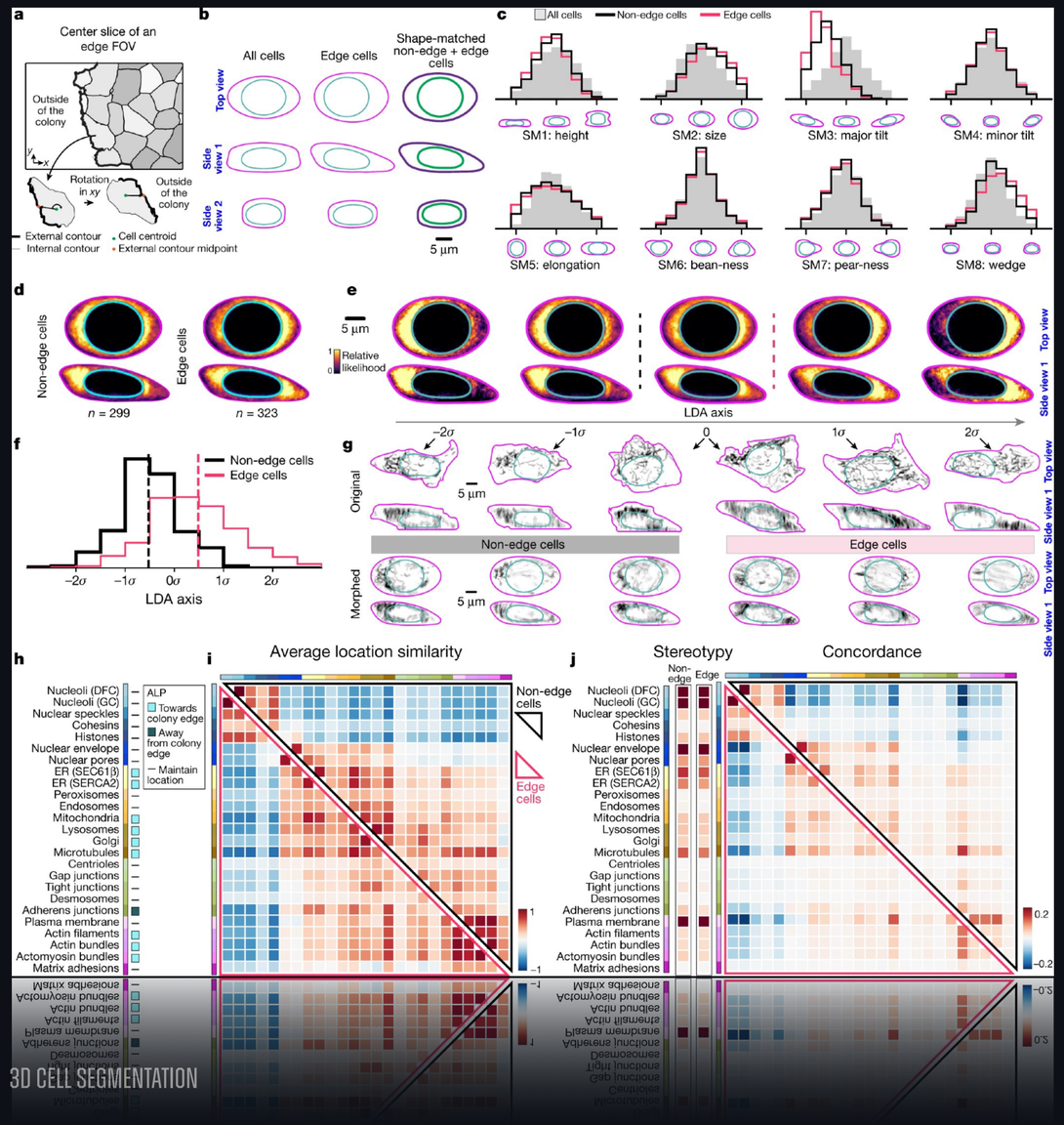
Calculating Cell Shape Modes

- Building a Cloud Pipeline
  - Build a web application that can store, analyze, and explore the CVAPIPE analysis at **petabyte scale** (Powered by AWS)
- Public Release
  - Users will be able to run the **entire** method/pipeline Matheus discussed in his talk on their own data



CVAPIPE

Calculating Cell Shape Modes



- **Pipeline Steps**
  - **Computing Single cell features**, i.e. compute the spherical harmonics coefficients for cell and nuclear shape
  - **Preprocessing** such as removing outliers and mitotic cells
  - **Computing Shapemodes** for cell and nuclear
  - **Create the parameterized intracellular location representation (PILR)**
  - **Create average PILRs**
  - **Correlate single cell PIRL**
  - **Stereotypy analysis**
  - **Concordance analysis**

Come to the Hackathon!

A web application for Cell Shape Analysis

Acknowledgments

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