# HTM SCA

## HTM Simple Cell Analyzer

*Minimal browser tool for holotomographic microscopy image analysis*

## Description

HTM SCA (HTM Simple Cell Analyzer) is a lightweight, browser-based image analysis tool designed for rapid morphological assessment of single cells in grayscale holotomographic microscopy images. The application runs entirely in a modern web browser without installation, server infrastructure, or data upload — all processing occurs locally on the user's device, preserving the confidentiality of unpublished experimental data.

The tool provides essential quantitative outputs for label-free cell morphology studies: cell area, perimeter, aspect ratio, circularity, solidity, and an optional count of intracellular bright granules. A three-category shape verdict (near-circular, moderately irregular, clearly irregular) offers an immediate human-readable interpretation suitable for initial screening of treatment effects, apoptotic morphology changes, or comparative condition analysis.

## Application summary

| **Property** | Value |
|---|---|
| **Application name** | HTM SCA — HTM Simple Cell Analyzer |
| **Version** | 1.0 |
| **Deployment model** | Single-file static HTML, client-side only |
| **Input formats** | PNG, JPG (grayscale microscopy images) |
| **Dependencies** | None (pure HTML5, Canvas API, JavaScript) |
| **Browser requirements** | Chrome, Firefox, Edge, Safari (any recent version) |
| **Installation** | None — open the HTML file or web link directly |
| **Data privacy** | 100% local processing, no server, no upload |
| **Typical runtime** | < 1 second per image (image downscaled to max 500 px) |
| **Export formats** | CSV (numeric results) |

## Functional features

### Image handling

- Drag-and-drop or file picker upload for PNG and JPG images
- Automatic conversion to grayscale, automatic downscaling to a maximum dimension of 500 pixels for fast processing
- Original image preserved alongside annotated overlay for visual comparison

### Segmentation pipeline

- **Light Gaussian-style blur:** separable box blur with user-controlled radius (0–30 px) to smooth noise

- **Background subtraction:** original image minus blurred background produces a high-pass filtered image, removing illumination gradients
- **Percentile-based threshold:** user-adjustable cutoff (30–98%) selects the brightest pixel fraction as candidate cell
- **Connected-component labelling:** 4-connectivity flood fill identifies distinct regions
- **Border-exclusion rule:** components touching the image edge are deprioritized, preventing background frame from being selected as the cell
- **Hole filling:** interior background holes within the cell mask are filled using border-BFS

### Quantitative outputs

- Area (pixels$^2$) — total number of pixels inside the cell mask
- Perimeter (pixels) — length of the cell boundary
- Bounding box dimensions — width and height of the axis-aligned rectangle enclosing the cell
- Aspect ratio — major / minor bounding box dimension, indicator of elongation
- Circularity — 4π·area / perimeter$^2$ (1.0 = perfect circle, < 0.5 = irregular)
- Solidity — cell area / bounding box area, indicator of concavity
- Mean intensity — average grayscale value inside the mask
- Granule count, mean area, and mean intensity — optional detection of bright intracellular puncta

### Shape interpretation

The circularity value is automatically classified into three categories for immediate interpretation: **near-circular** (> 0.78), **moderately irregular** (0.55–0.78), and **clearly irregular** (< 0.55). Ranges may be adjusted in the source code.

### Visualization

- Original image on the left, annotated overlay on the right
- Three toggleable overlays: binary segmentation mask, cell boundary contour, detected intracellular granules
- Live preview — moving the threshold slider automatically re-runs analysis after 250 ms

### Export

- Single-click CSV export of all numeric results named after the input image
- CSV is structured as a two-line table (header row + values row), directly usable in Excel, GraphPad, or R

## Deployment on website

HTM SCA is delivered as a single self-contained HTML file. To publish the application on a website, host the file at any URL and link to it from a dedicated launch button. The recommended button design is shown below.

### Launch button

The launch button (shown at the top of this document) features a stylized irregular cell silhouette with detection contour dots, intracellular granules, and nucleus — visually representing the analyzer's output. The two-tone blue-teal colour scheme aligns with scientific-software conventions and complements the Nanolive brand palette.

### Recommended HTML embedding

A minimal HTML snippet to embed the launch button on a website page:

```
<a href="/htm-sca/simple_cell_analyzer.html" target="_blank"
rel="noopener">   <img src="/assets/htm_sca_logo.png" alt="HTM SCA —
Launch"        width="150" height="150" style="cursor:pointer"> </a>
```

Place both files — the application HTML and the logo PNG — in the website's public assets directory. The anchor element opens the analyzer in a new tab, preserving the parent page. No server-side components, JavaScript frameworks, or database connections are required.

## Limitations and intended use

HTM SCA is a rapid, lightweight screening tool, not a replacement for publication-grade quantification. Key constraints:

- Single image per session — no batch processing or time-series analysis
- Single largest cell selected automatically — images with multiple separate cells will report metrics for only one
- Simple percentile threshold may fail on images with extreme intensity gradients; manual slider adjustment is required
- Granule detection uses a simple local-contrast threshold and does not distinguish vesicle types, lipid droplets, or acquisition artifacts
- Shape metrics are based on the 2D projection and do not capture out-of-plane information available in full holotomographic volumes
- Apoptosis, viability, and vesicle-class claims require orthogonal validation (Annexin V, caspase activity, PI exclusion, electron microscopy)

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