STEP UP YOUR MORPHOLOGICAL CELL PROFILING GAME WITH AI

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A fast approach for fully-automated Cell Painting image analysis and feature extraction from raw image data

Background and Motivation

Reproducible **morphological profiling**, particularly for drug discovery, has become an essential tool for **compound evaluation** [1]. We describe a novel approach for **cell profiling** using a **fully-automated** computer vision approach with IKOSA AI. Our main motivation is to make Cell Painting [2] easily accessible for biologists **without computer science knowledge**. The primary objective of this work is to create a parameter-free, robust, deep learning-based computer vision algorithm to achieve precise object segmentations for fully-automated high-content imaging.

Materials and Methods

- **Ground truth** label generation from Cell Painting Gallery JUMP-CP pilot dataset [3] using U2OS and A549 cell lines; 5 fluorescent (Mito, AGP, RNA, ER, DNA) and 3 brightfield channels
- Training a deep learning **instance segmentation model** using the IKOSA AI software [4] on a well-defined, diverse subset
- Morphological **feature extraction** based on CellProfiler [5] cell painting parameter groups
- **Feature prioritization** using StratoMineR software [6] by Core Life Analytics (SLAS EU 2023 poster number: 1084-A)
- **Validation & quality control**: Compare IKOSA AI with the CellProfiler output

Results

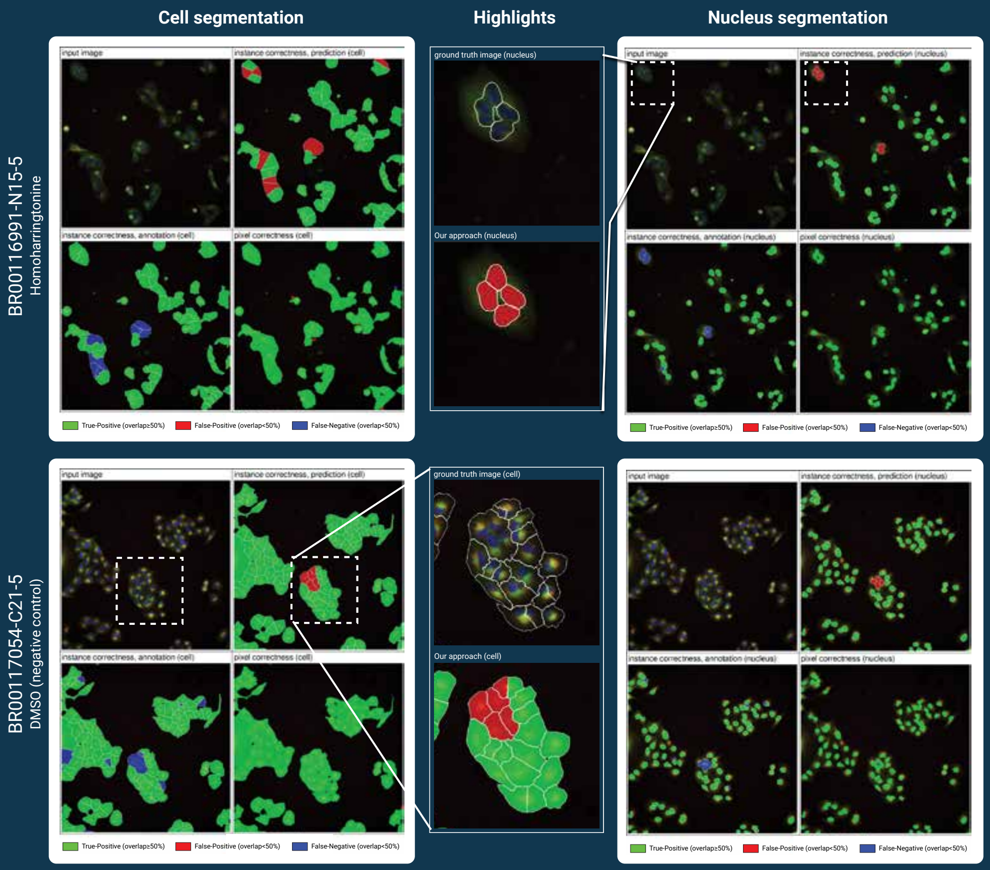
Instance segmentation

- Image dataset (n=2,780; 1,080x1,080 px)
  - 2,208 training images
  - 572 validation images
- Average runtime (GPU): 2.2s / image

Validation dataset	Cells (n=62,560)	Nuclei (n=58,290)
Precision higher is better	0.97	0.98
Recall higher is better	0.89	0.94
Average Precision higher is better	0.86	0.92
IoU Intersection over Union, higher is better	0.86	0.91

Feature extraction and validation

- Extracted groups: AreaShape, Correlation, Granularity, Intensity, Location, Neighbor, RadialDistribution, Texture, Zernike
- 1,145 of 3,664 features prioritized (31%)
- Quality control by comparing the results with CellProfiler features reporting normalized mean absolute error = 0.0298



Conclusions and Outlook

- Web-based software platform → High availability. Access anywhere, anytime.
- StratoMineR integration → Optimized feature selection
- Fully-automated feature extraction → No programming knowledge required
- Robust computer vision pipeline → Easily transfer to other datasets

We expect a significant impact on resource efficiency in drug discovery and personalized medicine.

Cell Painting will be **available soon on the IKOSA platform** for high-throughput scenarios.

References

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