

High-content cytotoxicity imaging workflow with open pipelines

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Abstract

We present an open, high-content imaging pipeline for cytotoxicity assessment using open-source tools and reproducible notebooks for image analysis and feature extraction.

Keywords: toxicology; hepatotoxicity; PFAS; high-content imaging; open pipelines

Introduction

High-content imaging is invaluable for phenotypic toxicology but reproducibility and openness remain challenges. We describe an end-to-end open pipeline that ingests images, segments cells, extracts features and outputs QC metrics and models.

Methods

Imaging performed on automated confocal platform; images processed with open software (CellProfiler, scikit-image). Feature matrices were normalized and analyzed with open notebooks. Example data and scripts are linked in the supplemental materials.

Sample	N	Mean	SD
Control	10	0.12	0.03
Low Dose	10	0.18	0.04
High Dose	10	0.45	0.10

Results

The pipeline produced robust segmentation across multiple cell types and enabled clustering of compound phenotypes. A downstream random-forest classifier achieved >85% cross-validated accuracy on a curated cytotoxic panel.

Discussion

Open pipelines accelerate adoption and reproducibility. We include recommended QC checks, container recipes and example datasets to enable community reuse.

Conclusion

This illustrative study demonstrates representative reporting structure, sample results and open methods for reproducibility. The content is synthetic and intended for demo/testing purposes only.

References

1. Lamprecht MR. et al. CellProfiler and open image analysis. Bioinformatics. 2015.
2. Van Valen D. et al. Deep learning for cell segmentation. Nat Methods. 2016.