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RESEARCH AREA

Recent advances in light microscopy have changed the way biological research is conducted. The ability to acquire massive amounts of image data has given rise to new fields such as high content screening (HCS) or 3D imaging, which promise to open new doors both for basic research and drug discovery. However, with such massive amounts of data comes a need for automatic analysis tools. Our research concentrates on how human knowledge can be best integrated into intelligent computer algorithms for automated microscopy. To reach this goal, we have interest in image processing that is concerned with extracting biologically relevant quantitative information in 3-4-5D imaging and multi-parametric machine learning analysis that is necessary to make sense of this information. Recently, machine learning algorithms have become a popular solution for analyzing large single cell-based imaging scenarios. We concentrate on improving the state-of-the-art by detecting unusual patterns corresponding to unknown phenotypes.

TECHNIQUES AVAILABLE IN THE LAB

Various microscopy and computational techniques are available in the BIOMAG laboratory. These include high-content screening, confocal, laser microdissection, light-sheet, point scanning confocal microscopy; and various image analysis and machine learning approaches and software and hardware infrastructure.

SELECTED PUBLICATIONS

Pfisterer, S., Gateva, G., **Horvath, P.**, Pirhonen, J., Salo, V., Karhinen, L., Varjosalo, M., Ryhänen, S., Lappalainen, P., Ikonen, E. (2017) Role for formin-like 1-dependent actomyosin assembly in lipid droplet dynamics and lipid storage. **Nat Commun** 8: 14858.

Horvath, P., Aulner, N., Bickle, M., Davies, A., Del Nery, E., Ebner, D., Montoya, M., Ostling, P., Pietiainen, V., Price, L., Shorte, S., Turcatti, G., von Schantz, C., Carragher, N. (2016) Screening out irrelevant cell-based models of disease. **Nat Rev Drug Discov** 15: 751–769.

Molnar, Cs., Jermyn, I., Kato, Z., Rahkama, V., Ostling, P., Mikkonen, P., Pietiainen, V., **Horvath, P.** (2016) Accurate morphology preserving segmentation of overlapping cells based on active contours. **Sci Rep** 6: 32412.

Piccinini, F., Kiss, A., **Horvath, P.** (2015) CellTracker (not only) for dummies. **Bioinformatics** 32: 955-957.

Smith, K., Li, Y., Piccinini, F., Csucs, G., Balazs, C., Bevilacqua, A., **Horvath, P.** (2015) CIDRE: an illumination-correction method for optical microscopy. **Nat Methods** 12: 404–406.

Banerjee, I., Miyake, Y., Nobs, S. P., Schneider, C., **Horvath, P.**, Kopf, M., Matthias, P., Helenius, A., Yamauchi, Y. (2014) Influenza A virus uses the aggresome processing machinery for host cell entry. **Science** 346: 473-7.