IA-27

Morphokinetic analysis of neutrophils from whole-blood infection assays

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01/10/2017

LIFE MEETS LIGHT First Scientific Conference of the Leibniz ScienceCampus InfectoOptics

Infecto Optics

Morphokinetic analysis of neutrophils from whole-blood infection assays

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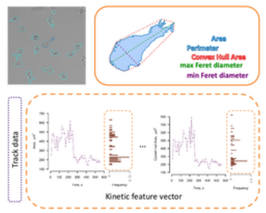
Project aim

Automated characterization of cells based on interpretable features, in order to construct classifier models based on dynamic cell properties.

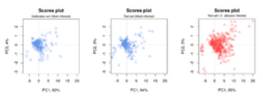
Project outline

Single cell description



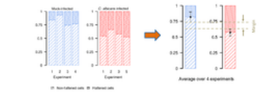
Classifier training

Based on visual inspection of live cell imaging data we introduced two types of morphological conditions for the cells (neutrophils): flattened and non-flattened. In the mock-infected scenario the last type dominates. This fact allows us to create a soft model of non-flattened cell using the data from mock-infected experiments and principal component decomposition.



Graphical representation of the model (left) and projections of new samples on this model (mid and right). The calibration set included 231 object, the mock-infected test set included 230 object, C. albicans infected set included 337 object. The data sets included only the cells with track duration not less than 10 time points.

Results

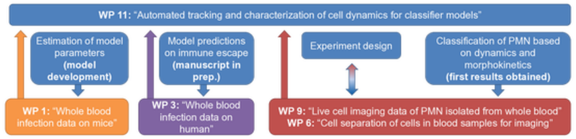


Classification results for paired experiments for each of the two conditions. The decision rule based on F-statistics. Averaged results demonstrate, that the fraction of flattened cells is significantly different between the two infection scenarios, because there is a clear margin with bandwidth of about one standard deviation.

Next steps

Identification of minimal requirements for comprehensive analysis.

Whole-blood infection model for other pathogens, immune cells and species.



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FUNDED BY Leibniz