Track-based analysis of cell migration

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The focus of this project is on the development of algorithms for automated characterization of cell tracks. The main objective is to find interpretable features and find groups of similarity in phenotypical sense, which allow to construct the classifier models based on dynamic cell properties.

This work is part of the project "Whole Blood Imaging" (BLOODi) within the framework of the Leibniz ScienceCampus InfectoOptics. The scientific aim of this project is to combat infectious diseases with advanced optical technologies by establishing the concept of a dynamic hemogram from whole blood infection assays. The dynamic hemogram goes beyond standard blood count examination in that information on the migration and interaction of immune cells is captured. This novel source of information will be investigated for its potential to function as a biomarker in the characterization of whole blood infections caused by various pathogens and in different species.
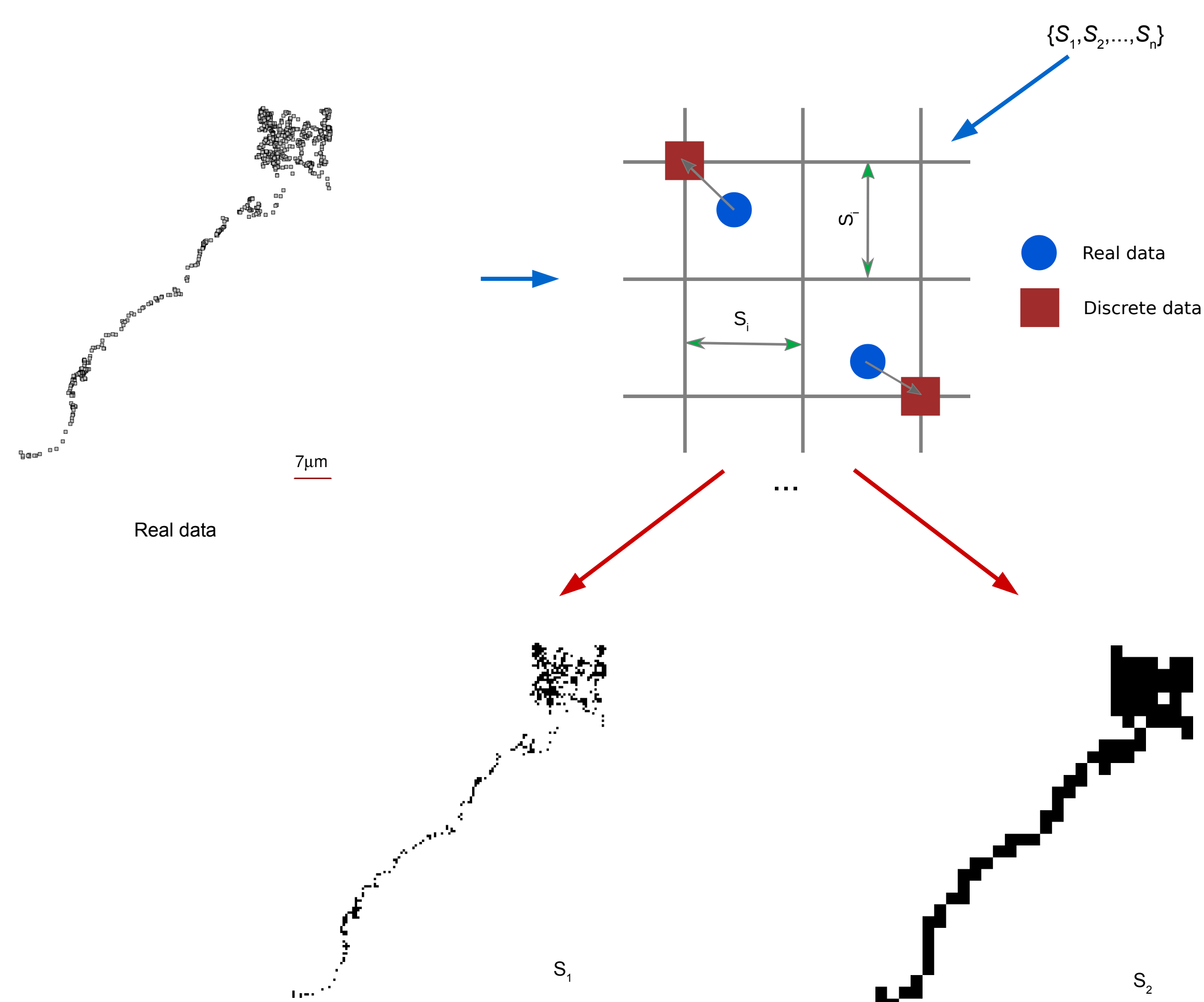
1. Data

The experimental data are 2D neutrophil tracks. Due to the rich diversity of cell tracks in general, their classification into different types of migration behavior can be a challenging task [1].
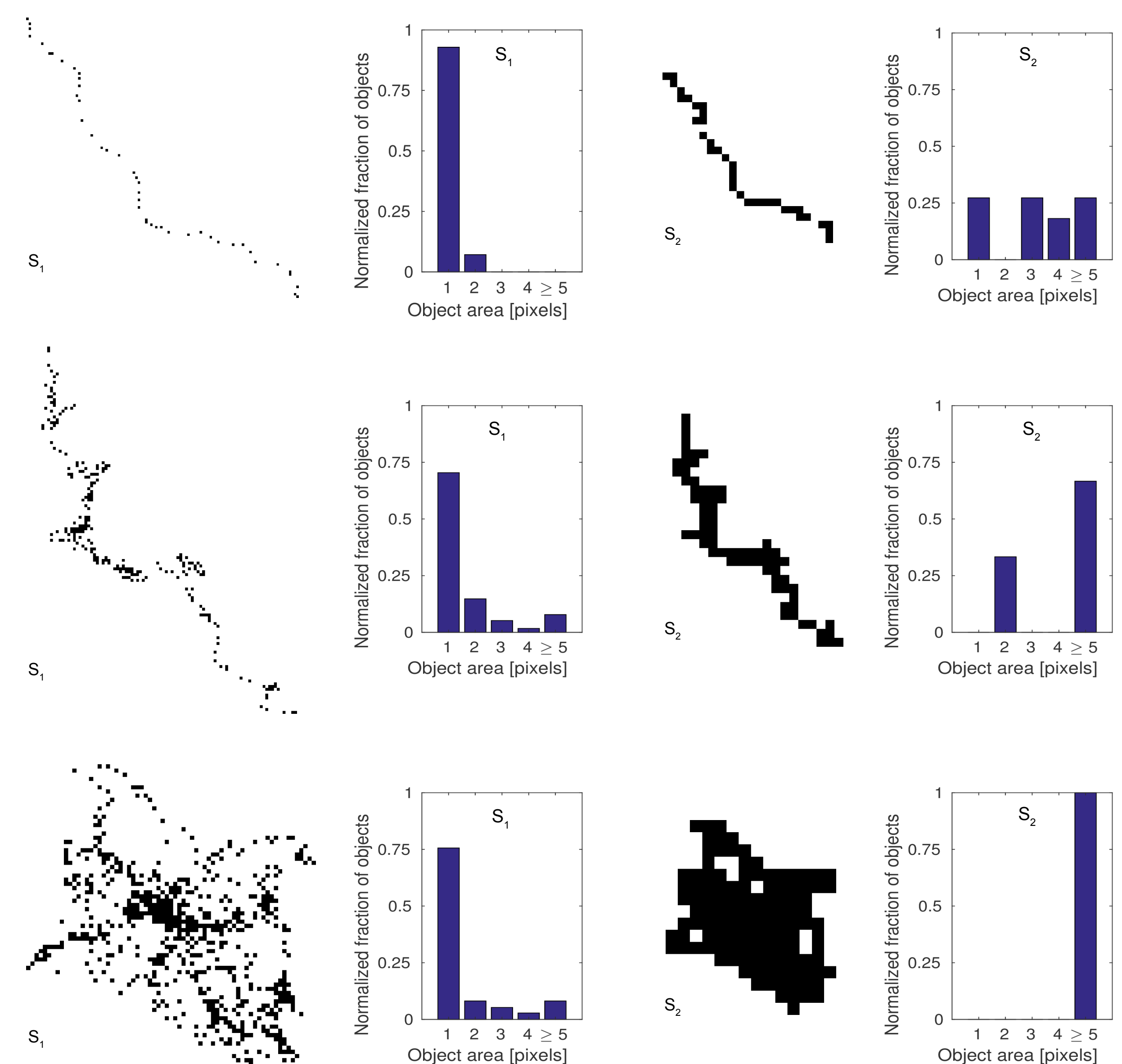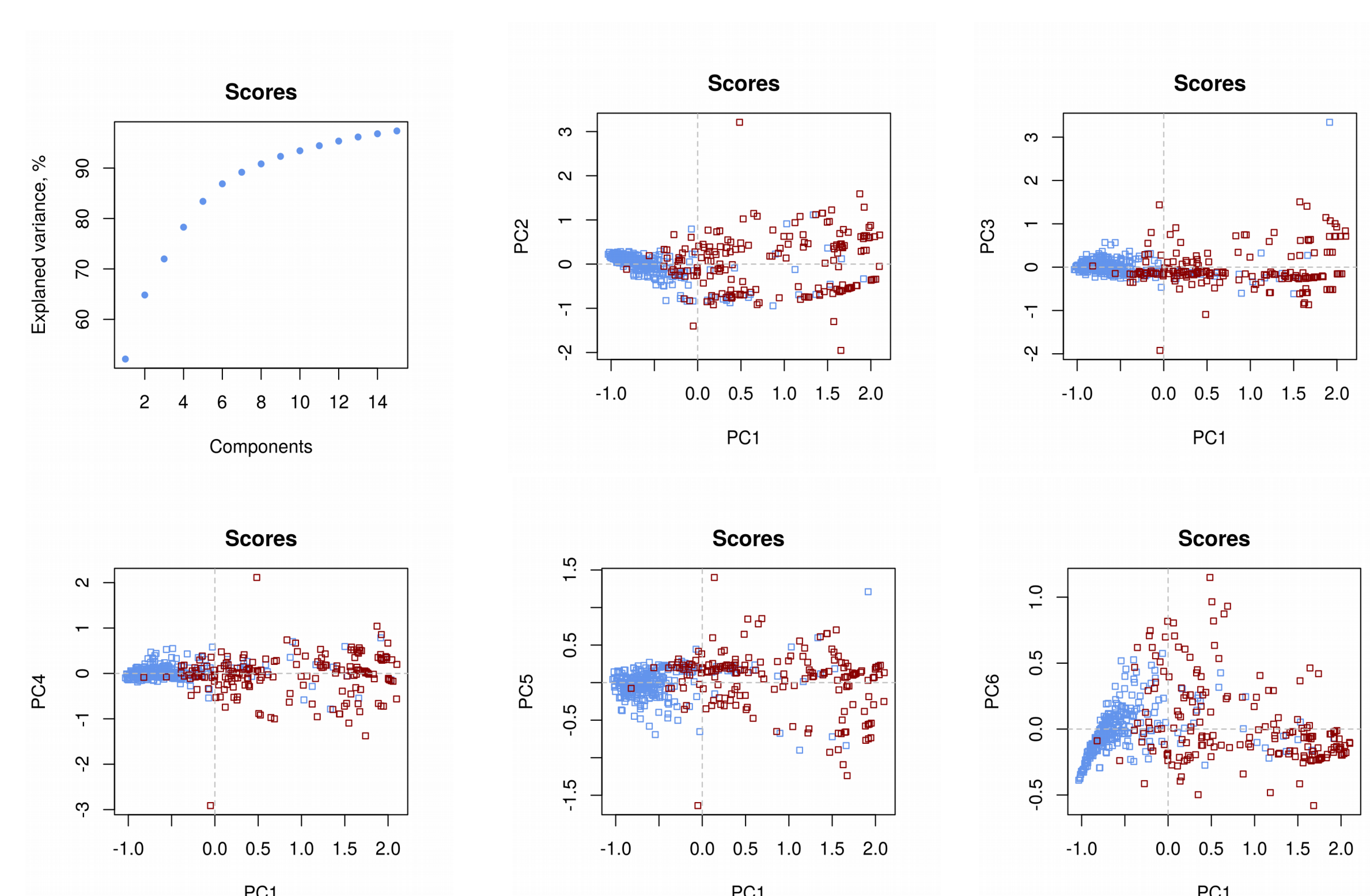
2. A coarse-grained view on the data

Representation on discrete lattice with different scales.

3. Descriptor

Distribution of object areas on the binary image on given scale.

4. PCA analysis

PCA-based clustering of two neuthrophil populations with different predominant types of migration.
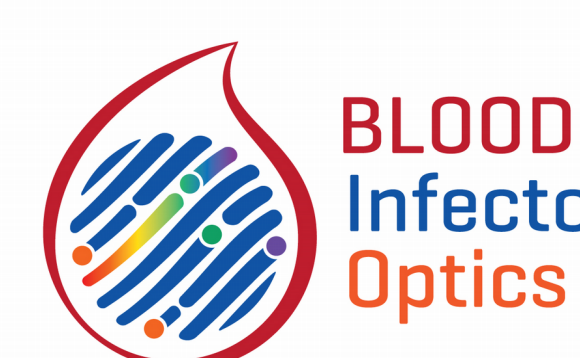
References

1. Mokhtari et al. PLoS One. 2013 Dec 6;8(12):e80808 doi:10.1371/journal.pone.0080808

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