Thomas Zerjatke, Nico Scherf, Ingmar Glauche, Ingo Roeder
Institute for Medical Informatics and Biometry
Medical Faculty C. G. Carus, Dresden University of Technology
Fetscherstrasse 74, D-01307 Dresden, Germany
e-mail: thomas.zerjatke@tu-dresden.de

Knowing their neighbours - correlation structures in the development of related stem cells

Time lapse video microscopy enables the tracking of stem cell development in bio-engineered culture conditions on a single cell level. The resulting cellular genealogies retain information on cellular characteristics, divisional history, and differentiation. Analysing the topology, the dynamical features, and the correlation structure within these pedigree-like genealogies provides information about underlying processes such as migration, cell growth, and differentiation.

For a systematic analysis of cellular genealogies we compare experimental data for different hematopoietic stem cell cultures with a single- cell based, mathematical model of hematopoietic stem cell organisation. In particular we illustrate how ancestral relation between cells influences their current behaviour and decision making. Furthermore we derive emerging contact networks based on spatial positioning of the cells within the time lapse video data. In particular we analyse whether ancestral information is conserved within the community structure of these networks and whether these mutual interactions between cells correlate with secondary read-outs such as cell cycle distribution or the occurrence of cell death events.

The presented framework for a comprehensive description and analysis of cellular development on the level of individual cells and their progeny is an important advancement to support experimental single cell tracking approaches. By combining experimental and modeling data our results demonstrate that the analysis of cellular genealogies and corresponding interaction networks can provide valuable insights into processes of cellular development and differentiation that can not be obtained on a population level.

References

[1] N. Scherf, JP. Kuska et al. (2009) *Spatio-temporal Analysis of Unstained Cells in vitro* Proceedings BVM 2009, 292- 296.

[2] N. Scherf, I. Roeder, and I. Glauche (2008) *Correlation patterns of cellular genealogies* Proceedings of the Fifth International Workshop on Computational Systems Biology, WCSB 2008, Leipzig, Germany, 161-164.