

# Multiscale Modeling and 3D Visualization of spatially-embedded Cytological Networks

Björn Sommer<sup>1,2</sup>

University of Konstanz, Konstanz, Germany<sup>1</sup>, Monash University, Melbourne, Australia<sup>2</sup>

Since decades, the visualization of cytological networks is an important branch of biological visualization. A famous example is Gerhard Michal's Biochemical Pathways map which was introduced in 1968; its success is today partly reflected by the establishment of databases like KEGG [KGSF12, Mich98]. However, these 2D visualization-based approaches are widely dissociated from the spatial reality of the cell. Recently, the arrival of stereoscopic 3D visualization in the consumer marked as well as the success of head-mounted displays – such as Oculus Rift – enables immersion into spatial data, with the large advantage to improve the understanding of cellular structures and their functioning.

Over the years, we developed a number of different *cell modeling approaches* which can be used to embed cytological networks into spatial structures, i.e., combining cell models segmented from 3D tomography with gene/protein-related data derived from databases such as KEGG or UniProt [Cons13, SKSH10].

Based on the generated models, we created a number of *cell visualization approaches* which can be explored on multiple scales: from the local computer, to web browsers, to mobile phones and Head-mounted displays, and to large-scale virtual environments like the CAVE2 [FNNT13, KoGS16, SBHG14, SHKC16, SWXC15].

In this talk we will give an overview of open source modeling, visualization and human-computer interaction techniques which can be used to create and present spatially-embedded biological networks in scientific as well as educational contexts.

## References

- [Cons13] CONSORTIUM, UniProt: Update on activities at the Universal Protein Resource (UniProt) in 2013. In: *Nucleic acids research* 41 (2013), no. D1, pp. D43–D47
- [FNNT13] FEBRETTI, Alessandro; NISHIMOTO, Arthur; THIGPEN, Terrance; et al.: CAVE2: a hybrid reality environment for immersive simulation and information analysis. In: *IS&T/SPIE Electronic Imaging* :, 2013, pp. 864903-864903–12
- [KGSF12] KANEHISA, M.; GOTO, S.; SATO, Y.; et al.: KEGG for integration and interpretation of large-scale molecular data sets. In: *Nucleic acids research* 40 (2012), no. D1, pp. D109–D114
- [KoGS16] KOVANI, Gökhan; GHAFAR, Mehmood; SOMMER, Björn: Web-based hybrid-dimensional Visualization and Exploration of Cytological Localization Scenarios. In: *Journal of Integrative Bioinformatics* 13 (2016), no. 4, p. 298
- [Mich98] MICHAL, Gerhard: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*. 1. ed. Heidelberg, Germany : Wiley-Spektrum, 1998. — Published: Hardcover — ISBN 0-471-33130-9
- [SBHG14] SOMMER, Björn; BENDER, Christian; HOPPE, Tobias; et al.: Stereoscopic cell visualization: from mesoscopic to molecular scale. In: *Journal of Electronic Imaging* 23 (2014), no. 1, pp. 011007-1-011007-10
- [SHKC16] SOMMER, Björn; HAMACHER, Andreas; KALUZA, Owen; et al.: Stereoscopic Space Map – Semi-immersive Configuration of 3D-stereoscopic Tours in Multi-display Environments. In: *Electronic Imaging, Proceedings of Stereoscopic Displays and Applications XXVII 2016* (2016), no. 5, pp. 1–9
- [SKSH10] SOMMER, Björn; KÜNSEMÖLLER, Jörn; SAND, Norbert; et al.: CELLmicrocosmos 4.1: an interactive approach to integrating spatially localized metabolic networks into a virtual 3D cell environment. In: FRED, Ana; FILIPE, Joaquim; GAMBOA, Hugo (eds.): *BIOSTEC 2010*, 2010, pp. 90–95
- [SWXC15] SOMMER, Björn; WANG, Stephen Jia; XU, Lifeng; et al.: Hybrid-Dimensional Visualization and Interaction - Integrating 2D and 3D Visualization with Semi-Immersive Navigation Techniques. In: *Big Data Visual Analytics (BDVA), 2015* : IEEE, 2015, pp. 1–8