**Biographical Sketch (Template)**

| Name: Silke Hauf | Title: Assistant Professor |
|---|---|
| Email: silke@vt.edu | Department: Biological Sciences |

**Education/Training:**

| Institution/Location | Degree/Postdoc | Year(s) | Field of Study |
|---|---|---|---|
| University of Würzburg, Germany | M.D. | 2000 | Medicine |
| Institute of Molecular Pathology (IMP), Vienna, Austria | Postdoc | 1999 – 2003 | Cell Biology |
| University of Tokyo, Japan | Postdoc | 2003 – 2005 | Genetics |

**Personal Statement:**

As a general rule, the more complex a machine is, the more likely it is to break - simply because there are more potential breaking points. Yet, cells are highly complex entities and are extremely robust, i.e. they perform their functions reliably even in variable intra- and extracellular milieus. We want to understand the underlying basis: what makes biological systems robust? To study this question, we look at cell division, a process that is essential for life and whose deregulation is common in cancer. When cells divide, a multitude of changes need to happen in a very short time, and any error can be fatal. Hence, reliability and robustness are crucial. To understand the underlying principles, we combine perturbations with high-end, quantitative microscopy, which allows us to obtain single-cell, time-resolved and spatial information. Computational modeling, for which we collaborate with experts in this field, helps us to interpret these experiments and to develop new hypotheses. We work with fission yeast, which is an excellent model for eukaryotic cells, and where we can easily introduce perturbations using CRISPR/Cas9 and other state-of-the-art technologies.

**Selected Publications:**


Geissen EM, Hasenauer J, Heinrich S, Hauf S, Theis FJ, Radde NE. MEMO: multi-experiment mixture model analysis of censored data. ***Bioinformatics***. 2016 Apr 19. pii: btw190 PMID: 27153627.

Kamenz J, Mihaljev T, Kubis A, Legewie S, Hauf S. Robust Ordering of Anaphase Events by Adaptive Thresholds and Competing Degradation Pathways. ***Mol Cell***. 2015 Nov 5;60(3):446-59. doi: 10.1016/j.molcel.2015.09.022. PMID: 26527280.

Carpy A, Krug K, Graf S, Koch A, Popic S, Hauf S, Macek B. Absolute proteome and phosphoproteome dynamics during the cell cycle of Schizosaccharomyces pombe (Fission Yeast). ***Mol Cell Proteomics***. 2014 Aug;13(8):1925-36. doi: 10.1074/mcp.M113.035824. PMID: 24763107

Kamenz J, Hauf S. Slow checkpoint activation kinetics as a safety device in anaphase. ***Curr Biol***. 2014 Mar 17;24(6):646-51. doi: 10.1016/j.cub.2014.02.005. PMID: 24583014.

Heinrich S, Geissen EM, Kamenz J, Trautmann S, Widmer C, Drewe P, Knop M, Radde N, Hasenauer J, Hauf S. Determinants of robustness in spindle assembly checkpoint signalling. ***Nat Cell Biol***. 2013 Nov;15(11):1328-39. doi: 10.1038/ncb2864. PMID: 24161933.

Koch A, Krug K, Pengelley S, Macek B, Hauf S. Mitotic substrates of the kinase Aurora with roles in chromatin regulation identified through quantitative phosphoproteomics of fission yeast. ***Sci Signal***. 2011 Jun 28;4(179):rs6. doi: 10.1126/scisignal.2001588. PMID: 21712547.

**Current and/or Recently Completed Research Grants:** (as applicable)

| | | | |
|---|---|---|---|
| NSF | 1616247 | Hauf | 07/2016 – 06/2019 |
| Title: The quantitative landscape of the mitotic checkpoint: from genes to function | | | |
| The mitotic checkpoint prevents dividing cells from making errors in chromosome segregation. Proper functioning of this checkpoint requires precise levels of the proteins that act in this signaling pathway. This project will determine how transcription and translation of mitotic checkpoint genes is quantitatively controlled to keep protein levels in the permissive range and will analyze why checkpoint functionality is restricted to this range. We combine our wet lab experiments with a bioinformatic analysis and computational modeling of the mitotic checkpoint - in collaboration with Lenwood Heath and Jing Chen, respectively. | | | |
| NIH | R35GM119723 | Hauf | 08/2016 – 05/2021 |
| Title: Molecular mechanisms of cell division robustness | | | |
| A remarkable feature of cells is their ability to divide accurately even when environmental or intracellular conditions vary. Thus, cells and organisms exhibit an intrinsic 'robustness' that buffers against fluctuations while allowing high-fidelity cell division. Our work will use intracellular and extracellular perturbations to identify the limits of cell division robustness and thereby identify fragile points. Our previous work (Kamenz et al., 2015) identified 'adaptive thresholds' as one mechanism that contributes to the robustness of mitotic exit. As part of this project, we will aim to identify the molecular basis of this phenomenon. Furthermore, we will continue to map the robustness landscape of cell division. The interpretation of our experimental results will be aided by computational modeling in a continuing collaboration with Stefan Legewie and his group at the IMB in Mainz, Germany. | | | |