

SEEWIESEN

LECTURE SERIES

FALL/WINTER 2018/19



THURSDAY | February 28th, 2019 | 13.00 | HOUSE 4 LECTURE ROOM

KATJA NOWICK

FU Berlin | Host: Kuepper Research Group

Human Evolution: How Gene Regulatory Factors and their networks might have shaped human specific phenotypes

Complex phenotypes are determined by many genes and can well be investigated using network methods. Hence, to study the evolution of complex phenotypes, comparative network approaches are very promising. Here we aim to shed light on the evolution of cognitive abilities in humans. To this end, we used transcriptome data from pre-frontal cortex samples of humans, chimpanzees, and rhesus macaques to calculate transcription factor (TF) co-expression networks. We revealed an overall increase in connectivity on the human lineage and that several TFs that are known to be involved in brain development or cognitive disorders have turned into hubs specifically in the human networks. These TFs are good candidates for further experimental studies on the evolution of cognition.

We developed several methods to facilitate comparative network analyses, among them a statistical framework to combine similar networks into consensus networks of high confidence, to assign p-values to links, and to define conserved, species-specific, and diverged links. Our methods are publicly available via two R packages, wTO and CoDiNA, and come along with sophisticated interactive visualization. We hope them to be useful for other evolutionary network studies.

WHO IS KATJA NOWICK?

Since 07/2017	Professor for Human Biology, Freie Universität Berlin, Berlin, Germany
01/2016 – 06/2017	Professor for Bioinformatics, University of Hohenheim, Germany
01/2011 – 12/2015	Independent research group leader: „TFome and Transcriptome Evolution“ (Research group awarded by the VolkswagenFoundation) University of Leipzig, Faculty of Mathematics and Computer Science, Bioinformatics group; Faculty of Medicine, Paul-Flechsig-Institute for Brain Research, Leipzig, Germany
02/2010 – 12/2010	Postdoc at the Max-Planck-Institute for Molecular Genetics, Dept. for Vertebrate Genomics headed by Prof. Hans Lehrach, Berlin, Germany
03/2008 – 12/2009	Postdoc at the Institute for Genome Biology, group of Prof. Lisa Stubbs, Urbana-Champaign, Illinois, USA
03/2006 – 03/2008	Postdoc at the Lawrence Livermore National Laboratory, group of Dr. Lisa Stubbs, Livermore, California, USA
10/2005 – 03/2006	Postdoc at the Max-Planck-Institute for Evolutionary Anthropology, Dept. for Evolutionary Genetics headed by Prof. Svante Pääbo, Leipzig, Germany
05/2001 – 09/2005	Doctoral student at the Max-Planck-Institute for Evolutionary Anthropology, Dept. for Evolutionary Genetics headed by Prof. Svante Pääbo, Leipzig, Germany

SELECTED RELEVANT PUBLICATIONS

- Gysi, D.M., Voigt, A., Fragoso, T. de M., Almaas, E., and Nowick, K. (2018). wTO: an R package for computing weighted topological overlap and consensus networks with an integrated visualization tool. *BMC Bioinformatics* 2018 Oct 24;19(1):392. doi: 10.1186/s12859-018-2351-7
- Kutsche, L.K., Gysi, D.M.*, Fallmann, J., Lenk, K., Petri, R., Swiersy, A., Klapper, S.D., Piracs, K., Khattak, S., Stadler, P.F., Jakobsson, J., Nowick, K. and Buskamp, V. (2018) Combined experimental and system-level analyses reveal the complex regulatory network of miR-124 during human neurogenesis, *Cell Systems* 2018 Oct 24;7(4):438-452.e8. doi: 10.1016/j.cels.2018.08.011 (*my PhD student is shared first author)
- Berto, S. and Nowick, K. (2018) Species-specific changes in a primate transcription factor network provide insights into the molecular evolution of the primate prefrontal cortex, *Genome Biology and Evolution* 2018 Jul 30. doi: 10.1093/gbe/evy149

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