# Tanja Stadler, Dr. rer. nat.

Theoretische Biologie

## Eidgenössische Technische Hochschule Zürich

Born in 1981 in Stuttgart

Studied Mathematics at the Technische Universität München

FELLOWSHIP

John Maynard Smith Prize-Fellow

ARBEITSVORHABEN

## Inferenz von Populations-Dynamiken in biologischen Systemen mithilfe von phylogenetischen Methoden

Genetic sequences of organisms are related through their evolutionary past. Therefore, genetic sequences cannot be treated as independent measurements, but their evolutionary past ( i.e., the phylogenetic tree - has to be considered in order to draw biological conclusions.

I am developing more realistic evolutionary models and more efficient computational tools to make it possible to infer and analyze phylogenies based on the large amount of sequence data becoming available. The methods are developed such that we can answer questions on both the macroevolutionary and the epidemiological level, which may lead e.g. to a better understanding of potential future extinction events, as well as of the effectiveness of public health interventions.

On the macroevolutionary level, my aim is to obtain a better understanding of which macroevolutionary processes shape the tree of life. So far, all commonly used models fail to explain the data in the sense that model trees differ significantly from the empirical trees. In the era of a vast amount of sequence data, we have the unique opportunity to use the sequence data to verify or reject novel macroevolutionary models.

On the epidemiological level, I am aiming to use the large amount of virus sequence data, which is obtained by routine drug resistance testing, to understand epidemiological and evolutionary dynamics of viruses in more detail. My future aim is to merge epidemiological and evolutionary models, such that both epidemiological and evolutionary parameters can be estimated on the basis of viral sequence data.

Addressing these open questions in macroevolution and epidemiology requires defining appropriate models for the different processes, which then need to be formalized in an inference framework. During my stay at the Wissenschaftskolleg, I am looking forward to broad discussions with evolutionary biologists, ecologists, and epidemiologists, which I expect to lead to more realistic models and testable hypotheses at the interface of these disciplines.

Recommended Reading

Stadler, Tanja (2011). "Mammalian phylogeny reveals recent diversification rate shifts." Proc. Nat. Acad. Sci. 108, 15: 6187-6192.

Stadler, Tanja, R. Kouyos, V. von Wyl, S. Yerly, J. Böni, P. Bürgisser, T. Klimkait, B. Joos, P. Rieder, D. Xie, H. Günthard, A. Drummond, and S. Bonhoeffer (2012). "Estimating the basic reproductive number from viral sequence data." Molecular Biology and Evolution 29, 1: 347-357.

PUBLIKATIONEN AUS DER FELLOWBIBLIOTHEK

Stadler, Tanja (London,2014)

Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth–death SIR model

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1680555472

Stadler, Tanja (Oxford,2014)

Using an epidemiological model for phylogenetic inference reveals density dependence in HIV transmission

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1680552481

Stadler, Tanja (London,2013)

Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1680554360

Stadler, Tanja (2013)

Recovering speciation and extinction dynamics based on phylogenies

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1046358588