

---

**CHRISTOPH WEITKAMP**, Universität Göttingen

*GROMOV-WASSERSTEIN BASED PHYLOGENETIC TREE SHAPE COMPARISON*

The shapes of phylogenetic trees carry important information about short and long-term evolutionary processes. In this talk, we propose to model the shapes considered as dissimilarity measure spaces and to compare them based on the Gromov-Wasserstein distance. We quantify their similarity on the basis of a dissimilarity-preserving soft assignment of the elements of the respective spaces. To reduce the computational complexity, we introduce several computationally efficient surrogates and illustrate in various examples that these represent powerful tools for the comparison of phylogenetic tree shapes. We compare our methods to the Colijn-Plazotta metric and illustrate the fundamental differences between these approaches.