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Symposium

Next generation phylogenetics – from gene trees to species trees

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In order to accomplish the ultimate goal of phylogenetics, being the reconstruction of the evolutionary history of the different lineages of organisms (the 'Tree of Life'), the usage of methods of molecular systematics have developed into indispensable tools of systematists. However, growing evidence for the importance of reticulation events among lineages by processes like hybridisation, homoploid or polyploid hybrid speciation in addition to the classically reconstructed bifurcations renders our gene-tree reconstructions to be only a local optimum on the path towards the long-standing conceptual goal of systematics, being rather a tree of species than a tree of genes. In addition, the advent of large multilocus datasets (phylogenomics) with their large numbers of independently segregating and individually evolving loci will also necessitate the application of new algorithms for estimating species trees from a number of often contradictory gene trees.

The present symposium will aim at a description of the present state of the art concerning the obstacles to receive species trees from gene trees and of methods to resolve these problems in the tension field between phylogenetics, phylogeography, and population genetics. Contributions to this symposium are invited from the different branches of the tree of life and either should demonstrate practical examples for reticulations in phylogenetic reconstructions due to biological processes like hybridisation or polyploidy or due to contradictions in large multilocus datasets or should report experiences with the application of novel methods for estimating species trees from gene trees.