The Aldous move on cladograms
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Abstract: A n-phylogenetic tree is a semi-labeled, unrooted and binary tree with n leaves labeled {1,2,...,n} and with n-2 unlabeled internal leaves and positive edge lengths representing the time spans between common ancestors. In biological systematics n-phylogenetic trees are used to represent the evolutionary relationship between n species. If one does focus only on the kinship (that is taking all edge length of unit length), a more precise term is cladogram.

Aldous constructed a Markov chain on cladograms and gave bounds on their mixing time. On the other hand, Aldous also gave a notion of convergence of cladograms which shows that the uniform cladogram with N leaves and edge length re-scaled by a factor of one over the square root of N converges to the so-called Brownian continuum random tree (CRT) which is the tree "below'' a standard Brownian excursion and can be thought of as the "uniform''
tree.
These two results suggest that if we re-scale edge lengths by a factor of one over the square root of N and speed up time by a factor of N to the power of 3/2 the Aldous move on cladograms converges in some sense to a continuous tree-valued diffusion.

The main emphasis of the talk is to give precise statements towards that direction.