**Database tools and other software for the study of transposable elements**

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Transposable elements are autonomously replicated repetitive sequences present in high numbers in eukaryotic genomes. In evolution of individual species and their genomes these sequences go through repeated rounds of multiplication and reduction, often producing and leaving behind only fragments of full-length sequences. The sequences are also mixed by nesting and recombination as well as mutated with time by normal biological processes. With the number of annotated genomes rapidly increasing, it is becoming very difficult to keep track of all the existing variants and their mutual positions and relationships in genomes. We are developing tools to deal with this kind of data. Specifically, we are building a CHADO ([www.gmod.org](http://www.gmod.org/)) based environment for storage and visualization of transposon annotations and developing a software tools for detection of ancient transposon copies fragmented by insertion of younger copies (nesting). Recent progress of our work on these tools will be presented.