

# Comparison of Alternative Splicing Structures in Eukaryotes

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Numerous databases of alternative splice forms have been generated over the recent years, which – beside of using heterogenous input data – differ substantially in the definition and in the representation of patterns. Motivated by this, we have developed a novel relative position notation system to univocally describe alternative splicing (AS) events, and a parsing and visualization tool (ASTALAVISTA) that, based on this notation, is able to automatically characterize AS events from gene annotations. We have used this tool to compare AS in different annotations for the human genome (i.e., GENCODE, REFSEQ and ENSEMBL) as well as across annotations for different eukaryotes. One outcome of our studies is that the impact of AS on the untranslated regions has probably been underestimated hitherto. We also show specific differences of the landscape of AS structures in UTR and in the CDS. Finally, we propose novel descriptive measures and metrics to compare AS structures in homologous genes. An online version of ASTALAVISTA is available at: <http://genome.imim.es/astalavista>.

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