Apr 21st, 1:15 PM - 2:15 PM

Determining New Consensus Sequences for Alternative Pre-mRNA Splicing

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Poster Presentation P22

DETERMINING NEW CONSENSUS SEQUENCES FOR ALTERNATIVE PRE-mRNA SPLICING

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It has been previously demonstrated that consensus for alternative pre-mRNA splicing occurs in the promoter and in the gene itself with respect to distance to the splice site. Mammalian genomic DNA sequences were aligned using BLAST2, the output parsed by a Perl script, and passed to a program that determines the probability of consensus for a sequence with respect to distance to a splice site or the TATA homology. Results of little significance and those that occur in genes that do not undergo alternative splicing in this output were then filtered out using another Perl script. Results will not only indicate the sequence for consensus, but also its location in the gene and the frequency with which it occurs, allowing us to infer what sequences are required for all alternative splicing genes, and which sequences regulate alternative splicing.