

***In Silico* Characterization of Novel Alternative Splice Products**

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Comprehensive searches for alternative splice products can involve gels of PCR products from known transcripts. The appearance of unexpected bands on the gel indicates novel products. Experimental characterization of the novel product can be time consuming and costly. Because the end points of the products are known based on the PCR primers that were used, and the length of the product can be estimated from the gel, a computational approach to determine the correct splicing pattern for all of the observed products seems feasible. We have a large collection of known alternative splice products with which to evaluate the prediction accuracy of different programs. Here we report a novel computational method for the direct identification of unknown splice products based only on their size and the genomic sequence from which they are derived. We evaluate our method using known alternatively spliced genes for the organism *Caenorhabditis elegans*.

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