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SÉMINAIRE

Predicting the functional consequences of alternative splicing variations

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Several protein isoforms can be produced from a single gene through alternative splicing. These isoforms have different protein sequences, and often diverse or even antagonistic functions. In the recent years,the use of high-throughput technologies has revealed that alternative splicing is massively deregulated in many experimental conditions. A proportion of the splicing events observed at the transcript level are also observed at the protein level. However, it is still difficult to decipher the functional consequences of these splicing variations because of the lack of functional information at the exon level. To circumvent that problem, we introduce a computational strategy that relies on the functional annotation of exons in order to predict the consequences of their inclusion or skipping.