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About half of the animal and plant genomes is composed by repetitive sequences. This huge amount of repetitive sequences suggests that they may play some significant role. Indeed, some recent studies have suggested that they might be involved in biological mechanisms such as gene expression regulation and formation of chimeric transcripts. Due their increasing relevance, in the last few years many databases and bioinformatics tools were released in order to identify and store repetitive sequences present in genomes. However, an important subset of repetitive sequences has received little attention. This subset is composed by those sequences within a gene locus which appear in different gene loci. They are mostly present in intronic regions, but may also be found within exons. In order to study this class of repetitive sequences, we have developed a Web-based software, called RepGraph, that identify and graphically display the intron-exon structure of those sequences for several model organisms. In this release, RepGraph supports *Homo sapiens*, *Bos taurus*, *Gallus gallus*, *Arabidopsis thaliana* and *Oryza sativa* genomes, but may be easily extended to other species. To the best of our knowledge, this is the first Web-based bioinformatics tool that performs these tasks.

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