**Abstract**

The aim of this work is to predict and describe the immunoglobulin (Ig) and T cell receptor (TR) genes in genomic DNA of vertebrates. Indeed, owing to their DNA rearrangements the Ig and TR variable, diversity and joining genes (V-, D- and J-GENE, respectively) have an unusual structure. Conventional bioinformatic software based on standard gene structure cannot identify them precisely. To solve this problem, a new tool named IMGT/LIGMmotif, specific for Ig and TR gene prediction and description, has been developed. This tool allows genomic annotation at IMGT®, the International ImMunoGeneTics Information system® [1]. The processing of the annotation is based on the DESCRIPTION concept established in IMGT-ONTOGY® [2], the first ontology in the domain of immunogenetics and immunoinformatics. The implemented algorithm combines a similarity search (BLASTN) for a rapid prediction with the matching of V-, D- and J-GENE for complete and accurate description of V-, D- and J-GENE.

**Objectives**

1. To predict efficiently Ig and TR germline vertebrate genes
2. To describe precisely genomic Ig and TR
3. To facilitate genomic annotation

**Approach**

Combines a similarity search (BLASTN) for a rapid prediction with the matching of V-, D- and J-GENE for completion and accurate description of V-, D- and J-GENE.

**Annotation algorithm**

1. Gene prediction

   **BLASTN**

   **Pattern matching**

   **Gene prediction**

   **Gene description**

   **Results association**

   **Results**

   **Conclusion and perspectives**

   **References**

**Conclusion and perspectives**

The combination of BLASTN and pattern matching in IMGT/LIGMmotif allows the prediction of Ig and TR genes in genomic sequences and the standardized description. This facilitates the annotation process by providing the delimitation of IMGT labels. The tool works on Ig and TR loci of human and mouse. Preliminary work shows that the software works for Ig and TR loci of other vertebrates sporcics. Sets of patterns will be added accordingly to the new genomic tools.

**References**


