The adaptive immune response is our ability to produce up to 2.10^12 different immunoglobulins (IG) or antibodies and T cell receptors (TR) per individual to fight pathogens. IMGT®, the international ImMunoGeneTics information system®, was created in 1989 by Marie-Paule Lefranc (Montpellier University and CNRS) to manage the huge and complex diversity of these antigen receptors [1].

IMGT® is at the origin of immunoinformatics [2], a science at the interface between immunogenetics and bioinformatics. IMGT® is built on the IMGT-ONTOLOGY concepts of identification (keywords), description (labels), classification (gene and allele nomenclature) and numeration (IMGT unique numbering) [3].

**IMGT/StatClonotype**: An R package with integrated web tool for pairwise evaluation and visualization of IMGT clonotype diversity and expression from IMGT/HighV-QUEST output

**User inputs**
- Choose IMGT/HighV-QUEST outputs
- Specify the range of CDR3-IMGT
- Select IMGT clonotype diversity or expression

**User outputs**
- CDR3-IMGT outer lengths elimination.
- Normalized bar graph of the proportions displays.
- Significance of the difference in proportions with 95% confidence interval (CI) for IMGT clonotype (AA) diversity and expression between two sets from IMGT/HighV-QUEST output.
- Testing difference in proportions of IMGT clonotype (AA) per gene of a given group (z-scores, Fisher-test).
- Adjustment of the p-values is made through a multiple testing procedure by the two strategies [8]:
  - Family-wise error rate (FWER): Bonferroni, Holm, Sidak (single stop and stop down) and Hochberg procedures.
  - False discovery rate (FDR): The Benjamini & Hochberg (BH) and Benjamini & Yekutieli (BY) procedures.
- Multiples testing procedure displays.
- Differences in proportions graph displays.
- IMGT/StatClonotype Shiny web application launch with 6 functionalities: 1) to 6) package dependencies: shiny, shinyjs, plotly, data.table, DT, reshape2, multtest, ggplot2, gridExtra, d3heatmap.

**IMGT/HighV-QUEST for NGS analysis**

**IMGT/HighV-QUEST** [4-7], the first web portal for next generation sequencing (NGS) analysis of IG and TR, provides the identification of the variable (V), diversity (D) and joining (J) genes and alleles, analysis of the V-(D)-J junction and characterization of the ‘IMGT clonotype (AA)’ (AA for amino acid).

**References**:

**Acknowledgments**: this work was granted access to the HPC resources of HPC@LR and of CINES and TGCC-CEA under the allocation 036029-(2010-2016) made by GENCI.

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