# BiERapp: A web-based interactive framework for the prioritization of disease candidate genes in whole exome sequencing studies

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## BIER we have a problem!

Whole-exome (WES) sequencing has become a fundamental tool for the discovery of disease-related genes of familiar diseases and the identification of somatic driver variants in cancer. However, finding the casual mutation among the enormous background of individual variability in a small number of samples is still a big challenge.

## The solution is:

Here we describe a web-based tool, **BiERapp [1]**, which efficiently helps in the identification of causative variants in familial and sporadic genetic diseases. The program uses predicted variants (SNVs and INDELs) in affected individuals or tumor samples and controls (in standard VCF format). In familial cases, different modes of inheritance can be easily defined to filter out variants that do not segregate with the disease along the family.

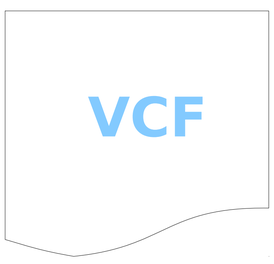
Moreover, **BiERapp** integrates additional information such as allelic frequencies in the general population and the most popular damaging scores to further narrow down the number of putative variants in successive filtering steps.

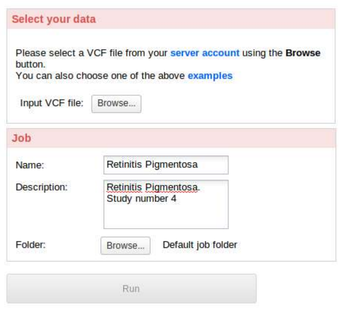
**BiERapp** provides an interactive and user-friendly interface that implements the filtering strategy used in the context of a large-scale genomic project carried out by the Spanish Network for Research, in Rare Diseases (CIBERER) in which more than 170 exomes have been analyzed.

**BiERapp** also offers a representation of the selected variants within the genomic context provided by an embedded version of the Genome Maps tool **[2]**.

**BiERapp** is currently used to present the results of the WES analysis carried out by the BiER. The version available within the CIBERER has, in addition, frequencies of Spanish populations, taken from the healthy unrelated samples analyzed so far.

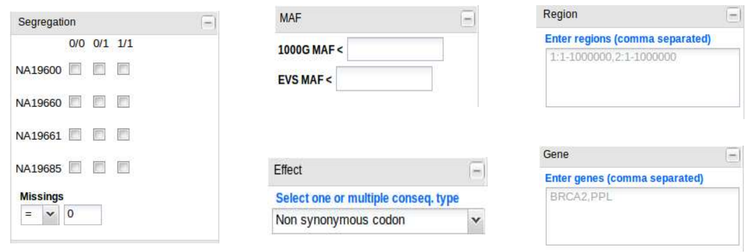
## How does it work?

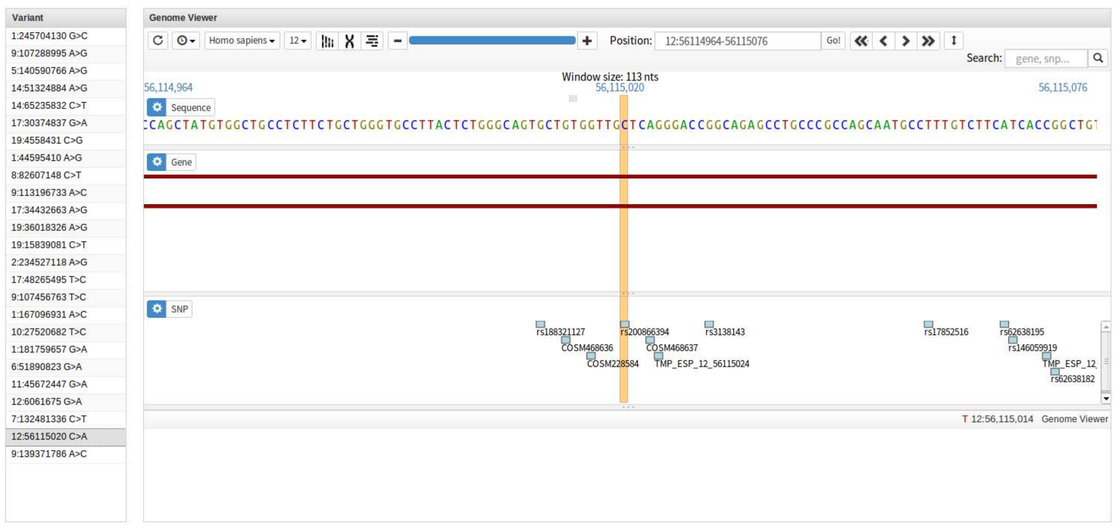


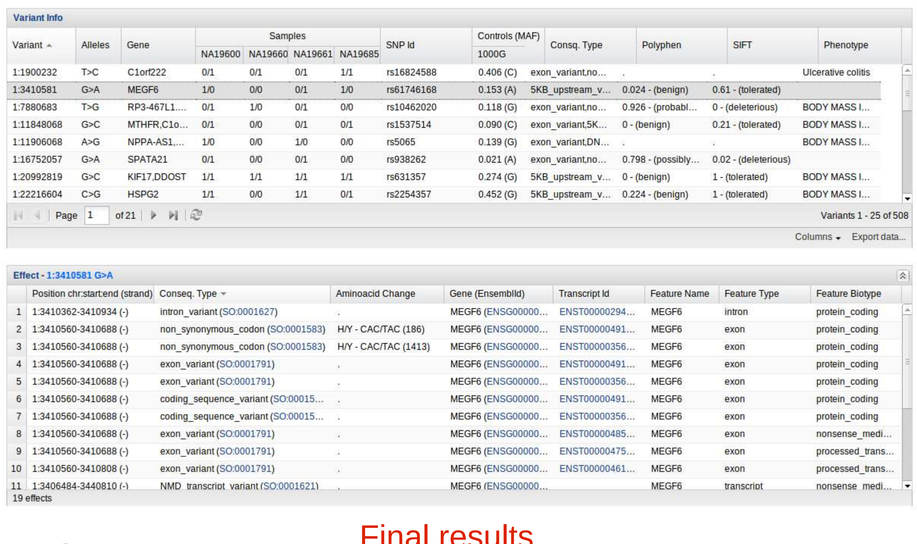

A few minutes later

**Apply some filters**




Visualizing variants in Genome Maps




Final results

**http://bierapp.babelomics.org/**

## Conclusions

- **BiERapp** has great potential to detect disease-related variants in familiar diseases as demonstrated by its successful use in the CIBERER.
- **BiERapp** is the first web-tool that provides the possibility of applying a consecutive filtering approach to variants coming from a WES study with this level of interactivity.

## References:

**[1]** A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. A. Aleman *et al. Nucleic Acids Res*, (2014) doi: 10.1093/nar/gku407.

**[2]** Genome Maps, a new generation genome browser. I. Medina *et al. Nucleic Acids Res*, **41**, W41-46 (2013).