

# Welcome to IVA

The Interactive Variant Analysis (IVA) tool is an open-source project implemented to facilitate the filtering, analysis and interpretation of whole genome variant data. This interactive tool allows the identification of genes affected by deleterious variants that segregate along family pedigrees, case-control or sporadic samples.

IVA has been developed as part of the [OpenCGA](#) project, making it easy to work with clinical and variant information stored in a Catalog and Variant storage instance.

## Latest news:



[IVA v1.0.0 coming soon!](#)

[Marta Bleda](#) posted on Feb 20, 2019 IVA v1.0.0 will be released next week with lots of improvements and new features.

## Main Features

- Allow to load VCF files and samples together with clinical data
- High-performance and scalable VCF and gVCF indexing
- VCF normalization and variant annotation
- Clinical interpretation analysis of samples and families

## Contact

- Ignacio Medina
- Joaquin Dopazo

IVA is developed and maintained at University of Cambridge and CIPF, it is freely available at <https://github.com/opencb/iva>

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## Variant Browser

You can efficiently browse annotated and indexed variant studies using a web-based application.

## Clinical Interpretation

You can select samples and families to perform an interpretation analysis... Disease panels are also available.

## Genome Browser

A genome browser based on Genome Maps allows for a interactive and smooth variant visualisation...

## Rich Configuration

You can highly customise your IVA installation thanks to the rich configuration implemented. You can easily customise the navigation bar, welcome page or the CSS.

## Who is Using

IVA is a novel application but it is already used in several top-level projects such as HGVA, BRIDGE, ...

## Developers

### Source Code

Web based on IVA project at <https://github.com/opencb/iva/tree/app/hgva>

Server based on OpenCGA at <https://github.com/opencb/opencga>

### Contributing

IVA is a collaborative project that aims to integrate as many reference human studies as possible, you can contact us for feature request. If you want to contribute to the code you are more than welcome to contribute to IVA and OpenCGA

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## Contributors

Dr. Joaquin Dopazo (CIPF)

Dr. Stefan Gräf (Clinical School, University of Cambridge)

Ignacio Medina (HPCS, University of Cambridge)

## Recent space activity

[Nacho Medina](#)

[Roadmap](#) updated Jan 27, 2020 • [view change](#)

[Marta Bleda](#)

[IVA v1.0.0 coming soon!](#) created Feb 20, 2019

[Welcome to IVA](#) updated Feb 20, 2019 • [view change](#)



[Alexis Martinez Chacón](#)

[How to Build](#) updated Nov 06, 2017 • [view change](#)

[Nacho Medina](#)

[About](#) updated Nov 06, 2017 • [view change](#)