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**Gigwa**  
Genotype Investigator for Genome-Wide Analyses  
V2

Interoperability Annotations Workflow Browsing Analytics Management  
Transcriptome GBS TSVCF HapMap Statistics INDEL SNP Conversion Visualization

Guilhem Sempère, UMR Intertryp, CIRAD

**SouthGreen** **cirad** **IRD** **INRA** **arcad**

## Appealing aspects

- Support for **haploid**, **diploid**, **polyploid** data
- Query **progress display**
- Ability to **abort running queries**
- No loss of **phasing information** when provided
- Ability to search for variants **discriminating 2 groups of individuals**
- Instant variant **density graph** display
- Easy **connection with external tools** (Galaxy, IGV, online genome browsers, ...)

## Application purpose

Providing a **graphical interface** allowing non-bioinformaticians to:

- **Host / share** large amounts of **genotyping data**, possibly enriched with metadata
- Applying **real-time filters** on this data
- **Browse** selected variants and genotypes
- Re-export thus defined **subsets** of data into various formats / **push into external tools**



## Publications

### V1

**Gigwa—Genotype investigator for genome-wide analyses**

Guilhem Sempère, Florian Philippe, Alexis Dereeper, Manuel Ruiz, Gautier Sarah and Pierre Larmande  
*GigaScience* 2016 5:25, <https://doi.org/10.1186/s13742-016-0131-8>

### V2\*

**Gigwa v2 – Extended and improved genotype investigator**

Guilhem Sempère; Adrien Pétré; Mathieu Rouard; Julien Frouin; Yann Hueber; F De Bellis; Pierre Larmande  
*\*Submitted at Gigascience, currently under revision*

## Main characteristics

- Supports datasets of tens of **billions of genotypes**
- Single instance handling **multiples databases**
- 2 setup modes: **local** instance / **data portal**
- 3 import formats / **7 export formats**
- **2 REST APIs** implemented: GA4GH & BrAPI
- Variant filtering based on:
  - marker features, functional annotations
  - **genotype patterns**, **data quality**



## Technical details

- Web-application in **Java / HTML / Javascript**
- Data hosted in **MongoDB**
- **Multi-platform** (Linux, Windows, MacOS)

## More on Gigwa homepage

<http://southgreen.fr/content/gigwa>  
(github URL, live instance list, installation bundles, etc...)

## Demonstration videos

### Video 1 - importing data (2'39)

[http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa\\_releases/1-gigwaV2-importing-commented.mp4](http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa_releases/1-gigwaV2-importing-commented.mp4)

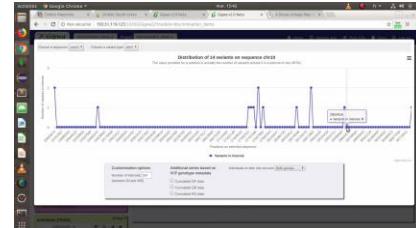


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## Demonstration videos

### Video 4 - phenotype-based discrimination (2'36)

[http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa\\_releases/4-gigwaV2-discrimination-commented.mp4](http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa_releases/4-gigwaV2-discrimination-commented.mp4)

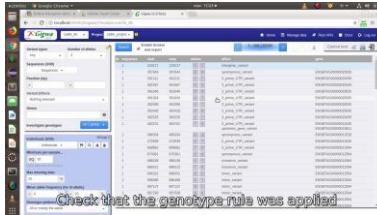


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## Demonstration videos

### Video 2 - filtering data (3'57)

[http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa\\_releases/2-gigwaV2-searching-commented.mp4](http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa_releases/2-gigwaV2-searching-commented.mp4)



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## Development context

**South Green**  
bioinformatics platform

<http://www.southgreen.fr>



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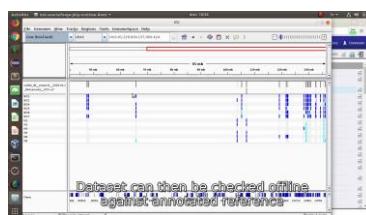
Local (Montpellier, France) network of bioinformaticians

- Multi-institute
- Focus: genetics / genomics of tropical & mediterranean plants
- Provides HPC + training & support to biologists
- Collaborative development: analysis pipelines & toolkits, web apps (Galaxy + in-house) & portals (genome hubs)

## Demonstration videos

### Video 3 - managing outputs (3'27)

[http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa\\_releases/3-gigwaV2-outputs-commented.mp4](http://southgreen.fr/sites/southgreen.fr/files/uploads/gigwa_releases/3-gigwaV2-outputs-commented.mp4)



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## Many thanks ...



... for your attention!

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