**Gigwa: Genotype Investigator for Genome Wide Analyses**

With the data deluge produced by Next Generation Sequencing (NGS) arise serious computational challenges in terms of storage, search, sharing, analysis, and data visualization, that redefine some practices in data management. Gigwa was mainly developed to manage genomic and genotyping data from NGS analysis.

### Main features
- Based on NoSQL technology (MongoDB)
- Handles VCF files (Variant Call Format) and annotations
- Supports multiple variant types: SNPs, InDels, SSRs, SV
- Optimized imports for specific genomic and genotyping data
- Takes phasing information into account when importing/exporting in VCF format
- Powerful genotyping queries
- Easily scalable with MongoDB sharding
- Efficient filters
- Web interface
- Responsive when working with millions of variants

### Export
- VCF, HapMap, PLINK, GFF, ...

### Security
- Multi-database application
- User control over execution
- Secure access to databases

### Availability
- http://www.southgreen.fr/content/gigwa

### Variant search interface
- Several types of selection:
  - Variant search is restricted to the selected reference sequences and subset of individuals

### Filters
Polymorphisms (SNPs, InDels, SSRs, SV) can be filtered using various criteria:
- Filter on read depth threshold
- Filter on missing data
- Filter on Minor Allele Frequency (MAF)
- Filter on number of alleles
- Filter on genomic positions
- Filter on gene name

### Sorted result tables
- Detailed genotyping information