# Version History

## Policy

See our versioning policy here.

## 3.0

**February 15, 2015**

- Ontology terms are now mapped to Ensembl Release 73 Genes.
- The mouse mm10 assembly is now supported.
- New ontologies of MSigDB Immunologic Signatures and MSigDB Oncogenic Signatures are now added. Ontologies of transcription factor targets and miRNA targets  have been dropped in GREAT 3.0 but are still in version 2.0.
- The hg18 human assembly is not supported in GREAT version 3.0 but is still supported in GREAT version 2.0.

## 2.0

**April 3, 2012**

- Mouse and human ontology data has been updated with new data so reproducing results prior to 2.0 need to be done using 1.8
- Extended programming interface to allow batch jobs to receive tsv output
- Added the export "All data as .tsv" option to "Global Export".
- The export for individual ontologies was also extended to output gene and regions hit and the FDR values.
- Added data visualization features to GREAT
    - Export tables as barplots
    - View enriched terms in hierarchy
- New modern CSS skin
- Zebrafish ontology data remains identical to GREAT 1.8 and thus can be reproduced using the 2.0 interface

## 1.8

**May 31, 2011**

- Added genomic region/gene association graphs to main results page.
- Enhanced the term details page to:
    - Include term-specific graphs,
    - Link specifically between genomic regions and genes, and
    - Open UCSC genome browser shots at a gene's regulatory domain.
- Added informative error messages when an input BED file has errors.
- All previously-existing ontology data remain identical to GREAT 1.5, 1.6, and 1.7, so reproducing GREAT 1.5, 1.6, or 1.7 runs happens automatically in 1.8.

## 1.7

**March 29, 2011**

- Added support for two phenotype ontologies (Human Phenotype and Osborne Annotated Disease Ontology) in the human and mouse assemblies.
- All previously-existing ontology data remain identical to GREAT 1.5 and 1.6, so reproducing GREAT 1.5 and 1.6 runs happens automatically in 1.7.

## 1.6

**Jan 27, 2011**

- Added support for the zebrafish Zv9 (UCSC danRer7, Jul/2010) assembly.
- All human- and mouse-related data remain identical to GREAT 1.5, so reproducing GREAT 1.5 runs happens automatically in 1.6.

## 1.5

**Nov 19, 2010**

- Added ability to download mapping between input regions and genes.
- Added support for the human GRCh37 (UCSC hg19, Feb/2009) assembly.
- Updated all ontologies from original data sources.

- Added filtering and display options to both whole genome and foreground/background tests.
- Enabled programmatic access to foreground/background test.
- Enabled submission of compressed data.
- Enabled submission of larger datasets.
- Slightly modified the basal+extension regulatory domain calculation logic.
- Created a versioning system for exact reproduction of analyses performed on any earlier date.

# 1.2

**May 2, 2010**

- First public release, coinciding with Nature Biotechnology paper publication.
- Supports the human NCBI build 36.1 (UCSC hg18, Mar/2006) and mouse NCBI build 37 (UCSC mm9, Jul/2007) genome assemblies.

# 1.0.0

**Apr 27, 2009**

- First internal release.