

Download

GREAT Source Code

Our implementation of the core calculation logic used by GREAT is now available for download. This package is written in C and includes two tools:

1. A tool to calculate computationally-defined gene regulatory domains.
2. A tool to calculate the genomic region-based binomial enrichment p-value for ontology terms given the regulatory domains of genes annotated with the term and the input regions associated with the term.

To download and compile the tools, perform the following steps:

1. [Download the source code tarball](#)
2. Unpack the tarball using the command `'tar xzvf greatTools.tar.gz'`
3. Follow the instructions given in the `README.txt` file

The logic for associating regions with genes and calculating enrichments is also fully described in our [Nature Biotechnology paper](#).

Ontology Data

All of the data included in the GREAT ontologies is publicly available, and we provide [links or references for every ontology](#). We do not offer these data for download, as all data is available from the original sources. Additionally, the GREAT web tool offers [numerous "Export" functions](#) to save all ontology data as it pertains to your sets.

GREAT Gene Sets

Please refer to [Genes](#) for instructions on how to download the gene set used by GREAT.