

# Home

## Welcome

The [Bejerano Lab](http://bejerano.stanford.edu) at Stanford University developed the Genomic Regions Enrichment of Annotations Tool (GREAT) and hosts the GREAT web server at <http://bejerano.stanford.edu/great>.

Many coding genes are well annotated with their biological functions. Non-coding regions typically lack such annotation. GREAT assigns biological meaning to a set of non-coding genomic regions by analyzing the annotations of the nearby genes. Thus, it is particularly useful in studying *cis* functions of sets of non-coding genomic regions. *Cis*-regulatory regions can be identified via both experimental methods (e.g. chromatin immunoprecipitation followed by massively parallel sequencing) and by computational methods (e.g. sequence conservation in a given clade).

## News

Read about our newly-available [GREAT Version 2.0](#) release which adds genomic region/gene distribution plots and improves the term details page.

## GREAT Help

### General

- [Overview](#) - When is GREAT useful, and for which uses should I prefer it to other annotation tools?
- [Video](#) - Watch a video presentation on GREAT
- [Citation](#) - How do I cite GREAT?
- [Publications & Reprints](#)
- [Version History](#)
- [About Us](#)
- [Download](#)
- [Contact Us](#) - forum information
- [Forums](#) - get help from the GREAT userbase

### Input

- [Genome Assemblies](#) - Which genome assemblies does GREAT support, and can I use other assemblies or species?
- [File Formats](#) - What should my test regions and background regions files contain?
- [File Size](#) - What data set sizes can GREAT handle?
- [Data Integrity](#) - What checks does GREAT perform to ensure my data is valid?
- [Background Sets](#) - When should I use an explicit background set in evaluating enrichments?

### Output

- [Statistics](#) - How does GREAT calculate enrichments, and how should I interpret my results?
- [Output](#) - What output does GREAT provide?
- [Genes](#) - Which set of genes does GREAT use, and how does GREAT determine a single transcription start site for a gene?
- [Visualizations](#) - How can GREAT help you visualize your data for publication or better analysis?
- [Ontologies](#) - What is an ontology, and what data do the ontologies in GREAT provide?

### Technical

- [Web Browsers](#) - Which web browsers does GREAT support, and how can I make my browser work best with GREAT?
- [Programming Interface](#) - How can I submit data sets to GREAT automatically through a script or directly from my web site?

### Troubleshooting

- [Troubleshooting](#)