Genome Assemblies

Which genome assemblies does GREAT support?

Currently, GREAT supports recent assemblies of the well-annotated human (UCSC hg19 and UCSC hg18), mouse (UCSC mm9) and zebrafish (UCSC danRer7) genomes.

Can I use a different species or assembly?

If you have genomic regions defined for a different species or assembly from the ones we currently support, you can use the UCSC LiftOver utility to convert to a supported assembly. The LiftOver typically works very well for within-species coordinate conversion (e.g. from one human assembly to another), but it can also be used as a best approximation of mapping regions in one genome to the orthologous regions of a genome for a different species (e.g., from chimpanzee to human), although more caution is obviously advised in these cases.

Will you consider expanding GREAT to support additional species?

We do hope to gradually expand the set of species we support. GREAT needs the following to consider adding a new species:

1. A decent genome assembly.
2. A decent reference gene set.
3. Gene annotations. Typically in the form of an ontology, and gene to ontology term mappings.
4. A user community for said species.

Vertebrates

For vertebrate species, you can help us consider additional species by sending us specific links to rich gene annotation resources unique to your species of interest.

Non-Vertebrate Species

For species more distantly related to human (e.g. drosophila or arabidopsis) we will likely not do the curation ourselves. However, if you are seriously interested and capable, we can consider sharing our file format requirements with you and have you contribute this species into GREAT.

Here's what you'll need to do:

1. Pick a reference genome, and describe it to GREAT.
2. Pick a reference gene set, and describe it to GREAT.
3. Pick a GREAT gene regulatory domain assignment default rule.
4. Identify (and/or generate from data) a set of ontologies with high-quality gene annotations for your species of interest.
5. For each such ontology:
    a. Describe the ontology structure to GREAT.
    b. Map the ontology gene annotations to the reference gene set you chose in #2 (in case they are tagged with another reference gene set from yours). This step can be tricky.
    c. Provide a format to link from GREAT to a term details page for each term in the ontology.

And that's it. Interested parties are welcome to contact us for more detailed instructions.