

A Short Tutorial for FUMGA Web Server

Last updated by K.Wu and C.Liu on August 13, 2014

FUMGA stands for Fungal Mitochondrial Genome Sequence Annotator. It allows automated annotation and analysis of newly sequenced mitochondrial genome. The web sever can be accessed at <http://www.medfungi.org/mitofungi>.

Step I. Upload a sequence for annotation.

1. Go to “AnnoGenome” page, download the sample fasta file.
2. Fill in the information for Project Name, Kingdom and Species Name.
3. Upload the sample fasta sequences for your genome.
4. Click the “Submit” button and you will see a message like the following.

“You job xxx has been submitted and it is under processing. It usually takes up to 60 minutes to finish the annotation of a 60kb long mitochondrial genome sequence. Please keep a note of your project id, as this is the only information by which you can access your data through <http://www.medfungi.org/mitofungi> under “ViewAnno”.

5. The best practice is to keep a note of the job ID or the URL and comes back, say, 60 minutes later to check the results.

Step II. Visualize and editing the annotations.

1. Once you come back, go to the “ViewAnno” page, enter the ID for your job. A report page will show up. Browse through this page to see the results for gene models in GFF3 format, circular map image in SVG format, sequences for predicted DNA and proteins in FASTA format and analysis reports organized in Tables.

2. Through our own research work, we become big fans of Apollo genome editor and believe that there is no need or it is not possible to reinvent a genome annotation editor just as powerful. As a result, we make FUMGA output compatible with Apollo for editing. Download the gene models in GFF format and edit it in genome editor like Apollo.
3. Edit the annotations using Apollo. Apollo is a very powerful editor that supports all sorts of editing of the predicted gene models. Of course, other editors can be used as well.

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