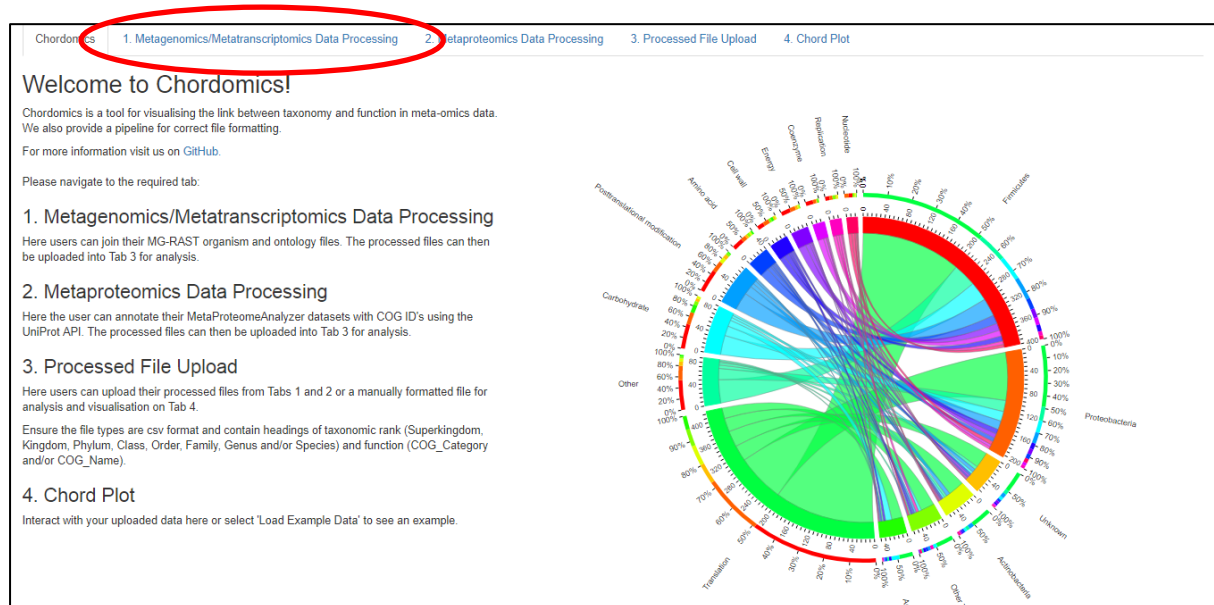


To process your data from MG-RAST click on Tab 2: Metagenomics/Metatranscriptomics Data Processing.



The software provides two options for data input:

1. Given an MG-RAST ID for a public repository, e.g. mgm4491407.3, relating to your dataset the app will automatically download the RefSeq taxonomy file and the COG functional file.
2. Alternatively you can manually upload your data from MG-RAST to Chordomics. Again, this requires the COG ontology file, the RefSeq or other organism file and also the input fasta file from MG-RAST. For more information read the [MG-RAST data walkthrough](#).

These are then combined by read ID and assigned taxonomy down to the lowest common ancestor of the possible species. Finally the COG IDs are labelled with their category and name.

Chordomics 1. Metagenomics/Metatranscriptomics Data Processing 2. Metaproteomics Data Processing 3. Processed File Upload 4. Chord Plot

### Automatic

**MG-RAST Identification**

mgm4491407.3

### Manual

**Upload MG-RAST COG file here**

Browse... No file selected

**Upload MG-RAST RefSeq or other organism file here**

Browse... No file selected

**Upload MG-RAST original input file (fasta) here**

Browse... No file selected

Prepare Data

### Metagenomics/Metatranscriptomics Data Processing

Before data can be explored using chordomics it must be presented in the correct format. Use this utility to merge both functional (COG) and phylogenetic information from MG-RAST as well as format your data for the next step (Tab3).

Please enter an MG-RAST ID to the upper section of the panel on the left OR upload the COG functional file, RefSeq or other phylogeny file and original input fasta file from your repository to the lower section.

Note, large files will take a long time to download using the Automatic pipeline.

Private projects cannot be accessed automatically, please download manually the relevant files from MG-RAST. For more information visit us on [GitHub](#). Once the ID is entered/datasets are uploaded press Prepare Data.

A download button will appear once the file is ready.

Progress:

Once an ID has been entered OR the three datasets are uploaded, pressing the Prepare Data button begins the processing.

The Progress window will post updates of what is happening in the processing pipeline.

Note large datasets will take a long time to download and process.

Once the data is ready a Download button will appear. Use this to save the processed file.

The processed data can then be uploaded to Tab 4: Processed File Upload for visualisation.

Chordomics

1. Metagenomics/Metatranscriptomics Data Processing

2. Metaproteomics Data Processing

3. Processed File Upload

4. Chord Plot

### Automatic

**MG-RAST Identification**

### Manual

**Upload MG-RAST COG file here**

Browse...

No file selected

**Upload MG-RAST RefSeq or other organism file here**

Browse...


No file selected

**Upload MG-RAST original input file (fasta) here**

Browse...

No file selected

Prepare Data

 Download

## Metagenomics/Metatranscriptomics Data Processing

Before data can be explored using chordomics it must be presented in the correct format. Use this utility to merge both functional (COG) and phylogenetic information from MG-RAST as well as format your data for the next step (Tab3).

Please enter an MG-RAST ID to the upper section of the panel on the left OR upload the COG functional file, RefSeq or other phylogeny file and original input fasta file from your repository to the lower section.

Note, large files will take a long time to download using the Automatic pipeline.

Private projects cannot be accessed automatically, please download manually the relevant files from MG-RAST. For more information visit us on [GitHub](#).

Once the ID is entered/datasets are uploaded press Prepare Data.

A download button will appear once the file is ready.

Progress:

```
Creating folder C:/Users/Kevin Mc/Documents/chordomics/mgm4443745.3
matching scientific name at the species level to taxid; this can take some time
complete
merging data
printing summary file
Finished getting data
Assigning LCA...
Adding names
File ready to download!
Click the 'Download' button on the side panel.
```