Computational methods for metagenomic data processing in the Metazoo Project

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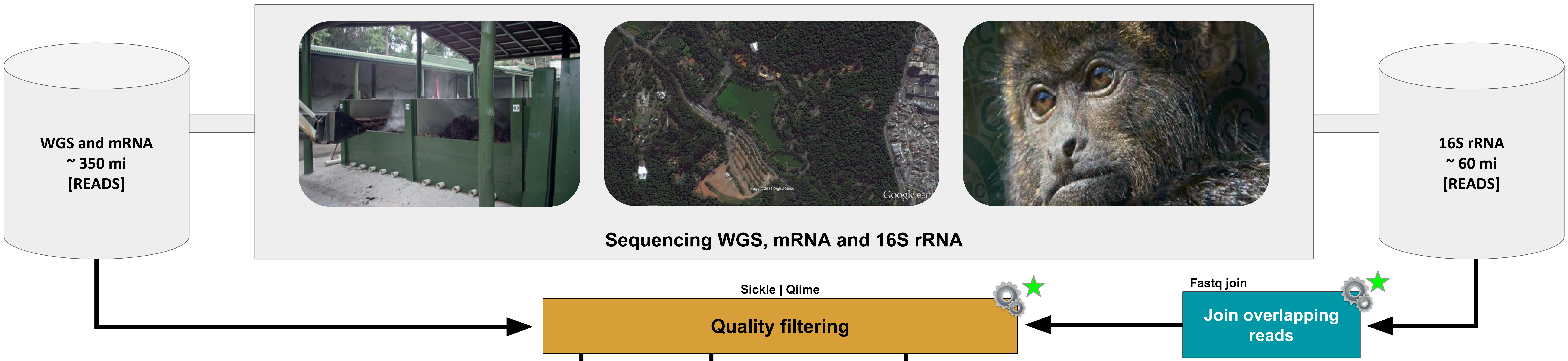
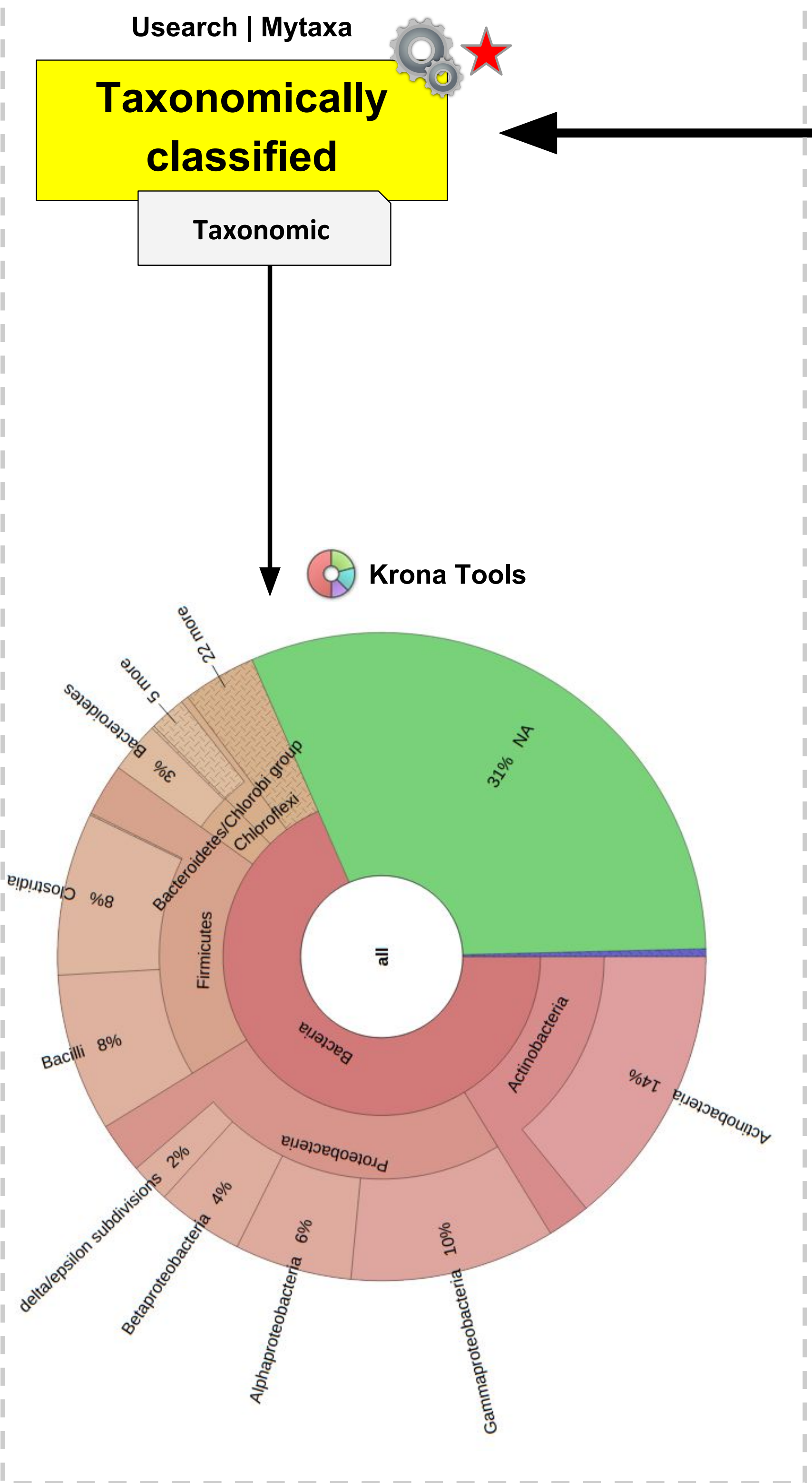
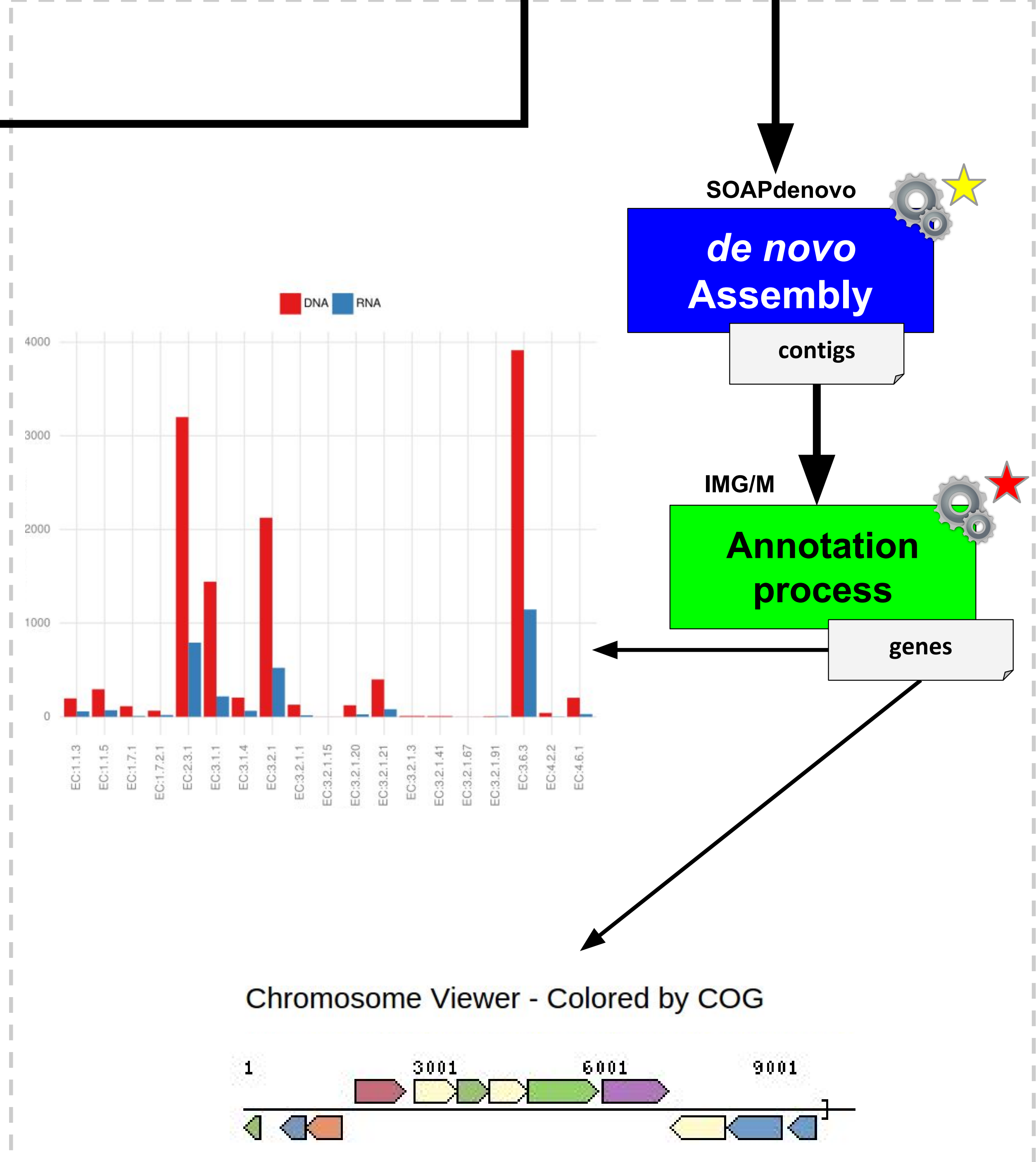
Introduction

The Metazoo project aims to study the **microbial communities** in three different environments of São Paulo's Zoo Park: a **composting process**, the **Sao Francisco Lake**, and **feces of resident howler monkeys**, by using a metagenomic approach. Different computational methodologies are being used to analyze the sequence datasets that were generated from sequencing total DNA (WGS - whole genome shotgun), amplicon 16S rRNA and mRNA (RNA-seq) with Roche-454 and/or Illumina. Besides analyzing the Metazoo project's datasets using computational methods, we are actively creating new computational tools, such as a metagenome browser and a conceptual framework and respective database to ease the integration of different types of data and metadata generated by metagenomic projects.

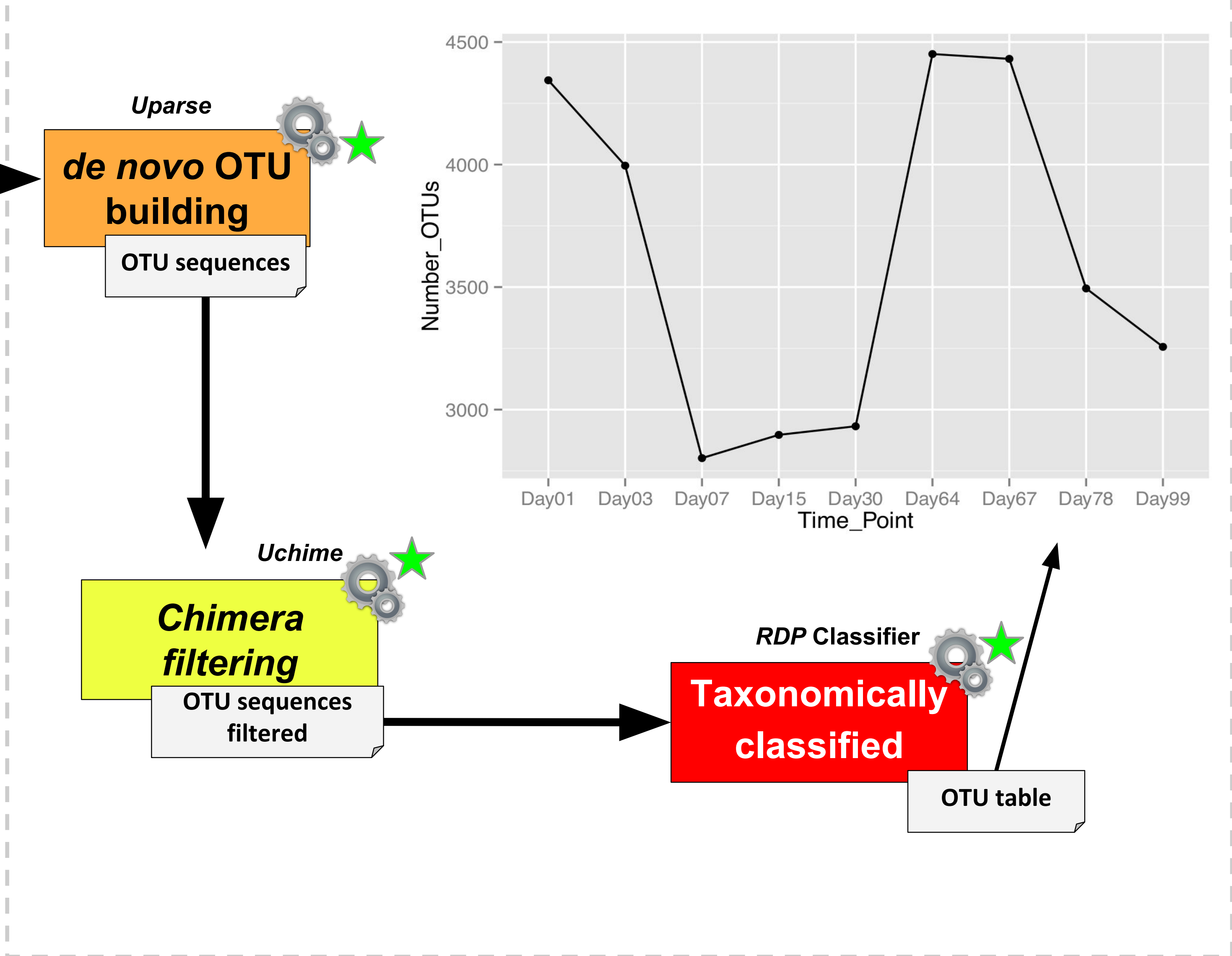




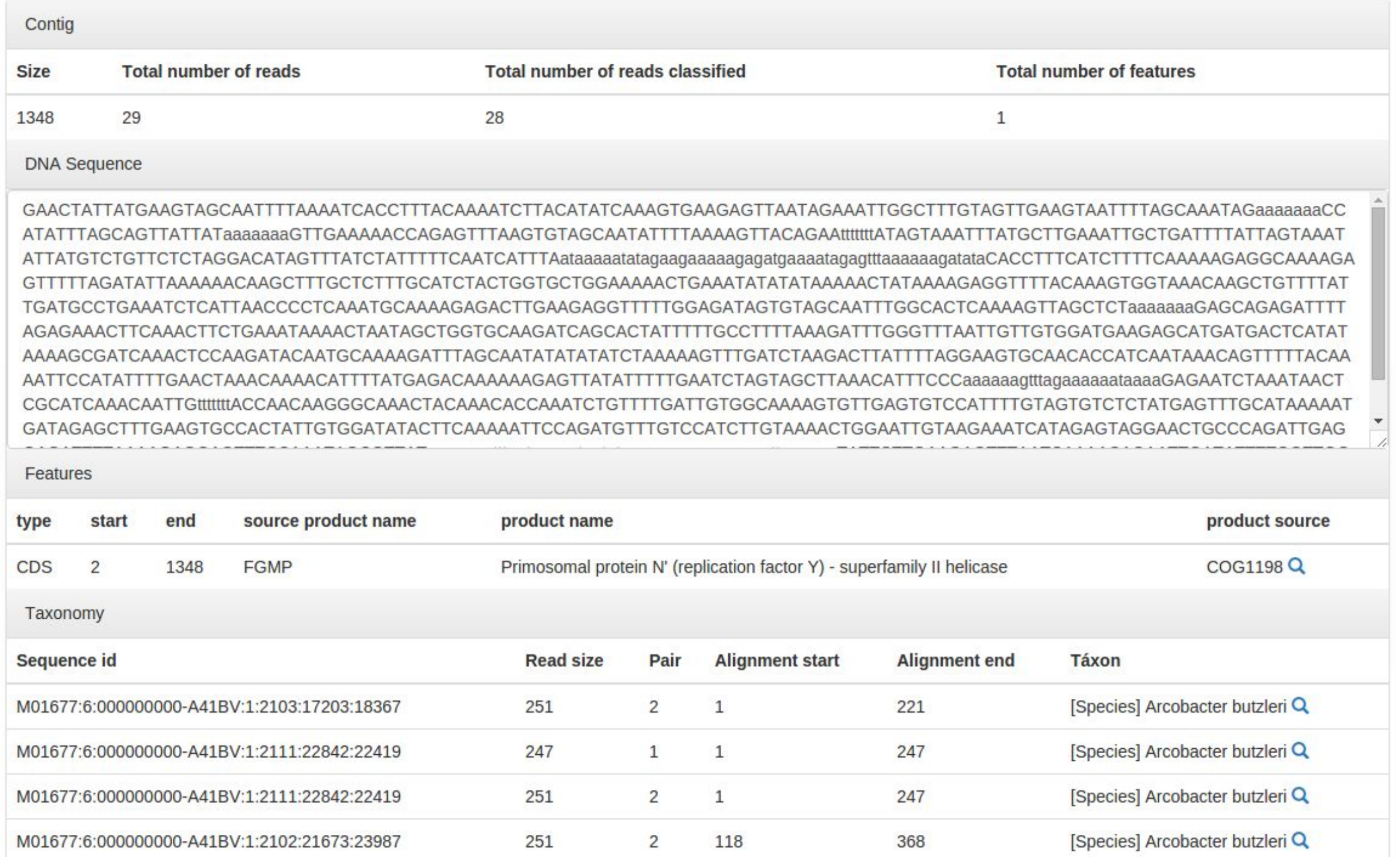


Chromosome Viewer - Colored by COG

★ ★ ★
low | medium | high
CPU cost



CARAVELA: a new approach to metagenomic browsing



Contig

Size	Total number of reads	Total number of reads classified	Total number of features
1348	29	28	1

DNA Sequence

```
GAACTATTATGAAGTAGCAATTTTAAAATCACCTTTACAAAATCTTACATATCAAAGTGAAGAGTTAATAGAAATTGGCTTTGTAGTTGAAGTAATTTTAGCAAATAGaaaaaaaCC
ATATTTAGCAGTTATTATaaaaaaaGTTGAAAAACCAGAGTTTAAGTGTAGCAATATTTTAAAAGTTACAGAAttttttATAGTAAATTTATGCTTGAAATTGCTGATTTTATTAGTAAAT
ATTATGTCTGTTCTCTAGGACATAGTTTATCTATTTTTCAATCATTTAataaaaatatagaagaaaaagagatgaaaatagagtttaaaaaagatataCACCTTTCATCTTTTCAAAAAGAGGCAAAAGA
GTTTTTAGATATTAAAAAACAAGCTTTGCTCTTTGCATCTACTGGTGCTGGAAAAACTGAAATATATATAAAAACTATAAAAGAGGTTTTACAAAGTGGTAAACAAGCTGTTTTAT
TGATGCCTGAAATCTCATTAACCCCTCAAATGCAAAAGAGACTTGAAGAGGTTTTTGGAGATAGTGTAGCAATTTGGCACTCAAAAGTTAGCTCTaaaaaaaGAGCAGAGATTTT
AGAGAAACTTCAAACTTCTGAAATAAAACTAATAGCTGGTGCAAGATCAGCACTATTTTTGCCTTTTAAAGATTTGGGTTTAATTGTTGTGGATGAAGAGCATGATGACTCATAT
AAAAGCGATCAAACTCCAAGATACAATGCAAAAGATTTAGCAATATATATATCTAAAAAGTTTGATCTAAGACTTATTTTAGGAAGTGCAACACCATCAATAAACAGTTTTTACAA
AATTCCATATTTTGAACTAAACAAAACATTTTATGAGACAAAAAAGAGTTATATTTTTGAATCTAGTAGCTTAAACATTTCCCaaaaaagtttagaaaaaataaaaGAGAATCTAAATAACT
CGCATCAAACAATTGttttttACCAACAAGGGCAAACTACAAACACCAAATCTGTTTTGATTGTGGCAAAAGTGTTGAGTGTCCATTTTGTAGTGTCTCTATGAGTTTGCATAAAAAT
GATAGAGCTTTGAAGTGCCACTATTGTGGATATACTTCAAAAATTCCAGATGTTTGTCCATCTTGTAAAACTGGAATTGTAAGAAATCATAGAGTAGGAACTGCCCAGATTGAG
```

Features

type	start	end	source product name	product name	product source
CDS	2	1348	FGMP	Primosomal protein N' (replication factor Y) - superfamily II helicase	COG1198

Taxonomy

Sequence id	Read size	Pair	Alignment start	Alignment end	Táxon
M01677:6:000000000-A41BV:1:2103:17203:18367	251	2	1	221	[Species] Arcobacter butzleri
M01677:6:000000000-A41BV:1:2111:22842:22419	247	1	1	247	[Species] Arcobacter butzleri
M01677:6:000000000-A41BV:1:2111:22842:22419	251	2	1	247	[Species] Arcobacter butzleri
M01677:6:000000000-A41BV:1:2102:21673:23987	251	2	118	368	[Species] Arcobacter butzleri

The CARAVELA tool is able to display a list of contigs and for each **contig**, it displays **annotated genes**, reads participating in its composition and **taxa associated with each read** (when such association exists).

Such a capability should enable manual/automated curation of assembly (identification of mis-assemblies) as well as taxonomic assignments (detection of possible mis-assignments)

References

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Support:

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