Meta-pipe analysis pipeline

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Tromsø, 2018

Outline

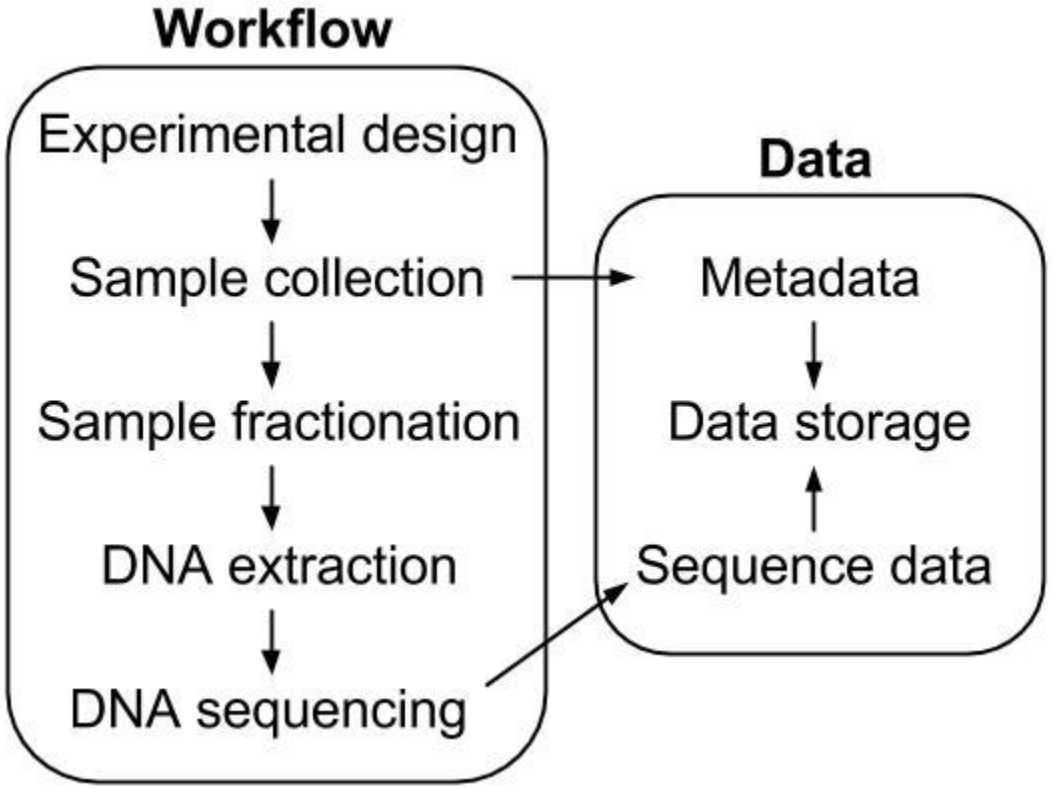
- Motivation / Why Meta-pipe
- Steps prior to bioinformatic analysis
- Overview of Meta-pipe
- Interfaces

Motivation behind META-pipe

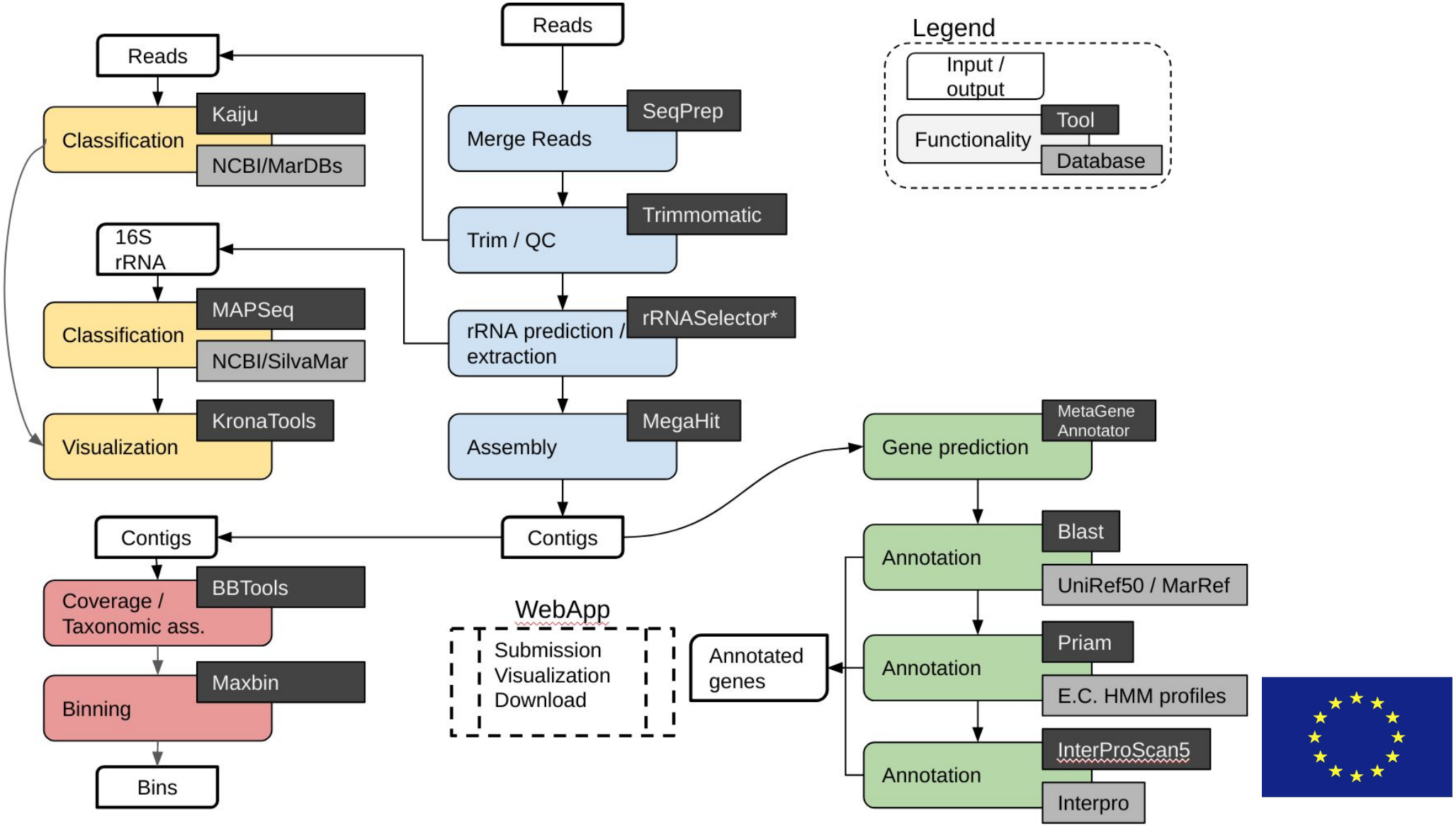
- Lack of metagenomics resources for the marine domain
- "Lack" of metagenomics resources for analysis of full-length genes
- User simplicity
- Resource availability

Mineta, Katsuhiko, Gojobori, Takashi 2016 Gene, ISSN: 1879-0038, Vol: 576, Issue: 2 Pt 1, Page: 724-8

Steps prior to bioinformatic analysis



Biological Overview of Meta-pipe



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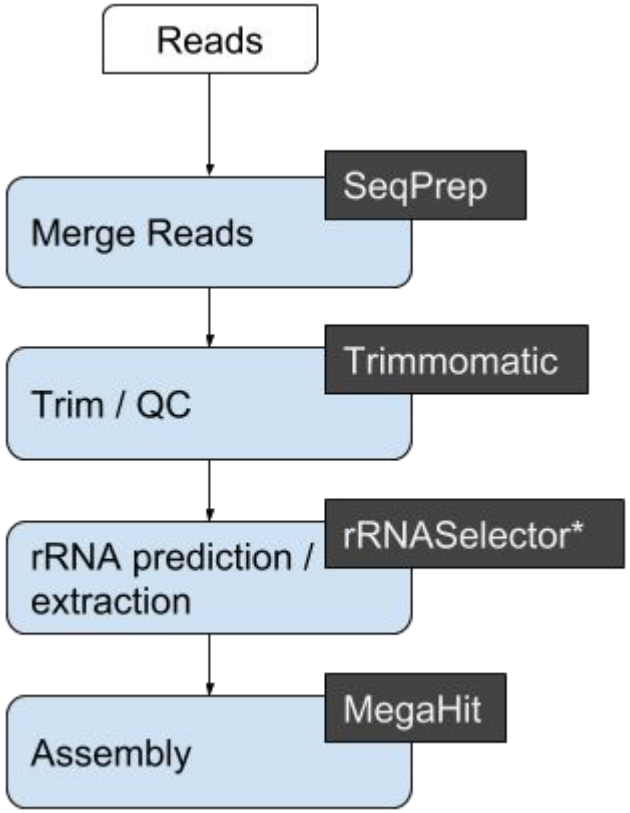
Biological Overview

Preprocessing

- SeqPrep – Merging of Illumina reads
- Trimmomatic – QC of reads
- (DeconSeq) – Filter unwanted sequences with reference
- rRNASelector – Removal/Extraction of rRNA sequences
- MEGAHIT – Assembly

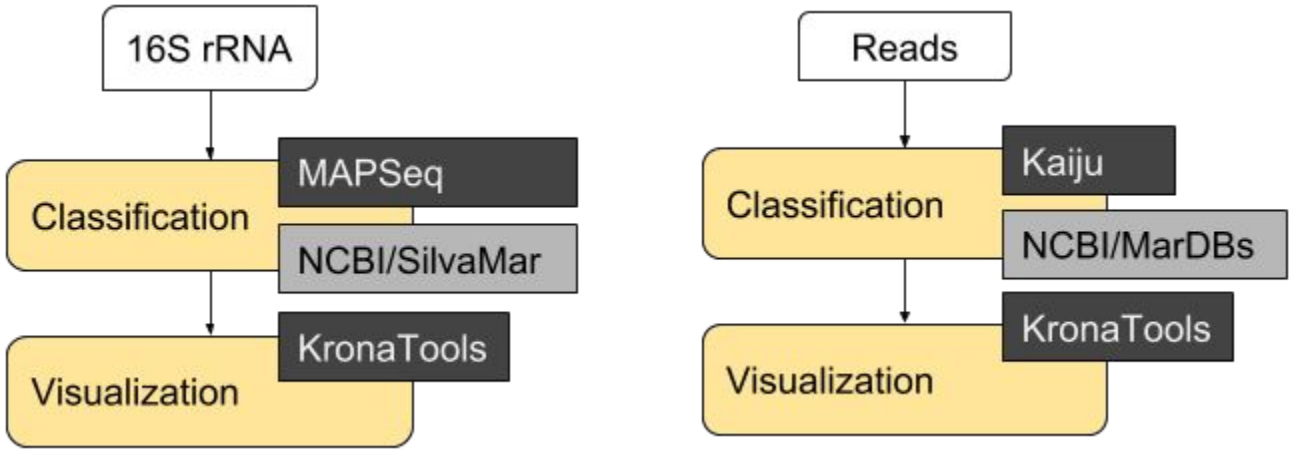


Biological Overview

Taxonomic Classification

- Kaiju - Classification of reads using protein reference databases
- Mapseq - High throughput rRNA sequence classification

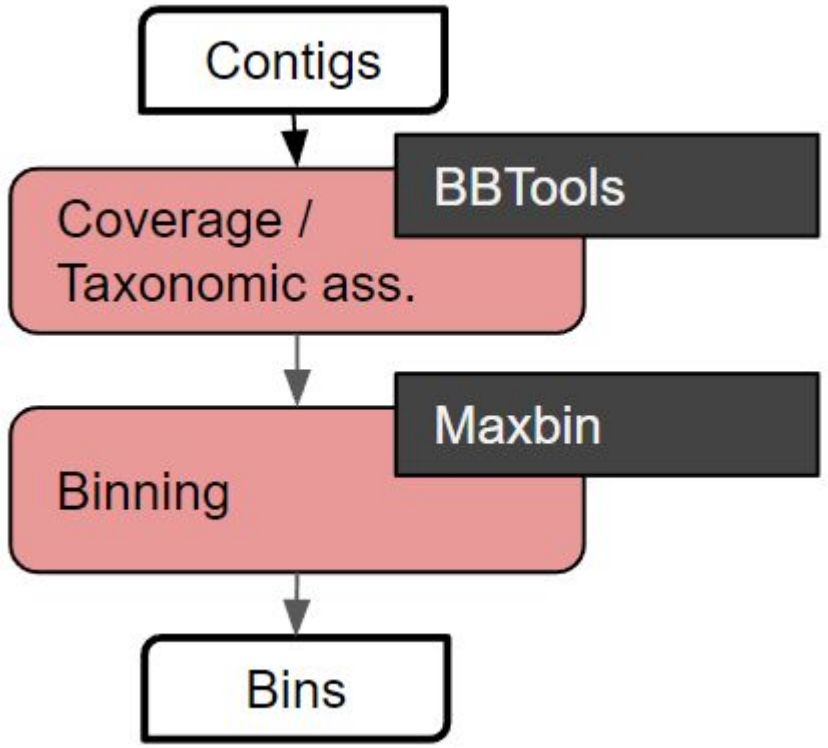
- KronaTools – Visualization of output



Biological Overview

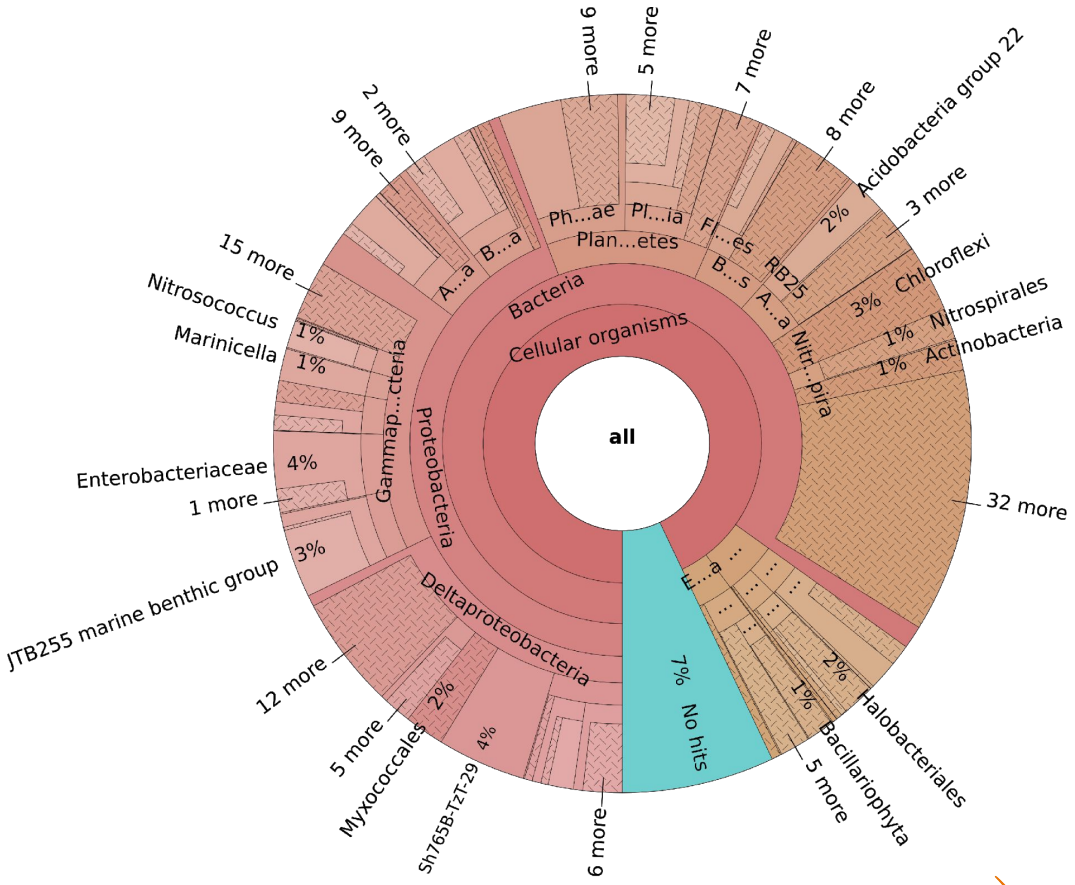
Binning

- BBMap - Coverage calculation
- MaxBin - Binning of contigs
- BBSketch - Taxonomic assignment of bins



Biological Overview

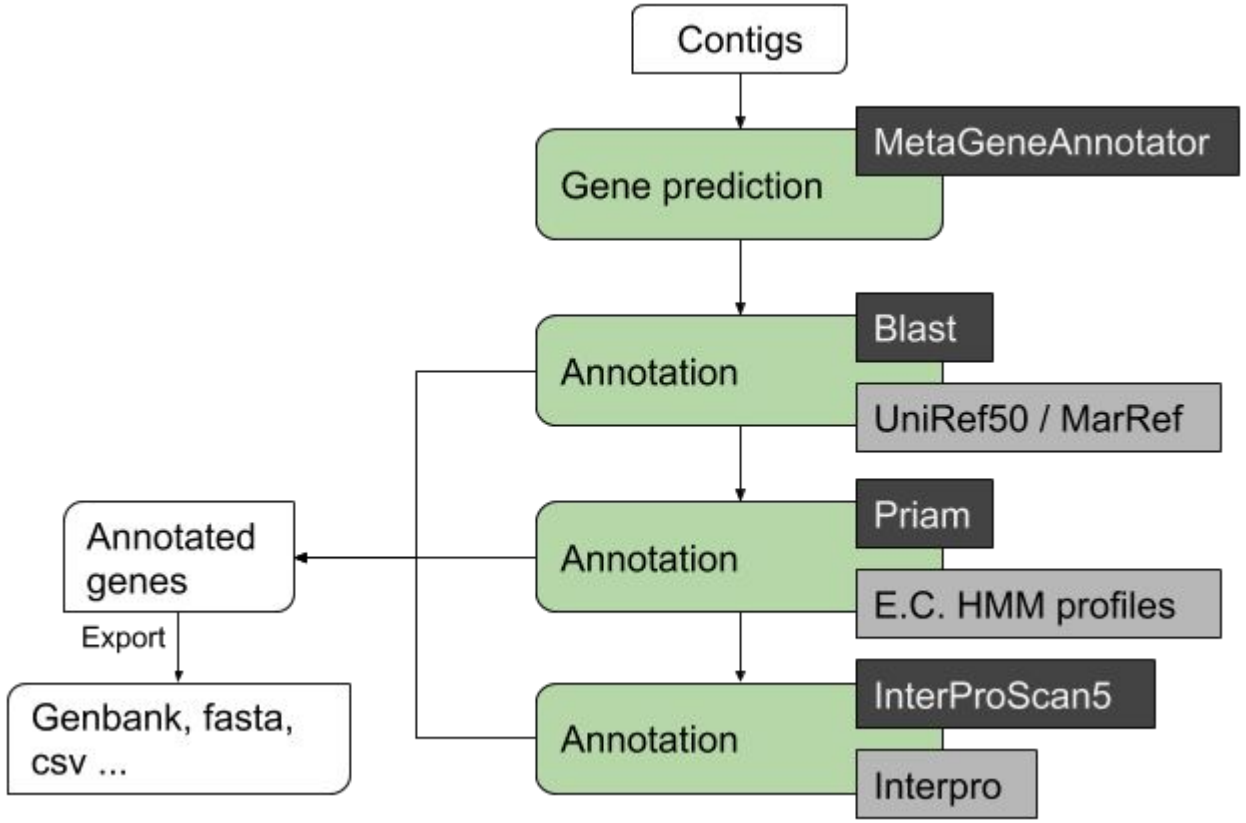
Taxonomic Classification



Biological Overview

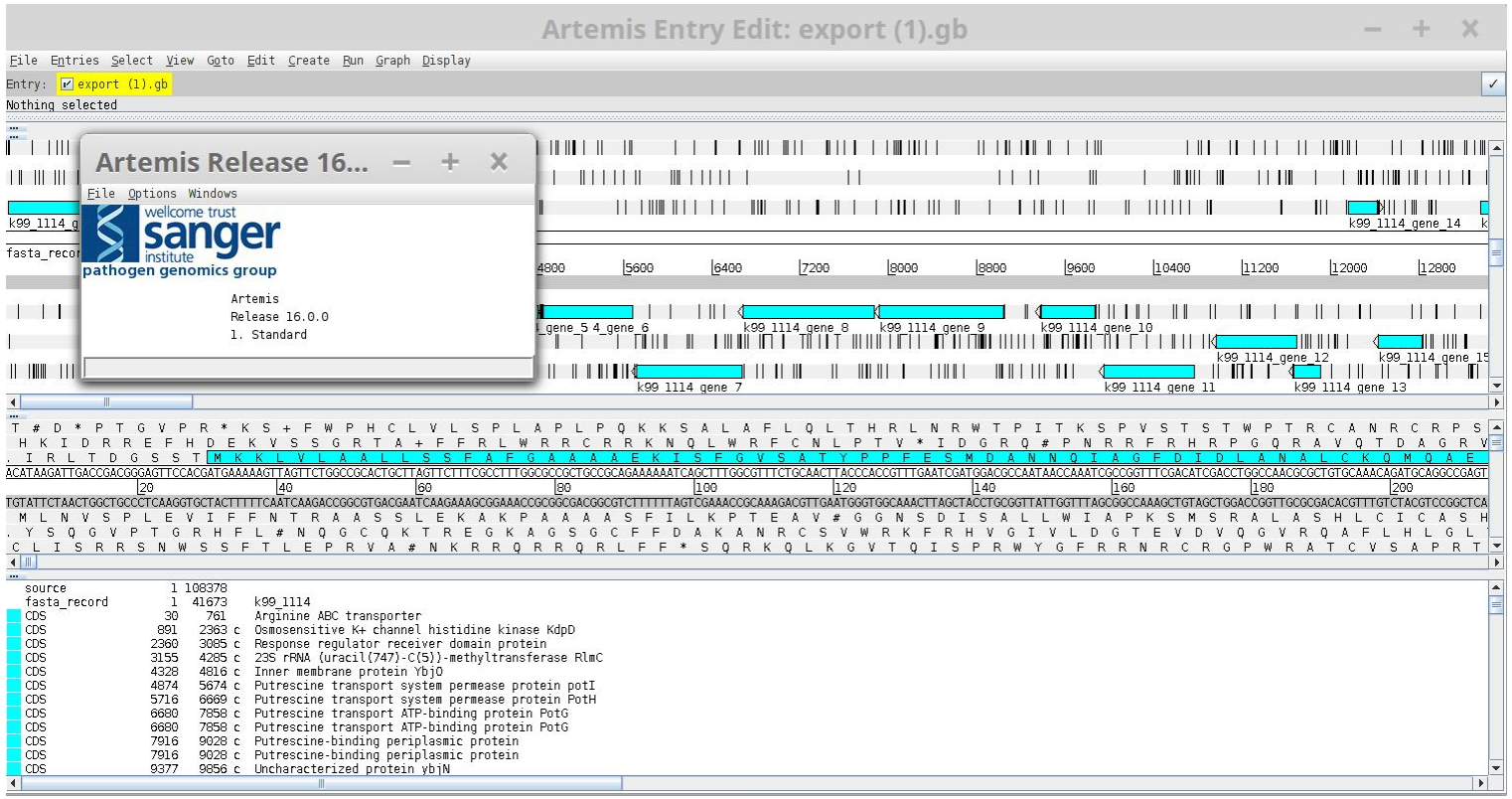
Functional Analysis

- PRIAM – Annotation of EC-numbers with RPS-blast
- Uniref50 – Clustered UniProt using Blast
- InterPro – Collection of 14 databases queried with InterProScan



Biological Overview

Functional Analysis



Inclusion and processing of MarDBs

- MarRef integrated with Meta-pipe
- MarDB scheduled for integration with Meta-pipe
- Meta-pipe currently processing samples for MarCat

MARINE
REFERENCE
DATABASES

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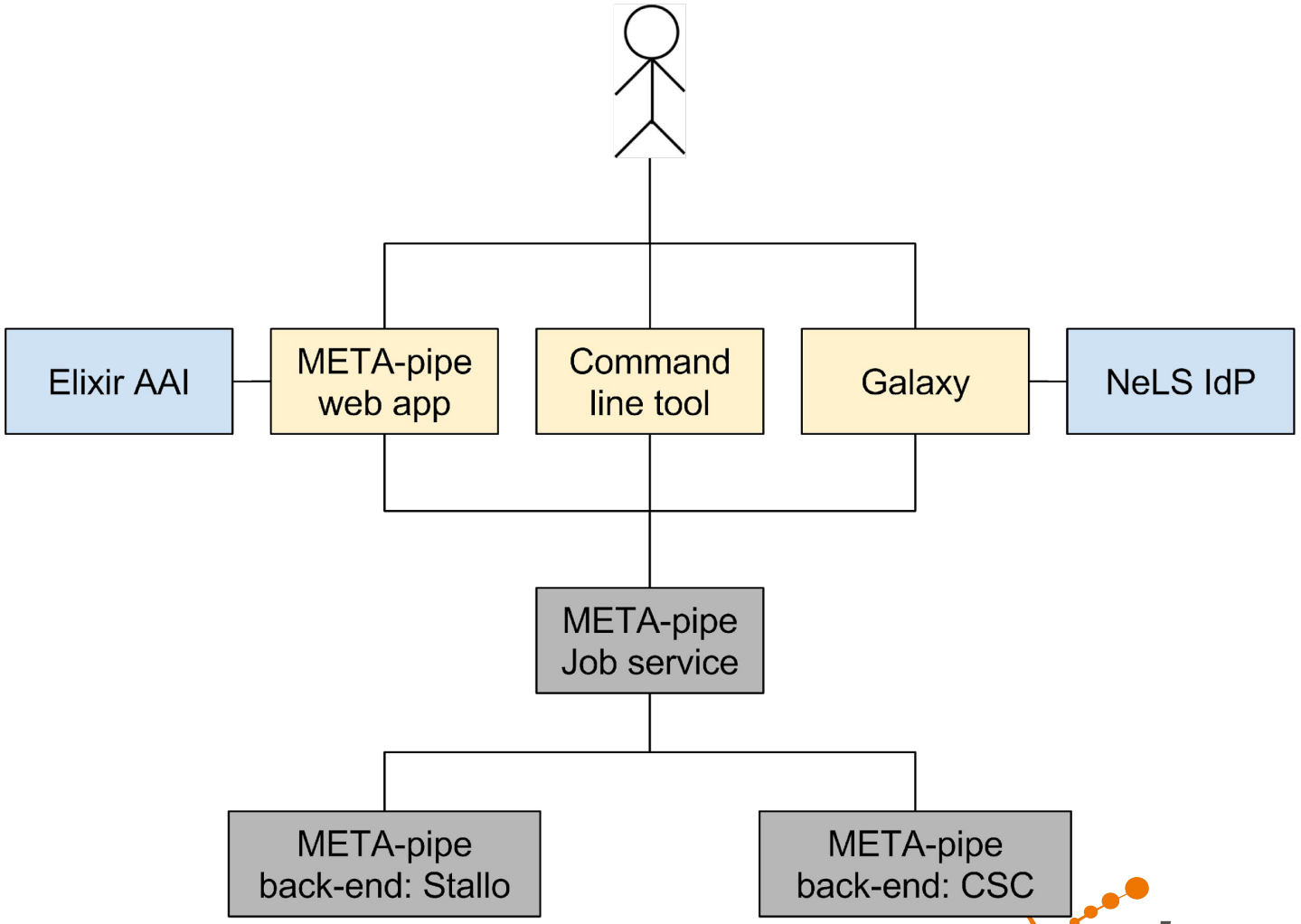
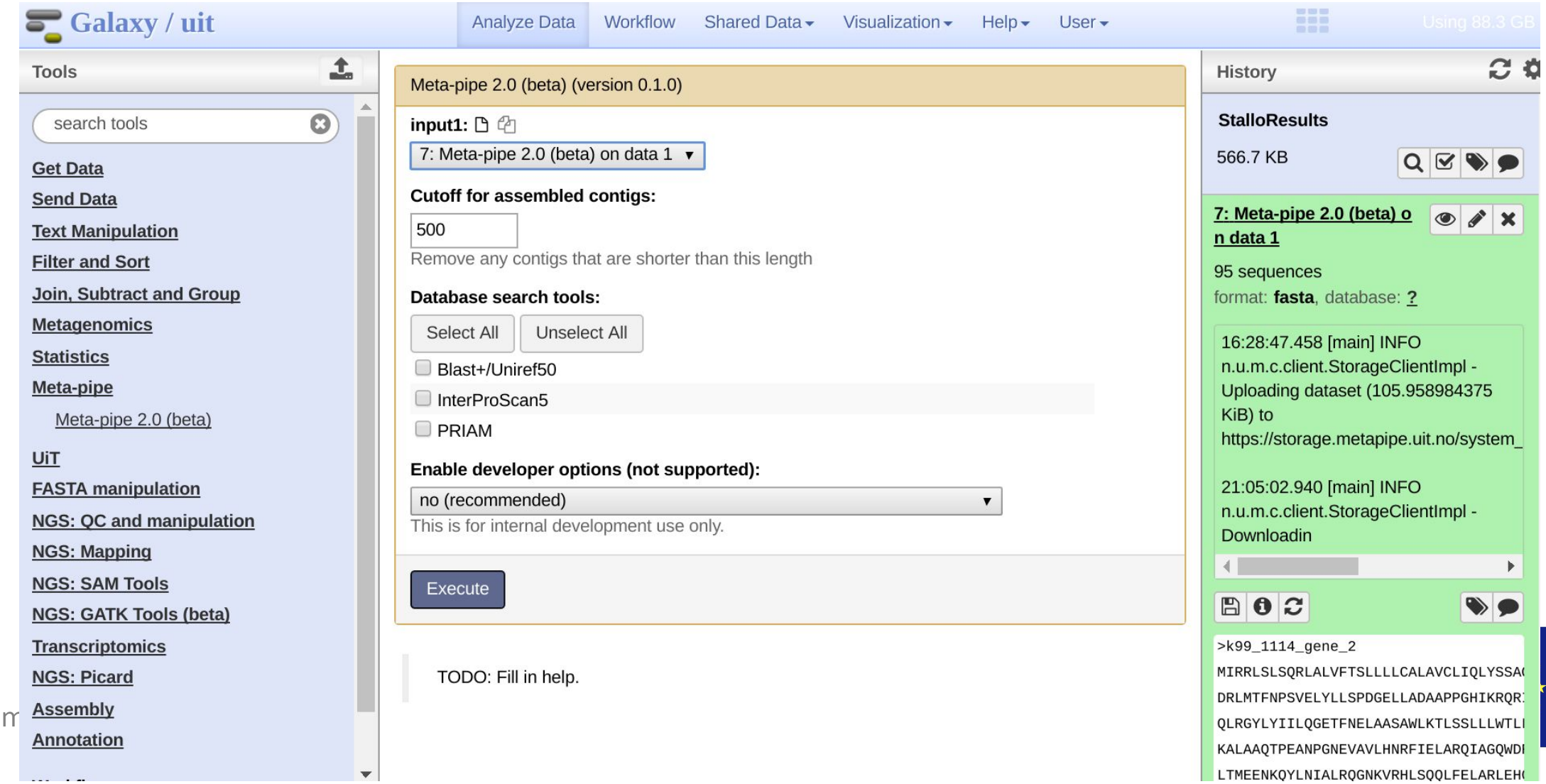
User Access


Elixir AAI
META-pipe web app
Command line tool
Galaxy
NeLS IdP
META-pipe Job service
META-pipe back-end: Stallo
META-pipe back-end: CSC

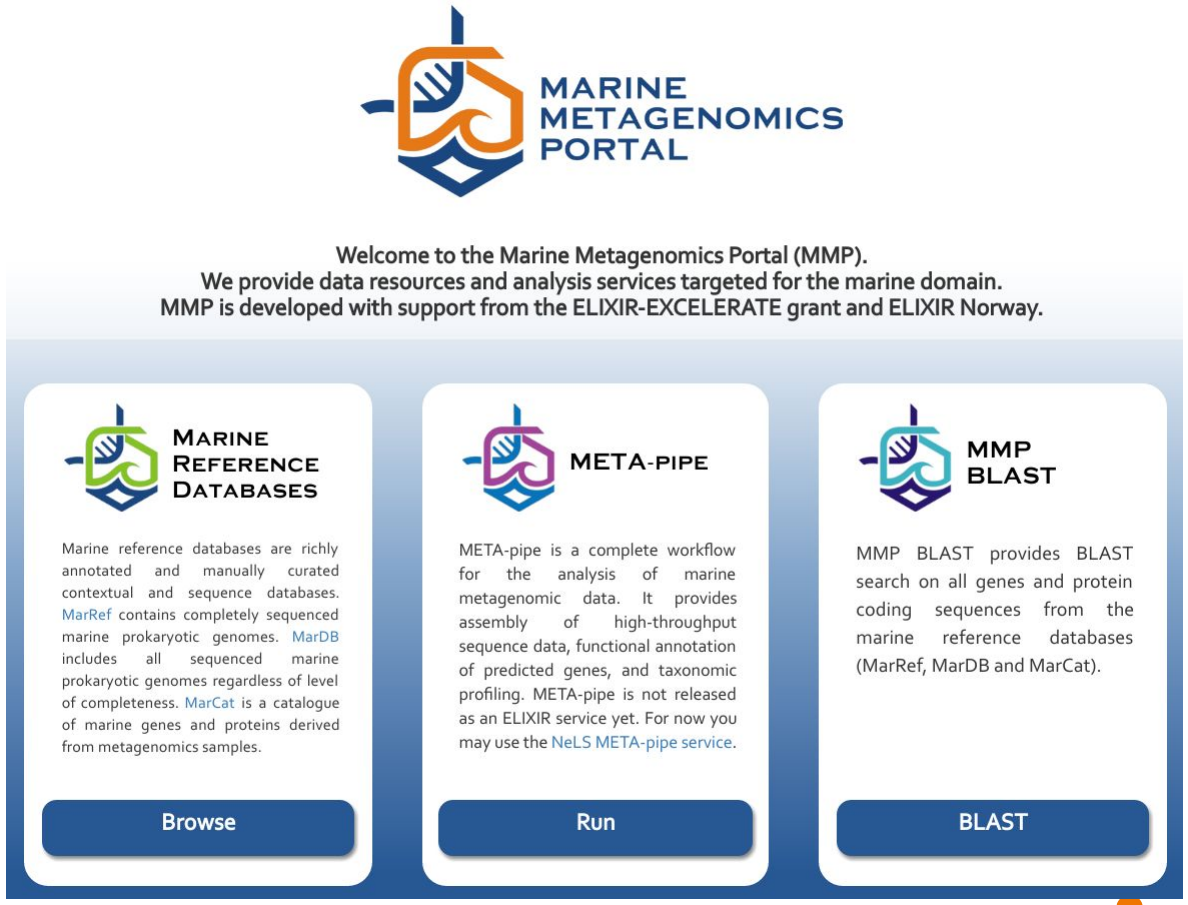
User Access

Galaxy with NeLS-idp



User Access

Webapp with ELIXIR-AAI



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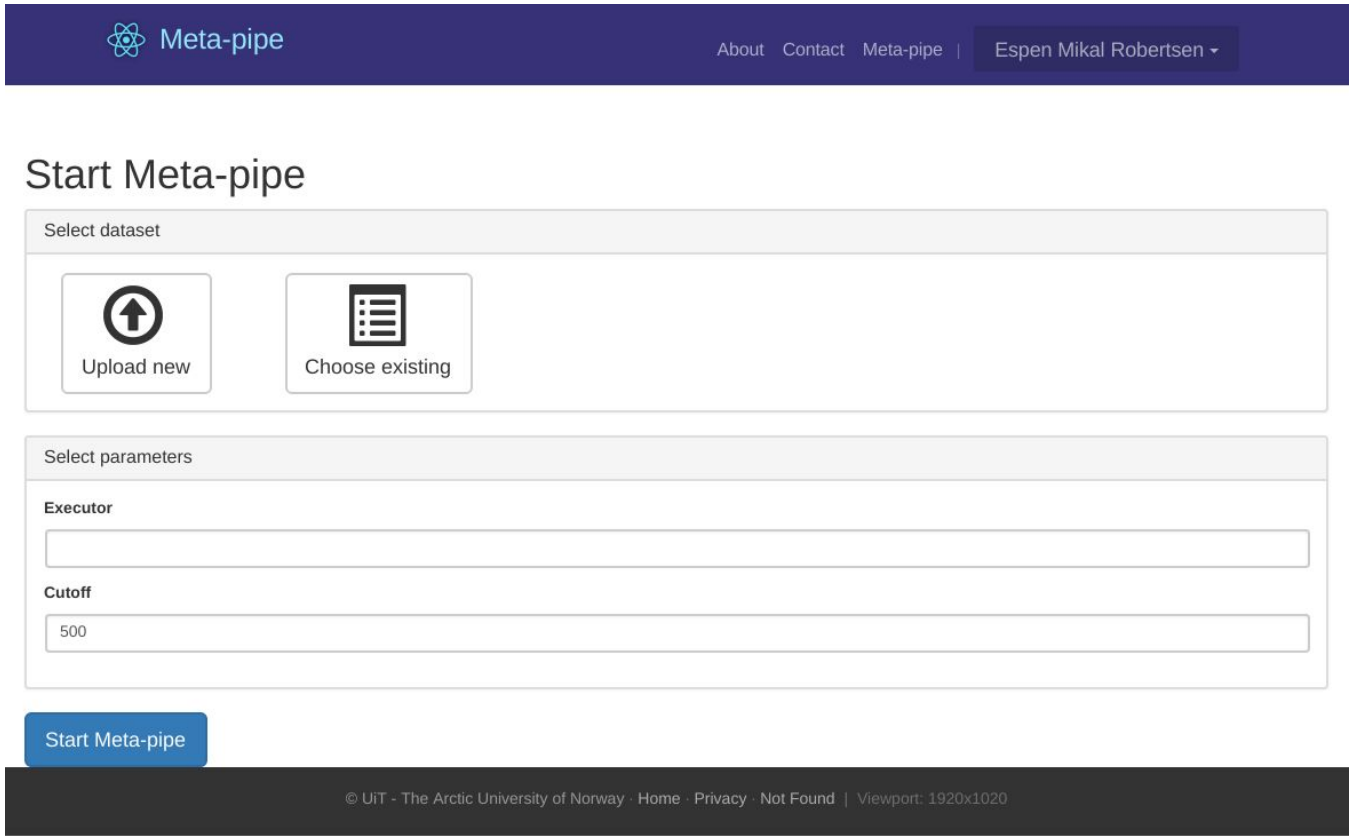
Webapp with ELIXIR-AAI



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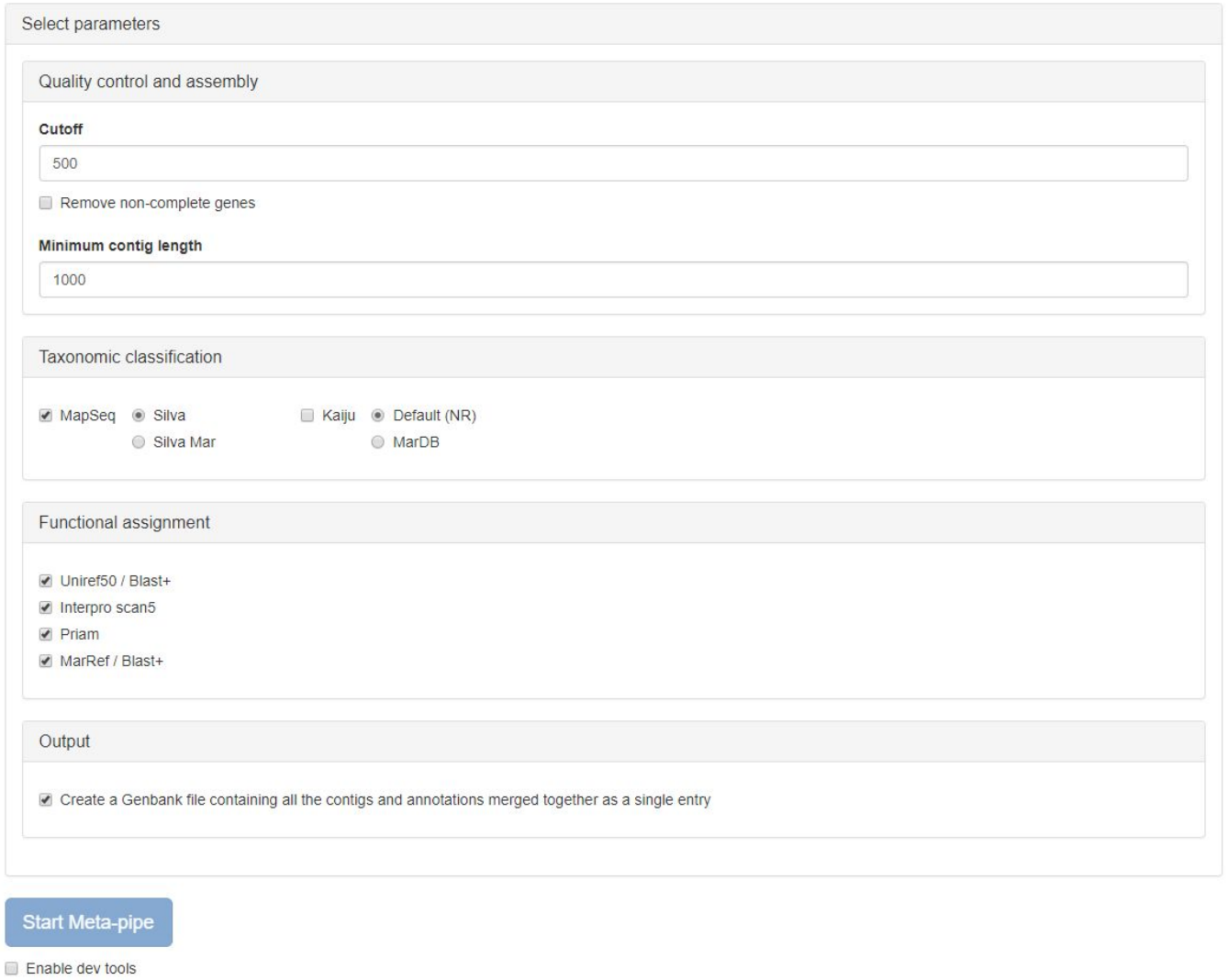
Webapp with ELIXIR-AAI



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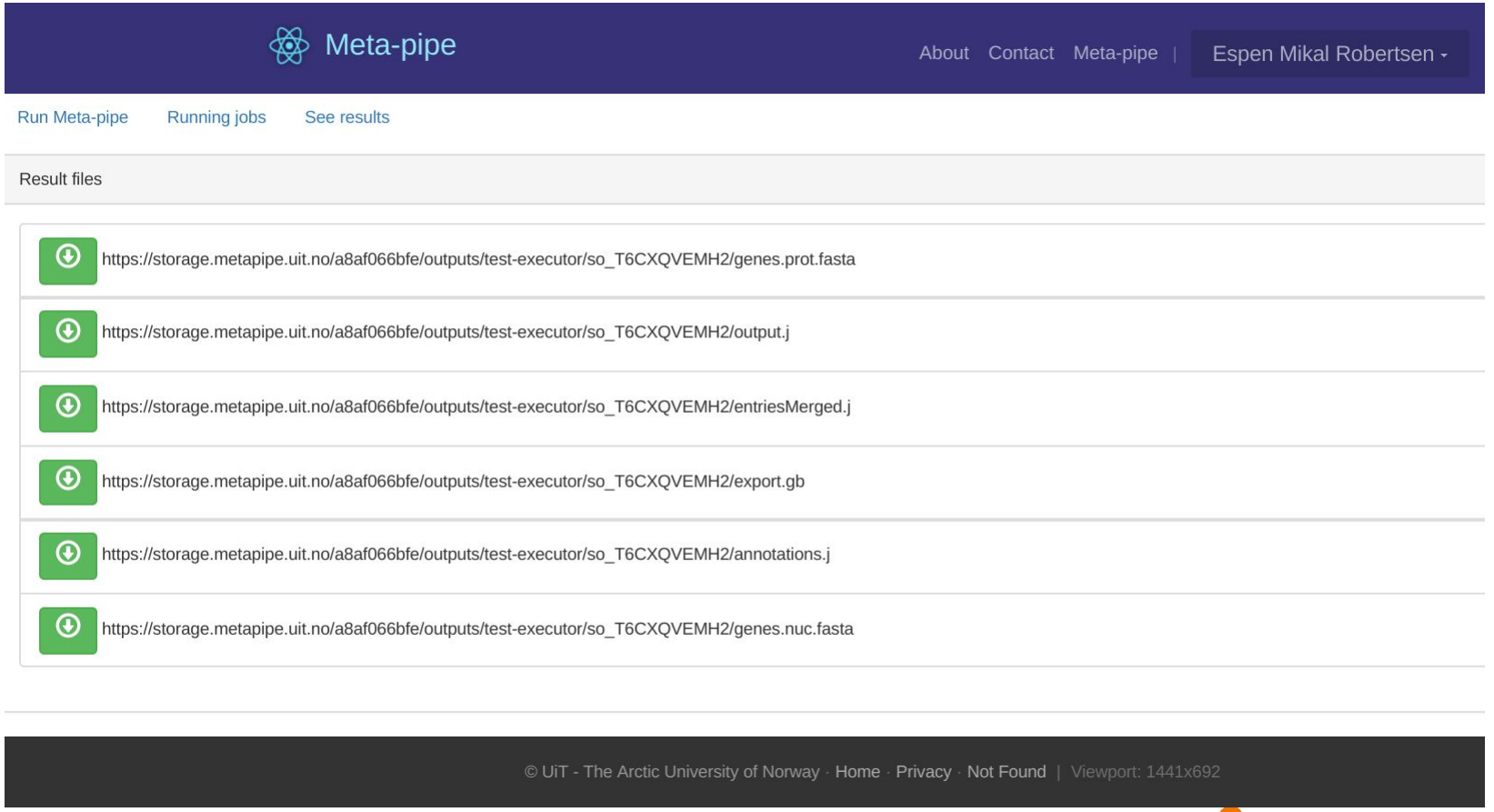
Output


Meta-pipe
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Espen Mikal Robertsen
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Running jobs
See results
Result files
https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/genes.prot.fasta
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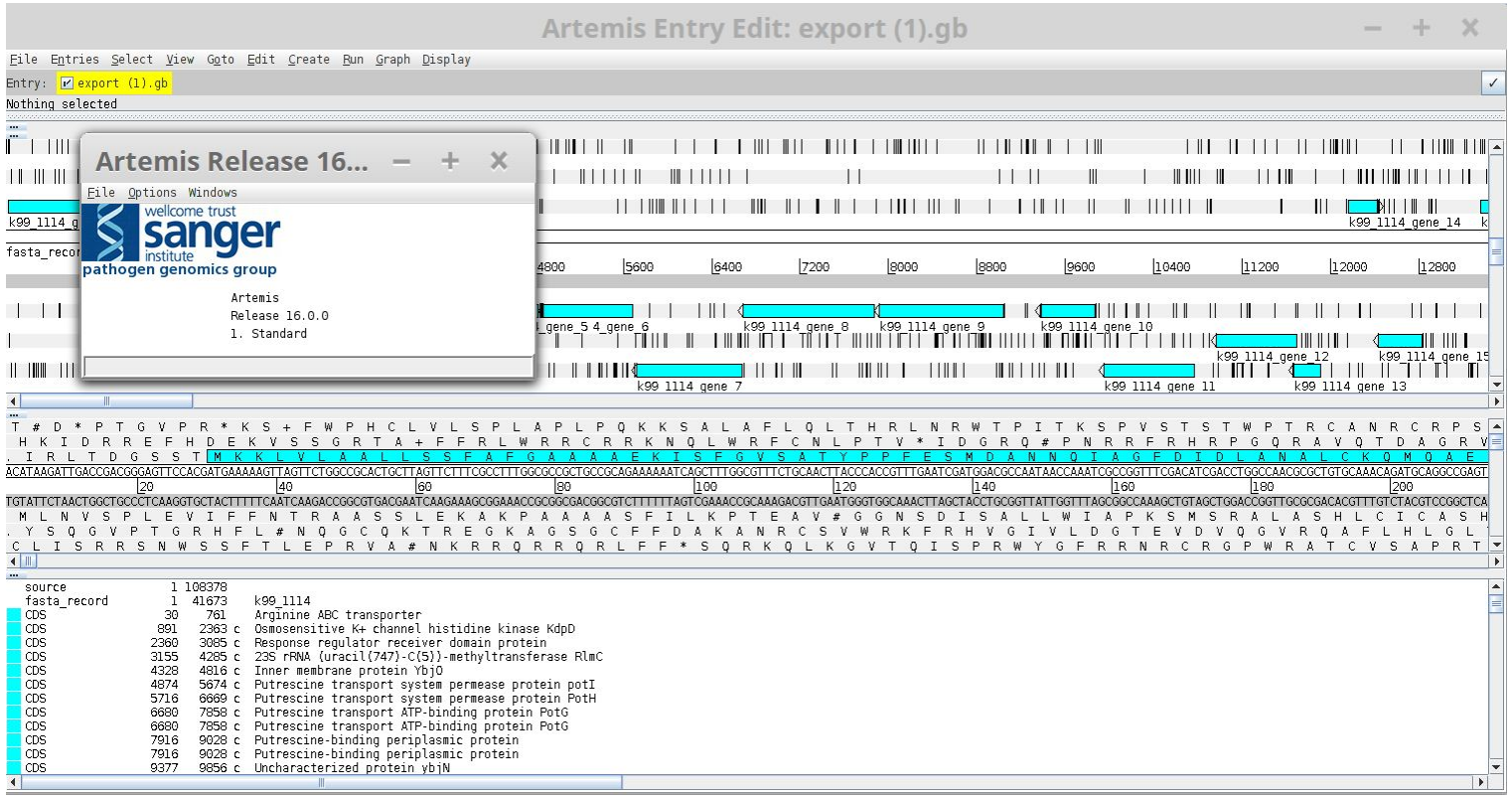
Output

Visualization of contigs in detail



Output

Visualization prototype

Overview | Sequence Distribution | Taxonomic Classification | Functional Assignment | Geographic Context To MarCat | Downloads

Histogram | Kernel density estimation

View histogram for:

Reads | Contigs | Genes, complete | Genes, truncated

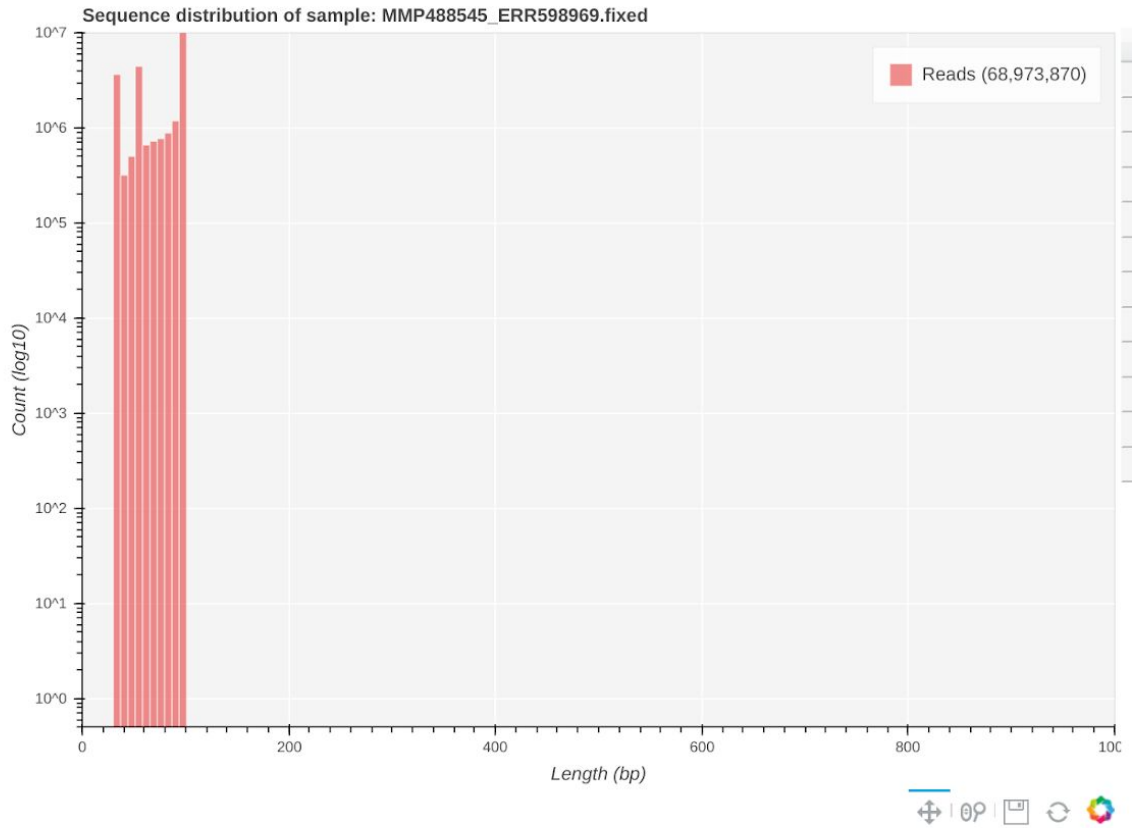
Y axis type

log

X scale: **0**

View KD-estimation for:

Reads | Contigs | Genes, complete | Genes, truncated



#	Metric	Reads	Contigs	Genes
0	Count (#)	68,973,870	162,298	62,591
1	Length (bp)	6,374,838,210	150,772,424	36,358,786
2	Over 100 bp	52,685,311	162,298	62,591
3	Over 500 bp	0	161,652	27,753
4	Over 1000 bp	0	39,001	8,392
5	Over 5000 bp	0	843	30
6	Over 10000 bp	0	177	0
7	Largest (bp)	101	166,928	8,936
8	Smallest (bp)	30	500	119
9	Average length (bp)	92	929	581
10	Median (bp)	101	708	452
11	N50	101	923	764

Thank you!

The Center for Bioinformatics team (SfB)

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Tromsø, May, 2018

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