



Hands on: Functional Assignment

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Short overview

3.Functional_assignment.html

- Logging in to the Meta-pipe web GUI
- Submitting metagenomic samples (reduced size)
- Over-night processing
- Functional analysis in Artemis



Hands on: Login and submission



Welcome to the Marine Metagenomics Portal (MMP).
We provide data resources and analysis services targeted for the marine domain.
MMP is developed with support from the ELIXIR-EXCELERATE grant and ELIXIR Norway.



MARINE REFERENCE DATABASES

Marine reference databases are richly annotated and manually curated contextual and sequence databases. [MarRef](#) contains completely sequenced marine prokaryotic genomes. [MarDB](#) includes all sequenced marine prokaryotic genomes regardless of level of completeness. [MarCat](#) is a catalogue of marine genes and proteins derived from metagenomics samples.

Browse



META-PIPE

META-pipe is a complete workflow for the analysis of marine metagenomic data. It provides assembly of high-throughput sequence data, functional annotation of predicted genes, and taxonomic profiling. META-pipe is not released as an ELIXIR service yet. For now you may use the [NeLS META-pipe service](#).

Run

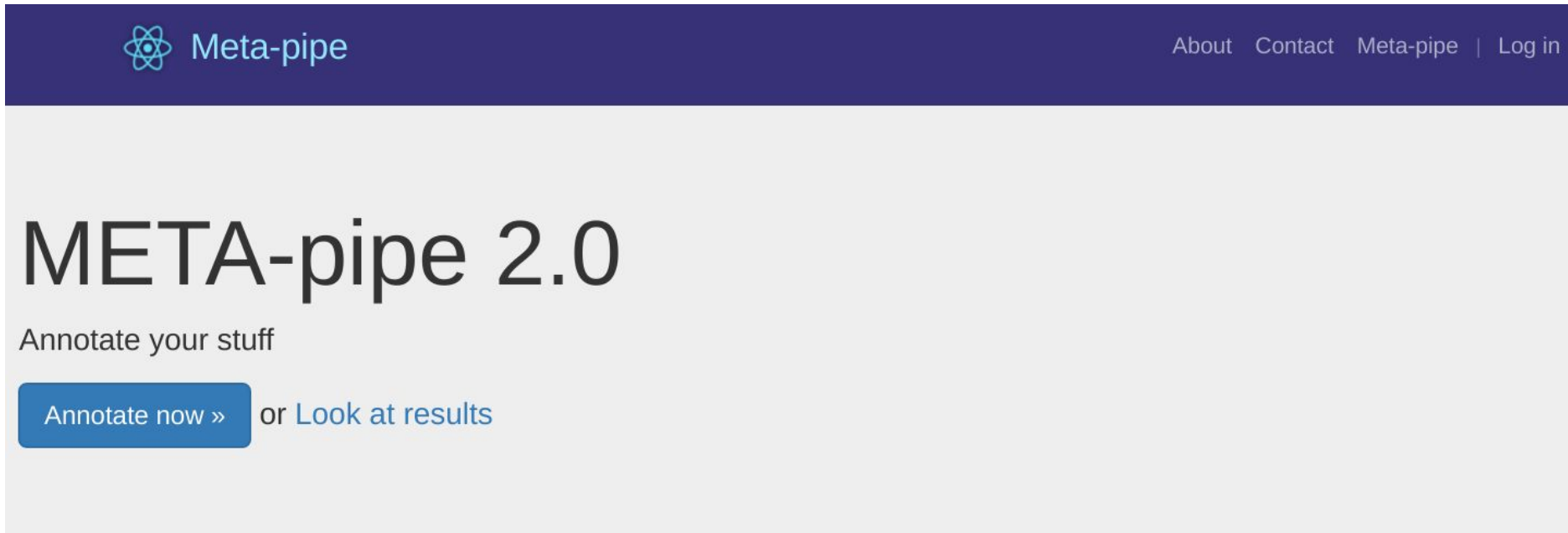


MMP BLAST

MMP BLAST provides BLAST search on all genes and protein coding sequences from the marine reference databases ([MarRef](#), [MarDB](#) and [MarCat](#)).

BLAST

Hands on: Login and submission



The screenshot shows the top portion of a web page. At the top is a dark blue navigation bar containing the Meta-pipe logo (a stylized atom symbol) and the text "Meta-pipe" on the left, and a list of links: "About", "Contact", "Meta-pipe", and "Log in" on the right. Below the navigation bar is a light gray main content area. The heading "META-pipe 2.0" is prominently displayed in a large, dark font. Underneath the heading is the text "Annotate your stuff". At the bottom of this section, there is a blue button with the text "Annotate now »" followed by the text "or Look at results" in a smaller, blue font.

Hands on: Login and submission



Log in using ...



or

your institutional account

A light blue rectangular input field with rounded corners and a thin border. Inside the field, on the left, is a small magnifying glass icon. To the right of the icon, the text "Type the name of your institution" is written in a light gray, sans-serif font.

Hands on: Login and submission

The screenshot shows the META-pipe 2.0 website. At the top, there is a dark blue navigation bar with the 'Meta-pipe' logo on the left and links for 'About', 'Contact', 'Meta-pipe', and a user profile 'Espen Mikal Robertsen' on the right. Below the navigation bar, the main content area has a light gray background. It features the title 'META-pipe 2.0' in a large font, followed by the subtitle 'Annotate your stuff'. There are two buttons: a blue 'Annotate now »' button and a blue 'Look at results' link. Below this, there are three columns, each with a heading, a 'Hello world' message, and a 'View details »' button. The columns are labeled 'Bigger', 'Faster', and 'Stronger'. At the bottom, there is a dark gray footer with copyright information: '© UIT - The Arctic University of Norway · Home · Privacy · Not Found | Viewport: 1920x922'.

Meta-pipe

About Contact Meta-pipe | Espen Mikal Robertsen

META-pipe 2.0

Annotate your stuff

Annotate now » or Look at results


Bigger
Hello world
View details »

Faster
Hello world
View details »

Stronger
Hello world
View details »


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Hands on: Login and submission

 Meta-pipe [About](#) [Contact](#) [Meta-pipe](#) | Espen Mikal Robertsen ▾

Start Meta-pipe

Select dataset


Upload new


Choose existing

Select parameters

Executor

Cutoff

[Start Meta-pipe](#)

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Hands on: Login and submission

Start Meta-pipe

Dataset type

Reads

Fasta

Select Fasta dataset

Fasta:

[Choose a different dataset](#)

subset_for_course.fasta



No description for this file

[dataset url](#)

Hands on: Login and submission

Select parameters

Quality control and assembly

Cutoff

500



Remove non-complete genes

Minimum contig length

1000



Taxonomic classification

MapSeq

Silva

Silva Mar

Kaiju

Default (NR)

MarDB

Hands on: Login and submission

Functional assignment

-  Uniref50 / Blast+
-  Interpro scan5
-  Priam
-  MarRef / Blast+

Output

-  Create a Genbank file containing all the contigs and annotations merged together as a single entry

Start Meta-pipe

-  Enable dev tools

Dev-Tools

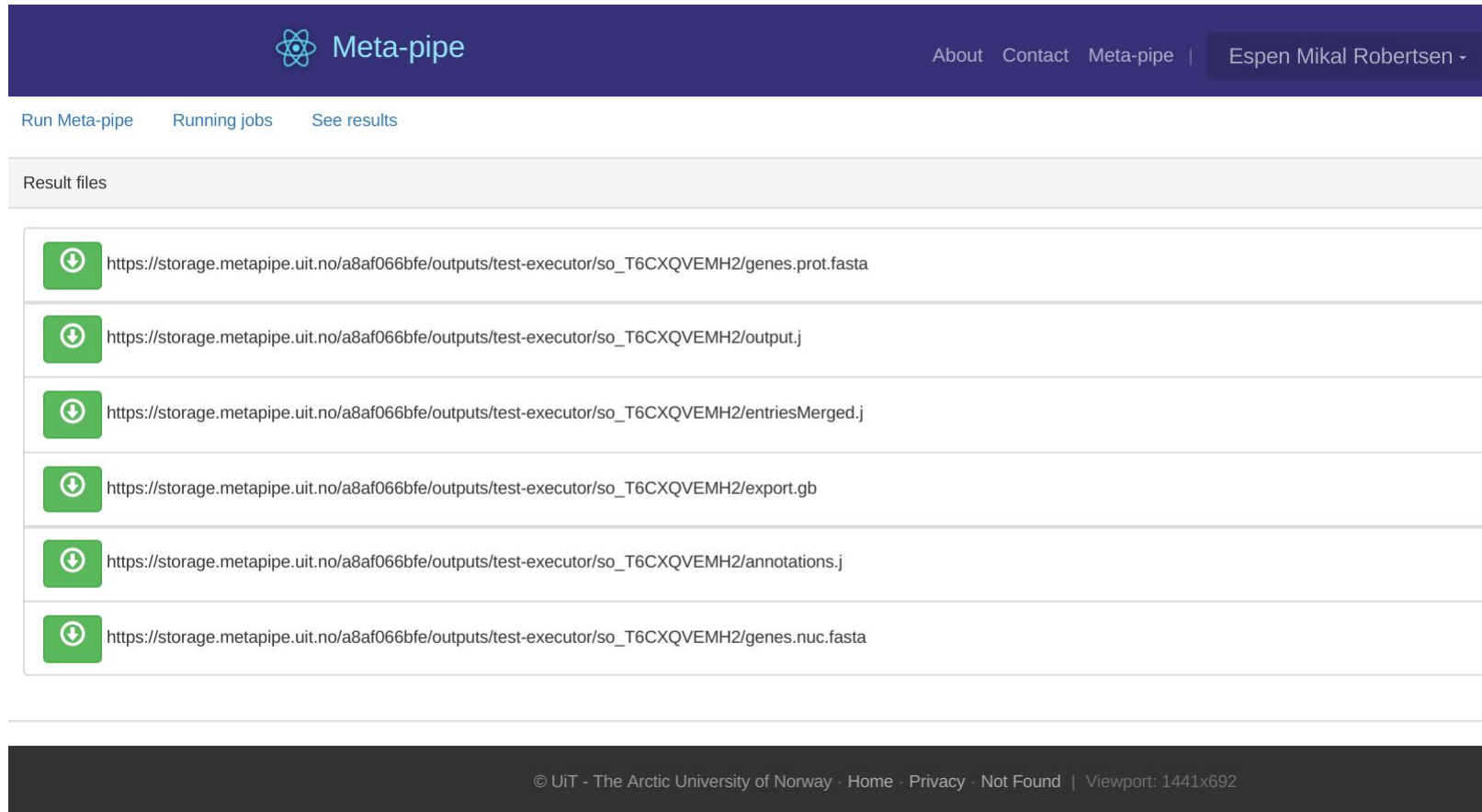
Job tag

morocco

Hands on: Functional analysis

The screenshot shows the Meta-pipe web interface. At the top, there is a dark blue header with the Meta-pipe logo and name on the left, and navigation links 'About', 'Contact', 'Meta-pipe', and a user profile 'Espen Mikal Robertsen' on the right. Below the header, there are links for 'Running jobs' and 'See results'. The main content area is titled 'Results' and contains four identical light green placeholder cards. Each card has the text 'Annotations', 'Submitted:', and a 'Go to results' link. At the bottom, there is a dark grey footer with copyright information: '© UiT - The Arctic University of Norway · Home · Privacy · Not Found | Viewport: 1441x692'.

Hands on: Functional analysis



The screenshot shows the Meta-pipe web interface. At the top, there is a dark blue header with the Meta-pipe logo and name on the left, and navigation links for 'About', 'Contact', 'Meta-pipe', and 'Espen Mikal Robertsen' on the right. Below the header, there are three links: 'Run Meta-pipe', 'Running jobs', and 'See results'. The main content area is titled 'Result files' and contains a list of six files, each with a green download icon and a URL. The footer is a dark grey bar with copyright information and navigation links.

Meta-pipe

About Contact Meta-pipe | Espen Mikal Robertsen ▾

[Run Meta-pipe](#) [Running jobs](#) [See results](#)

Result files

- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/genes.prot.fasta
- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/output.j
- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/entriesMerged.j
- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/export.gb
- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/annotations.j
- https://storage.metapipe.uit.no/a8af066bfe/outputs/test-executor/so_T6CXQVEMH2/genes.nuc.fasta

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Hands on: Functional analysis

Artemis Entry Edit: export (1).gb

File Entries Select View Goto Edit Create Run Graph Display

Entry: export (1).gb

Nothing selected

Artemis Release 16.0.0
1. Standard

wellcome trust
sanger institute
pathogen genomics group

fasta_record

4800 5600 6400 7200 8000 8800 9600 10400 11200 12000 12800

k99_1114_gene_5 k99_1114_gene_6 k99_1114_gene_7 k99_1114_gene_8 k99_1114_gene_9 k99_1114_gene_10 k99_1114_gene_11 k99_1114_gene_12 k99_1114_gene_13 k99_1114_gene_14 k99_1114_gene_15

T # D * P T G V P R * K S + F W P H C L V L S P L A P L P O K K S A L A F L Q L T H R L N R W T P I T K S P V S T S T W P T R C A N R C R P S
H K I D R R E F H D E K V S S G R T A + F E R L W R R C R R K N Q L W R F C N L P T V * I D G R Q # P N R R F R H R P G Q R A V Q T D A G R V
I R L L T D G S S T H K K L L V L L A A L L S E A F I G A A A A F K I L S F G V S A T Y P P F E S Y D A N N Q T A G F D I D L A N A L G K Q M G A E
ACATAAGATTGACCGACGGAGTTCCACGATGAAAAGTITAGTCTGGCCCACTGCTTGTCTTTCGCTTGGCCCGCTGCCGACAGAAAATCACTTGGCGTTCTGCACTTACCCACCGTTGAATGATGGACGCCAATAACCAATCGCCGTTTCGACATCGACCTGGCCACCGGCTGTGCAACAGATGCAGCCSAGT
TGTATTCTAACTGGCTGCCCTCAAGGTGCTACTTTTCAATCAAGACCGCGGTGACGAATCAAGAAAGCGGAAACCGCGGCAOCCGCTCTTTTGTAGTGGAAACCGCAAGACGTTGAATGGGTGGCAAACTTAGCTACCTGCGGTTATTGGTTTAGCGCCAAAGCTGTAGCTGGACCGGTTGGCGGACAGCTTTGTCTAGCTCCGGCTCA
M L N V S P L E V I F F N T R A A S S L E K A K P A A A A S F I L K P T E A V # G N S D I S A L L W I A P K S M S R A L A S H L C I C A S H
Y S Q G V P T G R H F L # N Q G C Q K T R E G K A G S G C F F D A K A N R C S V W R K F R H V G I V L D G T E V D V Q G V R Q A F L H L G L
C L I S R R S N W S S F T L E P R V A # N K R R Q R R Q R L F F * S Q R K Q L K G V T Q I S P R W Y G F R R N R C R G P W R A T C V S A P R T

source	1	109378
fasta_record	1	41673
CDS	30	761
CDS	891	2363
CDS	2360	3085
CDS	3155	4285
CDS	4328	4816
CDS	4874	5674
CDS	5716	6069
CDS	6690	7850
CDS	6890	7850
CDS	7816	9028
CDS	7816	9028
CDS	9377	9856

Arginine ABC transporter
Osmosensitive K+ channel histidine kinase KdpD
Response regulator receiver domain protein
23S rRNA (uracil(747)-C(5))-methyltransferase RlmC
Inner membrane protein YbjO
Putrescine transport system permease protein PotI
Putrescine transport system permease protein PotH
Putrescine transport ATP-binding protein PotG
Putrescine transport ATP-binding protein PotS
Putrescine-binding periplasmic protein
Putrescine-binding periplasmic protein
Uncharacterized protein ybjN