

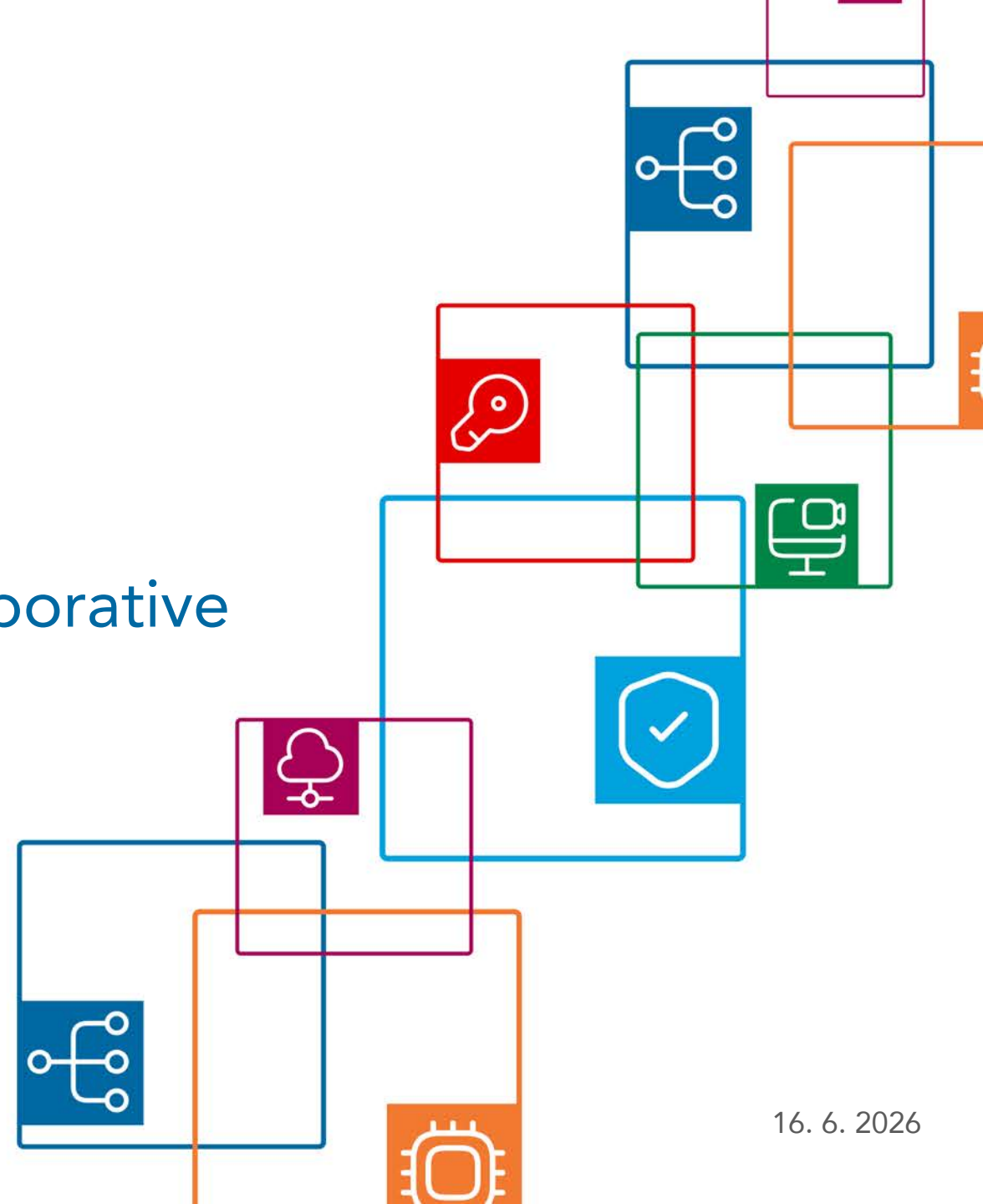
MetaCentrum NGI

For scientific computations, collaborative research and its support services

Jiří Vorel

Jan Evangelista Purkyně University in Ústí nad Labem

vorel@cesnet.cz meta@cesnet.cz



■ MetaCentrum is

- The activity of the CESNET association
- Part of the e-INFRA CZ e-infrastructure
- A national grid infrastructure (NGI)
- A provider of computational resources, application software (both commercial and free/open source) and data storage
- Available to the entire academic and research community (employees and students) in the Czech Republic
- Free of charge (users 'pay' by acknowledging the project 'e-INFRA CZ ID:90254' in their publications)
- For non-commercial academic research only

<https://www.cesnet.cz/>

<https://www.metacentrum.cz/>

<https://www.e-infra.cz/>

<https://docs.metacentrum.cz/>



■ MetaCentrum offers

- Access to all resources without submitted projects (with one exception)
- The possibility to apply for membership at any time
- Immediate access to hardware resources and licences (once an application has been approved)
- CPU/GPU resources, CLI access, GUI applications, Kubernetes and cloud services, etc.
- Various application software (commercial, free and open source)
- Data sharing
- Access is also possible for partners from industry and abroad

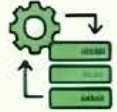


MetaCentrum in Numbers 2025



registered users

4 621



PBS (meta-pbs)



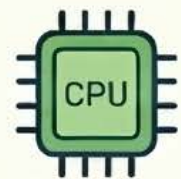
7.6 mil.
jobs



25 392
CPU years



283
GPU years



39 988
CPU cores /
332 GPU



OPENSTACK



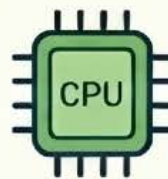
80.7 thous.
VM



10 586
CPU years



59
GPU years



9 670
CPU cores /
84 GPU



KUBERNETES



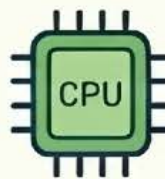
6.4 mil.
pods



1 760
CPU years



43
GPU years

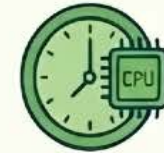


3 008
CPU cores /
47 GPU

SENSITIVE CLOUD



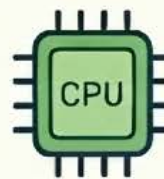
37.8 thous.
pods



657
CPU years



35
GPU years



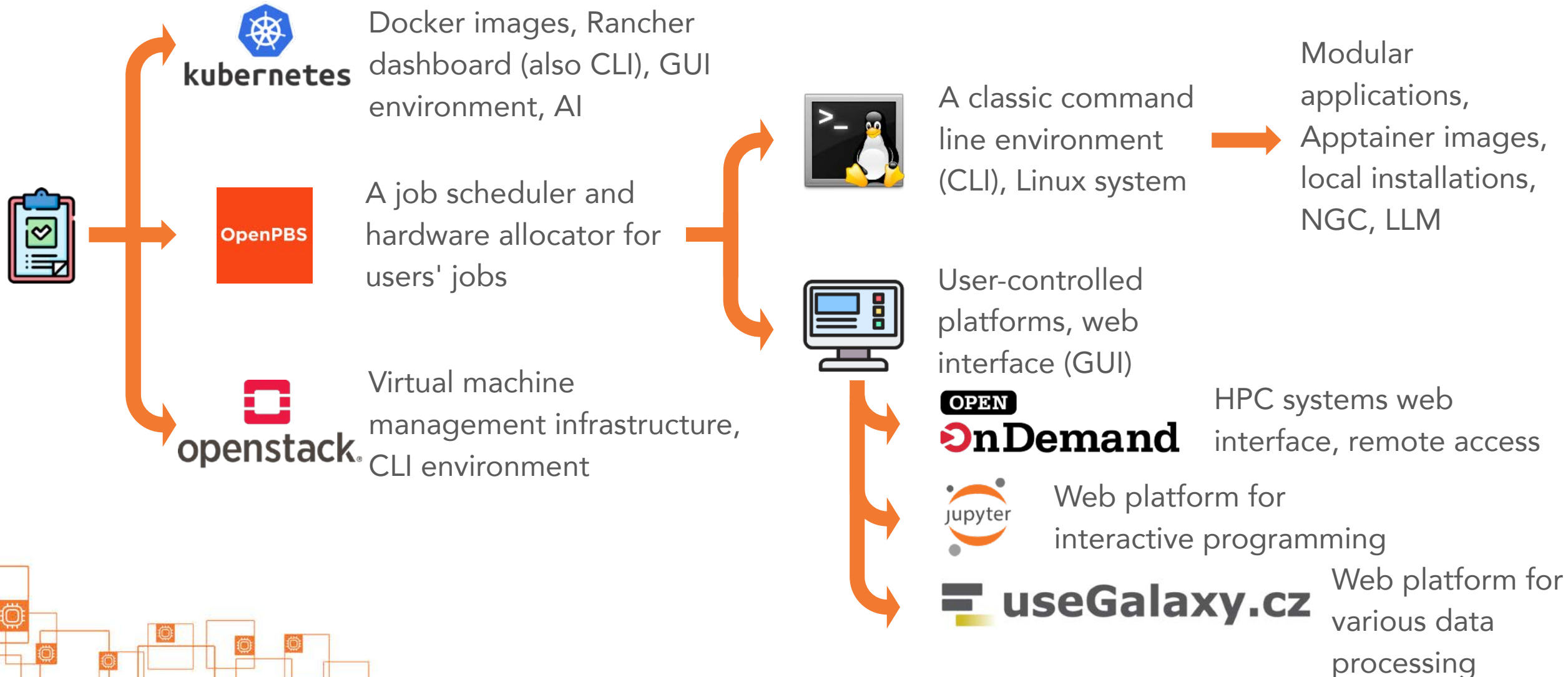
1 112
CPU cores /
40 GPU

A close-up, high-angle shot of the One Ring from J.R.R. Tolkien's Middle-earth. The ring is positioned diagonally across the frame, resting on a golden, textured surface that resembles a map or parchment. The ring's surface is highly reflective, showing bright highlights and a clear reflection of the surrounding environment. The Elvish script, known as Tengwar, is intricately engraved in a golden color onto the ring's band. The text is arranged in a circular pattern, following the curve of the ring. The lighting is warm and dramatic, creating deep shadows and bright highlights that emphasize the ring's metallic texture and the intricate details of the script. The overall composition is centered, with the ring as the primary focus.

ONE APPLICATION TO RULE THEM ALL

One application to rule them all

<https://docs.metacentrum.cz/en/docs/welcome>





MetaCentrum provides access to hundreds of software tools giving thousands of individual modules

Licence models

- We can run almost anything that doesn't violate the licence terms and is for Linux
- Most application software is open source, but...

<https://docs.metacentrum.cz/en/docs/software>

Paid licence



For registered individuals

For all users

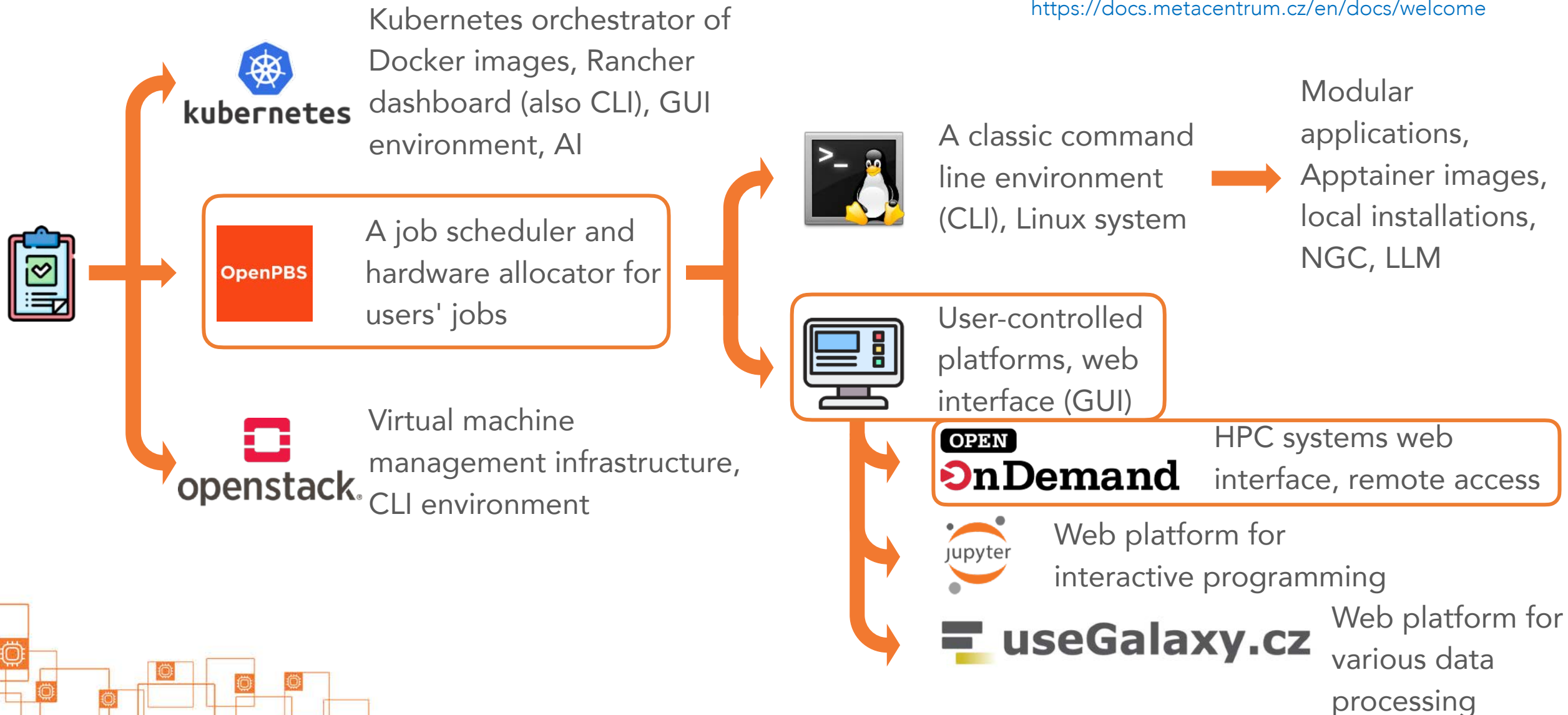


Free licence



How to use it

<https://docs.metacentrum.cz/en/docs/welcome>

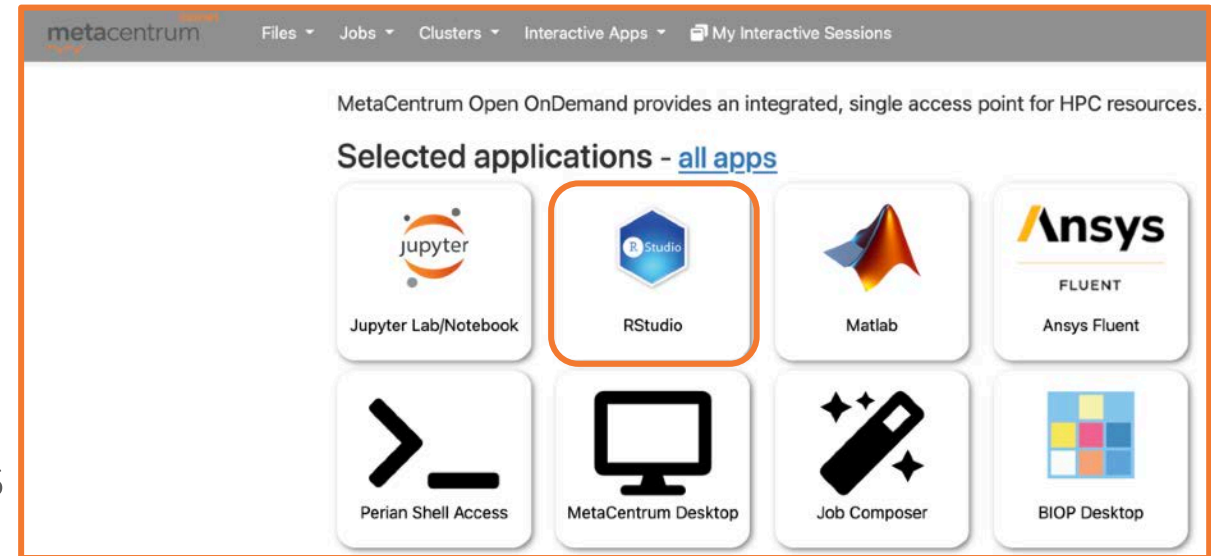


■ Open OnDemand



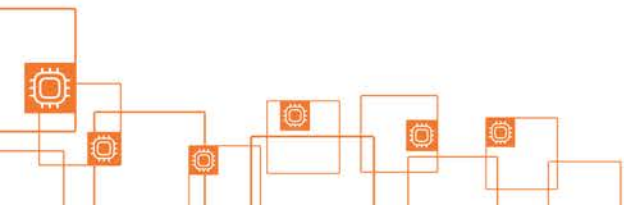
<https://ondemand.metacentrum.cz/>

- Web application on top of OpenPBS scheduler
- Running (not only) GUI applications



<https://docs.metacentrum.cz/en/docs/software/sw-list/rstudio>

<https://docs.metacentrum.cz/en/docs/software/sw-list/r>





R is a software environment for statistical computing and graphics

Open OnDemand



<https://ondemand.metacentrum.cz/>

- Web application on top of OpenPBS scheduler
- Running (not only) GUI applications

Home / My Interactive Sessions / RStudio Server

Interactive Apps

Cloud

- Kubernetes on OpenStack (KOST) (beta)
- OpenStack VM (beta)

Desktops

- Ansys/Enight
- Ansys/Fluent
- Ansys/Workbench
- BIOP Desktop
- CLCgenomicsWB
- MZMINE
- Matlab
- MetaCentrum Desktop
- QuPath
- VMD Desktop

Servers

- Julia Pluto.jl
- Jupyter - Evo2 (beta)
- Jupyter Notebook/Lab
- Matlab webapp (beta)
- RStudio Server**

RStudio Server

This app will launch an RStudio server on one or more nodes. Geospatial and Tensorflow packages are preinstalled.

Number of hours

2

Number of CPUs on single node

2

Memory (GB)

10

GPUs

0

Scratch local (GB)

10

RStudio Image version

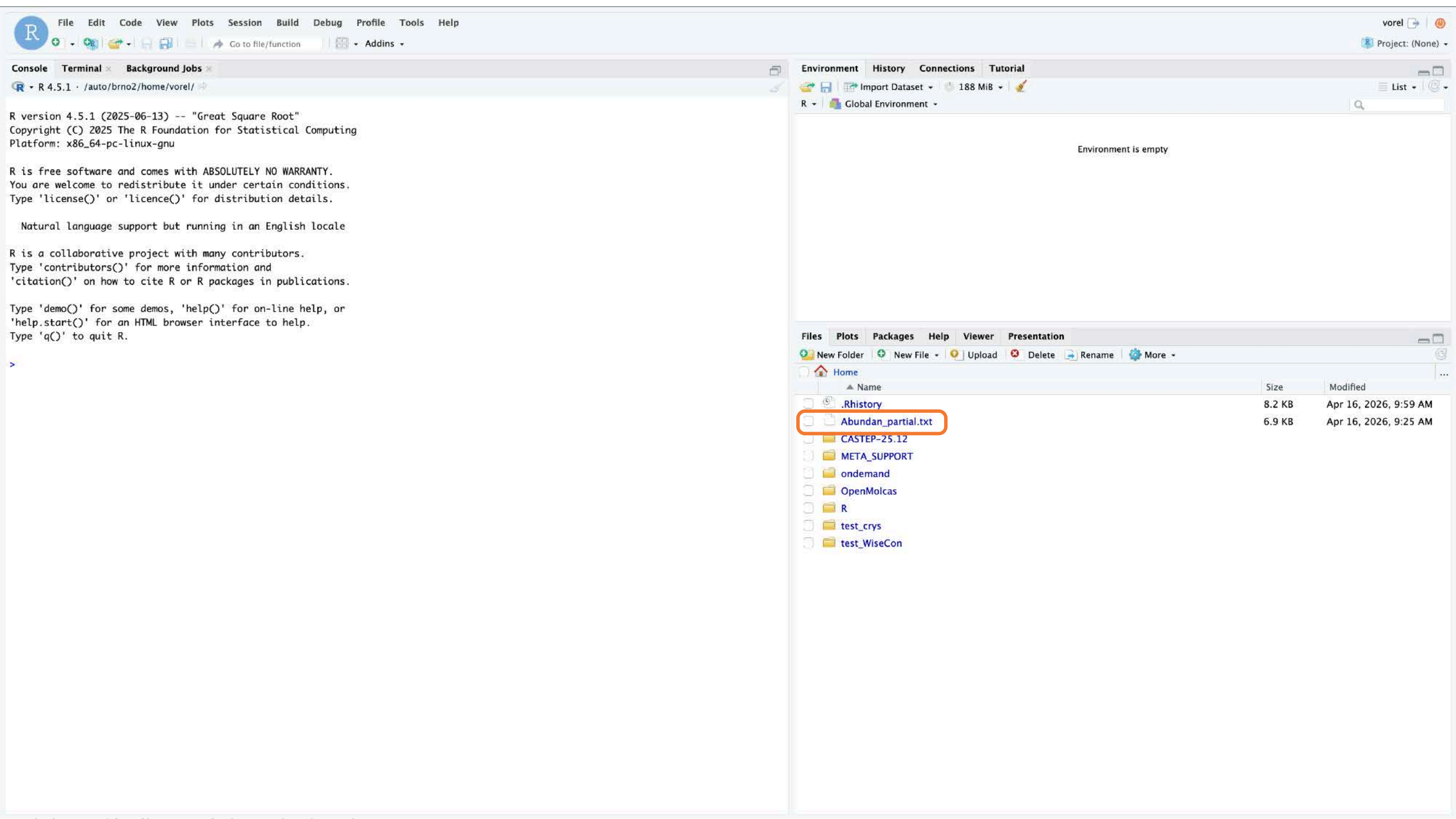
RStudio-geospatial-4.5.1

RStudio working directory location:

/storage/brno2

Launch

* The RStudio Server session data for this session can be accessed under the [data root directory](#).



Console Terminal Background Jobs

```
R 4.5.1 · /auto/brno2/home/vorel/

R version 4.5.1 (2025-06-13) -- "Great Square Root"
Copyright (C) 2025 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Environment History Connections Tutorial

Import Dataset 188 MiB

R Global Environment

Environment is empty

Files Plots Packages Help Viewer Presentation

New Folder New File Upload Delete Rename More

Name	Size	Modified
.Rhistory	8.2 KB	Apr 16, 2026, 9:59 AM
Abundan_partial.txt	6.9 KB	Apr 16, 2026, 9:25 AM
CASTEP-25.12		
META_SUPPORT		
ondemand		
OpenMolcas		
R		
test_crys		
test_WiseCon		

```

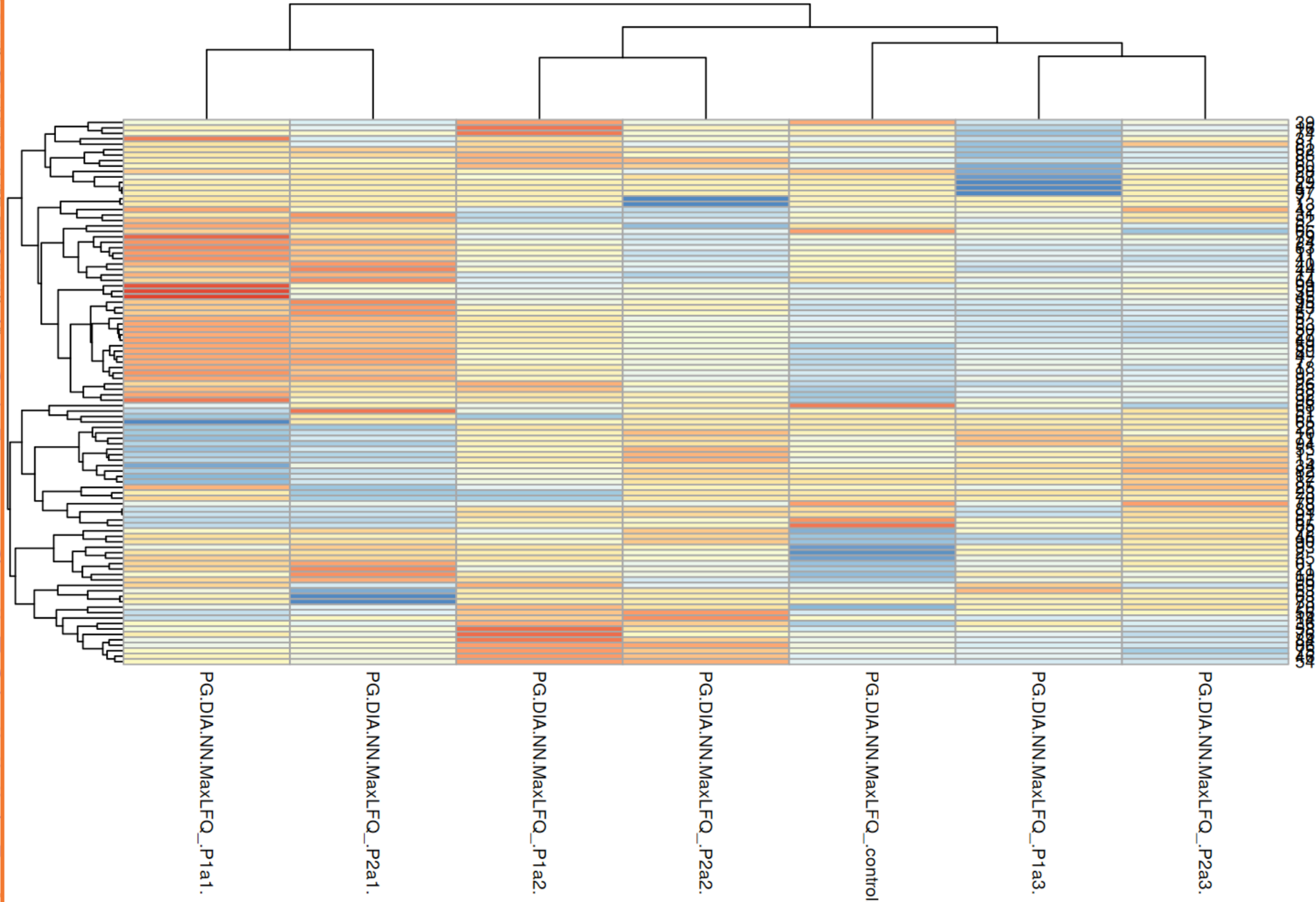
> library(pheatmap)
>
> # nacteni dat
> data <- read.delim("Abundan_partial.txt",
+                   sep = "\t",
+                   header = TRUE,
+                   stringsAsFactors = FALSE)
>
> # nastaveni rownames
> rownames(data) <- data$PG_ID
> data$PG_ID <- NULL
>
> # prevod desetinne carky na tecku
> data[] <- lapply(data, function(x) {
+   as.numeric(gsub(",", ".", x))
+ })
>
> # log transformace (bezpecna pro nuly)
> data_log <- log10(data + 1)
>
> # vykresleni heatmapy
> pheatmap(
+   data_log,
+   scale = "row",           # normalizace v ramci radku
+   clustering_distance_rows = "euclidean",
+   clustering_distance_cols = "euclidean",
+   clustering_method = "complete",
+   fontsize = 8,
+   main = "Protein abundance heatmap"
+ )

```

The screenshot shows the RStudio interface. The top bar indicates the user is 'vorel' and the project is '(None)'. The 'Environment' pane shows 'Global Environment' with 188 MiB of memory used. The 'Files' pane shows a directory listing:

Name	Size	Modified
.Rhistory	8.2 KB	Apr 16, 2026, 9:59 AM
Abundan_partial.txt	6.9 KB	Apr 16, 2026, 9:25 AM
CASTEP-25.12		
META_SUPPORT		
ondemand		
OpenMolcas		
R		
test_crys		
test_WiseCon		

Protein abundance heatmap



```
File Edit Co  
> library  
Console Terminal  
R ~ R 4.4.1 auto-brw  
> # nacte  
> data$P  
R version 4.4.1 (2025-03-18)  
Copyright (C) 2025 The R Foundation for Statistical Computing  
Platform: x86_64-pc-linux-gnu  
R is free software and you are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
Installing shared libraries: OK  
# nasta  
R is a collaborative effort by many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
> data$PG  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
> # prev  
> data[]  
+ as.  
+ })  
> # log t  
> data_lo  
> # vyk  
> pheatma  
+ dat  
+ sca  
+ clu  
+ clu  
+ clu  
+ fon  
+ mai  
+ )
```

vorel |

Project: (None) | |

List |

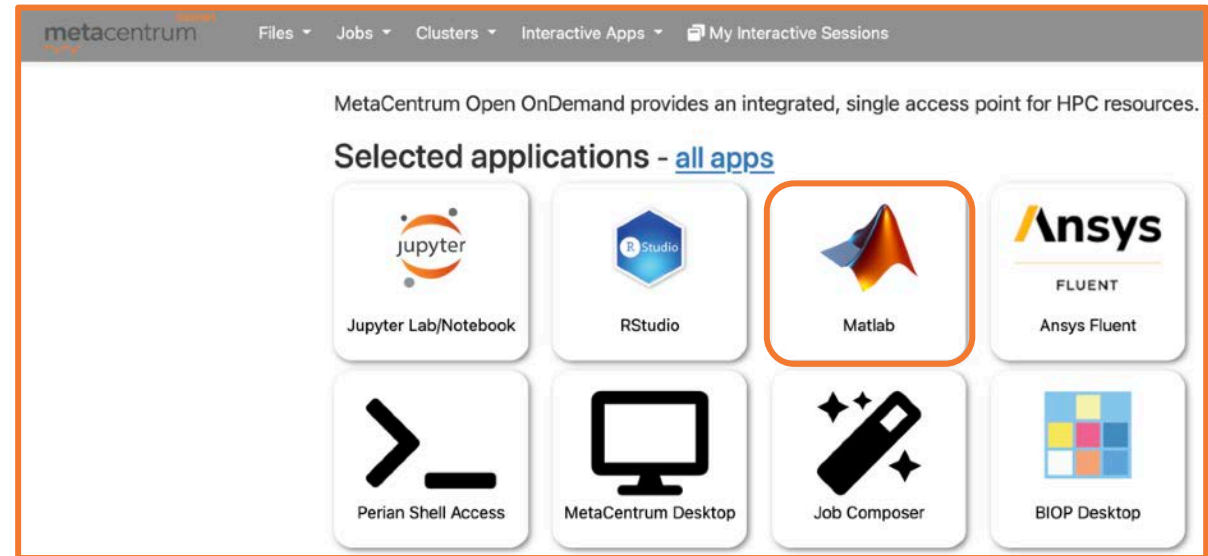
Modified
Apr 16, 2026, 9:59 AM
Apr 16, 2026, 9:25 AM

■ Open OnDemand



<https://ondemand.metacentrum.cz/>

- Web application on top of OpenPBS scheduler
- Running (not only) GUI applications



<https://docs.metacentrum.cz/en/docs/software/sw-list/rstudio>

<https://docs.metacentrum.cz/en/docs/software/sw-list/r>



MATLAB, the language of engineers and scientists, is a programming and numeric computation environment for algorithm development, data analysis, and visualisation

HOME PLOTS APPS EDITOR PUBLISH VIEW

New Open Save Compare Print Go To Find Bookmark Refactor Profiler Analyze Run Section Run and Advance Run Step Stop

FILE NAVIGATE CODE ANALYZE SECTION RUN

C:\Users\{user}\AppData\Roaming\MathWorks\MATLAB Add-Ons\Collections\Digilent Toolbox

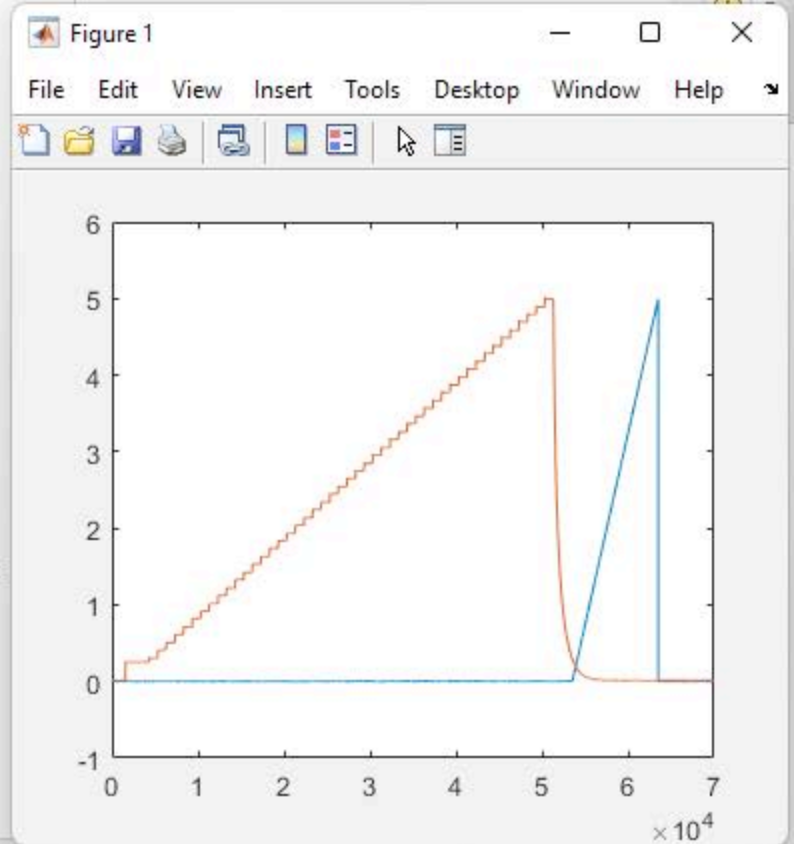
Current Folder

- digilent
 - + daq
 - doc
 - examples
 - all_systems.m
 - all_systems_AD3.m
 - analog_in_out_loop.m
 - analog_in_stream_blocking.m
 - analog_in_stream_nonblocking.m
 - analog_in_stream_nonblocking2...
 - analog_out_stream_blocking.m
 - analog_out_stream_nonblocking...
 - analog_out_stream_nonblocking...
 - analog_single_scan.m
 - digital_io_direction.m
 - digital_io_loop.m
 - digital_io_read.m
 - digital_io_write.m
 - fetchData.m
 - GSAcquiringAndGenerateData.mlx
 - GSAcquiringData.mlx
 - GSGeneratingData.mlx
 - quick_check.m
 - DigilentAdaptor.mexw64

```

1 % This example uses the two scope channels, one AWG channel, one power
2 % supply channel and all digital channels on the AD3
3 %
4 % W1 will generate a ramp from 0 to 5V for 1 second at 1KHz
5 % V+ will generate a ramp from 0 to 5V for 5 seconds at 10Hz
6 % Both will be acquired at 10KHz by scope channels 1 and 2
7 % DIO pins 0-7 will be used to output primes less than 128
8 % DIO pins 8-15 will acquire the primes generated by DIO0-7
9 %
10 % Connect W1 to 1+ and GND to 1-
11 % Connect V+ to 2+ and GND to 2-
12 % Connect DIO0 to DIO8, DIO1 to DIO9 ... DIO7 to DIO15
13 daqreset;
14 AI = daq("digilent") % DAQ session for the scope channels
15 AO = daq("digilent") % DAQ session for the AWG channel
16 VP = daq("digilent") % DAQ session for the V+ power supply
17 DI = daq("digilent") % DAQ session for the DIO channels used as input
18 DO = daq("digilent") % DAQ session for the DIO channels used as output
19
20 % add scope input channels
21 addinput(AI, "AD3_0", "ai0", "Voltage")
22 addinput(AI, "AD3_0", "ai1", "Voltage")
23
24 % add AWG1 output channel
25 addoutput(AO, "AD3_0", "ao0", "Voltage")

```



HOME PLOTS APPS EDITOR PUBLISH VIEW

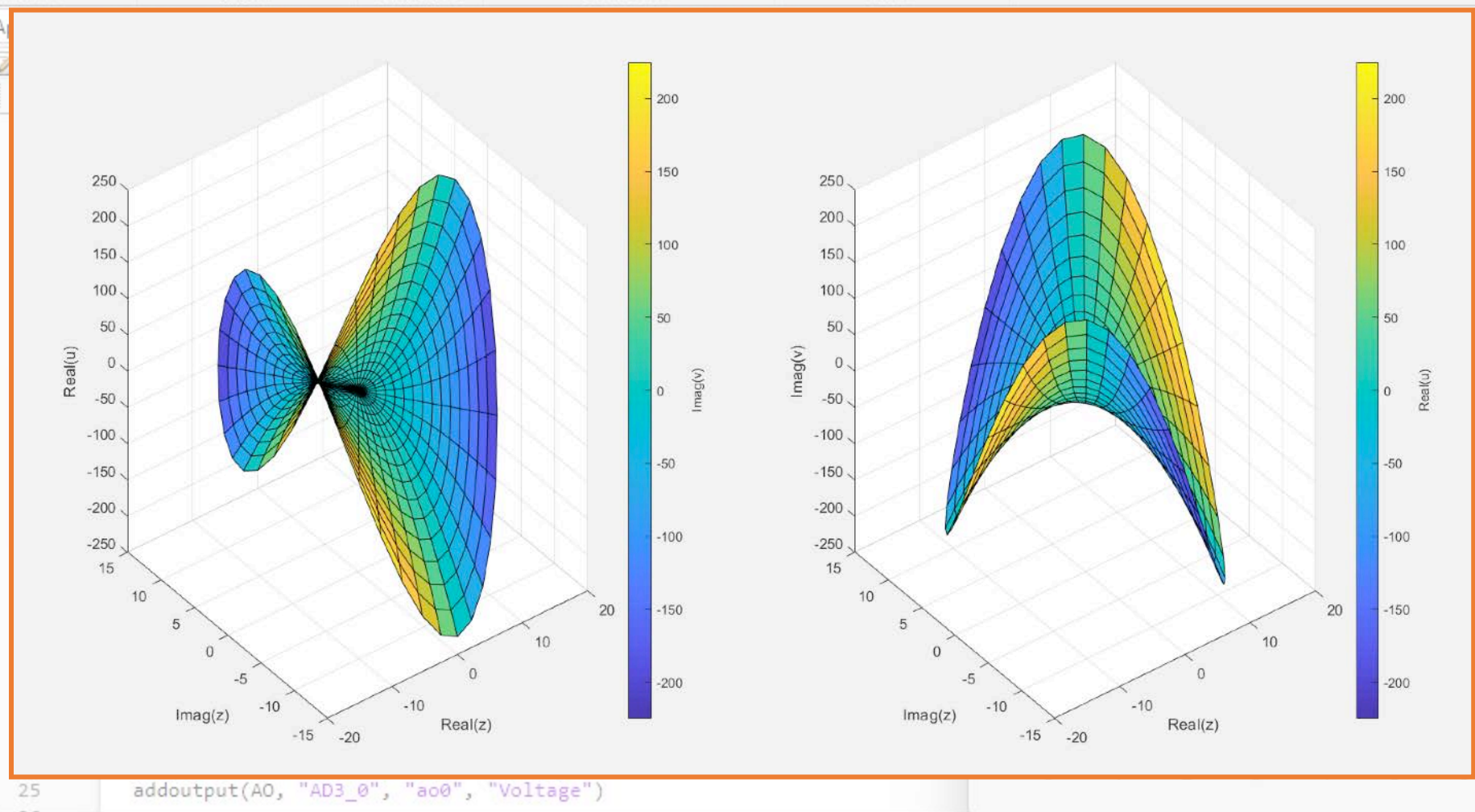
New Open Save Compare Print Go To Find Bookmark Refactor Analyze Run Section Run and Advance Run Step Stop

FILE NAVIGATE CODE ANALYZE SECTION RUN

C:\Users\{user}\A

Current Folder

- Name
- digilent
 - +daq
 - doc
 - examples
 - all_systems.m
 - all_systems_AD3.m
 - analog_in_out_loop.m
 - analog_in_stream_blocking.m
 - analog_in_stream_nonblocking.m
 - analog_in_stream_nonblocking2...
 - analog_out_stream_blocking.m
 - analog_out_stream_nonblocking...
 - analog_out_stream_nonblocking...
 - analog_single_scan.m
 - digital_io_direction.m
 - digital_io_loop.m
 - digital_io_read.m
 - digital_io_write.m
 - fetchData.m
 - GSAcquiringAndGenerateData.mlx
 - GSAcquiringData.mlx
 - GSGeneratingData.mlx
 - quick_check.m
 - DigilentAdaptor.mexw64

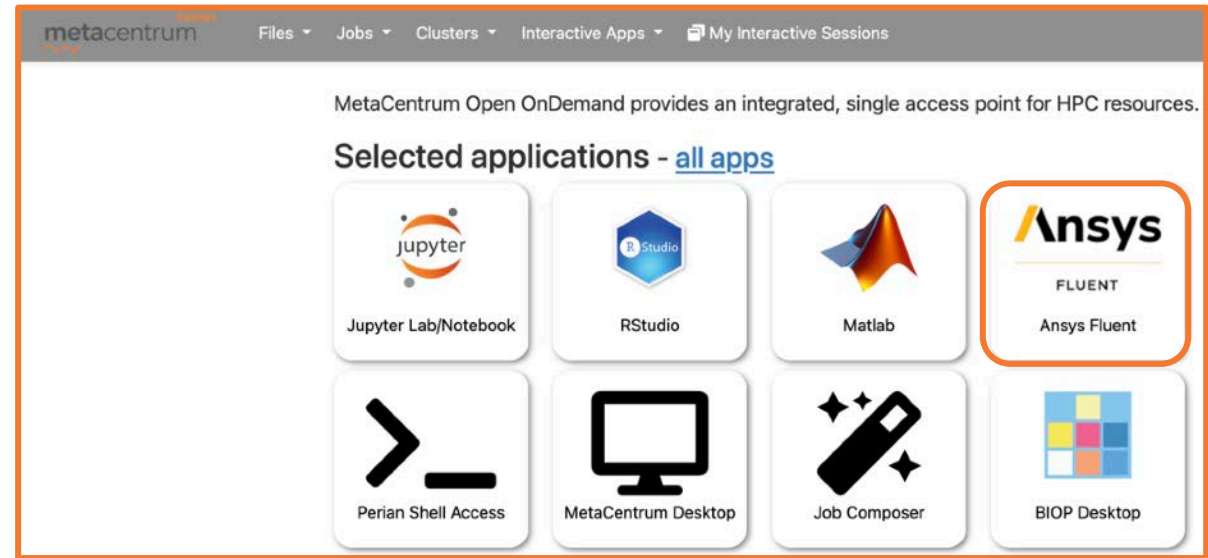


■ Open OnDemand



<https://ondemand.metacentrum.cz/>

- Web application on top of OpenPBS scheduler
- Running (not only) GUI applications



<https://docs.metacentrum.cz/en/docs/software/sw-list/rstudio>

<https://docs.metacentrum.cz/en/docs/software/sw-list/r>



ANSYS is engineering simulation software that integrates the physics of structural, fluid and electromagnetic systems to model real-world behaviour

Display

Views... Headlight Lighting

Options... Gouraud

Camera...

Graphics

Lights... Compose...

Colormap... Annotate...

Mouse

Left mouse-rotate Probe short description

Middle mouse-zoom Fluent Defaults

Right mouse-probe Workbench Defaults

Outline View

Filter Text

- Setup
 - General
 - Models
 - Materials
 - Cell Zone Conditions
 - Boundary Conditions
 - Mesh Interfaces
 - Dynamic Mesh
 - Reference Values
 - Reference Frames
 - Named Expressions
- Solution
 - Methods
 - Controls
 - Report Definitions
 - Monitors
 - Cell Registers
 - Initialization
 - Calculation Activities
 - Run Calculation
- Results
 - Surfaces
 - Graphics
 - Mesh
 - Contours
 - contour-2
 - contour-1
 - Vectors
 - Pathlines
 - Particle Tracks
 - Plots
 - Scene
 - Animations
 - Reports
- Parameters & Customization

Task Page

Run Calculation

Check Case... Update Dynamic Mesh...

Pseudo Transient Settings

Fluid Time Scale

Time Step Method: Automatic Time Scale Factor: 1

Length Scale Method: Conservative Verbosity: 0

Parameters

Number of Iterations: 420 Reporting Interval: 1

Profile Update Interval: 1

Solution Processing

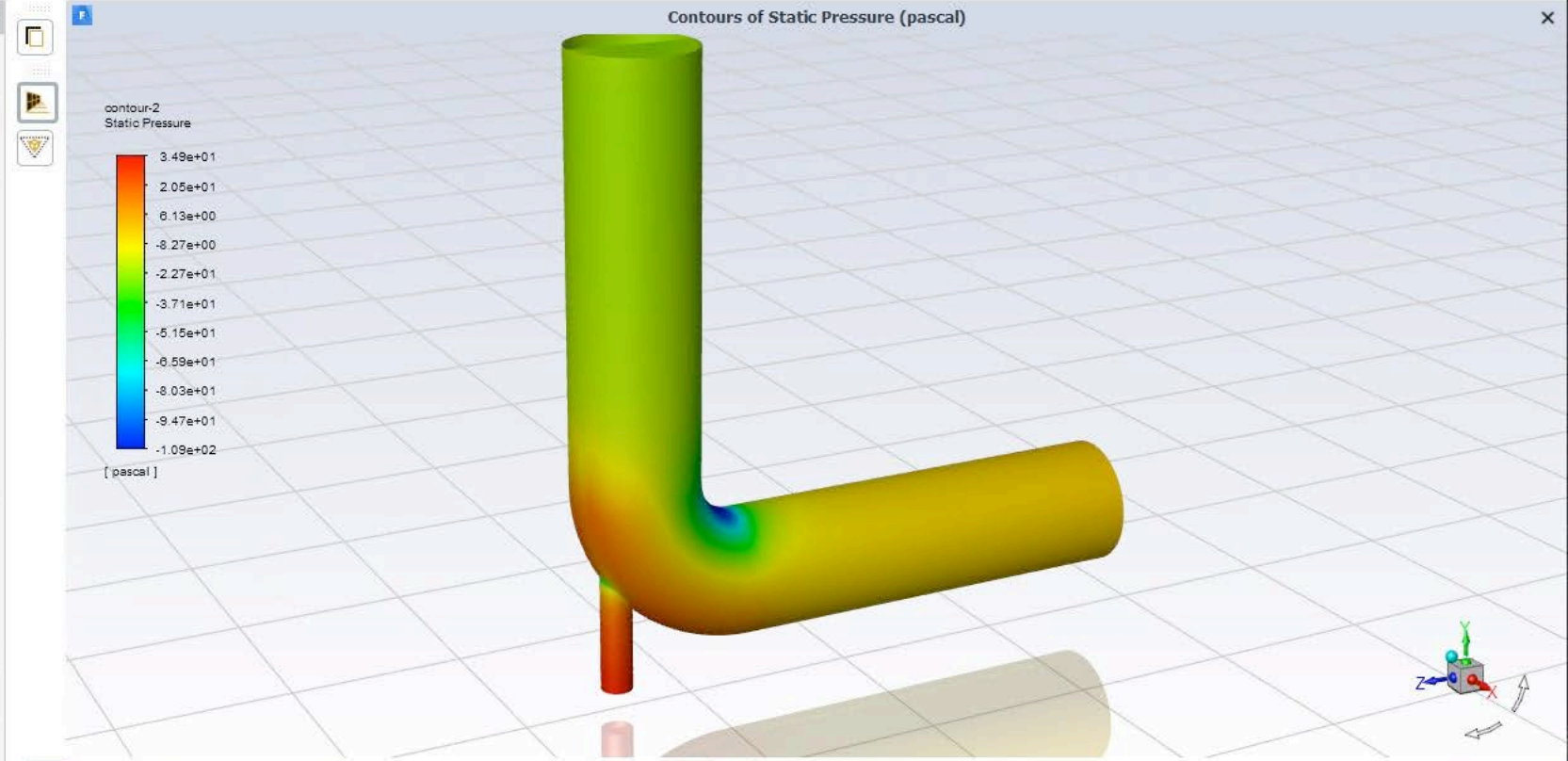
Statistics

Data Sampling for Steady Statistics

Data File Quantities...

Solution Advancement

Calculate



Console

Done.

Feature already enabled.

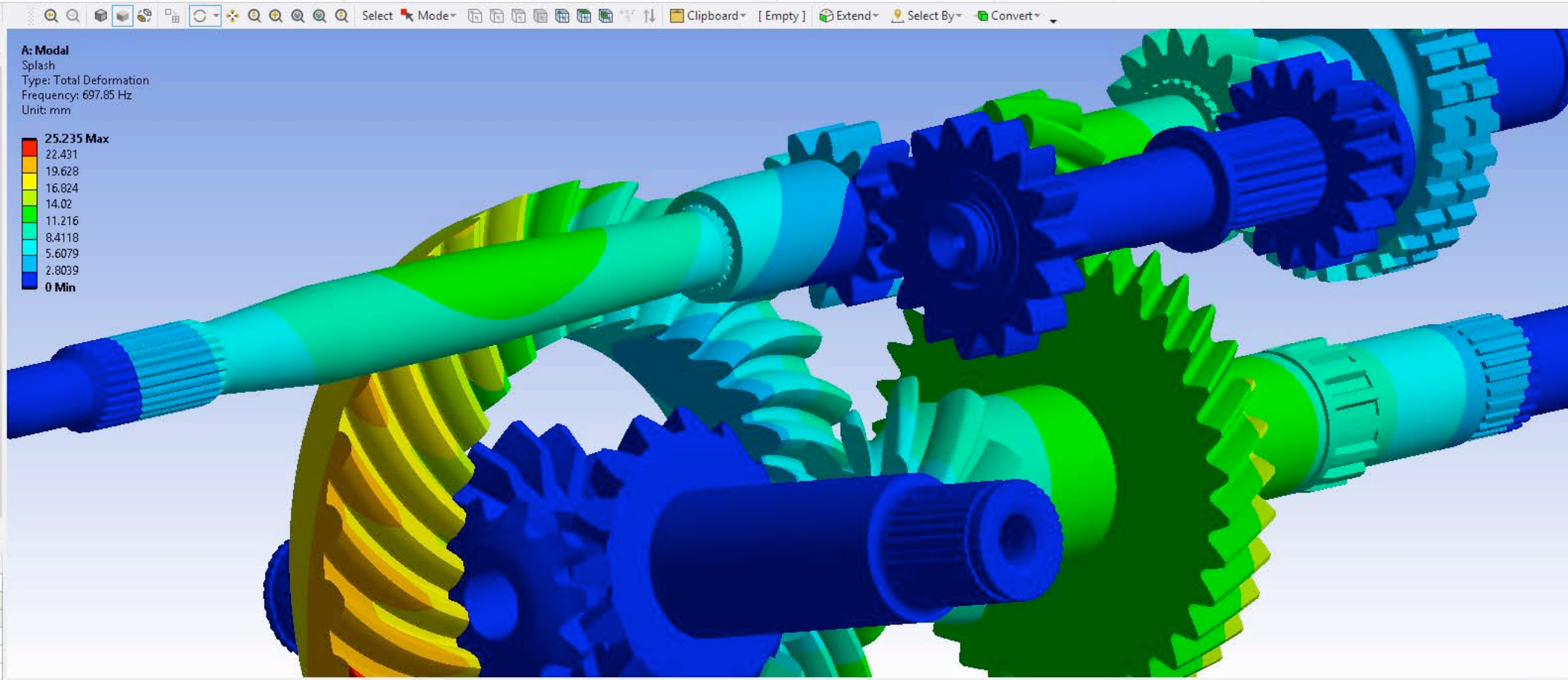
Reading "\\| gunzip -c \"D:\YOUTUBE\1. CFD.NINJA\ANSYS STUDENT\3. Fluent\Elbow\elbow3d_files\dp0\FLU\Fluent\SYS-1-00093.dat.gz\" \"\"...

Parallel variables...

Done.

Outline Panel

- Project
 - Model (A4)
 - Geometry
 - Materials
 - Coordinate Systems
 - Connections
 - Mesh
 - Named Selections
 - Modal (A5)
 - Pre-Stress (None)
 - Analysis Settings
 - Fixed Support
 - Fixed Support 2
 - Fixed Support 3
 - Fixed Support 4
 - Fixed Support 5
 - Fixed Support 6
 - Fixed Support 7
 - Solution (A6)
 - Solution Information
 - Total Deformation
 - Total Deformation 2
 - Total Deformation 3
 - Total Deformation 4
 - Splash
 - Total Deformation 6
 - Total Deformation 7
 - Total Deformation 8
 - Total Deformation 9
 - Total Deformation 10
 - Total Deformation 11
 - Total Deformation 12



Details of "Splash"

Scope

Scoping Method: Geometry Selection
 Geometry: All Bodies

Definition

Type: Total Deformation
 Mode: 5
 Identifier:
 Suppressed: No

Results

Minimum: 0. mm
 Maximum: 25.235 mm
 Minimum Occurs On: Shaft.Solid
 Maximum Occurs On: Ring Gear.3\Solid1

Information



Tabular Data

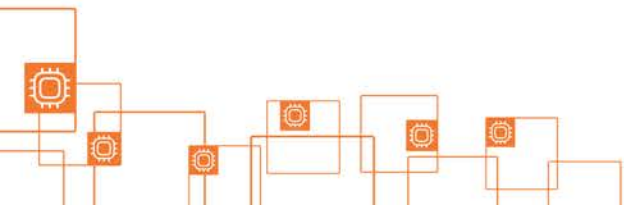
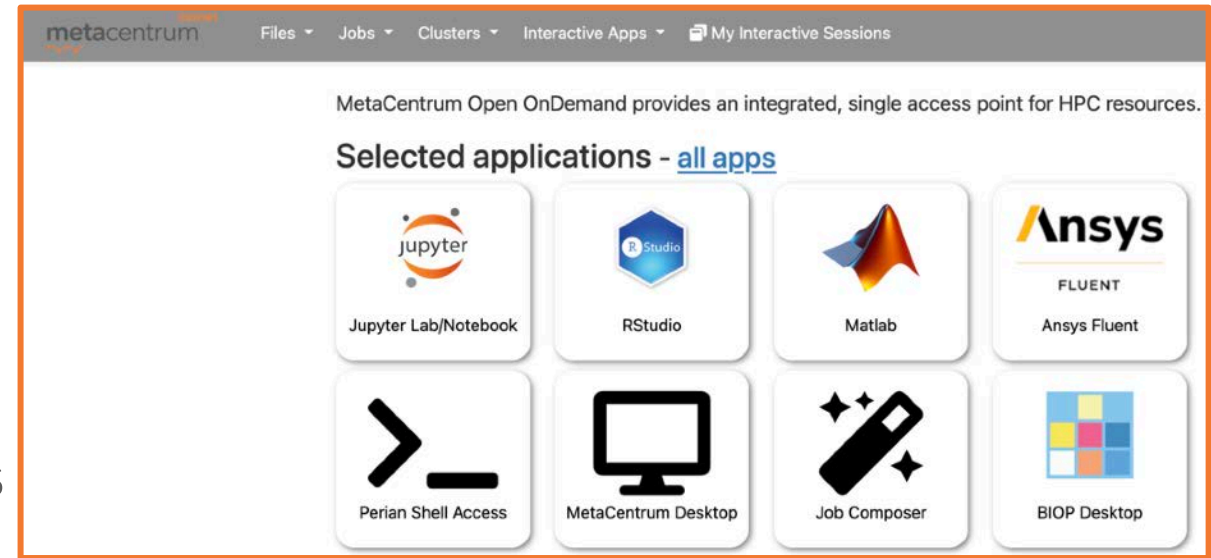
Mode	Frequency [Hz]
1.	184.09
2.	387.12
3.	395.05
4.	688.41
5.	697.85
6.	703.87
7.	917.9
8.	1064.
9.	1137.
10.	1188.3
11.	1303.4
12.	1542.4

■ Open OnDemand



<https://ondemand.metacentrum.cz/>

- Web application on top of OpenPBS scheduler
- Running (not only) GUI applications
- Browsing storages (tab 'Files')
- Launch a virtual desktop (MetaCentrum Desktop app)
- Command line (tab 'Clusters')



Themes: Cobalt2

- Default
- Bright**
 - CLRS
 - Github
 - Solarized Light
 - Tomorrow
- Dark**
 - ✓ **Cobalt2**
 - idleToes
 - Monokai Remastered
 - Pastel Dark
 - Red Alert
 - Tomorrow Night Blue
 - Tomorrow Night Bright
 - Tomorrow Night Eighties
 - Tomorrow Night



Your Home Directories

Avail space	DATA quota	DATA used	FILES quota	FILES used	Backup	Storage
227T	none	202G	none	4.88k	snap	brno12-cerit
23T	4.29T	79.8G	2.5M	141k	snap	brno2
17T	3.32T	24k	1M	9	full	budejovice1
30T	10.4G	12k	none	8	-	liberec3-tul
339T	4.29T	1.71T	3M	201k	snap	plzen1
60T	7.34G	44k	none	18	-	praha2-natur
11T	5.36T	942G	1.01M	122k	full	praha5-elixir
48T	7.34G	28k	none	11	full	pruhonice1-ibot
136T	2.14T	5.16G	2M	41.3k	snap	vestec1-elixir

CPUs

Free	Used	Total	Centre
8775	33677	42452	META

Contact

E-mail: meta@cesnet.cz
Web: http://www.metacentrum.cz/

Tip of the day: Explore our past seminars, lectures and hands-on courses with many valuable tips and tricks (<https://docs.metacentrum.cz/en/docs/tutorials>).

```
(BOOKWORM)vorel@zenith:~$ pwd  
/storage/brno12-cerit/home/vorel  
(BOOKWORM)vorel@zenith:~$ qstat -u vorel
```

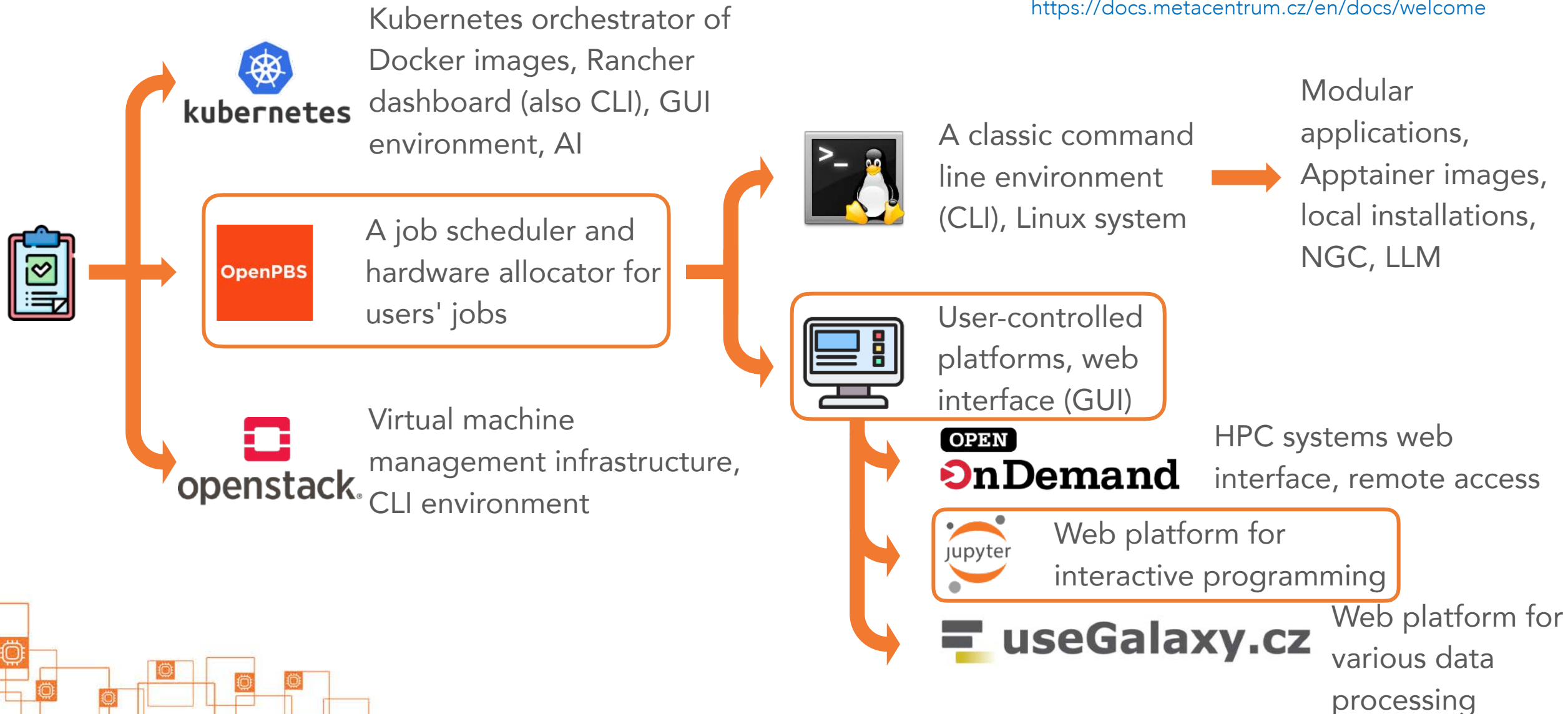
pbs-m1.metacentrum.cz:

Job ID	Username	Queue	Jobname	SessID	NDS	TSK	Req'd Memory	Req'd Time	Elap S	Time
19137135.pbs-m1.met*	vorel	interac*	STDIN	387033	1	1	400mb	18:00	R	00:00

(BOOKWORM)vorel@zenith:~\$

How to use it

<https://docs.metacentrum.cz/en/docs/welcome>

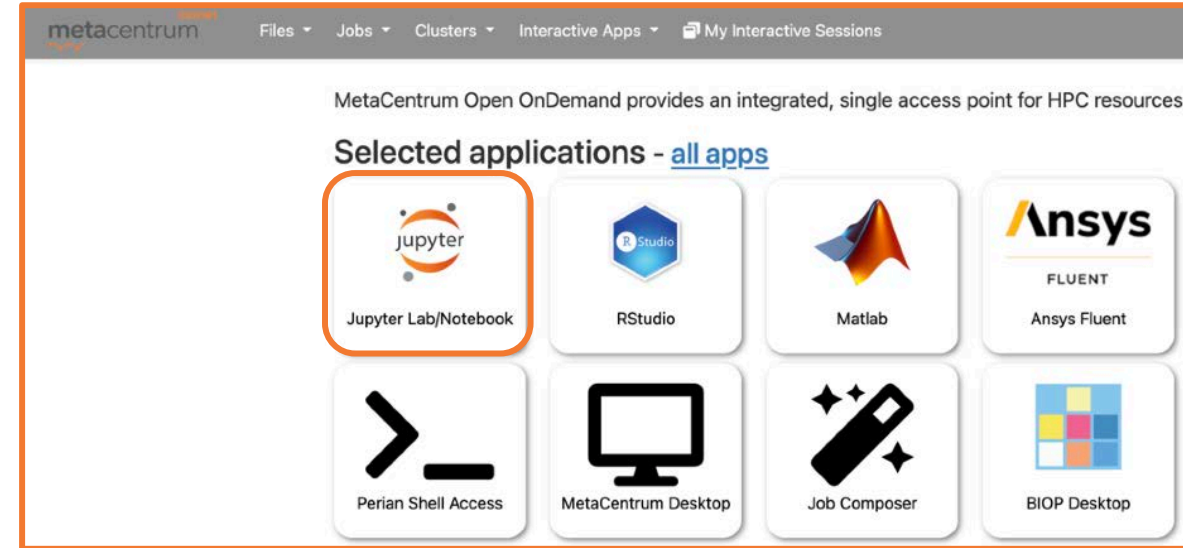


Jupyter Notebook in Open OnDemand

■ Jupyter Notebook

<https://ondemand.metacentrum.cz/>

- Web-based interactive environment mixing code, text, and visuals
- Excellent for step-by-step data analysis, machine learning, and prototyping
- Supports many languages (Python, R, Julia)
- Embeds plots, widgets, and equations directly
- Promotes reproducible, shareable work via version control and exports
- Also accessible in the Kubernetes service (with Claude Code)



<https://docs.cerit.io/en/docs/web-apps/jupyterhub>

Jupyter Notebook

<https://ondemand.metacentrum.cz/>



Jupyter

- Web-based interactive environment mixing code, text, and visuals
- Excellent for step-by-step data analysis, machine learning, and prototyping
- Supports many languages (Python, R, Julia, etc.)
- Embeds plots, widgets, and equations
- Promotes reproducible, shareable workflows
- Also accessible in the Kubernetes ecosystem

The screenshot shows the configuration interface for launching a Jupyter Notebook/Lab. On the left, a list of applications is shown, with "Jupyter Notebook/Lab" selected. On the right, the configuration options for "Jupyter Notebook/Lab" are displayed. The "Mode" is set to "Jupyter Notebook". The "Number of hours" is set to 1. The "Number of CPUs on single node" is set to 1. The "Memory (GB)" is set to 5. The "GPUs" is set to 0. The "Scratch local (GB)" is set to 5. The "Jupyter Image" is set to "Metacentrum/debian11.sif". The "Full path of custom singularity image with Jupyter notebook" is empty. The "PBS Queue" is set to "interactive". The "Jupyter working directory location" is set to "/storage/brno2". A "Launch" button is at the bottom.

Interactive Apps

- Cloud
 - Kubernetes on OpenStack (KOST) (beta)
 - OpenStack VM (beta)
- Desktops
 - Ansys/Enight
 - Ansys/Fluent
 - Ansys/Workbench
 - BIOP Desktop
 - CLCgenomicsWB
 - Matlab
 - MetaCentrum Desktop
 - QuPath
 - VMD Desktop
- Servers
 - Jupyter - Evo2 (beta)
 - Jupyter Notebook/Lab**
 - Matlab webapp (beta)
 - RStudio Server

Jupyter Notebook/Lab

This app will launch a Jupyter Notebook server on one or more nodes.

Mode

- Jupyter Notebook
- Jupyter Lab

Number of hours

1

Number of CPUs on single node

1

Memory (GB)

5

GPUs

0

Scratch local (GB)

5

Jupyter Image

Metacentrum/debian11.sif

Full path of custom singularity image with Jupyter notebook

PBS Queue

interactive

Jupyter working directory location:

/storage/brno2

Launch

Files

Running

Clusters

Select items to perform actions on them.

Upload

New ▾


 0 ▾ /

Name ▾

  CASTEP-25.12

  META_SUPPORT

  ondemand

  OpenMolcas

  test_crys

  Untitled.ipynb

Notebook:

 Python 3 (ipykernel)

 SMLv2

Other:

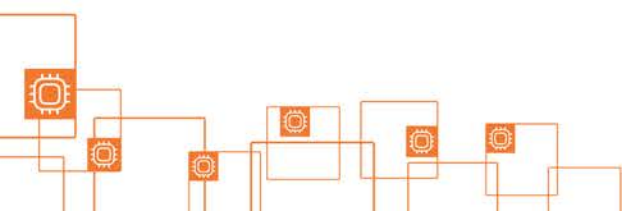
 Text File

 Folder

 Terminal

před hodinou

4.98 kB



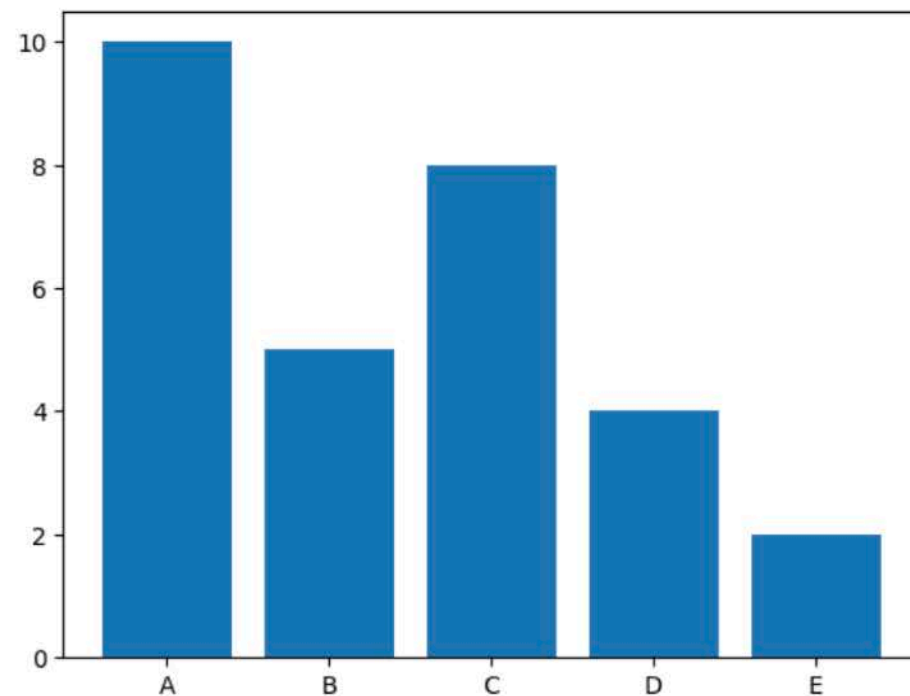
```
[1]: import os
current_working_directory = os.getcwd()
print(current_working_directory)

/auto/brno2/home/vorel
```

```
[2]: pip install matplotlib --quiet
```

Note: you may need to restart the kernel to use updated packages.

```
[3]: from matplotlib import pyplot as plt
x = ['A', 'B', 'C', 'D', 'E']
y = [10, 5, 8, 4, 2]
plt.bar(x, y)
plt.show()
```



Notebook Intelligence 

{"cell_index": 0}

(no content)

Perfect! I've successfully loaded your 'age_data.csv' file and displayed the first 5 rows. The data shows:

- **4 columns:** sex, age, city, and country
- **Data sample:**
 - Row 0: Male, age 64, from Houston, Brazil
 - Row 1: Female, age missing, from San Jose, Mexico
 - Row 2: Male, age 68, from San Antonio, Mexico
 - And so on...

I notice there are some missing age values (shown as NaN). Let me save the notebook:

Done! The notebook has been created and saved with your CSV data loaded. The first few rows are now displayed above.

Ask Notebook Intelligence...

exaple1.ipynb 

@



Launcher

exaple1.ipynb

age_data.csv



Code



git

Open in...



```
[3]: import pandas as pd

# Load the CSV file
df = pd.read_csv('age_data.csv')

# Display the first few rows
df.head()
```

```
[3]:
```

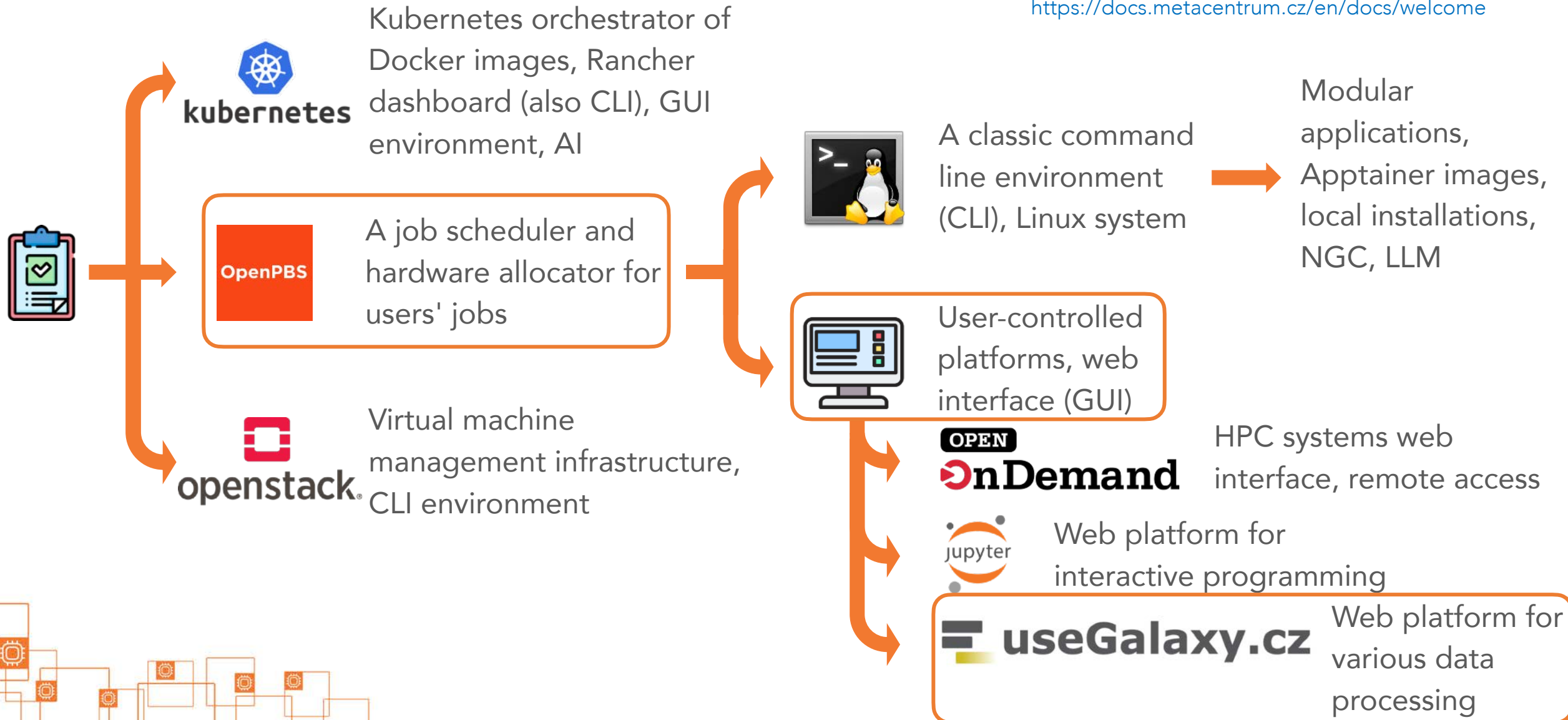
	sex	age	city	country
0	Male	64.0	Houston	Brazil
1	Female	NaN	San Jose	Mexico
2	Male	68.0	San Antonio	Mexico
3	Male	72.0	Dallas	USA
4	Male	81.0	San Antonio	Argentina

[]:



How to use it

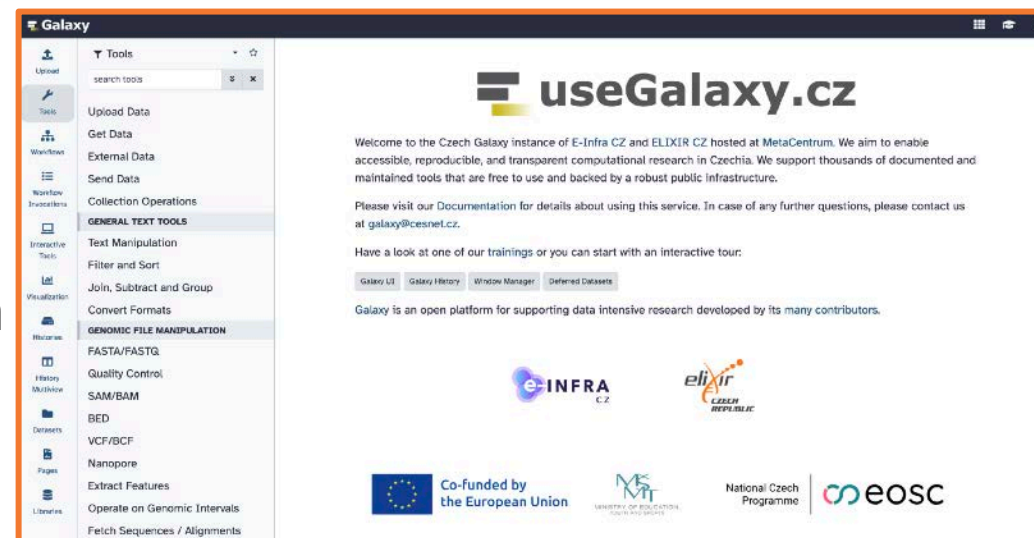
<https://docs.metacentrum.cz/en/docs/welcome>



Galaxy useGalaxy.cz

<https://usegalaxy.cz/>

- National instance hosted by MetaCentrum
- Web application based on OpenPBS
- A system for complex data analysis, workflow creation and sharing and teaching
- Processing of '-omic' data, LLM, ML, material science, ecology, chemistry, statistical analysis and humanities studies, and more
- Users do not need to worry about hardware reservation
- No programming required



The screenshot shows the Galaxy web interface. On the left is a navigation sidebar with categories like 'Tools', 'Workflows', and 'Interactive Tools'. The main content area displays the 'useGalaxy.cz' logo and a welcome message for the Czech instance. It includes a search bar, a list of tools (e.g., 'GENERAL TEXT TOOLS', 'GENOMIC FILE MANIPULATION'), and logos for funding partners: INFRA CZ, ELIXIR CZECH REPUBLIC, the European Union, and the National Czech Programme.





Upload



Tools



Workflows

Workflow
InvocationsInteractive
Tools

Visualization



Histories

History
Multiview

Datasets



Pages



Libraries

Tools

search tools

Upload Data

Get Data

External Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

GENOMIC FILE MANIPULATION

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

Extract Features

Operate on Genomic Intervals

Fetch Sequences / Alignments

GENOMICS ANALYSIS

Assembly



Welcome to the Czech Galaxy instance of [E-Infra CZ](#) and [ELIXIR CZ](#) hosted at [MetaCentrum](#). We aim to enable accessible, reproducible, and transparent computational research in Czechia. We support thousands of documented and maintained tools that are free to use and backed by a robust public infrastructure.

Please visit our [Documentation](#) for details about using this service. In case of any further questions, please contact us at galaxy@cesnet.cz.

Have a look at one of our [trainings](#) or you can start with an [interactive tour](#):

[Galaxy UI](#)[Galaxy History](#)[Window Manager](#)[Deferred Datasets](#)

Galaxy is an open platform for supporting data intensive research developed by its many contributors.



Co-funded by
the European Union



National Czech
Programme



Upload

Tools

Workflows

Workflow Invocations

Interactive Tools

Visualization

Histories

History Multiview

Datasets

Pages

Libraries

Tools

search tools

Upload Data

Get Data

External Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

GENOMIC FILE MANIPULATION

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

Extract Features

Operate on Genomic Intervals



Fetch Sequences / Alignments

GENOMICS ANALYSIS

Assembly

Upload from Disk or Web to **Unnamed history**

Regular Composite Collection Rule-based

 Drop files hereType (set all): Auto-detect Reference (set all): unspecified (?)  Choose local file Choose remote files Paste/Fetch data

Start

Pause

Reset

Close

Co-funded by
the European UnionNational Czech
Programme

Upload

Tools

Upload Data

Get Data

External Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

GENOMIC FILE MANIPULATION

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

Extract Features

Operate on Genomic Intervals

Fetch Sequences / Alignments

GENOMICS ANALYSIS

Assembly

Annotation

Mapping

Variant Calling

RNA Analysis

Multiple Alignments

Upload from Disk or Web to **Unnamed history**

Regular Composite Collection Rule-based

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

New File 115 b Auto-detect unspecified (?) 0%

Download data from the web by entering URLs (one per line) or directly paste content.

```
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/029/291/075/GCA_029291075.1_E_nip/GCA_029291075.1_E_nip_genomic.fna.gz
```

Type (set all): Auto-detect Reference (set all): unspecified (?)

Choose local file Choose remote files Paste/Fetch data **Start** Pause Reset Close

History

search datasets

Unnamed history

This history is empty.
You can load your own data or get data from an external source.



Co-funded by
the European Union



National Czech
Programme

eosc

- Upload
- Tools
 - search tools
- Upload Data
- Get Data
- External Data
- Send Data
- Collection Operations
- GENERAL TEXT TOOLS
 - Text Manipulation
 - Filter and Sort
 - Join, Subtract and Group
 - Convert Formats
- GENOMIC FILE MANIPULATION
 - FASTA/FASTQ
 - Quality Control
 - SAM/BAM
 - BED
 - VCF/BCF
 - Nanopore
 - Extract Features
 - Operate on Genomic Intervals
 - Fetch Sequences / Alignments
- GENOMICS ANALYSIS
 - Assembly
 - Annotation
 - Mapping
 - Variant Calling
 - RNA Analysis
 - Multiple Alignments

Upload from Disk or Web to Unnamed history

Regular Composite Collection Rule-based

New File 115 b Auto-detect unspecified (?) 100%

Download data from the web by entering URLs (one per line) or directly paste content.

```
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/029/291/075/GCA_029291075.1_E_nip/GCA_029291075.1_E_nip_genomic.fna.gz
```

Type (set all): Auto-detect Reference (set all): unspecified (?)

Choose local file Choose remote files Paste/Fetch data Start Pause Reset Close

History

search datasets

Unnamed history

0 B

1: GCA_029291075.1_E_nip_g
enomic.fna.gz



- Upload
- Tools
- Workflows
- Workflow Invocations
- Interactive Tools
- Visualization
- Histories
- History Multiview
- Datasets
- Pages
- Libraries
- Notifications
- More

- Tools
- search tools
- Upload Data
 - Get Data
 - External Data
 - Send Data
 - Collection Operations
 - GENERAL TEXT TOOLS**
 - Text Manipulation
 - Filter and Sort
 - Join, Subtract and Group
 - Convert Formats
 - GENOMIC FILE MANIPULATION**
 - FASTA/FASTQ
 - Quality Control
 - SAM/BAM
 - BED
 - VCF/BCF
 - Nanopore
 - Extract Features
 - Operate on Genomic Intervals
 - Fetch Sequences / Alignments
 - GENOMICS ANALYSIS**
 - Assembly
 - Annotation
 - Mapping
 - Variant Calling
 - RNA Analysis
 - Multiple Alignments

1: **GCA_029291075.1_E_nip_genomic.fna.gz** ok

21,044 sequences
format **fasta.gz** database ? size **281.4 MB**

[Preview](#) [Visualize](#) [Details](#) [Edit](#)

This dataset is large and only the first megabyte is shown below.
[Show all](#) | [Save](#)

```
>JAQBSW010000001.1 Eudiplozoon nipponicum isolate JV_EN_01 E_nip_1, whole genome shotgun sequence
gcaatgttctctcattcgagtaattaacctgctggctgatcgccctacgtaagttgatcgacaacttgcgcgtatctt
ggtaaaaaatatttgatattgacattaacgactgtttctctttgattactggtaaggcaagtggttacacataaac
actcgtagtttagctgcattaaatgctggttaagctgcttcaactttctttgtgctcattcgggaaactgcatcac
cataaattgggatgttaggtagacgcttttctttctggcgttaataagctgtttctgtttgattcctcttttaaat
tgattcaatataatgctTAGGATaccattagacataaactgcttaattgctttatataataatcttttagaatt
gactaaccaactgctcaattcttaaaagcaaccagcaactgtgataattatgaaatggtaacaaactgctgtat
aacaaatactgtgcagaccatgttggtttatggtaaatgttctgttttaatttaccattagttttttcattaatgata
tctaggaaaggcagacagtcattctctgctgctgctggaagcagatattcttatgtgctttgtgaaacttaag
taattgtgctgattgacacgttcttaagtaacaagaatataatcaccgtaccgtatatattgagcacatttaatta
tgattttctaggtgccctagaaaatctcagcaaacactggagataaggggctccattgacacacatttcaat
tactttgctgctccacttgtctatttcatctgatttatcgtctagacgtggaattttgtattgcatttaacacgttttc
catctttgtactgtagtcagatttgcattataaagtcgctctttctttgcttcttacttaagaacagggtcgaa
tcacgaacattgcttcaaggttcaacaagcacataaagaatcggcttcacgtcggagcagagaagatgactgtct
gcctttctagatgactattaaagaagaactaatggtaacttaaacgaaacatttacataaaccaacatggctg
cacagtttgcataaacagcagtttgtgctatttaaacataaattatcaacagttcgtggttcttcaagaatagac
aggttggttagcaagattctaaagaaaatgaatataaagaacaattaacggttaaatgtcctaatggctatcccagaca
attaattgaatcaattataaaaggggagttaacagaaaacagcgtattatgggcagaaaagaaaatagctaccta
acataccatttaagggggatgacgtctcccgaatggcacaagaagaagatgaagcagcattgacacacatttaagca
gccaaactcagagtgattatagggtaaacacactgcttactagcaatcaagagaaaacagcgttaattgctgatc
aaatattttaccatattgcatgcatgctgttgcgtcaacttaccgtaggcgcgaccagacgggttaattactcgaa
tgagagaacattgcaacttaaacgcccgttttaaatcaaatgggtaatacacgctgctgattgctgcaacacatcatgaa
gcatcgacgtatgttctcagacgtagcattcaagtaattactaaatgcaaaacaaaggagctagccacattatgg
ataaacaaattgacagcggatattgcaagcagaagaagcagctcaagcattgagcctgaactggatgtagggcagcga
atgtgattggttccgtgtttcacactctctatgttcacatattctatcttgttttgccttcaaatttatataaaa
atatgttcattagaagatatttcagaagacaatgcaagaagaatcttctgtactgataaattcaaatattttgca
taGGCTCTTATGAAACTAAGCTATAGGTGACATAGTTCGCTGTTTACGTATGCAACATTGATGAGCGAAATCGTGGC
AAAGAAAAGGCTGTAGGATGTTACCCGTTGTTAATGAATGCTTAAGCACTGCTGGTAAATAGGAAGGTGTTGTACCAAT
CGAACCTTAGTATTCCAGGAACCTCGGAACACGAGCACGAACCTTATGGTGTCCGTACTCGGAAAAAAGTATGCGCCA
ACATAGGCAACCTTCCAATTAGTCTATAAATCAACAATaatgtcattttataaataaacgaacattgtttgcggggcg
atcATAACCTTtttataatcagggttgcgaactgttataaaaacctgaccattaagttctAAAATTTAGTCATTATA
ATCTAAGatttgtagtgtagaaaaggcaattcaaccagtagaccggtttcgttcttatgggaactcatcatgactggc
ctgttagcatccatttagcgttaaagttcgaactaacatccacaactctgcatcaacgaAAGGATACACTGTTATATG
GGGAAATGGGatagttatttggaaacttagcgCTAAATGGATGATATATAGGCTCACaaaggaagactaaccaag
acgattagttagtataaactgaaattgtgctgtagtttgcggCACAGTGACTcggtagttagagcaccacattcggaa
acagacgttcccagggttgcgcCCTGACCGcttcaaatctggcaagtacatgaggagttctcaataaggcgaatcgg
tctactggcgaatttgcgtttctacactgtacaattcttagtttatactgcaaatgtatgcacttaattggatcaggtga
tcatatcaagttcgaacacttgattataaatttatgTCATTTTGTACTCAGTGTATGCAACATTTTTATCATCGTTTCC
TCACTATTTAACCCGCAAAAGAAACAAATGACACAGTAGAAAAAAAAGATCAGctaaaaattatogaaaattatagaaa
gcatgcataaaaaataaattagctcACTCACGAGAACACGCTGCCTATCCGCAATTAAGTACTGAGCAAATTTGATGCAC
```

History

search datasets

Unnamed history

295 MB

1: **GCA_029291075.1_E_nip_geno**

mic.fna.gz

- Upload
- Tools
- Workflows
- Workflow Invocations
- Interactive Tools
- Visualization
- Histories
- History Multiview
- Datasets
- Pages
- Libraries
- Notifications
- More

- Tools
- search tools
- Upload Data
 - Get Data
 - External Data
 - Send Data
 - Collection Operations
 - GENERAL TEXT TOOLS**
 - Text Manipulation
 - Filter and Sort
 - Join, Subtract and Group
 - Convert Formats
 - GENOMIC FILE MANIPULATION**
 - FASTA/FASTQ
 - Quality Control
 - SAM/BAM
 - BED
 - VCF/BCF
 - Nanopore
 - Extract Features
 - Operate on Genomic Intervals
 - Fetch Sequences / Alignments
 - GENOMICS ANALYSIS**
 - Assembly
 - Annotation
 - Mapping
 - Variant Calling
 - RNA Analysis
 - Multiple Alignments

1: **GCA_029291075.1_E_nip_genomic.fna.gz** ok

21,044 sequences
format **fasta.gz** database ? size **281.4 MB**

[Preview](#) [Visualize](#) [Details](#) [Edit](#)

This dataset is large and only the first megabyte is shown below.
[Show all](#) | [Save](#)

```
>JAQBSW010000001.1 Eudiplozoon nipponicum isolate JV_EN_01 E_nip_1, whole genome shotgun sequence
gcaatgttctctcattcgagtaattaaccgtctggctgatcgccctacgtaagttgatcgacaacttgcgcgatctt
ggtaaaaaatatttgatattgacattaacgactgtttctctttgattactggtaaggcaagtggttacacataaac
actcgtagtttagctgcattaaatgctggttaagctgcttcaactttctttgtgctcattcgggaaactgcatcac
cataaatgggatgttaggtagacgcttttctttctggcgttaataagctgtttctgtttgattcctcttttaaat
tgattcaatnaatagctTAGGATaccattagacataaactggttaattgctttatataatattttctttagaatatt
gaactaaccaactgtcaattcttaaaagcaaccacgaactgtgataattatattgaaatggtaacaaaactgctgat
aacaataactgtgcagaccatgttggtttatggtaaatgttctgtttaaattaccattagttttttcattaatagata
tctaggaaaggcagacagtcatttctcgtgctctgctgtaagcagatattcttatgtgctttgtgaaacttaag
taatgttctgtgattgcgacctgttcttaagtaacaagaatataatcaccgtaccgtatatattgagcacatttaatta
tgatatttctaggtgccctagaaaatctcagccaactggagataaggggctccattgagcacaccatttcaat
tactttgctcctccacttgtctatttcatctgatttctgcttagacgtggaatttggattgcatthaacacgcttttc
catcttttgcctagctagctagatttgcattataagtcgctctttctttgcttcttacttaagaacagggtcgaa
tcacgaacattgcttcaaggttcaacaagcacataagaatctcggcttccagctggagcagagaagatgactgtct
gcctttcctagatgactatnaagaagaactaatggtaacttaaacgaaacatttacataaaccaacatggctg
cacagtttgcataaacagcagtttgtgctatttaacataaattatcaacagttcgtggttcttcaagaatagac
aggttggttagcaagattctaaagaaaatgaatataataaagcaattaacggttaaatgtcctaatggctatcccagaca
attaattgaatcaattataaaaggggagttaacagaaaacagcgtattatgggcagaaaagaaaatagctaccta
acataccatttaagggggatgcatctcccgaatggcacaagaagaagatgaagcagcattgacacacacattaatgca
gccaaactcagagtgattattagggttaacacacttgcctttactagcaatcaagagaaaacagccttaattgctgatc
aaatattttaccatattgcatgcatggttgcgacacttaactagcagcagcagcagcagcagcagcagcagcagcagc
tgagagaaacattgcaacttaaacgcccgttttaaatcaaatgggtaatacacgctgctgattgagcaacacatcatcgaa
gcatcgacgctgatttctcagacgtagcattcaagtaattactaaatgcaaaaagggagctagccacattatgg
ataaacaaattgacagcggatattgcaagcagaagaagcagctcaagcattgagcctgaactggatgtagggcagcga
atgtgattggtttccgtgtttcacactctctatgttcacatatttctatcttgttttgccttcaaatttatataaaa
atatgttcatagaaagatatttcagaagacaatgcaagaagaaattttctgtactgataaattcaaatattttgca
taGGCTCTTATGAAACTAAGCTATAGGTGACATAGTTCGCTGTTTACGTATGCAACATTGATGAGCGAAATCGTGGC
AAAGAAAAGGCTGTAGGATGTTACCCGTTGTTAATGAATGCTTAAGCACTGCTGGTAAATAGGAAGGTGTTGTACCAAT
CGAACCTTAGTATTCCAGGAACCTCGGAACACGAGCACGAACTTTATGGTGTCCGTACTCGGAAAAAAGTATGCGCCA
ACATAGGCAACCTTCCAATTAGTCTATAAATCAACAATaatgtcattttataaataaacgaacattgtttgcgpggcg
atcATAACCTTttttataatcagggttgcgaactgtttataaaaacctgaccattaagttctAAAATTTAGTCATTATA
ATCTAAGatttgtagtgtagaaaaggcaattcaaccagtagaccggtttcgttcttatgggaactcatcatgactggc
ctgttagcatccatttagcgttaaaattcgaactaacatccacaactctgcatcaacgaAAGGATACACTGTTATATG
GGGAAATGGGatagttatttggaaacttagcgCTAAATGGATGATATATAGGCTCACaaaaggaagactaaccaag
acgatttagttatataaactgaaattgtgctagtttgcgCACAGTGACTcggtagttagagcaccacattcggaa
acagacgttccagggttgcgCCTGACCGcttcaaatctggcaagtacatgaggagttctcaataaggcgaatcgg
tctactggcaaatgtgctttctacactgtacaattcttagtttatactgcaaatgtatgcacttaattggatcaggtga
tcatatcaagttcgaacacttgattataaatttatgTCATTTTGTACTCAGTGTATGCAACATATTTTATCATCGTTTCC
TCACTATTTAACCCGCAAAAGAAACAAATGACACAGTAGAAAAAAAAGATCAGctaaaaattatogaaaattatagaaa
gcatgcataaaaaataaattagctcACTCACGAGAACACGCTGCCTATCCGCAATTAAGTACTGAGCAAATTTGATGCAC
```

History

search datasets

Unnamed history

295 MB

1: GCA_029291075.1_E_nip_geno mic.fna.gz

Tools

statistics

Show Sections

Statistics on presence-absence of a numeric variable

Summary Statistics for any numerical column

FASTQ Summary Statistics by column

Fasta Statistics display summary statistics for a FASTA file

SeqKit statistics of FASTA/Q files

Compute quality statistics

Genome annotation statistics

Read length statistics from a set of FAST5 files

BAM Index Statistics

Stacks: statistics on stacks found for multiple samples

MiModD Coverage Statistics calculates coverage statistics for a BCF file as generated by the MiModd Variant Calling tool

ProteomIQon PSMStatistics utilizes semi supervised machine learning techniques to integrate search engine scores as well as the mentioned quality scores into one single consensus score.

MapStatistics Extract extended statistics on the features of a map for quality control

zonal statistics over each area

Boxplot of quality statistics

Dr. Disco (classify) Classifies detected break-points in RNA-seq based on corresponding statistics and blacklists

cmstat Summary statistics for covariance model

BAM/SAM Mapping Stats reads mapping statistics for a provided BAM or SAM file.

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz ok

21,044 sequences

format **fasta.gz** database ? size **281.4 MB**

Preview

Visualize

Details

Edit

Edit Dataset Attributes

Attributes

Datatypes

Permissions

Name

renamed_GCA_029291075.1_E_nip_genomic.fna.gz

Info

My genome file

Annotation - optional

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Nullam justo enim, consectetur nec, ullamcorper ac, vestibulum in, elit. Maecenas aliquet accumsan leo.

Add an annotation or notes to a dataset, annotations are available when a history is viewed.

Database/Build - optional

unspecified (?)

Save

Auto-detect

History

search datasets

Unnamed history

Unnamed history

Annotation (optional)

Add Tags

Save

Cancel

295 MB

1

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz

Tools

statistics

Show Sections

Statistics on presence-absence of a numeric variable

Summary Statistics for any numerical column

FASTQ Summary Statistics by column

Fasta Statistics display summary statistics for a FASTA file

SeqKit statistics of FASTA/Q files

Compute quality statistics

Genome annotation statistics

Read length statistics from a set of FAST5 files

BAM Index Statistics

Stacks: statistics on stacks found for multiple samples

MiModD Coverage Statistics calculates coverage statistics for a BCF file as generated by the MiModd Variant Calling tool

ProteomIQon PSMStatistics utilizes semi supervised machine learning techniques to integrate search engine scores as well as the mentioned quality scores into one single consensus score.

MapStatistics Extract extended statistics on the features of a map for quality control

zonal statistics over each area

Boxplot of quality statistics

Dr. Disco (classify) Classifies detected break-points in RNA-seq based on corresponding statistics and blacklists

cmstat Summary statistics for covariance model

BAM/SAM Mapping Stats reads mapping statistics for a provided BAM or SAM file.

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz ok

21,044 sequences

format **fasta.gz** database ? size **281.4 MB**

Preview

Visualize

Details

Edit

Edit Dataset Attributes

Attributes

Datatypes

Permissions

Name

renamed_GCA_029291075.1_E_nip_genomic.fna.gz

Info

My genome file

Annotation - optional

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Nullam justo enim, consectetur nec, ullamcorper ac, vestibulum in, elit. Maecenas aliquet accumsan leo.

Add an annotation or notes to a dataset; annotations are available when a history is viewed.

Database/Build - optional

unspecified (?)

Save

Auto-detect

History

search datasets

Unnamed history

Unnamed history

Annotation (optional)

Add Tags

Save

Cancel

295 MB

1

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz

Tools

statistics

Show Sections

Statistics on presence-absence of a numeric variable

Summary Statistics for any numerical column

FASTQ Summary Statistics by column

Fasta Statistics display summary statistics for a FASTA file

SeqKit statistics of FASTA/Q files

Compute quality statistics

Genome annotation statistics

Read length statistics from a set of FAST5 files

BAM Index Statistics

Stacks: statistics on stacks found for multiple samples

MiModD Coverage Statistics calculates coverage statistics for a BCF file as generated by the MiModd Variant Calling tool

ProteomIQon PSMStatistics utilizes semi supervised machine learning techniques to integrate search engine scores as well as the mentioned quality scores into one single consensus score.

MapStatistics Extract extended statistics on the features of a map for quality control

zonal statistics over each area

Boxplot of quality statistics

Dr. Disco (classify) Classifies detected break-points in RNA-seq based on corresponding statistics and blacklists

cmstat Summary statistics for covariance model

BAM/SAM Mapping Stats reads mapping statistics for a provided BAM or SAM file.

Fasta Statistics display summary statistics for a FASTA file (Galaxy Version 2.0)

Run Tool

Tool Parameters

FASTA or Multi-FASTA file *

Select a dataset

accepted formats

FASTA dataset to get sta

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz (as fasta)

Estimated genome size - optional

This parameter is optional. If provided, it will be used for calculating the NG50 statistic. (--genome_size)

Generate gap stats

 No

(--gaps_option)

Additional Options

Email notification

 No

Send an email notification when the job completes.

Attempt to re-use jobs with identical parameters?

 No

This may skip executing jobs that you have already run.

Run Tool

Help

Purpose

Displays the summary statistics for a FASTA file.

Outputs

This tool generates two outputs: a general summary and an optional gap stats file.

The general summary includes the following information:

- Lengths: n50, min, max, median and average
- Number of base pairs: A, C, G, T, N, Total and Total_not_N
- Number of sequences
- GC content

In addition the optional gap stats BED file includes the information about gaps localization.

History

search datasets

Unnamed history

Unnamed history

Annotation (optional)

Add Tags

Save Cancel

295 MB

1

1: renamed_GCA_029291075.1_E_nip_genomic.fna.gz

Upload

Tools

Workflows

Workflow Invocations

Interactive Tools

Visualization

Histories

History Multiview

Datasets

Pages

Libraries

Notifications

More

Tools

statistics

Show Sections

Statistics on presence-absence of a numeric variable

Summary Statistics for any numerical column

FASTQ Summary Statistics by column

Fasta Statistics display summary statistics for a FASTA file

SeqKit statistics of FASTA/Q files

Compute quality statistics

Genome annotation statistics

Read length statistics from a set of FAST5 files

BAM Index Statistics

Stacks: statistics on stacks found for multiple samples

MiModD Coverage Statistics calculates coverage statistics for a BCF file as generated by the MiModd Variant Calling tool

ProteomIQon PSMStatistics utilizes semi supervised machine learning techniques to integrate search engine scores as well as the mentioned quality scores into one single consensus score.

MapStatistics Extract extended statistics on the features of a map for quality control

zonal statistics over each area

Boxplot of quality statistics

Dr. Disco (classify) Classifies detected break-points in RNA-seq based on corresponding statistics and blacklists

cmstat Summary statistics for covariance model

BAM/SAM Mapping Stats reads mapping statistics for a provided BAM or SAM file.

Started tool **Fasta Statistics** and successfully added 1 job to the queue.

It produces this output:

• 2: **Fasta Statistics on data 1: summary stats**

You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

Here is a link to the job: [83e4c30195971270](#)

History

search datasets

Unnamed history

Unnamed history

Annotation (optional)

Add Tags

Save Cancel

295 MB

2

2: **Fasta Statistics on data 1: summary stats**

1: renamed_GCA_02929107
5.1_E_nip_genomic.fna.gz

- Upload
- Tools
- Workflows
- Workflow Invocations
- Interactive Tools
- Visualization
- Histories
- History Multiview
- Datasets
- Pages
- Libraries
- Notifications
- More

Tools

[Show Sections](#)

Statistics on presence-absence of a numeric variable

Summary Statistics for any numerical column

FASTQ Summary Statistics by column

Fasta Statistics display summary statistics for a FASTA file

SeqKit statistics of FASTA/Q files

Compute quality statistics

Genome annotation statistics

Read length statistics from a set of FAST5 files

BAM Index Statistics

Stacks: statistics on stacks found for multiple samples

MiModD Coverage Statistics calculates coverage statistics for a BCF file as generated by the MiModd Variant Calling tool

ProteomIQon PSMStatistics utilizes semi supervised machine learning techniques to integrate search engine scores as well as the mentioned quality scores into one single consensus score.

MapStatistics Extract extended statistics on the features of a map for quality control

zonal statistics over each area

Boxplot of quality statistics

Dr. Disco (classify) Classifies detected break-points in RNA-seq based on corresponding statistics and blacklists

cmstat Summary statistics for covariance model

BAM/SAM Mapping Stats reads mapping statistics for a provided BAM or SAM file.

2: Fasta Statistics on data 1: summary stats ok

30 lines 2 columns

format **tabular** database ? size **664 b**
[Preview](#)
[Visualize](#)
[Details](#)
[Edit](#)

Column 1	Column 2
Scaffold L50	3219
Scaffold N50	87067
Scaffold L90	11600
Scaffold N90	19508
Scaffold len_max	557136
Scaffold len_min	4973
Scaffold len_mean	44658
Scaffold len_median	23894
Scaffold len_std	52885
Scaffold num_A	305506036
Scaffold num_T	305603756
Scaffold num_C	164346741
Scaffold num_G	164346396
Scaffold num_N	0
Scaffold num_bp	939802929
Scaffold num_bp_not_N	939802929
Scaffold num_seq	21044
Scaffold GC content overall	34.97
Contig L50	3219
Contig N50	87067
Contig L90	11600
Contig N90	19508
Contig len_max	557136
Contig len_min	4973
Contig len_mean	44658

History

Unnamed history

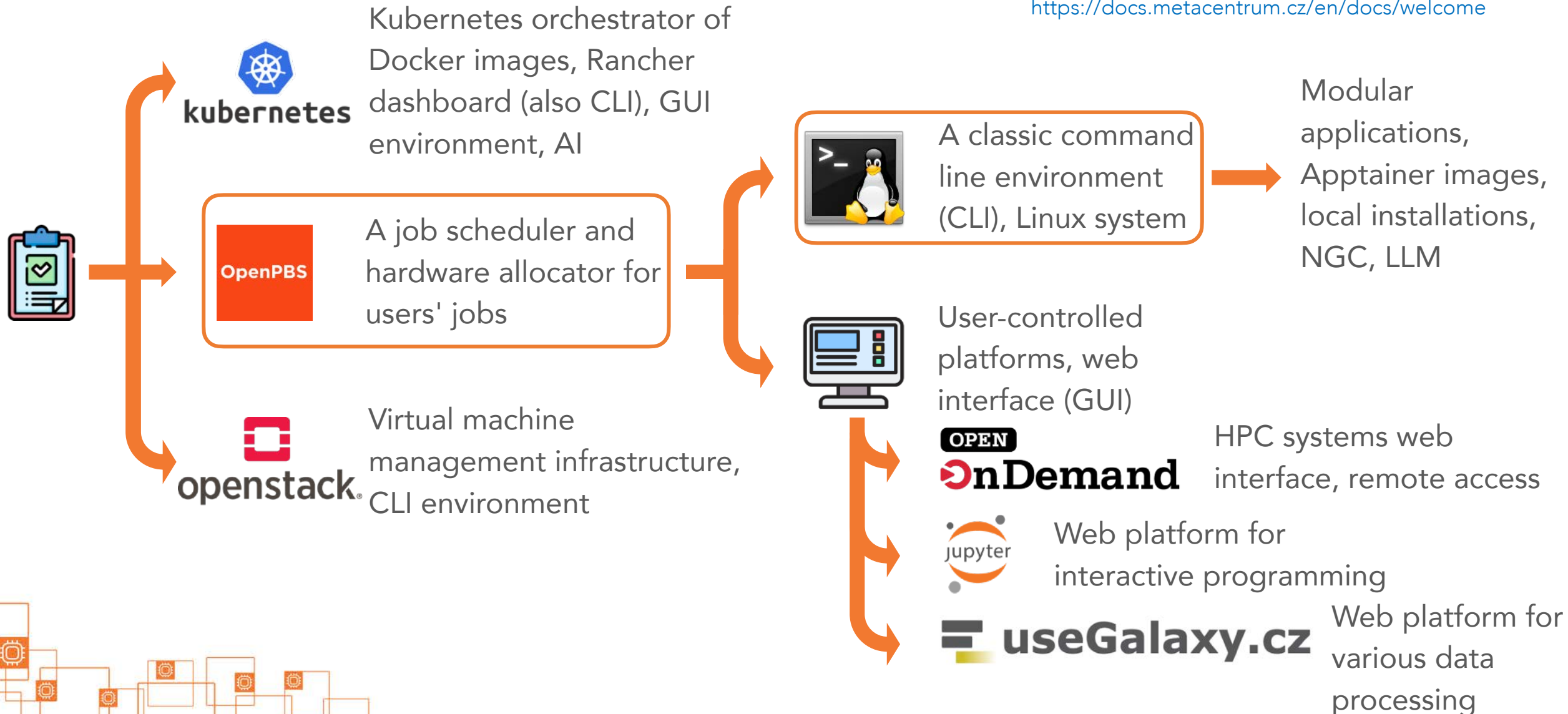
1.25 GB

2: Fasta Statistics on data 1: summary stats

1: renamed_GCA_02929107
5.1_E_nip_genomic.fna.gz

How to use it

<https://docs.metacentrum.cz/en/docs/welcome>



- Grid computing (OpenPBS scheduler)
 - Maximum flexibility
 - Long batch jobs (days/weeks)
 - Interactive jobs
 - Parallel and multi-node computing
 - GPU acceleration (NVIDIA H100, 96 GB)
 - SSH access on a dedicated nodes

```

cesnet
[BOOKWORM]vorel@skirit:~$ ssh vorel@skirit

Your Home Directories
-----
Avail |   DATA   |  FILES  | Backup | Storage
space | quota  used | quota  used |         |
-----|-----|-----|-----|-----|
313T  none  375G   none  4.88k   snap  brno12-cerit
50T   4.29T 60.3G  2.5M  18.6k  snap  brno2
17T   3.32T 24k    1M    9      full  budejovice1
30T   10.4G 12k    none   8      -     liberec3-tul
353T  4.29T 1.73T  3M   192k   snap  plzen1
60T   7.34G 44k    none   18     -     praha2-natur
12T   5.36T 941G  1.01M 113k   full  praha5-elixir
55T   7.34G 28k    none   11     full  pruhonice1-ibot
145T  2.14T 5.16G  2M   41.2k  snap  vestec1-elixir

CPUs
-----
Free  Used  Total  Centre
7568 32132 39700  META

Contact
-----
E-mail:  meta@cesnet.cz
Web:    http://www.metacentrum.cz/

Tip of the day:  Have you ever heard about a Chipster? Chipster is a web-based interactive analysis software for NGS and microarray data. More information at https://docs.metacentrum.cz/en/docs/related/chipster.

(BOOKWORM)vorel@skirit:~$

```


Batch job script example

```
#!/bin/bash
#PBS -q default@pbs-m1.metacentrum.cz
#PBS -l walltime=24:0:0
#PBS -l select=1:ncpus=8:mem=100gb:scratch_ssd=50gb:mpiprocs=1:omphreads=8
#PBS -N my_job_name
#PBS -M my_email@xyz
#PBS -m e

ulimit -s unlimited
trap "clean_scratch" TERM EXIT
export TMPDIR=$SCRATCHDIR

# test if a scratch directory exists
# variable SCRATCHDIR is set automatically
test -n "$SCRATCHDIR" || { echo >&2 "Variable SCRATCHDIR is not set!"; exit 1; }

# set a DATADIR variable
DATADIR="/storage/brno12-cerit/home/vorel/data/"

# copy input file "data.fa" to the scratch directory
cp $DATADIR/data.fa $SCRATCHDIR || { echo >&2 "Error while copying input file(s)!!"; exit 2; }

# move into the scratch directory
cd $SCRATCHDIR

# load a module for your application
module add blast-plus/blast-plus-2.12.0-gcc-8.3.0-ohlv7t4

# run the calculation
# do not forget to use reserved CPUs by '-num_threads' flag
# variable PBS_NCPUS is a number of CPUs requested for the entire job
blastp -query data.fa <other_parameters> -num_threads $PBS_NCPUS -out results.txt

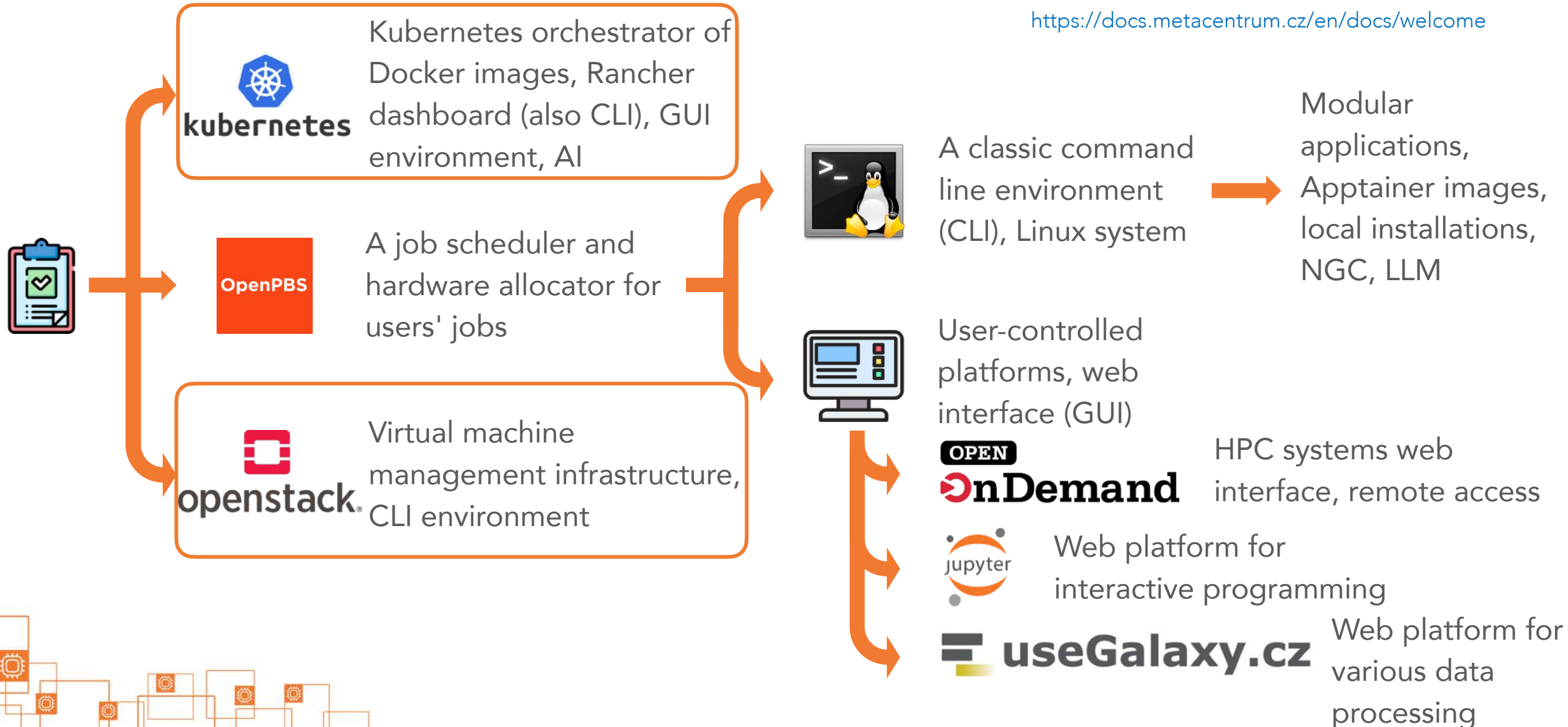
#copy results
cp results.txt $DATADIR || export CLEAN_SCRATCH=false
```

- Define HW resources (-l), queue (-q), and walltime (-l), set the job name (-N) and email alert (-m)
- You can define as many variables as you want
- Available modules can be listed by command `module avail *key_word*` on any frontend
- The scratch directory will be cleaned automatically



How to use it

<https://docs.metacentrum.cz/en/docs/welcome>



■ Kubernetes

<https://docs.cerit.io/en/docs/platform/overview>

- Open-source container orchestration engine that automates the deployment, scaling and management of containerised applications
- A Docker image is an essential part of container infrastructure. It contains an application and all its necessary components, such as libraries and other files

<https://docs.cerit.io/en/docs/news>

Rancher apps

Rancher Applic

Ansys

Desktop

Matlab

Minio

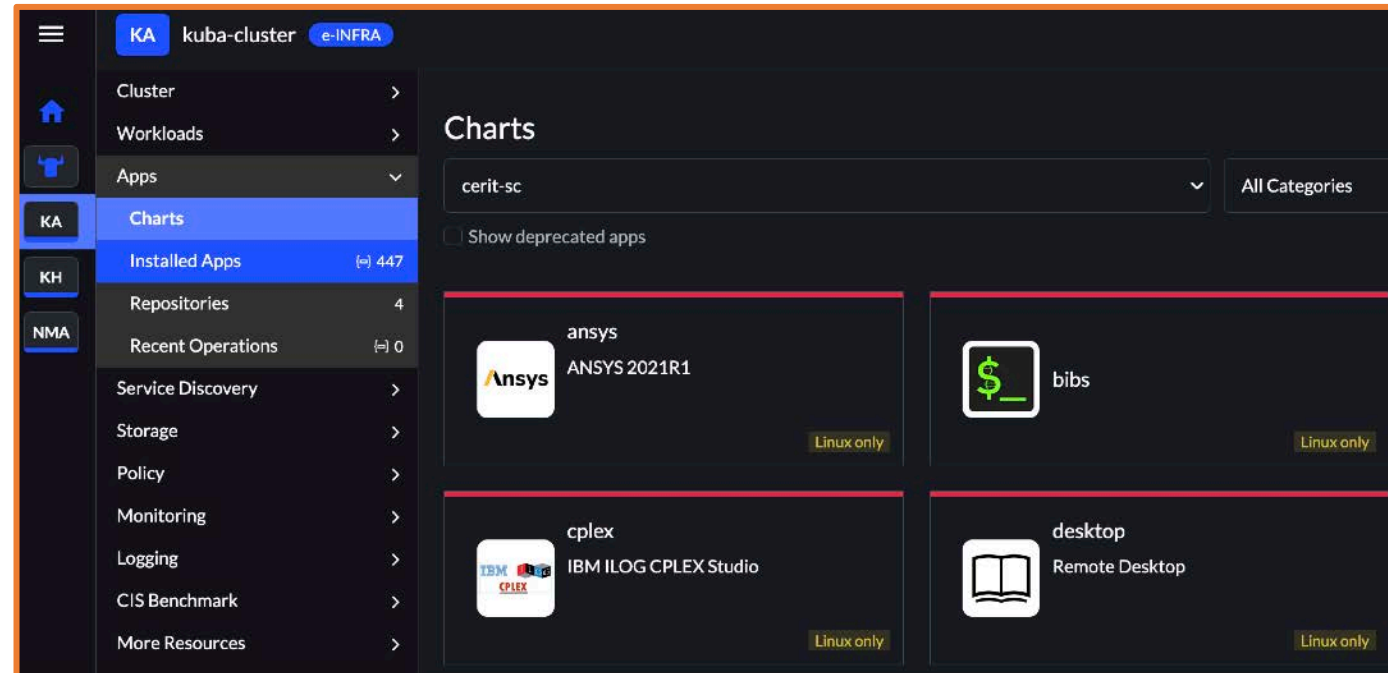
Workflows

Running Nextflow Pipelines in
Kubernetes

Argo Workflows

TES/WES

Snakemake



KA kuba-cluster e-INFRA

Cluster >

Workloads >

Apps >

KA Charts

KH Installed Apps (447)

NMA Repositories 4

Recent Operations (0)

Service Discovery >

Storage >

Policy >

Monitoring >

Logging >

CIS Benchmark >

More Resources >

Charts

cerit-sc All Categories

Show deprecated apps

ansys ANSYS 2021R1 Linux only

bibs Linux only

cplex IBM ILOG CPLEX Studio Linux only

desktop Remote Desktop Linux only



It can also run as a batch job in the MetaCentrum grid infrastructure

■ Foldify

- A web application based on the Alphafold tools



AlphaFold 3

AlphaFold 2

ColabFold

OmegaFold

ESMFold

Mgr. Jiří Vorel Ph.D. ▾

Powered by Advanced AI

Protein Folding Platform

3D Result Comparison Multiple Tools Powerful Hardware

Get Started →

View Examples

2000+

Predicted Proteins

5

Prediction Tools

24/7

Processing

Select Prediction Tool & Start Your Computation

Select a tool to predict protein or molecule structures. New to this? Try **AlphaFold 2** for reliable results, or **MultiFold** to compare multiple prediction tools.

MultiFold
Compare multiple prediction tools

Compare Tools

AlphaFold 3
Latest version with advanced capabilities

Latest

AlphaFold 2
Reliable and proven protein structure prediction

Stable

ColabFold
Fast and efficient protein predictions

Fast Prediction

OmegaFold
End-to-end protein structure prediction

ESMFold
Fast folding with language models

Running & Completed Computations (0)

🕒 Compare Multiple Results

Select multiple completed jobs to compare their results in a single view. The first selected job will be used as reference.

Select jobs to compare

🔍 Search Jobs

Type job name...



View

My Jobs

Public Jobs



Visibility

Job Name

Service

Started

Status

Actions

[← Back to Dashboard](#)

AlphaFold 3

Predict protein structures with enhanced accuracy using AlphaFold 3. Configure your job parameters below and submit for computation.



Input Form

Guided step-by-step configuration

Use JSON instead?

[JSON Mode](#)

1 Basic Information

Job Name * ⓘ

test-job

Model Seeds * ⓘ

1

2 Sequences and Ligands

1 Entity 1 • Protein

Type * ⓘ

Protein

IDs * ⓘ

A

Sequence *

```

MGSFAKMFVAASFVLCFCIIGCFSADQNESPFQKNFIINSNTASKGVDYVSQSWSMFKNFFKRNFENAIEEGERFFFIFARNFFMIS
SHNAEYASGGKIYELTLNKFSDAKESELMKLRGYKAVMKKHKDAPKGSTYISPSVDFKLPTDVDWRNDGAVTDVKNQGCGCGSC
WAFSTTGSLEGQHRKTGNLVSLEQQLVDCSSSYGNMGCNGGLMDNAFAYIKATNGIDYEDKYPPYSGDTGSAEDTCYFKE
EDIGAVDTGYVDIPTEDEAALQEAVANVGPVSVAINAGRADFMMYKOGIYKPDECPGQMNDLDHGVLVVGYGSENGODYWI
VKNSWGPDWGESGYIRMARNSGNLCGIATAASYPLV

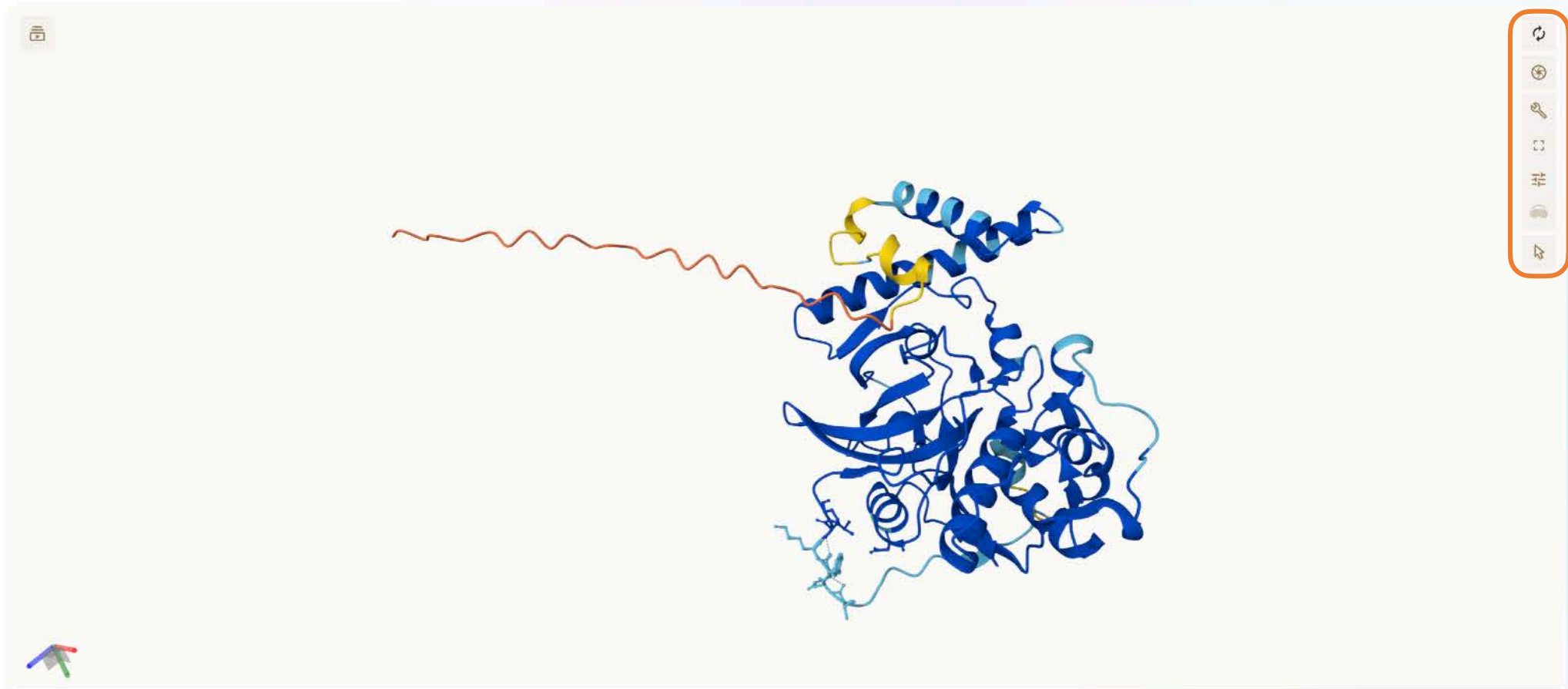
```



Protein sequence (no FASTA header). Copy IDs must be unique.

▼ Show 168 more characters

Very low (pLDDT < 50) Low (70 > pLDDT > 50) Confident (90 > pLDDT > 70) Very high (pLDDT > 90)



Open in 

PLDDT data not available.

MGSFAKMFVAASFVLCFCIIIGCF SADQNESPFQKNFIINSNTASKGV D VYSQSWMFKNFFKRN FENAIIEEGERFFIFARNFFMIS SHNAEYASGKKIYELTLNKFSDAKESELMKLRGYKAVMKKHKDAPKGSTYISPSVDFKLP TDVDWRNDGAVTDVK
NQGCQCGSCWAFSTTGSLEGQHFRKTGNL VSLSEQQLVDC...

▼ Show 168 more characters

Very low (pLDDT < 50) Low (70 > pLDDT > 50) Confident (90 > pLDDT > 70) Very high (pLDDT > 90)

Sequence of test-job Chain 1: A

1 11 21 31 41 51 61 71 81 91 101 111 121 131 141 151
MGSFAKMFVAASFVLCFCIIIGCF SADQNESPFQKNFIINSNTASKGV D VYSQSWMFKNFFKRN FENAIIEEGERFFIFARNFFMIS SHNAEYASGKKIYELTLNKFSDAKESELMKLRGYKAVMKKHKDAPKGSTYISPSVDFKLP TDVDWRND
161 171 181 191 201 211 221 231 241 251 261 271 281 291 301
GAVTDVKNQGCQCGSCWAFSTTGSLEGQHFRKTGNL VSLSEQQLVDCSSSYGNMCGGLMDNAPAYIKATNGIDYEDKYPVYSGDTGSASDTCYFKREDTGAVDTGYVDI PTEDEAAIQEAVANVGPVSVATNAGRADPFMMYKQGIYKPDCECPG
311 321 331 341 351 361
QMNDLDHGVLVVGYSSENGQDYWIVKNSWGPDWGESGYIRMARNSGNLCGIATAASYPLV

Structure Tools

Structure

test-job

Type Model

MET 1 | A [+ 14 other Residues]

Measurements

+ Add

Quick Styles

Apply Representation

Default Cartoon Spacefill Surface

Apply Style

Default Illustrative

Components test-job

Preset + Add

Polymer Cartoon

[Focus] Target Ball & Stick

[Focus] Surroundings (5 Å)

Export Models

11:00:57 Updated Structure Focus Representation in 0ms.

11:00:57 Updated Cartoon in 16ms.

11:00:57 Updated Structure Focus Representation in 1ms.

Open in MolS

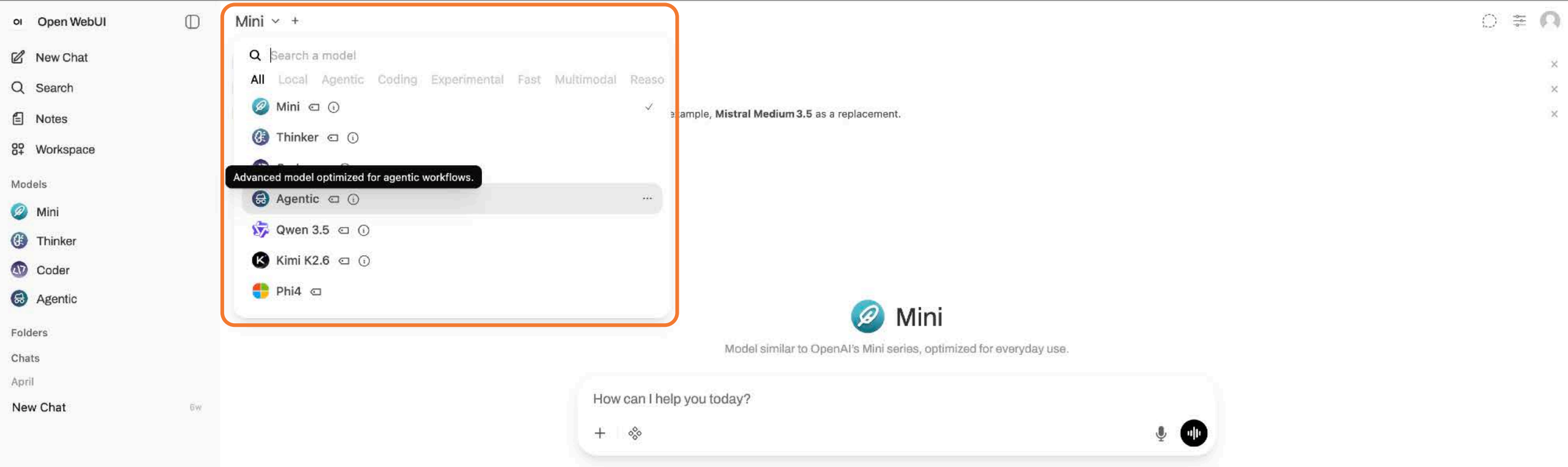
■ AI chatbot (Open WebUI, LLMs)

<https://docs.cerit.io/en/docs/ai-as-a-service/chat-ai>

<https://chat.ai.e-infra.cz/>

- The AI-powered chatbot interface runs strictly on local hardware
- Open WebUI itself logs at the 'INFO' level by default, meaning that request/response data is not logged
- Only system administrators have access to these logs, which are not transmitted anywhere else
- Data does not leave the infrastructure
- Image generator and picture editor included
- Can extract text from images
- Programming languages proficiency
- Visit documentation for the description of available models





You can select any available model and view its notes



The primary uses of different models vary. For general computing, coding, image creation, test processing, etc.



Please note that the available models may change over time

Guaranteed Models

Model	Model Name	Capability	Description	Context Size
GPT-OSS-120B	gpt-oss-120b	tool	A 120B language model from OpenAI. Superior performance.	128k
DeepSeek V4 Pro	deepseek-v4-pro-thinking	coder, reasoning, tool	A 1.6T total / 49B active parameters, 1M-token context. Excels at complex tasks, including mathematics, logical reasoning, and code generation.	1M
Qwen3.5	qwen3.5-122b	multimodal, coder, tool	A 122B language model from Qwen. Succeeds the Qwen3-coder with significantly enhanced performance in coding tasks.	256k

Experimental Models

Model	Model Name	Capability	Description	Context Size
GLM 5	glm-5	multimodal, coder, tool	The 744B GLM 5 fp4 language model for advanced "agentic" reasoning and superior multi-step task handling	200k
Kimi K2.6	kimi-k2.6	agentic, multimodal, coder, tool	Large-scale MoE model with roughly 1 trillion parameters with significantly enhanced performance in coding tasks.	256k
Qwen 3.5	qwen3.5	agentic, multimodal, coder, tool	397B Multimodal advanced model for coding, tool use, and agentic workflows	262k
Mistral-Medium-3.5	mistral-medium-3.5	multimodal, coder, tool	128B Multimodal advanced model for coding, tool use, and agentic workflows	262k
whisper-large-v3	whisper-large-v3 (API only)	audio, speech recognition	OpenAI's 1.55-billion parameter automatic speech recognition (ASR) and speech translation model. It supports 99+ languages and offers a 10-20% reduction in Word Error Rate (WER) over previous versions, achieving robust transcription even in noisy conditions	

⚡ Suggested

Give me ideas
for what to do with my

Help me study
vocabulary for a colleg

Show me a code
of a website's sticky he

Czech Language Proficiency

We evaluated selected models using the [BenCzechMark](#) benchmark. Full results are available at the provided link.

For reference, key scores are summarized below:

Model	Mean Score
DeepSeek-R1-0528	85.3
Command-A	82.8
LLaMA-3.3	73.5
LLaMA-4-Scout	71.5
Aya Expanse	63.5
Gemma 3	59.2
Phi-4	58.2

	Context Size
Advanced "agentic" coding	200k
on parameters with coding tasks.	256k
ng, tool use, and	262k

Mistral-Medium-3.5	mistral-medium-3.5	multimodal, coder, tool	128B Multimodal advanced model for coding, tool use, and agentic workflows	262k
whisper-large-v3	whisper-large-v3 (API only)	audio, speech recognition	OpenAI's 1.55-billion parameter automatic speech recognition (ASR) and speech translation model. It supports 99+ languages and offers a 10-20% reduction in Word Error Rate (WER) over previous versions, achieving robust transcription even in noisy conditions	

Czech Language Proficiency

We evaluated selected models using the [BenCzechMark](#) benchmark. Full results are available at the provided link.

For reference, key scores are summarized below:

- Models
- Mini
- Thinker
- Model
- Coder
- Agentic
- DeepSeek-R1-0
- Folders
- Chats
- Command-A
- April
- New Chat
- LLaMA-3.3
- LLaMA-4-Scou
- Aya Expanse
- Gemma 3
- Phi-4

Programming Languages Proficiency

We evaluated selected models using [Aider Polyglot Benchmark](#). For reference, key scores are summarized below:

Model	C++ Score	Go Lang Score	Java Score	Javascript Score	Python Score	Rust Score
GPT-OSS-120B	50.0	59.0	40.4	61.2	70.6	53.3
DeepSeek V3.2 (think)	88.5	84.6	66.0	89.9	82.4	76.7
DeepSeek V3.2 (nothink)	92.3	82.1	59.6	79.6	79.4	66.7
GLM 5.1 (think)	84.6	87.2	72.3	83.7	88.2	83.3
Kimi K2.5 (think)	92.3	84.6	74.5	93.9	91.2	90
Kimi K2.5 (nothink)	92.3	82.1	76.6	89.8	82.4	90
Kimi K2.6 (think)	96.2	89.7	89.4	91.8	97.1	93.3
Qwen 3.5 (think)	96.2	79.5*	80.9	89.8	79.4	63.3

Open WebUI

New Chat

Search

Notes

Workspace

Models

Folders

Chats

Today

- Hello Line Extractor

Previous 30 days

- SMASH Simulation Crash 1w
- Software Installation Method... 4w

únor

- Language Improvement R... 4w
- Jak interpretovat "select=1:n... 4w
- OpenStack Cloud Overview 4w
- Data Privacy Assurance 4w
- Sticky Header Demo 4w

Qwen3-Coder-480B

Write a Python (Python3) script that extracts all lines with the string "hello" from an input file named "input.txt". Place the selected lines in an output text file named "output.txt".

Qwen3-Coder-480B

Here's a Python3 script that extracts all lines containing the string "hello" from input.txt and writes them to output.txt :

```
python
1 def extract_hello_lines():
2     try:
3         # Read from input.txt and filter lines containing "hello"
4         with open("input.txt", "r", encoding="utf-8") as infile:
5             lines_with_hello = [line for line in infile if "hello" in line]
6
7         # Write the filtered lines to output.txt
8         with open("output.txt", "w", encoding="utf-8") as outfile:
9             outfile.writelines(lines_with_hello)
10
11        print(f"Successfully extracted {len(lines_with_hello)} lines containing 'hello' to output.txt")
12
13    except FileNotFoundError:
14        print("Error: 'input.txt' not found. Please ensure the file exists in the current directory.")
15    except Exception as e:
16        print(f"An error occurred: {e}")
17
18 if __name__ == "__main__":
19    extract_hello_lines()
```

How it works:

- Case-sensitive matching:** "hello" in line matches only exact lowercase "hello" (e.g., won't match "Hello" or "Hello!").
 - To make it case-insensitive, change to:

```
python
1 if "hello" in line.lower()
```

- Line endings preserved:** Original line endings (e.g., \n) are kept in the output.
- Error handling:** Catches missing input.txt and other exceptions.
- Efficient:** Uses a list comprehension for filtering and \n \n \n for writing.

Open WebUI



RedHatAI Scout ▼ +

Set as default

INFO Use <https://llm.ai.e-infra.cz/v1> as API endpoint

New Chat

Search

Notes

Workspace

Models

Folders

Chats



How can I help you today?



Upload Files

Capture

Attach Webpage

Attach Notes >

Attach Knowledge >

Reference Chats >

of a website's sticky header

✍ New Chat

🔍 Search

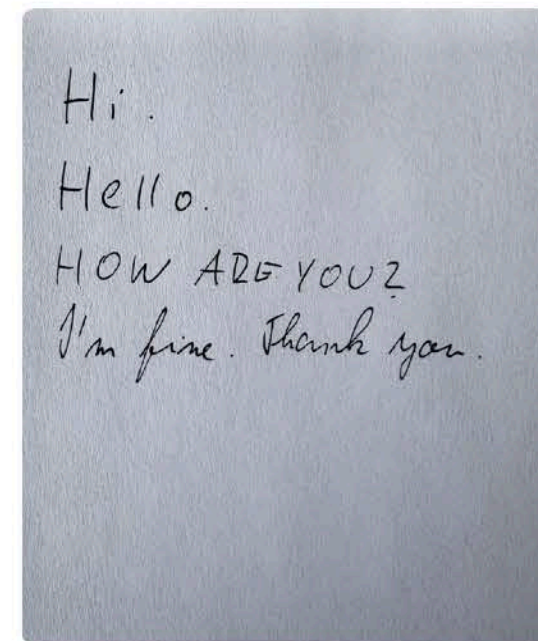
📄 Notes

🗑 Workspace

Models

Folders

Chats



Read it.

**RedHatAI Scout**

The image presents a handwritten note on a gray background, featuring a mix of typed and written text. The note is divided into five lines:

- "Hi."
- "Hello."
- "HOW ARE YOU?"
- "I'm fine. Thank you."

The first three lines are written in black ink, with the first two lines in a smaller font and the third line in a larger font. The last line is written in cursive.

The background of the image is a light gray color, resembling paper or cardboard. The overall appearance of the image suggests that it may be a photograph of a handwritten note or a piece of artwork created using digital tools.



Thinker ▾ +

Set as default

INFO Use <https://llm.ai.e-infra.cz/v1> as API endpoint

Model for advanced reasoning and analytical tasks.

Thinker ⓘ



Thinker

Model for advanced reasoning and analytical tasks.

2025_Sreibr.pdf

9.4 MB

Do a short summary (max. 20 sentences) from the article.



Upload Files

Capture

Attach Webpage

Attach Notes >

Attach Knowledge >

Reference Chats >



Open WebUI · v0.8.10

Do a short summary (max. 20 sentences) from the article.



Thinker

Retrieved 1 source

- Querying
- Retrieved 1 source

Thought for 9 seconds

This study characterizes the activation of *Heterorhabditis bacteriophora* infective juveniles (IJs) and their release of excreted/secreted products (ESPs) in response to various stimuli [2025_Sreibr.pdf](#). The researchers compared insect-derived activation materials—including homogenates from live larvae (H1), frozen larvae (H2), and heat-inactivated frozen larvae (H3)—with non-biological stimuli such as filtered water (H2O) and phosphate-buffered saline (PBS) [2025_Sreibr.pdf](#). None of the tested materials induced complete recovery of the IJ population, consistent with the phased infectivity hypothesis observed in entomopathogenic nematodes [2025_Sreibr.pdf](#). However, all activation materials triggered the release of ESPs, with comparable protein concentrations across treatments despite significant differences in protein composition [2025_Sreibr.pdf](#). Notably, PBS exposure resulted in the highest number of identified proteins (over 200), whereas bioactive homogenates from live and frozen larvae yielded the fewest proteins (65 and 48, respectively) [2025_Sreibr.pdf](#). The study identified several protein families associated with host-parasite interactions, including alpha-2-macroglobulins, trypsin inhibitor-like (TIL) domain proteins, and metalloendopeptidases, which were significantly upregulated in response to insect-derived materials [2025_Sreibr.pdf](#). Heat-inactivated homogenate (H3) showed distinct characteristics, including lower protein content and altered protein profiles due to denaturation of host proteins during heating [2025_Sreibr.pdf](#). Interestingly, nematodes exposed to water also released numerous proteins, though these reflected stress responses rather than host-parasite interaction mechanisms [2025_Sreibr.pdf](#). The findings demonstrate that both host-derived cues and non-biological stressors can induce IJ activation and ESP release, revealing a complex interplay between environmental stimuli and nematode physiology [2025_Sreibr.pdf](#). These insights into the molecular mechanisms of *H. bacteriophora* parasitism may contribute to optimizing mass production and biocontrol applications [2025_Sreibr.pdf](#).

1 Source



Follow up



- New Chat
- Search
- Notes
- Workspace

- Models
- Folders
- Chats

Do a short summary (max. 20 sentences) from the article.



Thinker

Retrieved 1 source

- Querying
- Retrieved 1 source

Thought for 9 seconds



This study characterizes the activation of *Heterorhabditis bacteriophora* infective juveniles (IJs) and their release of excreted/secreted products (ESPs) in response to various stimuli [2025_Sreibr.pdf](#). The researchers compared insect-derived activation materials—including homogenates from live larvae (H1), frozen larvae (H2), and heat-inactivated frozen larvae (H3)—with non-biological stimuli such as filtered water (H2O) and phosphate-buffered saline (PBS) [2025_Sreibr.pdf](#). None of the tested materials induced complete recovery of the IJ population, consistent with the phased infectivity hypothesis observed in entomopathogenic nematodes [2025_Sreibr.pdf](#). However, all activation materials triggered the release of ESPs, with comparable protein concentrations across treatments despite significant differences in protein composition [2025_Sreibr.pdf](#). Notably, PBS exposure resulted in the highest number of identified proteins (over 200), whereas bioactive homogenates from live and frozen larvae yielded the fewest proteins (65 and 48, respectively) [2025_Sreibr.pdf](#). The study identified several protein families associated with host-parasite interactions, including alpha-2-macroglobulins, trypsin inhibitor-like (TIL) domain proteins, and metalloendopeptidases, which were significantly upregulated in response to insect-derived materials [2025_Sreibr.pdf](#). Heat-inactivated homogenate (H3) showed distinct characteristics, including lower protein content and altered protein profiles due to denaturation of host proteins during heating [2025_Sreibr.pdf](#). Interestingly, nematodes exposed to water also released numerous proteins, though these reflected stress responses rather than host-parasite interaction mechanisms [2025_Sreibr.pdf](#). The findings demonstrate that both host-derived cues and non-biological stressors can induce IJ activation and ESP release, revealing a complex interplay between environmental stimuli and nematode physiology [2025_Sreibr.pdf](#). These insights into the molecular mechanisms of *H. bacteriophora* parasitism may contribute to optimizing mass production and biocontrol applications [2025_Sreibr.pdf](#).

1 Source



Follow up





Thinker Today at 17:01

Retrieved 1 source

- Querying
- Retrieved 1 source

Thought for 9 seconds ^

"The user wants a short summary (max. 20 sentences) from the article provided in the context.

First, I need to identify the key points of the article:

1. The study investigates the activation of *Heterorhabditis bacteriophora* infective juveniles (IJs) and their release of excreted/secreted products (ESPs).
2. They tested various activation materials: H1 (homogenate from live larvae), H2 (homogenate from frozen larvae), H3 (heat-inactivated homogenate from frozen larvae), H2O (filtered water), and PBS (phosphate-buffered saline).
3. None of the materials induced 100% recovery, but all triggered ESP release.
4. Protein concentrations were consistent across treatments, but protein composition varied significantly.
5. PBS induced the highest number of proteins (over 200), while insect-derived materials (H1, H2) induced the fewest.
6. Key proteins identified include alpha-2-macroglobulins, trypsin inhibitor-like proteins, and metalloendopeptidases, which are important for host-parasite interactions.
7. Heat inactivation (H3) reduced protein content and altered protein profiles compared to live/frozen homogenates.
8. The study reveals that both host-derived and non-biological stimuli can trigger IJ activation and ESP release.
9. ESPs play roles in immune suppression, melanization inhibition, and tissue migration.
10. The findings provide insights for optimizing biocontrol strategies.

Now I need to condense this into maximum 20 sentences, using inline citations [id] only when the <source> tag includes an explicit id attribute. Looking at the context, all sources have id="1", so I should cite as `2025_Sreibr.pdf` when referencing specific information.

2025_Sreibr.pdf 9.4 MB

20 sentences) from the article.

and their release of excreted/
d insect-derived activation
l frozen larvae (H3)—with non-
. None of the tested materials
is observed in entomopathogenic
comparable protein concentrations
PBS exposure resulted in the
frozen larvae yielded the fewest
sociated with host-parasite
metalloendopeptidases, which
vated homogenate (H3) showed
uration of host proteins during
ns, though these reflected stress
strate that both host-derived
interplay between environmental
f *H. bacteriophora* parasitism

Follow up

- Search
- Notes
- Workspace
- Models
- Folders
- Chats

Let me draft the summary:

This study characterizes the activation of *Heterorhabditis bacteriophora* infective juveniles (IJs) and their release of excreted/secreted products (ESPs) in response to various stimuli (2025_Sreibr.pdf). The researchers compared insect-derived activation materials—including homogenates from live larvae (H1), frozen larvae (H2), and heat-inactivated frozen larvae (H3)—with non-biological stimuli such as filtered water (H2O) and phosphate-buffered saline (PBS) (2025_Sreibr.pdf). None of the tested materials induced complete recovery of the IJ population, consistent with the phased infectivity hypothesis observed in entomopathogenic nematodes (2025_Sreibr.pdf). However, all activation materials triggered the release of ESPs, with comparable protein concentrations across treatments despite significant differences in protein composition (2025_Sreibr.pdf). Notably, PBS exposure resulted in the highest number of identified proteins (over 200), whereas bioactive homogenates from live and frozen larvae yielded the fewest proteins (65 and 48, respectively) (2025_Sreibr.pdf). The study identified several protein families associated with host-parasite interactions, including alpha-2-macroglobulins, trypsin inhibitor-like (TIL) domain proteins, and metalloendopeptidases, which were significantly upregulated in response to insect-derived materials (2025_Sreibr.pdf). Heat-inactivated homogenate (H3) showed distinct characteristics, including lower protein content and altered protein profiles due to denaturation of host proteins during heating (2025_Sreibr.pdf). Interestingly, nematodes exposed to water also released numerous proteins, though these reflected stress responses rather than host-parasite interaction mechanisms (2025_Sreibr.pdf). The findings demonstrate that both host-derived cues and non-biological stressors can induce IJ activation and ESP release, revealing a complex interplay between environmental stimuli and nematode physiology (2025_Sreibr.pdf). These insights into the molecular mechanisms of *H. bacteriophora* parasitism may contribute to optimizing mass production and biocontrol applications (2025_Sreibr.pdf).

es) from the article.

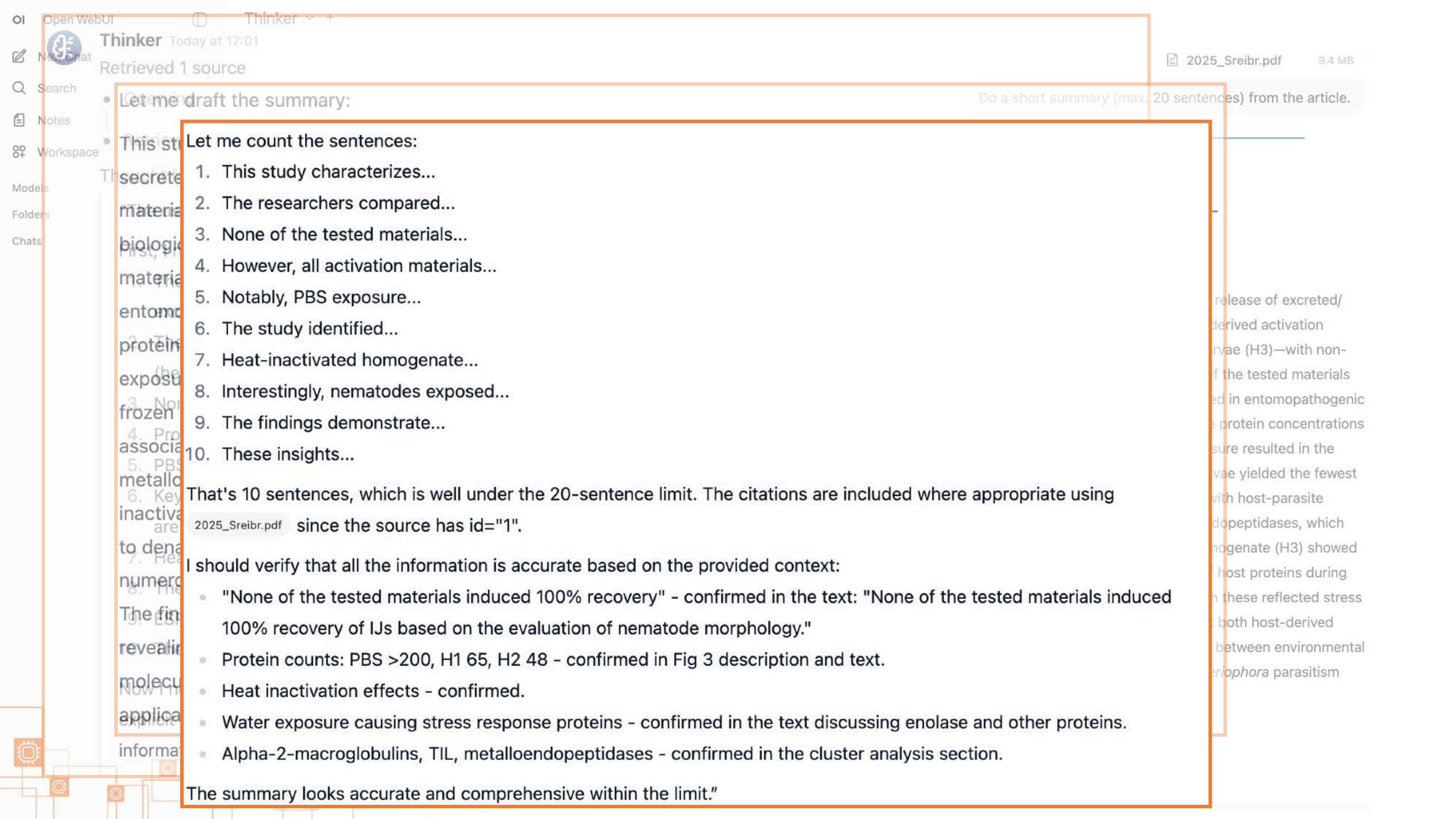
release of excreted/
 rived activation
 ae (H3)—with non-
 he tested materials
 in entomopathogenic
 protein concentrations
 re resulted in the
 e yielded the fewest
 h host-parasite
 peptidases, which
 generate (H3) showed
 ost proteins during
 hese reflected stress
 oth host-derived
 between environmental
 ophora parasitism

information.



Follow up





Let me draft the summary:

This st

Let me count the sentences:

1. This study characterizes...
2. The researchers compared...
3. None of the tested materials...
4. However, all activation materials...
5. Notably, PBS exposure...
6. The study identified...
7. Heat-inactivated homogenate...
8. Interestingly, nematodes exposed...
9. The findings demonstrate...
10. These insights...

That's 10 sentences, which is well under the 20-sentence limit. The citations are included where appropriate using `2025_Sreibr.pdf` since the source has `id="1"`.

I should verify that all the information is accurate based on the provided context:

- "None of the tested materials induced 100% recovery" - confirmed in the text: "None of the tested materials induced 100% recovery of IJs based on the evaluation of nematode morphology."
- Protein counts: PBS >200, H1 65, H2 48 - confirmed in Fig 3 description and text.
- Heat inactivation effects - confirmed.
- Water exposure causing stress response proteins - confirmed in the text discussing enolase and other proteins.
- Alpha-2-macroglobulins, TIL, metalloendopeptidases - confirmed in the cluster analysis section.

The summary looks accurate and comprehensive within the limit."

Do a short summary (max. 20 sentences) from the article.

release of excreted/
derived activation
ryae (H3)—with non-
of the tested materials
ed in entomopathogenic
e protein concentrations
sure resulted in the
vae yielded the fewest
with host-parasite
dopeptidases, which
nogenate (H3) showed
of host proteins during
n these reflected stress
t both host-derived
between environmental
eriphora parasitism

■ OpenAI API

<https://docs.cerit.io/en/docs/ai-as-a-service/introduction>

- Integrate LLMs into local applications, scripts, or AI workflows (Open AI, Anthropic API, OpenCode, Clade Code, VS Code)

■ AI coding assistant (Claude Code)

- A coding tool that lives in your terminal, understands your codebase and helps you code faster by executing routine tasks and explaining complex code

■ Vibe Coding (DeepSite)

- Web-based AI web page and application generator that creates fully functional websites directly from your descriptions, powered by DeepSeek 3.2



■ Compute cloud

<https://docs.platforms.cloud.e-infra.cz/en/docs>

- Runs on OpenStack (allows users to create and manage their own cloud computing resources)
- 17 computational clusters with 8,968 cores, 96 GPU cards, and 178 TB RAM
- Virtual machines are accessed using SSH keys

■ Sensitive cloud

<https://docs.cerit.io/en/docs/sensitivecloud/account>

- Provides a secure computing and storage environment for sensitive data processing and research, operated by CERIT-SC (part of e-INFRA CZ)
- Follows security standards such as ISO 27000, C5, ISO 15189, and ECRIN
- Relies on container technology via Kubernetes, MFA required



■ CESNET S3 service

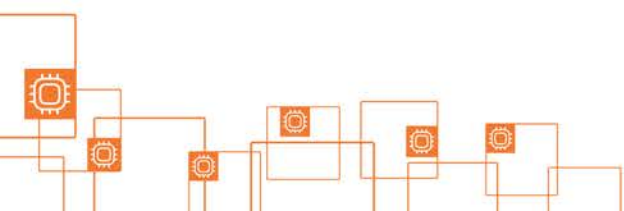
<https://docs.du.cesnet.cz/en/docs/object-storage-s3/s3-service>

- Personal space has a quota of 2 TB (increasable)
- Personal accounts do not support sharing between users and/or groups (by default, all objects and buckets are private)
- Data (buckets) can be shared via the manually generated temporary URLs

<https://docs.du.cesnet.cz/en/docs/object-storage-s3/s3-features#sharing-an-s3-object-using-presigned-url>

- Or by setting up bucket policies for sharing

<https://docs.du.cesnet.cz/en/docs/object-storage-s3/s3-features#set-up-bucket-policies-for-sharing-aws-cli-s3-plugin>



<https://docs.du.cesnet.cz/en/docs/object-storage-s3/s3-service>

■ CESNET S3 service

- S3 storage can be accessed from the MetaCentrum disk storages via CLI
- For example *s3cmd*, *s5cmd* (faster version of *s3cmd*) or *aws* tools
- Tools needs to be configured with access keys



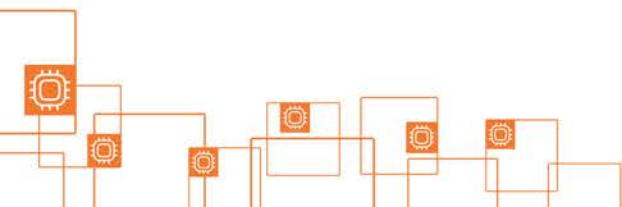
■ CESNET S3 service

Configuring the S3cmd Tool

Add the following lines to the configuration file located at `/home/user/.s3cfg`.

```
[default]
host_base = https://s3.clX.du.cesnet.cz
use_https = True
access_key = xxxxxxxxxxxxxxxxxxxxxxxx
secret_key = xxxxxxxxxxxxxxxxxxxxxxxx
host_bucket = s3.clX.du.cesnet.cz
```

the `host_base` and `host_bucket` refer to the S3 endpoint URL, which you received via email along with your `access_key` and `secret_key`. This information is sent to you during the S3 account creation process.



Amazon S3_test
NIQXAT6VO43DPEXD1MN...

Open Connection New Folder View

- elmo.metacentrum.cz - SFTP - praha5
elmo.metacentrum.cz
vorel
- nympha.metacentrum.cz - SFTP - plzen1
nympha.metacentrum.cz
vorel
- zenith.metacentrum.cz - SFTP - brno12
zenith.metacentrum.cz
vorel
- storage-brno11 - SFTP
storage-brno11-elixir.metacentrum.cz
vorel
- Amazon S3**
s3.cl4.du.cesnet.cz
NIQXAT6VO43DPEXD1MNM
- skirit.metacentrum.cz - SFTP - brno2
skirit.metacentrum.cz
vorel

Amazon S3

Nickname: Amazon S3

Labels:

URL: <https://s3.cl4.du.cesnet.cz/meta-archive>

Server: s3.cl4.du.cesnet.cz Port: 443

Access Key ID: [REDACTED]

Anonymous Login

Secret Access Key: [REDACTED]

SSH Private Key: None

Client Certificate: None

More Options

Path: /meta-archive

Web URL: <https://s3.cl4.du.cesnet.cz/>

Download Folder: Downloads

Transfer Files: Default

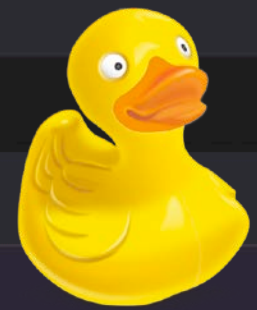
Timezone: UTC

Encoding: Default

Connect Mode: Default

Notes:

 The SFTP client can access various types of storage



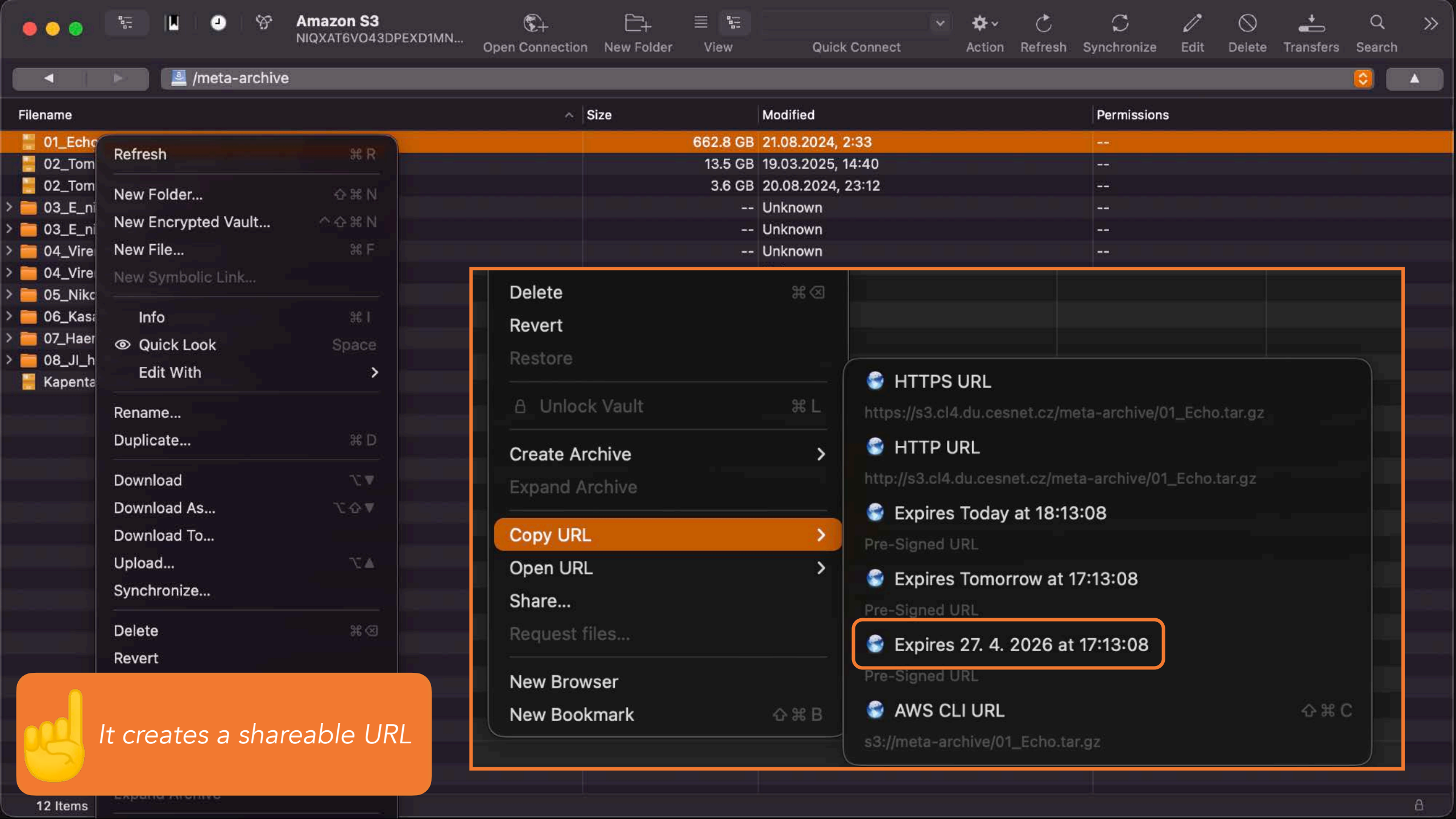
Filename	Size	Modified	Permissions
01_Echo.tar.gz	662.8 GB	21.08.2024, 2:33	--
02_TomasPakosta_posledni_vymysl.zip	13.5 GB	19.03.2025, 14:40	--
02_TomasPakosta.tar.gz	3.6 GB	20.08.2024, 23:12	--
> 03_E_nip_genom	--	Unknown	--
> 03_E_nip_trans	--	Unknown	--
> 04_Viremie_AV_Kapr_Karas	--	Unknown	--
> 04_Viremie_AV_Plotice_Cejn	--	Unknown	--
> 05_Nikol_Kmentova	--	Unknown	--
> 06_Kasa_mansoni_hepatica_vejce	--	Unknown	--
> 07_Haem_cont_metylacDNA	--	Unknown	--
> 08_JI_hetero_trans	--	Unknown	--
Kapentagyryus_July2022.tar.gz	473.7 GB	21.08.2024, 2:00	--

Filename	Size	Modified	Permissions
01_Echo.tar.gz	662.8 GB	21.08.2024, 2:33	--
02_TomasPakosta_posledni	13.5 GB	19.03.2025, 14:40	--
02_TomasPakosta.tar.gz	3.6 GB	20.08.2024, 23:12	--
> 03_E_nip_genom	--	Unknown	--
> 03_E_nip_trans	--	Unknown	--
> 04_Viremie_AV_Kapr_Karas	--	Unknown	--
> 04_Viremie_AV_Plotice_Ceji	--	Unknown	--
> 05_Nikol_Kmentova	--	Unknown	--
> 06_Kasa_mansoni_hepatica	--	Unknown	--
> 07_Haem_cont_metylaceDN	--	Unknown	--
> 08_JI_hetero_trans	--	Unknown	--
Kapentagyrus_July2022.tar.	473.7 GB	21.08.2024, 2:00	--

- Refresh ⌘ R
- New Folder...
- New Encrypted Vault... ⌘ ⌘ N
- New File... ⌘ F
- New Symbolic Link...
- Info ⌘ I
- Quick Look Space
- Edit With >
- Rename...
- Duplicate... ⌘ D
- Download ⌘ ⌘
- Download As... ⌘ ⌘
- Download To...
- Upload... ⌘ ⌘
- Synchronize...
- Delete ⌘ ⌘
- Revert
- Restore
- Unlock Vault ⌘ L
- Create Archive >
- Expand Archive

Filename	Size	Modified	Permissions
01_Echo	662.8 GB	21.08.2024, 2:33	--
02_Tom	13.5 GB	19.03.2025, 14:40	--
02_Tom	3.6 GB	20.08.2024, 23:12	--
03_E_ni	--	Unknown	--
03_E_ni	--	Unknown	--
04_Vire	--	Unknown	--
04_Vire	--	Unknown	--
05_Niko	--	Unknown	--
06_Kasa	--	Unknown	--
07_Haer	--	Unknown	--
08_JI_h	--	Unknown	--
Kapenta	473.7 GB	21.08.2024, 2:00	--

- Refresh ⌘ R
- New Folder... ⌘ N
- New Encrypted Vault... ⌘ N
- New File... ⌘ F
- New Symbolic Link...
- Info ⌘ I
- Quick Look Space
- Edit With >
- Rename...
- Duplicate... ⌘ D
- Download ⌘ ⌵
- Download As... ⌘ ⌵
- Download To...
- Upload... ⌘ ⬆
- Synchronize...
- Delete ⌘ ⌫
- Revert
- Restore
- Unlock Vault ⌘ L
- Create Archive >
- Expand Archive



 It creates a shareable URL

Filename	Size	Modified	Permissions
01_Echo	662.8 GB	21.08.2024, 2:33	--
02_Tom	13.5 GB	19.03.2025, 14:40	--
02_Tom	3.6 GB	20.08.2024, 23:12	--
03_E_ni	--	Unknown	--
03_E_ni	--	Unknown	--
04_Vire	--	Unknown	--
04_Vire	--	Unknown	--
05_Niko	--	Unknown	--
06_Kasa	--	Unknown	--
07_Haer	--	Unknown	--
08_JI_h	--	Unknown	--
Kapenta	--	Unknown	--

URL Type	URL
HTTPS URL	https://s3.cl4.du.cesnet.cz/meta-archive/01_Echo.tar.gz
HTTP URL	http://s3.cl4.du.cesnet.cz/meta-archive/01_Echo.tar.gz
Expires Today at 18:13:08	Pre-Signed URL
Expires Tomorrow at 17:13:08	Pre-Signed URL
Expires 27. 4. 2026 at 17:13:08	Pre-Signed URL
AWS CLI URL	s3://meta-archive/01_Echo.tar.gz



■ FileSender

<https://du.cesnet.cz/en/navody/filesender/start>

- Web service for sending files
- A download link is sent to the recipient and the file is stored for a maximum of one month before being automatically deleted
- Connection with MetaCentrum is possible

■ OwnCloud

- Cloud storage with 100 GB of space per user (increasable)
- Clients are available for all OS (Windows, Linux, OS X, iOS, Android)
- Automatic data synchronisation between multiple devices

<https://du.cesnet.cz/en/navody/owncloud/start>



Access is granted without the need for further registration



<https://www.cesnet.cz/>

<https://www.metacentrum.cz/>

<https://www.e-infra.cz/>

<https://docs.metacentrum.cz/>

- Free and immediately accessible, no grant proposals
- All we ask: acknowledge e-INFRA CZ (ID:90254) in your publications
- For everyone, no programming skills required
- Scales with your needs, from a small interactive session to large and long-term parallel jobs
- Hundreds of tools included, ready to use
- Dedicated user support and step-by-step documentation

vorel@cesnet.cz meta@cesnet.cz