

# MetaCentrum NGI

For scientific computations, collaborative  
research & its support services

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June 26th, 2025

Czech Agrifood Research Center, Prague

## ■ MetaCentrum is

<https://metacentrum.cz>

- ... National Grid Infrastructure (NGI) <https://metavo.metacentrum.cz>
- ... the activity of the CESNET association (coordinator) <https://docs.metacentrum.cz>
- ... part of e-INFRA CZ
- ... a provider of computational resources, application software (commercial and free/open source) and data storage
- ... free of charge (users "pay" by acknowledgement in their publications)

## ■ MetaCentrum is available for

- ... employees and students from Czech universities, the Czech Academy of Sciences, non-commercial research facilities, abroad partners, etc..
- ... industry users (non-profit and public research, upon individual request)

## ■ MetaCentrum targets

- ... individual users (we can offer resources) <https://metacentrum.cz>
- ... projects (cooperation, sharing data in a group) <https://metavo.metacentrum.cz>
- ... organisations (incorporate their resources under central management) <https://docs.metacentrum.cz>

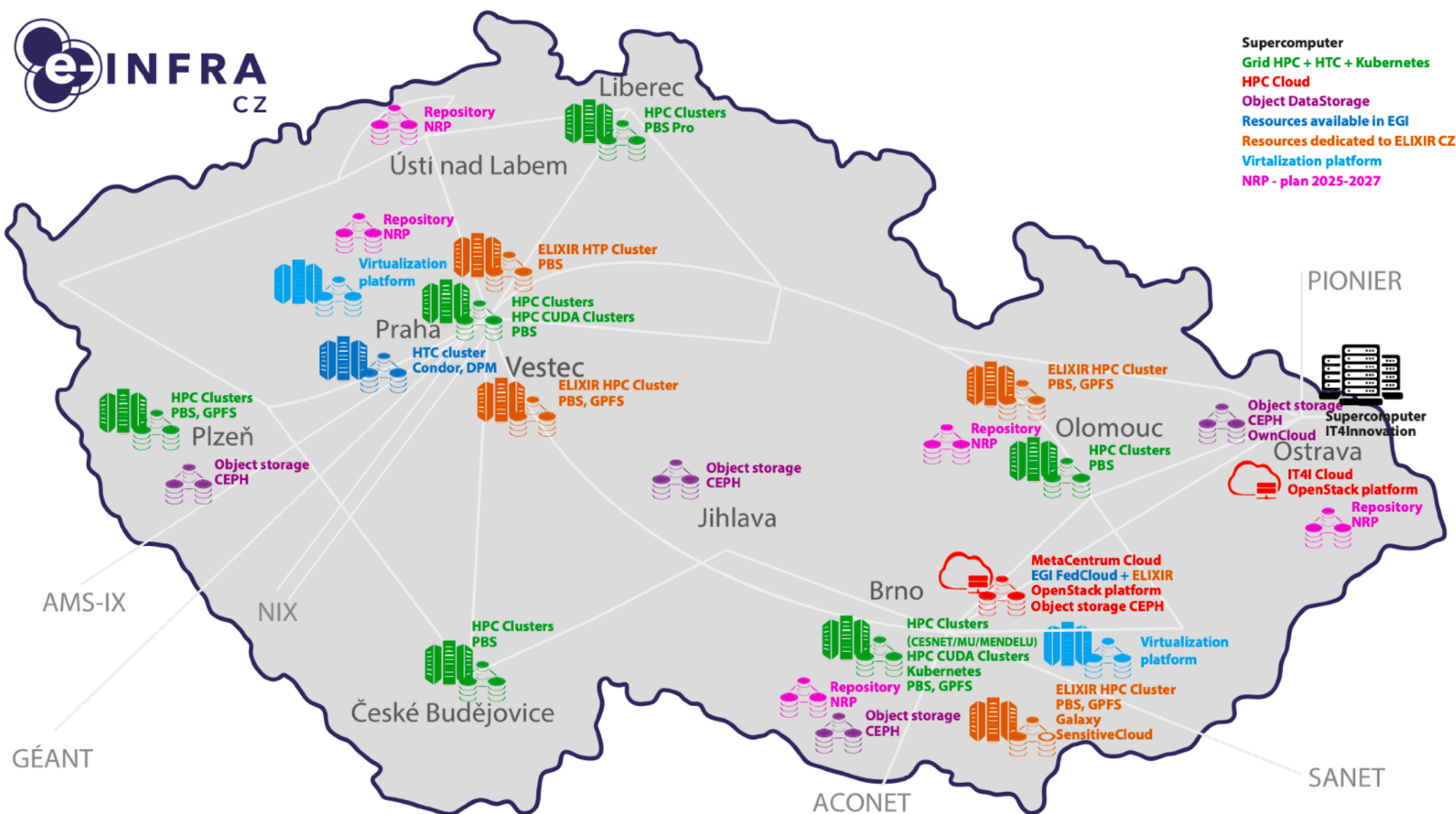
## ■ MetaCentrum offers

- ... possibility of applying at any time without grant competitions
- ... access without submitted projects (with one exception)
- ... immediate access to HW resources and licences
- ... the principle of grid (shared) usage (privileged access for cluster owners)
- ... various application software (commercial, free, open source)
- ... CPU/GPU resources, GUI applications and access, cloud services

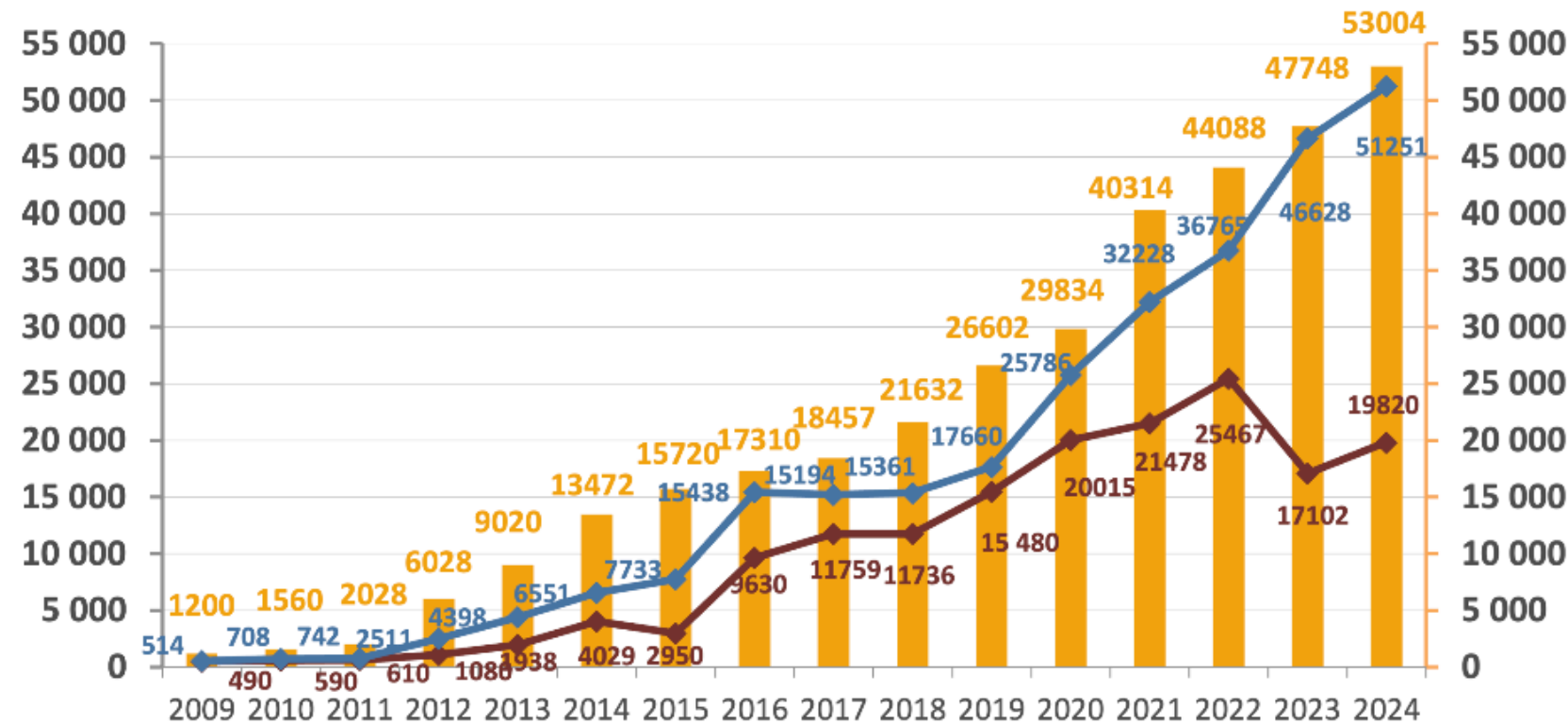


- **Compute resources are provided by the CESNET association and its partners (universities, CAS institutes), and**
  - ... are freely available for research and academic usage
  - ... are shared among all users (community approach)
  - ... are with privileged access for cluster owners
  - ... can be used in case of urgent/heavy load extensively
  - ... are replaceable during an outage
  - ... are centrally managed (AAI)
  - ... are dedicated to grid HPC/HTC and containerised computing, cloud computing, and data storage capacities
  - ... are designed to process all types of data





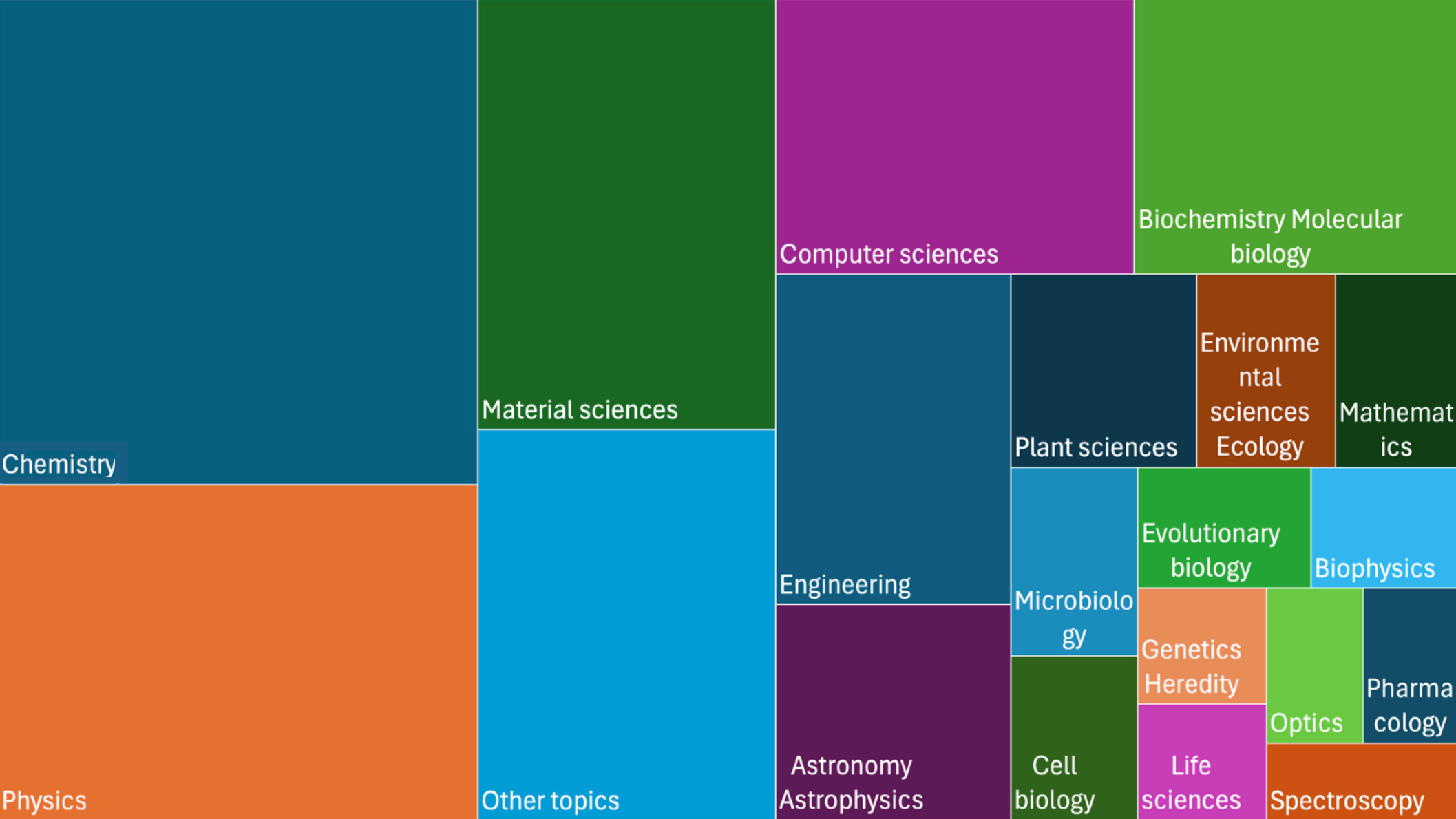
Number of CPUs, executed jobs and corresponding CPU years  
(PBS, cloud, K8s, EGI)



MetaCentrum leden – prosinec 2024	Celkem MetaCentrum
Počet úloh / spuštěných VM strojů / kontejnerů	15 mil
Propočítaný CPU čas (walltime) [CPU let]	37552
Propočítaný GPU čas (walltime) [GPU let]	357
Počet uživatelů	3490
Počet CPU jader konec 2024	47132
Počet evidovaných GPU karet ke konci roku 2024	480

<https://metavo.metacentrum.cz/cs/state/stats/2024/index.html>

- CPU cores
- thousand jobs / VM
- CPU years





- Hundreds of available SW tools in many versions (circa 5,000 different modules)

PAID LICENCE








FOR INDIVIDUALS/  
PERSONAL

FOR EVERYONE



FREE LICENCE



- Submission of the application is conditional on academic affiliation (eduID)
- Access is granted to the MetaCentrum and its services
  - Grid computing (CLI, OpenPBS scheduler) <https://docs.metacentrum.cz>
  - Open OnDemand (GUI, remote web access)  <https://ondemand.grid.cesnet.cz>
  - Galaxy (GUI, web-based platform for computational analyses) <https://usegalaxy.cz>
  - Jupyter notebook (GUI)  <https://docs.cerit.io/en/docs/web-apps/jupyterhub>  **useGalaxy.cz**
  - Cloud/Sensitive cloud computing (OpenStack, Kubernetes) <https://docs.platforms.cloud.e-infra.cz/en/docs>
  - Container platform Kubernetes (GUI, for Docker images)  **openstack.**
  - Nextflow pipelines <https://docs.cerit.io/en/docs/workflows/nextflow>  **kubernetes**
  - AI chatbot (on local HW) <https://docs.cerit.io/en/docs/web-apps/chat-ai>



MetaCentrum Grid	Kubernetes	OpenStack Cloud
Centrally managed infrastructure (restrictive in some cases)	Centrally managed infrastructure (containers can be modified)	Images provided by MetaCentrum, EGI, projects, users,...
Batch/interactive (long) jobs with reserved resources (OpenPBS)	Individually started non-root containers with reserved HW	Long-term running VMs with HW reserved via specific flavours
Compute nodes and storages are distributed across the CZE	Central localisation in Brno (CERIT-SC)	Central OpenStack installation in Brno
Mainly CLI, also GUI approaches (OnDemand, Galaxy, Jupyter)	Considerable interactive support (mostly remote GUI applications)	CLI management
Limitations given by OS and system libraries	Potentially problematic container incorporation to K8s/Rancher	High level of user freedom, independent work with VMs
Easily supported	Easily supported	Problematic access into users' VMs
Kerberos authentication	Web application (AAI)	SSH keys

## ■ Fill out and submit the registration form

- Select your organisation (through the eduID)
- Use your local/institutional username and password
- Fill out the form and create a strong (and unique) MetaCentrum password
- Applications are approved manually (and almost immediately)
- All accounts are valid till 02. 02. YYYY
- Users must extend MetaCentrum membership from the beginning of each calendar year (during January)



<https://docs.metacentrum.cz/en/docs/access/account>

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

E-mail: [meta@cesnet.cz](mailto:meta@cesnet.cz)  
Web: <http://www.metacentrum.cz/>

```
*****
* O  R  C  A *
*****
```

[illegible]





## ■ Access through t

```
jirivorel@MacBook ~$ ssh vorel@nympha.metacentrum.cz
vorel@nympha.metacentrum.cz's password:
Linux nympha.meta.zcu.cz 6.1.0-34-amd64 #1 SMP PREEM
```

```
10 updates could not be installed automatically. For
see /var/log/unattended-upgrades/unattended-upgrades
Last login: Tue Jun 24 11:16:06 2025 from gtx121.ces
```

### Your Home Directories

Avail	DATA	FILES	Backup	Storage
space	quota	used	quota	used
134T	5.36T	3.91T	2M	9.43k
592T	none	201G	none	40
113T	4.29T	30.8G	2.5M	15.0k
22T	3.32T	24k	1M	9
39T	10.4G	12k	none	8
399T	4.29T	1.71T	3M	90.8k
66T	7.34G	44k	none	18
237T	5.36T	933G	1.01M	30.5k
72T	7.34G	32k	none	12
59T	2.14T	80k	2M	36

Free	Used	Total	Centre
15764	20905	36669	META

### Contact

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

```
#!/bin/bash
#PBS -q default@meta-pbs.metacentrum.cz
#PBS -l walltime=24:0:0
#PBS -l select=1:ncpus=8:mem=100gb:scratch_ssd=50gb
#PBS -N my_awesome_job
#PBS -m e

# 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

# 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 forgeto 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

# clean the scratch directory
clean_scratch
```

[metacentrum.cz/en/docs/welcome](http://metacentrum.cz/en/docs/welcome)

```
c-10.2.1-rg2lpmk xz/5.2.5-gcc-10.2.1-fteagxc
a/11.6.2-gcc-10.2.1-nwpmxyy
hwloc/2.7.1-gcc-10.2.1-a7ilbqg
opa-psm2/11.2.206-gcc-10.2.1-q4gu6pl
psm/2017-04-28-gcc-10.2.1-hrczaup
copy/2.3-gcc-10.2.1-evvrzi ucx/1.12.1-gcc-10.2.1-ixjcks
```



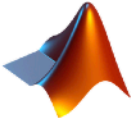









```
##,
###,
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'##
',,,'',
#####',',
',,,'
###,
' '#
: #
', #
####'
```

- Access through the web browser <https://ondemand.grid.cesnet.cz>
- In the future, primary access for new users (replacement of CLI)
- Frontend servers and storages can be accessed through the OnDemand
  - Web-based CLI access to selected frontends (with all functionalities)
  - Web-based interactive access to storages (mainly for browsing)
- Deployment of VMs and containers
- S3, OneData browser
- Singularity images (NGC, Pytorch,...)



MetaCentrum Open OnDemand provides an integrated, single access point for HPC resources.

## Selected applications - [all apps](#)

 Jupyter Lab/Notebook	 RStudio	 Matlab	 FLUENT Ansys Fluent	 ENSIGHT Ansys Ensight	 WORKBENCH Ansys Workbench
 Frontend shell	 Meta Desktop	 Job Composer	 BIOP Desktop	 CLC Genomics WB	 VMD Desktop

## Announcements

### 23-04-2024

OnDemand has been upgraded to version 3.1.4. Jobs are now submitted to OpenPBS server [pbs-m1.metacentrum.cz](#).

### 21-08-2023

OnDemand has been upgraded to the major version 3.



Home Directory

brno11-elixir /storage/brno11-elixir/home/vorel

brno12 /storage/brno12-cerit/home/vorel

brno14-ceitec /storage/brno14-ceitec/home/vorel

brno2 /storage/brno2/home/vorel

brno3-cerit /storage/brno3-cerit/home/vorel

budejovice1 /storage/budejovice1/home/vorel

liberec3 /storage/liberec3-tul/home/vorel

plzen1 /storage/plzen1/home/vorel

plzen4-ntis /storage/plzen4-ntis/home/vorel

praha1 /storage/praha1/home/vorel

praha2-natur /storage/praha2-natur/home/vorel

praha5-elixir /storage/praha5-elixir/home/vorel

praha5-elixir /storage/praha5-elixir/home/vorel

praha6-fzu /storage/praha6-fzu/home/vorel

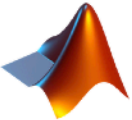
projects /storage/projects

projects2 /storage/projects2


pruhonice1-ibot /storage/pruhonice1-ibot/home/vorel

is an integrated, single access point for HPC resources.


os




Matlab




FLUENT  
Ansys Fluent




ENSIGHT  
Ansys Ensignt




WORKBENCH  
Ansys Workbench




Job Composer



BIOP Desktop



CLC Genomics WB



VMD Desktop

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# 21-08-2023

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Open in Terminal

Refresh

New File

New Directory

Upload

Download

Copy/Move

Delete

- Home Directory
- brno2
- brno12
- praha5-elixir
- brno11-elixir
- brno14-ceitec
- brno3-cerit
- budejovice1
- liberec3
- plzen1
- plzen4-ntis
- praha1
- praha2-natur
- praha5-elixir
- praha6-fzu
- pruhonice1-ibot
- projects
- projects2

↑ / storage / brno12-cerit / home / vorel /

Change directory

Copy path

☐ Show Owner/Mode

☐ Show Dotfiles

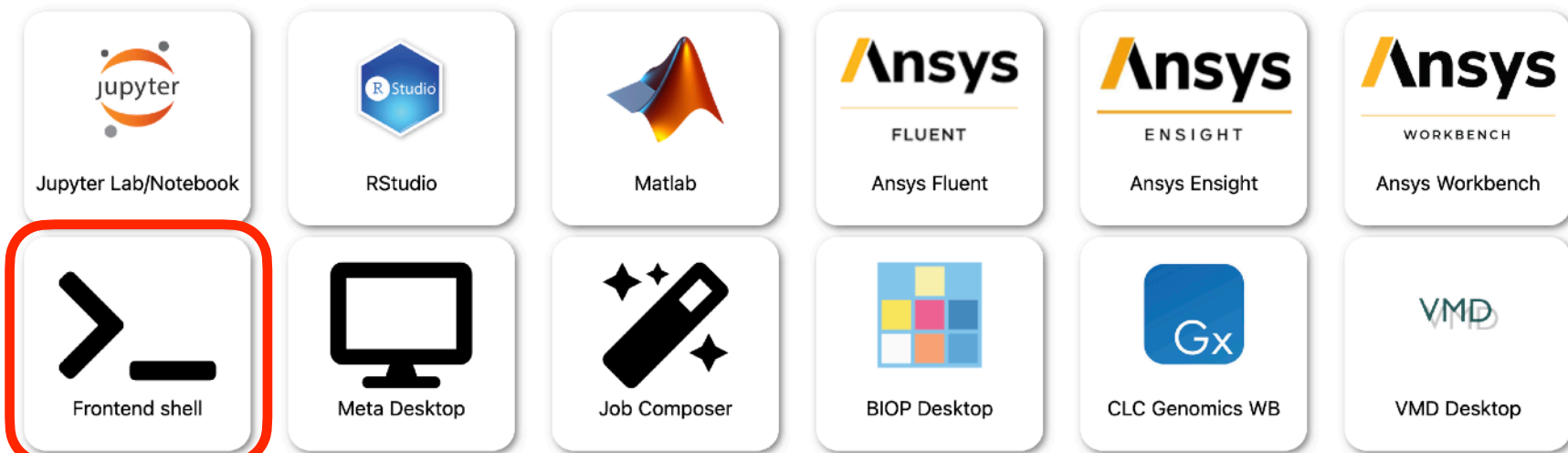
Filter:

Showing 4 of 15 rows - 0 rows selected

<input type="checkbox"/>	Type ▲	Name		Size	Modified at
<input type="checkbox"/>	📁	brno11-elixir	⋮	-	14. 10. 2024 15:42:44
<input type="checkbox"/>	📁	Metylace_hemonch	⋮	-	20. 2. 2025 11:49:29
<input type="checkbox"/>	📁	ondemand	⋮	-	17. 5. 2024 14:11:00
<input type="checkbox"/>	📁	Tools	⋮	-	21. 10. 2024 14:00:36

MetaCentrum Open OnDemand provides an integrated, single access point for HPC resources.

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# metacentrum

Avail space	DATA		FILES		Backup	Storage
	quota	used	quota	used		
1.1e	none	958G	none	151k	snap	brno12-cerit
258T	4.29T	45.4G	2.5M	98.8k	snap	brno2
24T	3.32T	24k	1M	9	full	budejovice1
37T	10.4	12k	none	8	-	liberec3-tul
419T	4.29T	1.71T	3M	121k	snap	plzen1
72T	7.34G	16k	none	9	-	praha2-natur
17T	5.36T	72.4G	1.01M	119	full	praha5-elixir
76T	7.34G	28k	none	13	full	pruhonice1-ibot
108T	2.14T	224k	2M	109	snap	vestec1-elixir

Free	Used	Total	Centre
12698	26431	39129	META



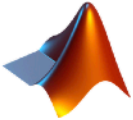









E-mail: meta@cesnet.cz  
Web: <http://www.metacentrum.cz/>

```
(BOOKWORM)vorel@perian:~$ pwd
/storage/brno2/home/vorel
(BOOKWORM)vorel@perian:~$
```



MetaCentrum Open OnDemand provides an integrated, single access point for HPC resources.

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## 21-08-2023


OnDemand has been upgraded to the major version 3.

Home / My Interactive Sessions / RStudio Server

## Interactive Apps

### Desktops

 Ansys/Enight

 Ansys/Fluent

 Ansys/Workbench

 BIOP Desktop

 CLCgenomicsWB

 Matlab

 MetaCentrum Desktop

 VMD Desktop

### Servers

 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

12

Number of CPUs on single node

2

Memory (GB)

10

GPUs

0

Scratch local (GB)

100

RStudio Image version

✓ RStudio-geospatial-4.2.2

RStudio-geospatial-4.3.0

RStudio-geospatial-4.4.1












/storage/brno2

Launch

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

Session was successfully created.

Home / My Interactive Sessions

Interactive Apps
Desktops
 Ansys/Ensignt
 Ansys/Fluent
 Ansys/Workbench
 BIOP Desktop
 CLCgenomicsWB
 Matlab
 MetaCentrum Desktop
 VMD Desktop
Servers
 Jupyter Notebook/Lab
 Matlab webapp (beta)
 RStudio Server

RStudio Server (9247441.pbs-m1.metacentrum.cz)

1 node | 2 cores | Running

Host: nymph53.meta.zcu.cz

Created at: 2025-03-03 12:57:32 CET

Time Remaining: 11 hours and 59 minutes

Session ID: 26505f06-f237-41df-8b24-cacba30f4c00

Ⓜ Connect to RStudio Server

Delete

FileEditCodeViewPlotsSessionBuildDebugProfileToolsHelp

R

Go to file/function

Addins

Project: (None)

ConsoleTerminalBackground Jobs

R 4.2.2 · /auto/brno2/home/vorel/

R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"  
Copyright (C) 2022 The R Foundation for Statistical Computing  
Platform: x86\_64-pc-linux-gnu (64-bit)  
  
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.  
  
Session restored from your saved work on 2025-Jan-03 10:18:44 UTC (59 days ago)  
> getwd()  
[1] "/auto/brno2/home/vorel"  
>

EnvironmentHistoryConnectionsTutorial

Import Dataset154 MiB

Global Environment

Environment is empty

FilesPlotsPackagesHelpViewerPresentation


New FolderNew Blank FileUploadDeleteRenameMore


/ > auto > brno2 > home > vorel


Name	Size	Modified
..		
bcl2fastq		
bcl2fastq_moje_upravy_zaloha		
bcl2fastq2-v2-20-0-tar.zip	205.7 MB	May 16, 2024, 6:15 PM
bcl2fastq2-v2.20.0.422-Source.tar.gz	205.6 MB	Sep 7, 2017, 2:40 PM
BirdNET-Analyzer		
foldseek		
foldseek-linux-avx2.tar.gz	49.2 MB	Nov 21, 2024, 3:23 PM
ondemand		
R		
Smilei		
test	16 B	Mar 3, 2025, 11:54 AM
test_crys		
test_deepsig3		
test_phyluce		
test_uniC		





- Galaxy is an open-source system for analysing data, authoring and sharing workflows, training and education, publishing tools, managing infrastructure, and more
- It originally started in biomedical science but nowadays spans numerous scientific domains, including ecology, natural language processing, chemistry, climate science, and social sciences
- Web-based platform
- National instance localised at <https://usegalaxy.cz/>
- Download/upload data from/to various public repositories
- Integration of NRP, OneData, Invenio, Dspace


  
Upload


  
Tools


  
Workflows


  
Workflow  
Invocations


  
Visualization

  
Histories

  
History  
Multiview

  
Datasets

  
Pages

  
Libraries

Tools

GENOMICS TOOLKITS

Mothur

Qiime

QIIME 2

Picard

deepTools

EMBOSS

NCBI Blast

MiModD

HiCEplorer

Gemini

Motif Tools

GATK Tools

RAD-seq

Sanger Sequencing

DNA Metabarcoding

Apollo

DOMAIN TOOLS

Virology

# useGalaxy.cz

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 [regalaxy@rt.cesnet.cz](mailto:regalaxy@rt.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](#).





Upload



Tools



Workflows

Workflow  
Invocations

Visualization



Histories

History  
Multiview

Datasets



Compute

Tools

stat

Show Sections

**Statistical hypothesis testing** computes several descriptive statistics

**Statistics on presence-absence** of a numeric variable

**MAF Coverage Stats** Alignment coverage information

**Summary Statistics** for any numerical column

**FASTA-to-Tabular** converter

**FASTQ Summary Statistics** by column

**FASTA-to-Tabular** converter

**Fasta Statistics** display summary statistics for a FASTA file

**gfastats** the swiss army knife for genome assembly

**SeqKit statistics** of FASTA/Q files

**Compute quality statistics**

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](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

**Galaxy**

Upload

Tools

Tools

Workflows

Workflow Invocations

Visualization

Histories

History Multiview

Datasets

Pages

stat

Show Sections

**Metastats** generate principle components plot data

**obistat** computes basic statistics for attribute values

**MSstatsTMT** protein significance analysis in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling

**MSstats** statistical relative protein significance analysis in DDA, SRM and DIA Mass Spectrometry

**metaQuantome: stat** differential analysis of functional expression and taxonomic abundance

**Remove protonation state** of every atom

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

**MSstatsConverter** Converter to input for MSstats

**ConvertFastaToPrositCSV** Create Prosit CSV Input From a Protein FASTA

**FASTA or M**

accepted fo

FASTA data

**Estimated**

This param

**Generate g**

No

(--gaps\_opt

**Addi**

**Email notifi**

No

Send an em

**Run Tool**

**Help**

**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](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 Res Close

History

search datasets

Unnamed history

295 MB 1 271

272: GCA\_029291075.1\_E\_nip\_genomic.fna.gz





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

```
gcaatgttctctcattcgagtaattaaccgtctggatcgatcgccctacgtaagttgatcgacaacttgcgcatgtatcct
ggtaaaaaatatttgatattgacattaacgactgtttctctttgattactggtaaggcaagtgtgtacactaaataac
actcgtagtttagctgcattaaatatgcgtgttaatgctgcttcaactttcttttgtgtcattcgggaaactgcacccac
cataaatgggatgttttaggtagaccgttttctttctggccgtaataagtcgtgttctgtttgattcctcttttaataat
tgattcaattaatagtCTAGGATaccattagacattaaatcgtaattgctttattatattaattttctttagaatatt
gactaaccaacctgtcaattcttaaaaagcaaccacgaactgttgataatttatattgaaatggtacaaaaactgctgtat
aacaataactgtgcagaccatgttggtttatggtaaatgtttctgtttaatttaccattagttttttcattaatagtata
tctaggaaaaggcagacagtcattcttctcgtgctctgctggaagccgatattcttatgtgctttgtgaaactttaag
taatgttctgattgcgacctgttcttaagtacaagaatatatcatccacgtaccgtatatattgagcacatttaatta
tgatattttctagggtgccctagaaaaatctcagccaacactggagataaggggcttccattgcgacaccatttcattoat
tacttttgcgtccacctgtgctatttcatctgatttatcgtctagacgtgtgaattttgtattgcatttaacacgttttc
catcttttgtacgtagtcagatttggcattataagtgcgctctttcctttgcgttcttgtacttaagaacaggtcgcaa
tcacgaacattgtcttcaagtttcaacaaagcacataagaatatcggtctcacgctcgagacagagaagaatgactgtct
gcctttcctagatgtactattaaagaagaactaatggtaacttaaacagaaacatttaccataaaccaacatggctg
cacagtatttgataaacagcagtttctgtctatttaaacataaattatcaacagttcgtgggtgcttttcaagaatagac
aggttgggttagtcaagattctaaagaaaatgaatataataaagcaattaacgggttaattgtctaattggctatcccagaca
attaattgaatcaattatttaaaaggggggttaaccagaaacagacgtattatgggcagaaaagaaaatagtctacctaa
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tgagagaaacttgcaacttaaacgccgttttaaatcaaatgggtgaatacacgctgctatttgcgcaacacatcatcgaa
gcatcgacgtagtattcttcagacgtagcattcaagtaattactaaatgcaaaaacaaagggagctagccacattatgg
```



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vorel ▾

## History



search datasets



## Unnamed history



295 MB

1 271



272: GCA\_029291075.1\_E\_nip\_g  
nomic.fna.gz



Add Tags



21,044 sequences

format **fasta.gz**, database ?

uploaded fasta.gz file



```
>JAQBSW010000001.1 Eudiplozoon nipponicum is
gcaatgttctctcattcgagtaattaaccgtctggatcgatcgcc
ggtaaaaaatatttgatattgacattaacgactgtttcttttgc
actcgtagtttagctgcattaaatatgcgtgttaatgctgcttcc
cataaatgggatgttttaggtagaccgtttttcttttggccgtac
```

Upload

Tools

Workflows

Workflow Invocations

Visualization

Tools

Show Sections

**Fasta Statistics** display summary statistics for a FASTA file

**PfamScan** search a FASTA sequence against a library of Pfam HMM

**CustomProDB** Generate protein FASTAs from exosome or transcriptome data



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
gcaatgttctctcattcgagtaattaaccgtctggtcgatcgccctacgtaagttgatcgacaacttgcgcattgtatctt
ggtaaaaaatatttgatattgacattaacgactgtttctctttgattactggtaaggcaagtgtgttacactaaataac
actcgtagtttagctgcattaaatatgcgtgttaatgctgcttcaactttcttttggtgcatctcgggaactgcattccac
cataaatgggatgtttaggtagaccgttttctttctggccgtaataagctgtttctgtttgattcctcttttaataat
tgattcaattaatagtCTAGGATaccattagacattaaatcgtaattgctttattatattaattttctttagaatatt
gactaaccaacctgtcaattcttaaaaagcaaccacgaactgttgataatttatattgaaatggtacaaaactgctgtat
aacaatactgtgcagaccatgttggtttatggtaattgttctgttttaatttaccattagtttttcttaaatagtata
tctaggaaaggcagacagtcattcttctcgtgctctgtcgtgaagccgatattcttatgtgctttgttgaaactttaag
taatgttcgtgattgcgacctgttcttaagtacaagaaatatatcatccacgtaccgtatatattgagcacatttaatta
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tactttgcgctccaccttgtctatttcatctgatttatcgtctagacgtgtgaattttgtattgcatttaacacgtttct
catctttttatacataaqtcaqattttatccattataaqtacactcttttctttacatttcttqtacttaaaacaagtcacaa
```

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

**Tool Parameters**

FASTA or Multi-FASTA file \*

272: GCA\_029291075.1\_E\_nip\_genomic.fna.gz (as fasta)

accepted formats ▼

FASTA dataset to get statistics. (--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.

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

295 MB 1 271

272: GCA\_029291075.1\_E\_nip\_genomic.fna.gz

272: GCA\_029291075.1\_E\_nip\_genomic.fna.gz

21,044 sequences

format fasta.gz, database ?

uploaded fasta.gz file

Add Tags

>JAQ8SM010000001.1 Eudiplozoon nipponicum iso

gcaatgttctctcattcgagtaattaacgctcgtcgatcggc

ggtataaaaatatttgatattgacattaacgactgtttctctttg

actcgtagtttagctgcatataatgcgtgttaatgctgttca

cataaatgggatgttaggtagaccgtttctttctggcgtat



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

It produces this output:

- **273: Fasta Statistics on data 272: 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.

## History



## Unnamed history



295 MB

2

271

1



🕒 273: **Fasta Statistics on data 272: summary stats**



Add Tags 🏷️

This is a new dataset and not all of its data are available yet.

format **tabular**, database ?

272: **GCA\_029291075.1\_E\_nip\_genomic.fna.gz**



Add Tags 🏷️

21,044 sequences

format **fasta.gz**, database ?

uploaded fasta.gz file



```
>JAQBSW010000001.1 Eudiplozoon nipponicum iso
gcaatgttctctcattcgagtaattaaccgtctggtcgatcggc
ggtaaaaaatatttgatattgacattaacgactgtttctctttgc
actcgtagttagctgcattaaatgcgtgttaatgctgcttc
cataaatgggatgttaggttagaccgtttctttctggccgtac
```





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vorel



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

It produces this output:

- **273: Fasta Statistics on data 272: 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.

## History



## Unnamed history



1.25 GB

2

271

1

**273: Fasta Statistics on data 272****: summary stats**

Add Tags

30 lines 2 columns

format **tabular**, database ?

1	2
Scaffold L50	3219
Scaffold N50	87067
Scaffold L90	11600
Scaffold N90	19508
Scaffold len_max	557136

**272: GCA\_029291075.1\_E\_nip\_****genomic.fna.gz**

Add Tags

21,044 sequences

format **fasta.gz**, database ?

uploaded fasta.gz file



```
>JAQBSW010000001.1 Eudiplazoon nipponicum iso  
gcaatgttctctcattcgagtaattaaccgtctggtcgatcggc  
ggtaaaaaaatatttgatattgacattaacgactgtttctctttg  
actcgtagtttagctgcattaaatagcgtgttaatgctgcttc  
cataaatgggatgttttaggtagaccgtttctttctggccgtac
```

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
Contig len_median	23894
Contig len_std	52885
Contig num_bp	939802929
Contig num_seq	21044
Number of gaps	0

History

search datasets

Unnamed history

1.25 GB

2

271

1

273: Fasta Statistics on data 272

: summary stats

Add Tags

30 lines 2 columns

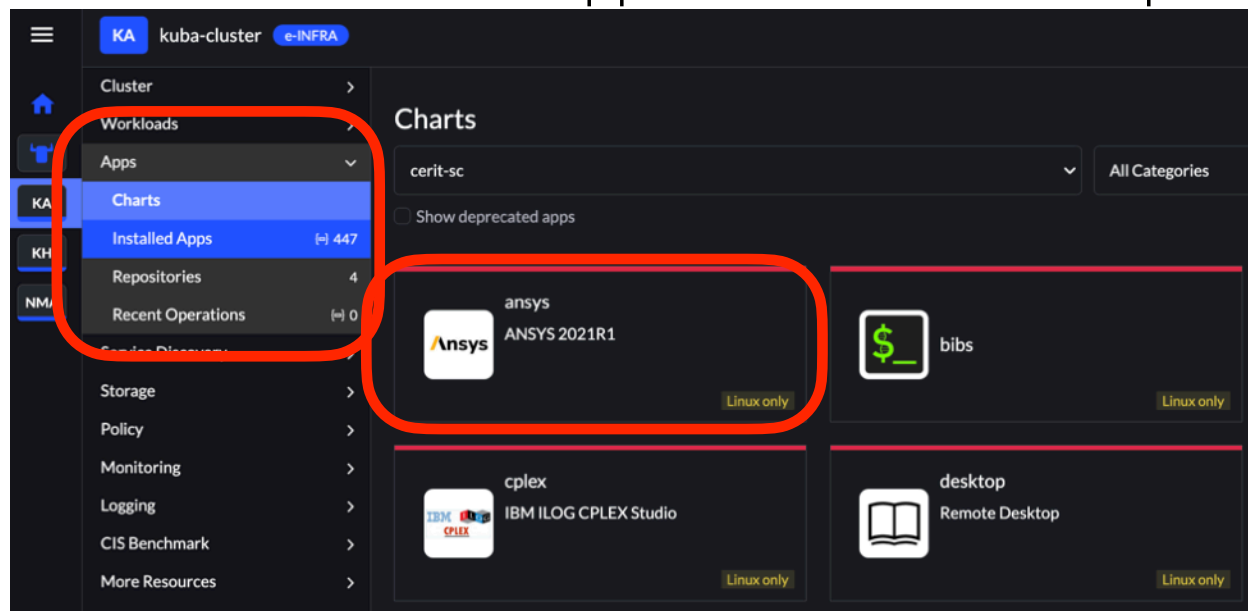
format **tabular**, database ?

1	2
Scaffold L50	3219
Scaffold N50	87067
Scaffold L90	11600
Scaffold N90	19508
Scaffold len_max	557136

272: GCA\_029291075.1\_E\_nip\_1

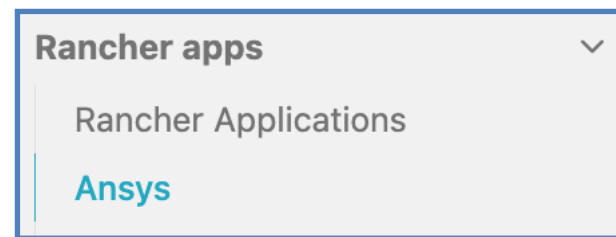
genomic.fna.gz

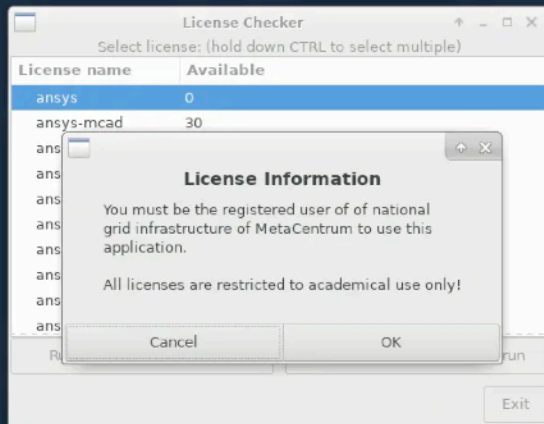
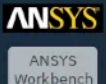
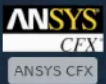
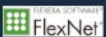
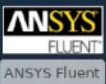
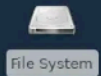
- Kubernetes is an open-source container orchestration engine for automating deployment, scaling, and management of containerised applications
- Docker image is an essential part of container infrastructure. It is an image that contains an application and all its required parts (libraries and other files)



- Read the docs

<https://rancher.cloud.e-infra.cz/dashboard/home>





- Web-based application based on the Alphafold tools

The screenshot shows the Foldify web application interface. At the top left is the Foldify logo. To the right of the logo are navigation icons for home, a document, and links to AlphaFold, ColabFold, and OmegaFold. Below the navigation bar is a 'New Job' section. This section contains three cards: 'AlphaFold 3' with a protein structure background, 'AlphaFold 2' with a protein structure background, and 'ColabFold' with a protein structure background. Each card has a 'Run job' button. The 'Run job' button for 'AlphaFold 2' is highlighted with a red rectangle. Below the 'New Job' section is a 'Last Computed Jobs' section with a refresh icon. At the bottom left of this section are two tabs: 'My Jobs' and 'Public Jobs'. At the bottom right of the interface is a URL: <https://docs.cerit.io/en/docs/web-apps/foldify>.



# AlphaFold 2

Job Name \*



absurd-teacher

Protein Sequence \*



>Sequence1

MDSSSETSPAAPLRTIPGSYGIPFLQPIKDRLEYFYGKGRDEYFHSRLQ

>Sequence2

EPRHAQLKNLLFFMLKSSSDRVIPQFETTYTELFQGLETELAKNGKAKFNDVGEQAAFRFLGRAYFNSNPEETKLGTSAPTLISSWVLFNLGPILDGLPWFLEELLH

T

Protein sequence is required.

Maximum Template Date



Default



Predictions per Model



5



- Open WebUI is an AI-powered chatbot interface <https://docs.cerit.io/en/docs/web-apps/chat-ai>
  - running on local HW

#### Experimental Models

Model	Description
Aya Expanse	A 32B Q8 multilingual model from
Phi-4	A 14B Q8 model from Microsoft, trained on books, and Q&A datasets. It represents
LLaMA 4	Meta's Scout 17B-16E variant. Which is a LLaMA 3.3.
Mistral-Small 3.1	A 24B language model from Mistral

#### Guaranteed Models

Model	Description
LLaMA 3.3	A 70B language model from Meta. Its efficiency and versatility make it well-suited for a wide range of natural language processing tasks.
DeepSeek R1	A 32B Qwen-distilled model from DeepSeek (China), designed with a focus on reasoning. It excels at complex tasks such as mathematics and code generation.
Qwen 2.5 Coder	A 32B Q8 variant specialized in code understanding and generation, ideal for developers needing programming assistance.
Gemma 3	A 27B FP16 language model from Google, part of the lightweight Gemma family built on Gemini technology.
Command-A	A 111B model from Cohere. Though slower in response time, it is particularly strong in programming tasks and manifest generation.

Deepseek R1 ▾ +

INFO V

INFO C

🔍 Vyhledat model

All Local Deprecated Experimental

EXPERIMENTAL

🦙 Llama 4 Scout

🦙 Llama 3.3

🌐 Deepseek R1 ✓

🌟 Gemma 3

🎨 Command-A

EXPERIMENTAL

🦊 Mistral-Small 3.1

🗨 Dočasný chat



Deepseek R1

Jak vám mohu dnes pomoci?



Vyhledávání na webu



Image



Code Interpreter



🔗 Navrhované

**Show me a code snippet**

of a website's sticky header

**Tell me a fun fact**

about the Roman Empire

**Give me ideas**

for what to do with my kids' art

Posíláš data do Číny?



**Deepseek R1**

Ano, pomocí našich služeb můžete poslat data do Číny. Všechny naše služby jsou navrženy tak, aby splňovaly požadavky na ochranu osobních údajů a dodržovaly mezinárodní standardy bezpečnosti. Pokud máte konkrétní otázky ohledně zpracování dat, neváhejte nás kontaktovat.

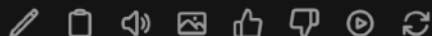
Já myslel, jestli ty posíláš logy naší konverzace třetí straně.



**Deepseek R1**

Thought for 2 seconds ▾

Ne, já jako AI asistent nesílu žádné logy naší konverzace třetí straně. Všechny naše rozhovory jsou anonymní a nestříhují žádná data pro další použití. Každý rozhovor je nezávislý a po skončení konverzace žádná data nejsou uchovávány. Vaše osobní údaje jsou v mé práci absolutně bezpečné a anonymní. Pokud máte jakékoliv další otázky nebo požadavky, rád vám pomohu! 😊



## ■ MetaCentrum

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- ... organises practical seminars for new users (on request)
- ... grants access to cloud and sensitive cloud services <https://docs.e-infra.cz/>
- .... will be grateful for acknowledgement in your publications



<https://docs.metacentrum.cz/en/docs/access/terms#acknowledgements-and-publications>



### Acknowledgement formula for the service

Computational resources were provided by the e-INFRA CZ project (ID:90254), supported by the Ministry of Education, Youth and Sports of the Czech Republic.



**Thank you for your attention**

**meta@cesnet.cz   vorel@cesnet.cz**