Bilgisayardan Galaxy'e Veri Yükleme

Hazırlayanlar: Halit Kemal Aydın, Şahin Öztürk, Tolga Leyla

Workflow   Visualize   Shared Data ▾   Help ▾   User ▾

Tools

search tools

⬆ Upload Data

Download from URL or upload files from disk

Get Data

Send Data

GENERAL TEXT TOOLS

Text Manipulation

Convert Formats

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Operate on Genomic Intervals

Fetch Sequences / Alignments

GENOMICS ANALYSIS

Annotation

Multiple Alignments

Assembly

Mapping

Variant Calling

Genome editing

⬆ Upload Data

...dated list of laboratories that can host Ukrainian scientists at all career levels. If your lab can host a scientist -- add ...s a number of positions at its EU and US sites. Contact us at ukraine@galaxyproject.org. German organisations are organising accommodation here.

Світова наукова спільнота створила список лабораторій, що постійно оновлюється та які можуть прийняти українських науковців усіх рівнів, у тому числі й аспірантів. Якщо ваша лабораторія має можливість запросити -- ви можете додати ваше ім'я до списку тут. Окрім того, Galaxy Project має відкриті вакансії у своїх європейських та американських осередках. Пишіть нам на ukraine@galaxyproject.org

Научное сообщество создало постоянно обновляемый список лабораторий, которые могут принять украинских ученых (включая аспирантов). К тому же, Galaxy Project имеет открытые позиции на своих европейских и американских сайтах. Контактируйте нас используя ukraine@galaxyproject.org uA

"Anyone, anywhere in the world should have free, unhindered access to not just my research, but to the research of every great and enquiring mind across the spectrum of human understanding." – Prof. Stephen Hawking

📣 News

The European Galaxy Team is hiring a Bioinformatics training officer
Are you passionate about training in life sciences? The Freiburg Galaxy Team is looking for a team member who will develop, coordinate and implement training programs within international communities, especially via BioNT, a new multi-organization project funded by the European Commission, and via the Galaxy Training Network (GTN).

Impact on Galaxy of OpenSSL 3.0.x Vulnerabilities CVE-2022-3602 and CVE-2022-3786 ("Spooky SSL")
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UseGalaxy.eu Tool Updates for 2022-10-23

Research Data Management in Galaxy
How Galaxy manages your (meta)data

Galaxy as a cross-EOSC platform
New scientific collaboration agreement between EOSC-Life and EOSC-Pillar

📅 Events

Oct 31 - Dec 19 Analysis of biological data with Galaxy
Learn how to use Galaxy in YOUR research

Nov 7 - Nov 11 Galaxy @ BioHackathon-Europe 2022
BioHackathon activities are driven by practical sessions where people gather, discuss, and implement ideas and projects during intensive and productive coding sessions

Nov 17 Galaxy Community Call: The new GTN course builder
A forum to share updates and discuss community-wide topics

Feb 6 - Feb 10 Single-cell RNA-seq analysis using Galaxy
Participants will be guided through the droplet-based scRNA-seq analysis pipelines from raw reads to trajectories.

Apr 25 - Apr 26 Galaxy Introduction for Life Scientists
This 1.5-day course will give a general introduction on the galaxy web-page structure, how to import data, run tools, share analyses and build workflows. Participants will run a whole NGS analysis using an RNA-seq dataset as an example.

The European Galaxy server

The European Galaxy server UseGalaxy.eu is maintained primarily by the Freiburg Galaxy Team in collaboration with other academic groups across Europe and with the US Galaxy team. Please check our Terms of Service and data retention police before using the server. We offer thousands of tools, increased quota on temporary basis.

History

search datasets

Unnamed history

📦 24.8 kB   📍4   👁1

4 : NCBI Accession Download on : Log

3 : NCBI Accession Download on : Downloaded Files
a list with 1 fasta dataset

2 : dizi.fna

1 : dizi-fasta.xlsx

Galaxy ana sayfasının sol üst köşesinde bulunan "tools" alanınındaki "Upload Data" butonuna tıklayarak yükleme alanına ulaşırız.

Tools

search tools

⬆ Upload Data

Get Data
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Collection Operations

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Download from web or upload from disk

Regular   Composite   Collection   Rule-based

📄 Drop files here

Type (set all): Auto-detect ▾   🔍 Genome (set all): unspecified (?) ▾

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Peace to Uk...

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Світова науков...
аспірантів. Які...
європейських ...

Научное сооб...
Project имеет о...

"Anyone, anywhere...
understanding." –...

📢 New...

The European ...
Are you passionate...
member who will o...
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"Choose local files" Butonuna tıklayarak;

Workflow Visualize Shared Data ▾ Help ▾ User ▾

Using 0%

Tools

search tools

⬆ Upload Data

Flymine server
modENCODE modMine server
MouseMine server
Ratmine server
YeastMine server
metabolicMine server
modENCODE worm server
WormBase server
ZebrafishMine server
EuPathDB server
HbVar Human Hemoglobin Variants and Thalassemias
Faster Download and Extract Reads in FASTQ format from NCBI SRA
Download and Extract Reads in BAM format from NCBI SRA
Unipept retrieve taxonomy for peptides
NCBI Accession Download Download sequences from GenBank/RefSeq by accession through the NCBI ENTREZ API
Download and Generate Pileup Format from NCBI SRA
UniProt download proteome as XML or fasta
Get species occurrences data from GBIF, ALA, iNAT and others
NCBI ESearch search NCBI Databases by text query
NCBI EGQuery Provides the number of records retrieved in all Entrez

Executed NCBI Accessio

The tool uses this input:

It produces this output:

• 8: NCBI Accessio

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successfully or 'error' if p

Download from web or upload from disk

Regular   Composite   Collection   Rule-based

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Galaxy Eur

This page contains a
community and ad

Also see the _Galacti_

Contribute

To add a news item, create a new folder within the _news folder_
other existing news items as a template.

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Open

← → ↑ | This PC > Downloads

Organize ▾   New folder

Pc YEDEK
Screenshots
OneDrive - Person
This PC
3D Objects
Desktop
Documents
Downloads
Music
Pictures
Videos
S (B:)
OS (C:)
Network

Search Downloads

Name	Date modified	Type	Size
∨ **Today (3)**			
tree	11/5/2022 3:13 PM	Text Document	1 KB
clustalo-I20221105-120625-0326-6188579...	11/5/2022 3:07 PM	CLUSTAL_NUM File	5 KB
example	11/5/2022 3:06 PM	FNA File	2 KB
› **Earlier this week (8)**			
› **Last week (4)**			
› **Last month (19)**			
› **Earlier this year (7)**			

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Open   Cancel

History

search datasets

Unnamed history

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dataset

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Yüklemek istediğiniz verinin bulunduğu konuma gidip, verimizi seçerek sisteme ekleriz.

Tools

search tools

Upload Data

Flymine server
modENCODE modMine server
MouseMine server
Ratmine server
YeastMine server
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Faster Download and Extract Reads in FASTQ format from NCBI SRA
Download and Extract Reads in BAM format from NCBI SRA
Unipept retrieve taxonomy for peptides
NCBI Accession Download Download sequences from GenBank/RefSeq by accession through the NCBI ENTREZ API
Download and Generate Pileup Format from NCBI SRA
UniProt download proteome as XML or fasta
Get species occurrences data from GBIF, ALA, iNAT and others
NCBI ESearch search NCBI Databases by text query
NCBI EGQuery Provides the number of records retrieved in all Entrez

Executed **NCBI Accession**

The tool uses this input:

It produces this output:

- **8: NCBI Accession**

You can check the status successfully or 'error' if p

Download from web or upload from disk

Regular   Composite   Collection   Rule-based

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

	Name	Size	Type	Genome	Settings	Status
	example.fna	1.9 KB	fasta	unspecified (?)	⚙	0%	🗑

Type (set all): [Auto-detect]   Genome (set all): [unspecified (?)]

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

Galaxy Eur

This page contains **community** and ad

Also see the *Galactic*

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History

search datasets

Unnamed history

29.5 kB   📍6 🗑1 👁2

8 : NCBI Accession Download on : Log

7 : NCBI Accession Download on : Downloaded Files
a list with 1 dataset

4 : NCBI Accession Download on : Log

3 : NCBI Accession Download on : Downloaded Files
a list with 1 fasta dataset

2 : dizi.fna

1 : dizi-fasta.xlsx

Gerekli bütün işlemleri gerçekleştirdikten sonra "start" butonuna tıklayarak yüklemeyi başlatabiliriz.

Download from web or upload from disk

Regular	Composite	Collection	Rule-based

	Name	Size	Type	Genome	Settings	Status
🖥	example.fna	1.9 KB	fasta 🔍	unspecified (?)	⚙	100% ✓

Type (set all): Auto-detect 🔍   Genome (set all): unspecified (?)

[🖥 Choose local files] [📁 Choose remote files] [📋 Paste/Fetch data] [Start] [Pause] [Reset] [Close]

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The tool uses this input:

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You can check the status successfully or 'error' if

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⏳ 10 : example.fna   👁 ✎ 🗑
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a list with 1 fasta dataset
2 : dizi.fna   👁 ✎ 🗑
1 : dizi-fasta.xlsx   👁 ✎ 🗑

Veri sisteme tanımlanmıştır. Yükleme aşamasına geçilmiştir.

Workflow   Visualize   Shared Data ▾   Help ▾   User ▾

Using 0%

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NCBI ECitMatch search NCBI for citations in PubMed

✅ Executed **NCBI Accession Download** and successfully added 1 job to the queue.

The tool uses this input:

It produces this output:

- **8: NCBI Accession Download on : Log**

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 s... successfully or 'error' if problems were encountered.

⬚ **10 : example.fna**

Galactic News

Galaxy Europe News

This page contains announcements of interest to the Galaxy Community. These include **items from the Galaxy Team or the Galaxy community** and address anything that is of wide interest to the community.

Also see the *Galactic Blog* for more.

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16 October 2022	UseGalaxy.eu Tool Updates for 2022-10-16	

History

search datasets

Unnamed history

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⬚ **10 : example.fna**   👁 ✏ 🗑

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```
>ENA|BAA20512|BAA20512.1_Cyprinus_carpio
ATGAGTCTCTCTGATAAGGACAAGGCTGCTGTGAAAGCCCTATGGGCTAAGATCAGCCCC
AAAGCCGATGATATCGGCGCTGAAGCTCTCGGCAGAATGCTGACCGTCTACCCTCAGACC
AAGACCTACTTCGCTCACTGGGATGACCTGAGCCCTGGGTCCGGTCCTGTGAAGAAGCAT
GGCAAGGTTATCATGGGTGCAGTGGCCGATGCCGTTTCAAAAATAGACGACCTTGTGGGA
GGTCTGGCCTCCCTGAGCGAACTTCATGCTTCCAAGCTGCGTGTTGACCCGGCCAACTTC
AAGATCCTCGCACACAATGTCATCGTGGTCATCGGCATGCTCTTCCCTGGAGACTTCCCC
CCAGAGGTTCACATGTCAGTTGACAAGTTTTTCCAGAACTTGGCTCTGGCTCTCTCTGAG
AAGTACCGCTAA
>ENA|CAA23748|CAA23748.1_Homo_sapiens
ATGGTGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCG
CACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGATGTTCCTGTCCTTCCCCACCACC
AAGACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCAAGTTAAGGGCCACGGC
AAGAAAGGTGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGCG
CTGTCCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAG
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TACCGTTAA
>ENA|CAA24095|CAA24095.1_Mus_musculus
ATGGTGCTCTCTGGGGAAGACAAAAGCAACATCAAGGCTGCCTGGGGGAAGATTGGTGGC
CATGGTGCTGAATATGGAGCTGAAGCCCTGGAAAGGATGTTTGCTAGCTTCCCCACCACC
AAGACCTACTTTCCTCACTTTGATGTAAGCCACGGCTCTGCCCAGGTCAAGGGTCACGGC
AAGAAAGGTGCCGATGCGCTGGCCAGTGCTGCAGGCCACCTCGATGACCTGCCCGGTGCC
TTGTCTGCTCTGAGCGACCTGCATGCCCACAAGCTGCGTGTGGATCCCGTCAACTTCAAG
CTCCTGAGCCACTGCCTGCTGGTGACCTTGGCTAGCCACCACCTCGCCGATTTCACCCCC
GCGGTACATGCCTCTCTGGACAAATTCCTTGCCTCTGTGAGCACCGTGCTGACCTCCAAG
TACCGTTAA
>ENA|CAA28435|CAA28435.1_Capra_hircus
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CAGGCAGACGTCATTGGCACCGAGACCCTGGAGAGGCTCTTCTCCTGCTACCCGCAGGCC
AAGACCTACTTCCCGCACTTCGACCTGCACTCGGGCTCCGCGCAGCTGCGCGCGCACGGC
TCCAAGGTGGTGGCCGCCGTGGGCGACGGCGGTCAAGGACATCGACAACGTGACGAGCGCG
CTGTCCAAGCTGAGCGAGCTGCACGCCTACGTGCTGCGCGTGGACCCGGTCAACTTCAAG
TTCCTGTCCCACTGCCTGCTGGTCACGTTGGCCTCACGTTCCCCGCCGACTTCACGGCC
GACGCGCACGCCGCCTGGGACAAGTTCCTGTCCATCGTGTCCGGCGTCCTGACGGAGAAG
TACCGCTGA
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Multiple Alignments

Assembly

Mapping

Variant Calling

Edit Dataset Attributes

≡ Attributes   ⚙ Convert   ▤ Datatypes   ▲ Permissions

Name

example.fna

Info

uploaded fasta file

Annotation

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

Database/Build

unspecified (?)

Save   ↻ **Auto-detect**

History

search datasets

Unnamed history

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10 : example.fna

Kalem ikonuna ile verinin adını değiştirebilirsiniz, açıklama vs. ekleyebilirsiniz.