

Chipster

Data analysis platform for biosciences



*CSC - Suomalainen tutkimuksen, koulutuksen, kulttuurin ja julkishallinnon
ICT-osaamiskeskus*

Chipster

- User-friendly analysis software for high-throughput data
- Provides an easy access to over 450 analysis tools
- Command line tools
- R/Bioconductor packages
- Free, open source software

- What can I do with Chipster?
 - analyze high-throughput data
 - visualize data efficiently
 - share analysis sessions

Chipster website

(<https://chipster.csc.fi/>)



Chipster

Open source platform for data analysis



- Home
- Getting access
- Analysis tool content
- Screenshots
- Manual
- Tutorial videos
- Course material
- Cite
- FAQ
- Contact

- For developers:
 - Open source project
 - Tool editor

Welcome to Chipster

Chipster is a user-friendly analysis software for high-throughput data such as RNA-seq and single cell RNA-seq. It contains over 450 analysis tools and a large collection of reference genomes. Up to version 3.x Chipster is a desktop application requiring Java Web Start. Chipster version 4 is a Web application which runs on your browser. Both run the actual analysis in the cloud and the analysis tool content is the same, but **we encourage users to move to the Web App. The Java desktop application will be phased out in November 2020** because many universities don't provide Java Web Start any more due to the change in Oracle's Java licensing policy.

If you would like to use Chipster running on CSC's server, you need a [user account](#). Please note that both the [v3 server](#) and the [v4 server](#) are also available for local installations free of charge.



Launch Chipster v4

Chipster web application, no Java needed (watch introductory video)



Launch Chipster v3.16.3

...or launch with more memory: 3 GB or 6 GB

Java desktop application. If you have trouble launching it, read the [FAQ](#)

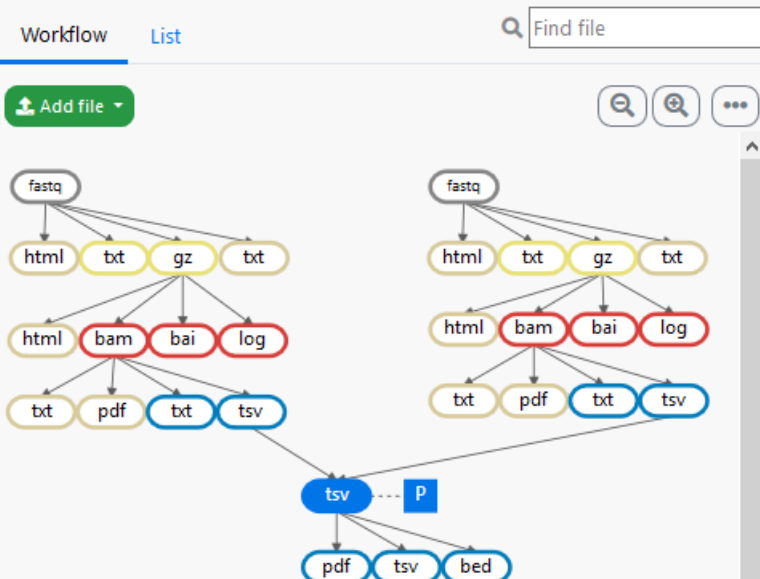
News and resources:

- 14.10.2020 [Lecture videos of single cell RNA-seq data analysis with Chipster course](#)
- 20.5.2020 [Instructions for moving data from Puhti to Chipster](#)
- 14.5.2020 [Chipster Web App video](#)
- 01.4.2020 [Lecture videos of 16S microbiome data analysis course](#)
- 24.1.2020 [Version 3.16.3 released](#)
- [Lecture videos of advanced single cell RNA-seq data analysis course](#)

Chipster user interface



Files



Tools

NGS Microarray Misc Find tool Job: 0

Category

- Quality control
- Preprocessing
- Utilities
- Matching sets of genomic regions
- Alignment
- Variants
- RNA-seq
- Small RNA-seq
- Single cell RNA-seq
- ChIP- and DNase-seq
- 16S rRNA sequencing
- CNA-seq

Tool

- Read quality with FastQC
- Read quality with MultiQC for many FASTQ files
- Read quality statistics with FASTX
- Read quality statistics with PRINSEQ
- RNA-seq quality metrics with RseQC
- RNA-seq strandedness inference and inner distance estimation using RseQC
- Collect multiple metrics from BAM
- PCA and heatmap of samples with DESeq2
- Check FASTQ file for errors
- Combine reports using MultiQC

Parameters Run

The tool runs FastQC on multiple FASTQ files, and then combines the reports using MultiQC. Input file is a single Tar package containing all the FASTQ files, which can be gzipped. This tool is based on the FastQC and MultiQC packages. [More info...](#)

File

ngs-data-table.tsv ...

Spreadsheet Text Expression Profile Scatter Plot Phenodata Details

First 101 rows of 58396 View in full screen to see all the rows.

Full Screen

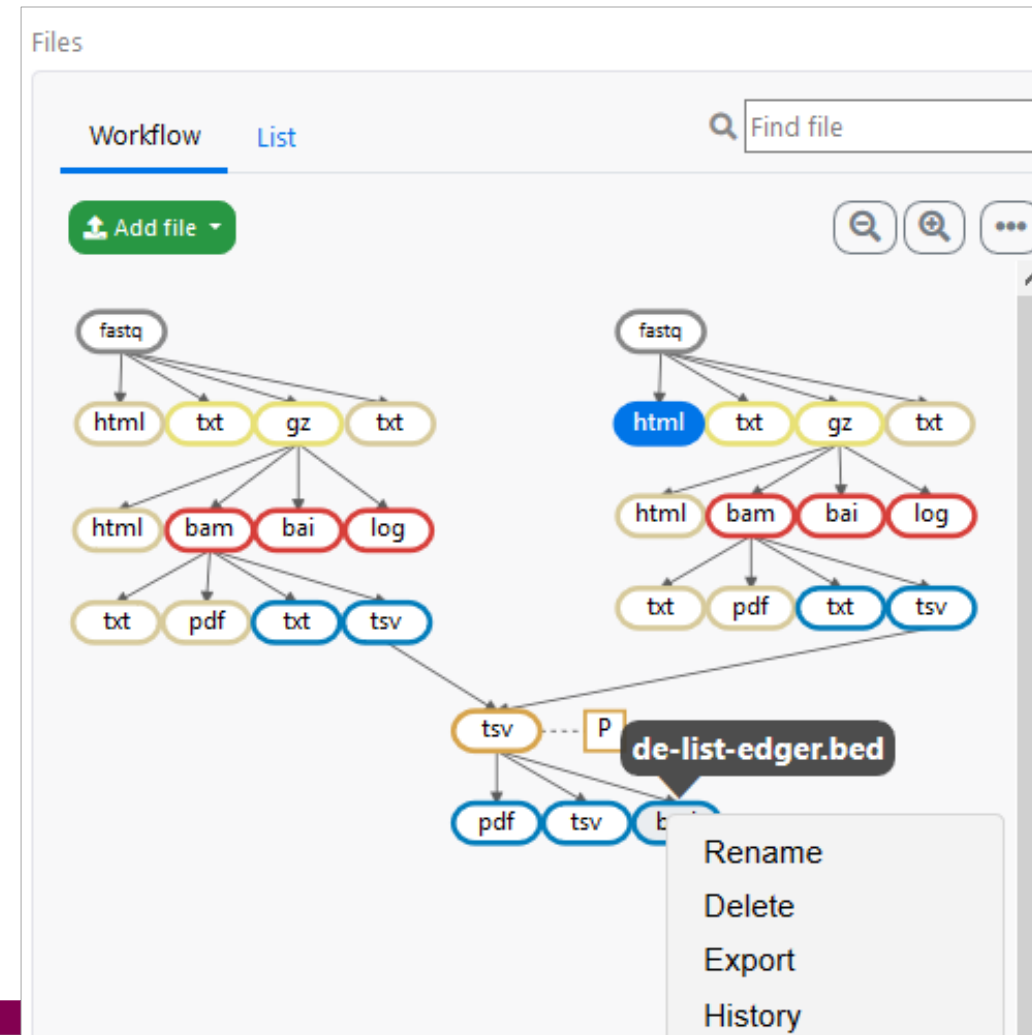
identifier	chr	start	end	length	sequence	chip.sample001.tsv	chip.sample002.tsv
ENSG000000000003	X	100627108	100639991	12883	NA	0	0
ENSG000000000005	X	100584801	100599885	15084	NA	0	0
ENSG000000000419	20	50934866	50958555	23689	NA	0	0

Analysis sessions

- Your analysis is saved automatically in the cloud
 - Session includes all the files, their relationships and metadata (what tool and parameters were used to produce each file).
 - Session is a single .zip file.
 - Note that cloud sessions are not stored forever! Remember to download the session when ready.
- You can share sessions with other Chipster users
 - You can give either read-only or read-write access
- If your analysis job takes a long time, you don't need to keep Chipster open:
 - Wait that the data transfer to the server has completed (job status = running)
 - Close Chipster
 - Open Chipster later and the results will be there

Workflow view

- Shows the relationships of the files
- You can move the boxes around, and zoom in and out.
- Several files can be selected by
 - keeping the Ctrl key down
 - Drawing a box around them
- Right click allows you to
 - Download a file ("Export")
 - Delete a file



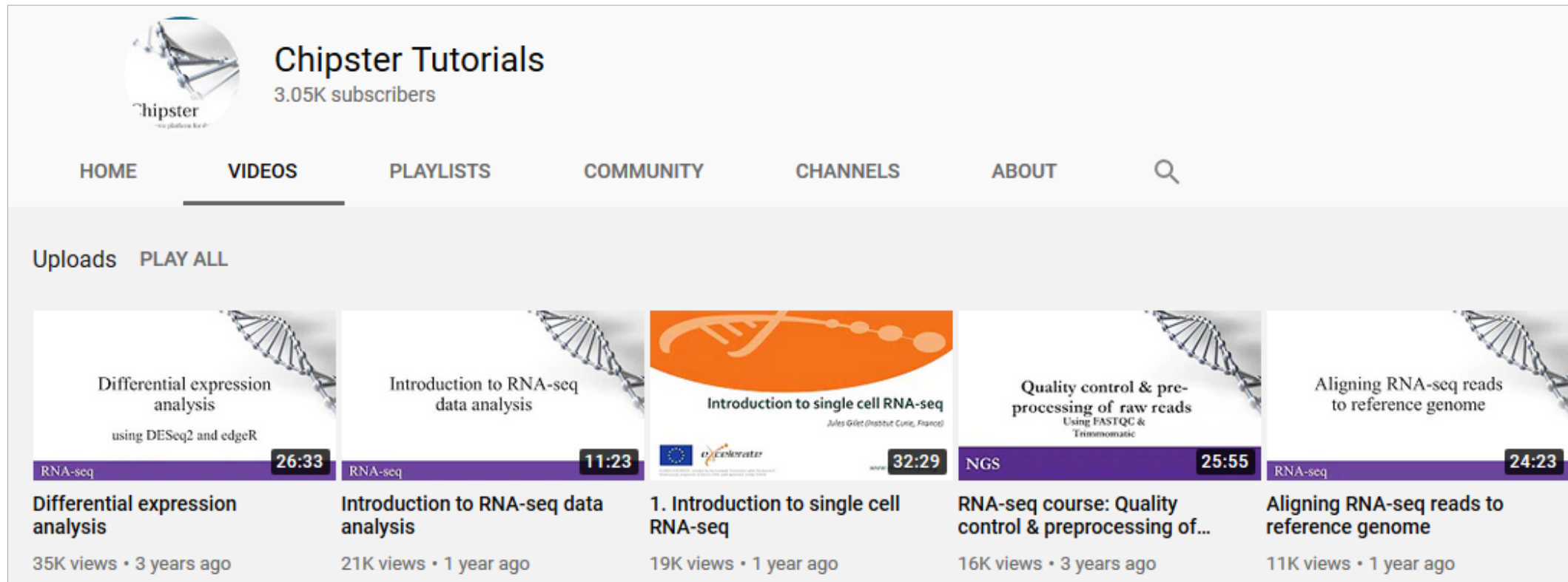
Options for importing data to Chipster



- Add file button
 - Upload files
 - Upload folder
 - Download from URL
- Sessions tab
 - Import session file
- Tools
 - Import from Illumina BaseSpace
 - Utilities / Retrieve data from Illumina BaseSpace
 - Access token needed
 - Import from SRA database
 - Utilities / Retrieve FASTQ or BAM files from SRA
 - Import from Ensembl database
 - Utilities / Retrieve data for a given organism in Ensembl
 - Import from URL
 - Utilities / Download file from URL directly to server

More info

- chipster@csc.fi
- <http://chipster.csc.fi>
- Chipster tutorials in YouTube
- <https://chipster.csc.fi/manual/courses.html>



The screenshot shows the YouTube channel page for 'Chipster Tutorials', which has 3.05K subscribers. The navigation menu includes HOME, VIDEOS, PLAYLISTS, COMMUNITY, CHANNELS, and ABOUT. The 'Uploads' section is active, displaying a grid of five video thumbnails. Each thumbnail includes the video title, a duration badge, and view/viewer information.

Video Title	Duration	Views	Time Ago
Differential expression analysis using DESeq2 and edgeR	26:33	35K views	3 years ago
Introduction to RNA-seq data analysis	11:23	21K views	1 year ago
1. Introduction to single cell RNA-seq	32:29	19K views	1 year ago
RNA-seq course: Quality control & preprocessing of...	25:55	16K views	3 years ago
Aligning RNA-seq reads to reference genome	24:23	11K views	1 year ago

How to access Chipster?

- CSC maintains Chipster server at <https://chipster.csc.fi>
 - This service is free of charge only for researchers working in Finland
- Your institute may already have Chipster server
- EGI provides Chipster:
 - <https://marketplace.eosc-portal.eu/services/chipster>



How to access Chipster?

- Code base is open source: You can install you own Chipster server.
- Based on Kubernetes running on Ubuntu.
- Recommended server: at least 4 cores, 16 GB RAM and 1 TB Storage space.
 - <https://github.com/chipster/chipster-openshift/blob/k3s/k3s/prerequisites.md>
(VM, Firewall, Ansible, Docker, K3s, Helm)
 - <https://github.com/chipster/chipster-openshift/blob/k3s/k3s/README.md>
(Chipster instructions)
- Downloading Tools-bin (containing 200 GB of software and reference data) is most time consuming step. Can be replaced with CVMFS mount.