CSC

Bioinformatics data analysis using Chipster

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

Chipster: User-friendly analysis software for high-throughput data

- Over 500 analysis tools, inc tools for single-cell RNA-seq and Visium data
  - Command line tools, R/Bioconductor packages
  - Free, open source software
- Users can share analysis sessions, analysis metadata is tracked
- Training resources
  - Course material (slides, videos, exercises, data sets) available
  - Training accounts available, email chipster@csc.fi
- Technical
  - Angular based web app and cloud native scalable backend
  - Ansible playbooks and Helm templates for setting up a K3s container orchestration system and Chipster containers on a virtual machine or on a physical server
- https://chipster.csc.fi/

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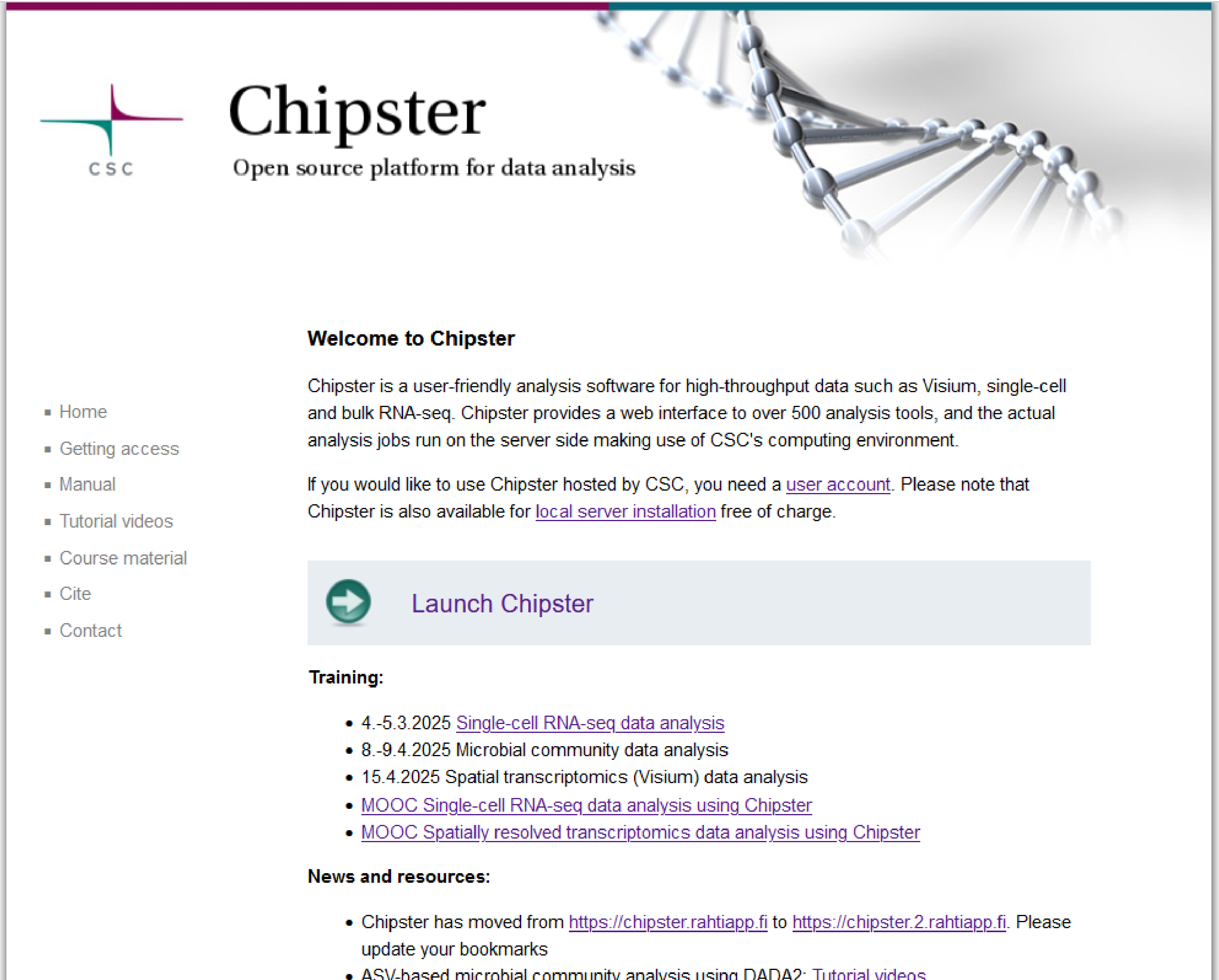


Welcome to Chipster

Chipster is a user-friendly analysis software for high-throughput data such as Visium, single-cell and bulk RNA-seq. Chipster provides a web interface to over 500 analysis tools, and the actual analysis jobs run on the server side making use of CSC's computing environment.

If you would like to use Chipster hosted by CSC, you need a user account. Please note that Chipster is also available for local server installation free of charge.

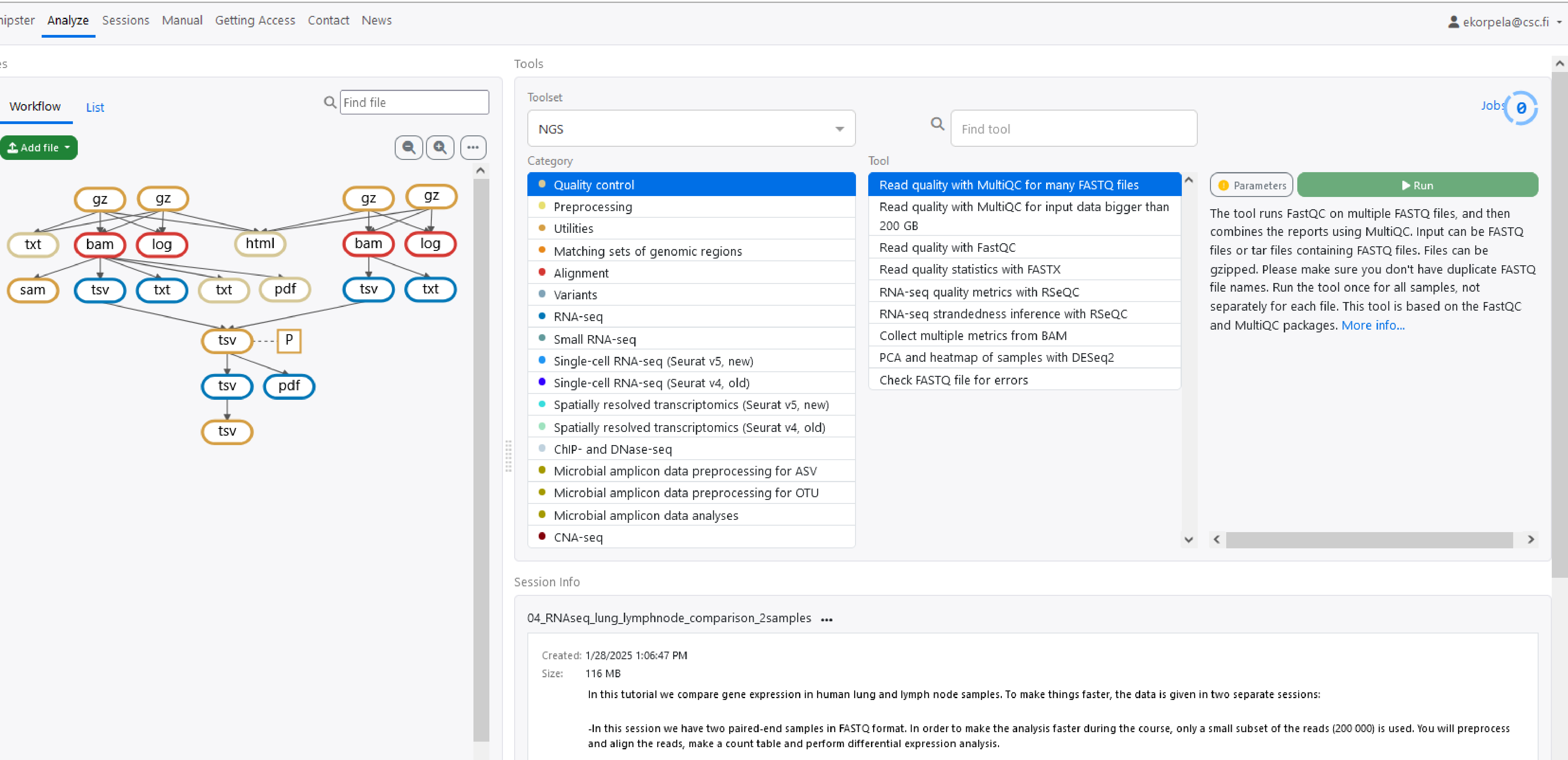
Training:

- 4.-5.3.2025 Single-cell RNA-seq data analysis
- 8.-9.4.2025 Microbial community data analysis
- 15.4.2025 Spatial transcriptomics (Visium) data analysis
- MOOC Single-cell RNA-seq data analysis using Chipster
- MOOC Spatially resolved transcriptomics data analysis using Chipster

News and resources:

- Chipster has moved from https://chipster.rahtiapp.fi to https://chipster.2.rahtiapp.fi. Please update your bookmarks
- ASV-based microbial community analysis using DADA2: Tutorial videos

Chipster user interface (chipster.2.rahtiapp.fi)



Toolset: NGS

Find tool

Category

- Quality control
- Preprocessing
- Utilities
- Matching sets of genomic regions
- Alignment
- Variants
- RNA-seq
- Small RNA-seq
- Single-cell RNA-seq (Seurat v5, new)
- Single-cell RNA-seq (Seurat v4, old)
- Spatially resolved transcriptomics (Seurat v5, new)
- Spatially resolved transcriptomics (Seurat v4, old)
- ChIP- and DNase-seq
- Microbial amplicon data preprocessing for ASV
- Microbial amplicon data preprocessing for OTU
- Microbial amplicon data analyses
- CNA-seq

Tool

- Read quality with MultiQC for many FASTQ files
- Read quality with MultiQC for input data bigger than 200 GB
- Read quality with FastQC
- Read quality statistics with FASTX
- RNA-seq quality metrics with RSeQC
- RNA-seq strandedness inference with RSeQC
- Collect multiple metrics from BAM
- PCA and heatmap of samples with DESeq2
- Check FASTQ file for errors

Parameters ▶ Run

The tool runs FastQC on multiple FASTQ files, and then combines the reports using MultiQC. Input can be FASTQ files or tar files containing FASTQ files. Files can be gzipped. Please make sure you don't have duplicate FASTQ file names. Run the tool once for all samples, not separately for each file. This tool is based on the FastQC and MultiQC packages. More info...

Session Info

04_RNAseq_lung_lymphnode_comparison_2samples ...

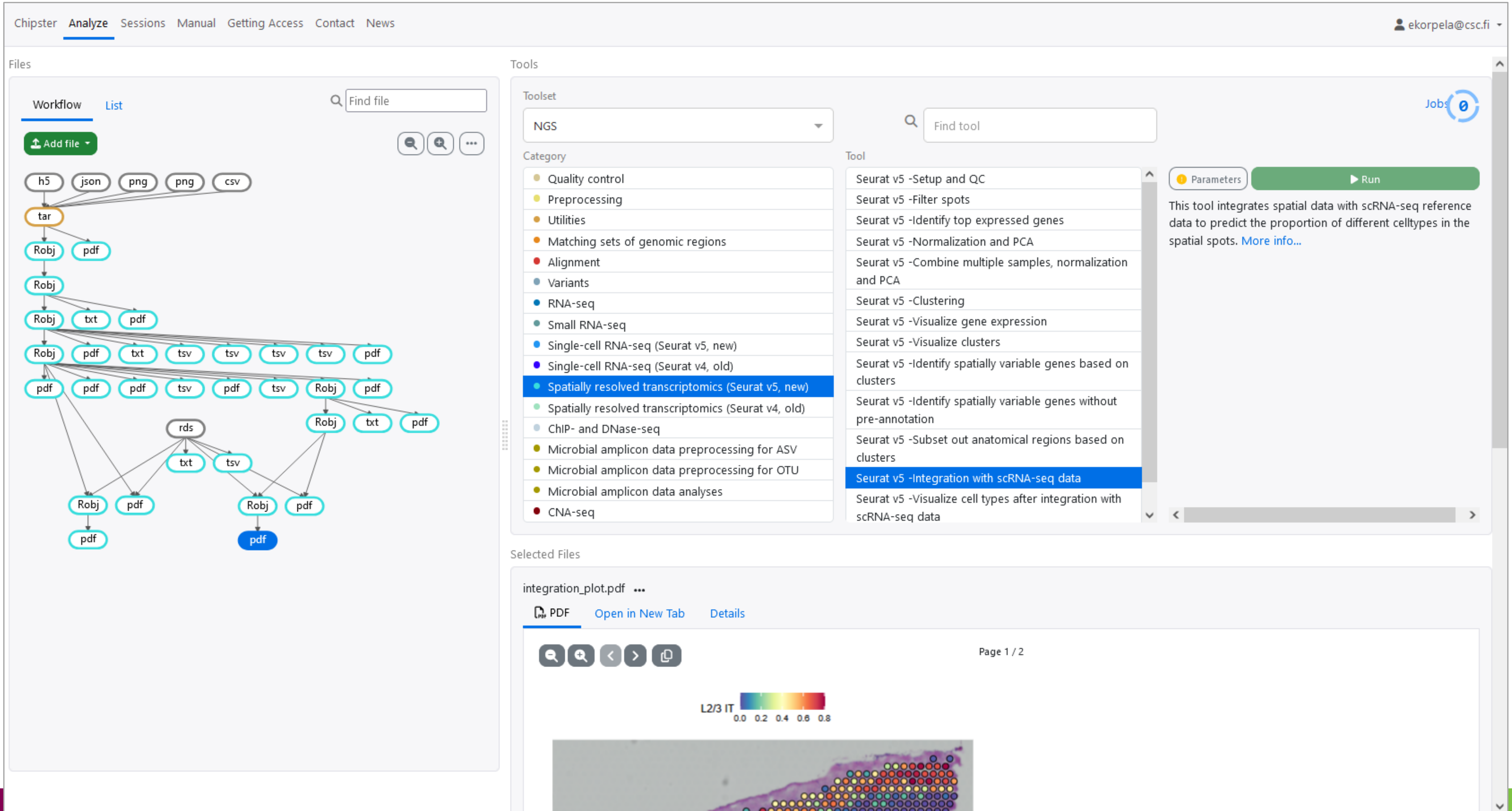
Created: 1/28/2025 1:06:47 PM

Size: 116 MB

In this tutorial we compare gene expression in human lung and lymph node samples. To make things faster, the data is given in two separate sessions:

-In this session we have two paired-end samples in FASTQ format. In order to make the analysis faster during the course, only a small subset of the reads (200 000) is used. You will preprocess and align the reads, make a count table and perform differential expression analysis.

Chipster GUI, continued



Toolset: NGS

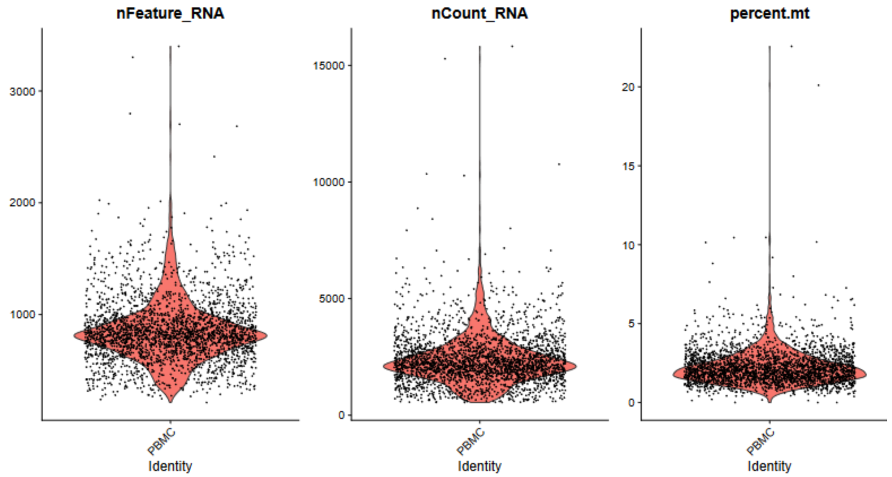
Category: Spatially resolved transcriptomics (Seurat v5, new)

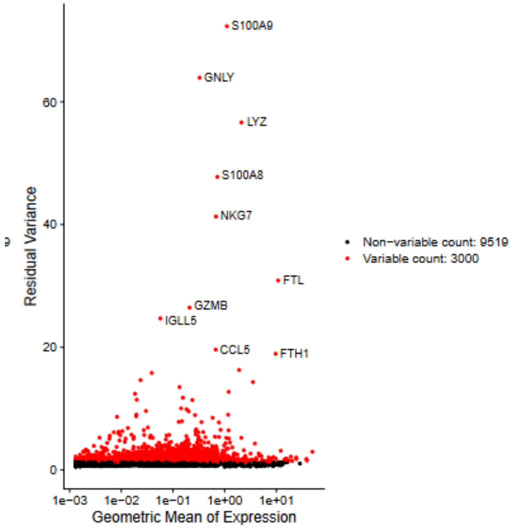
Tool: Seurat v5 -Integration with scRNA-seq data

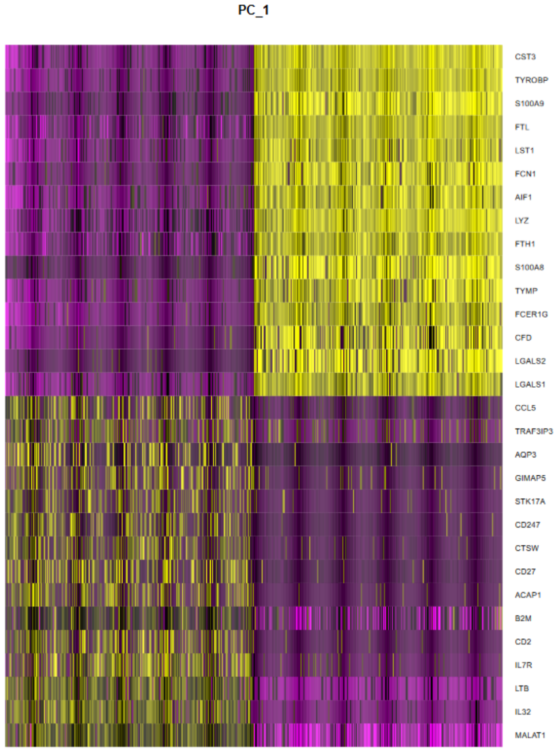
This tool integrates spatial data with scRNA-seq reference data to predict the proportion of different celltypes in the spatial spots. More info...

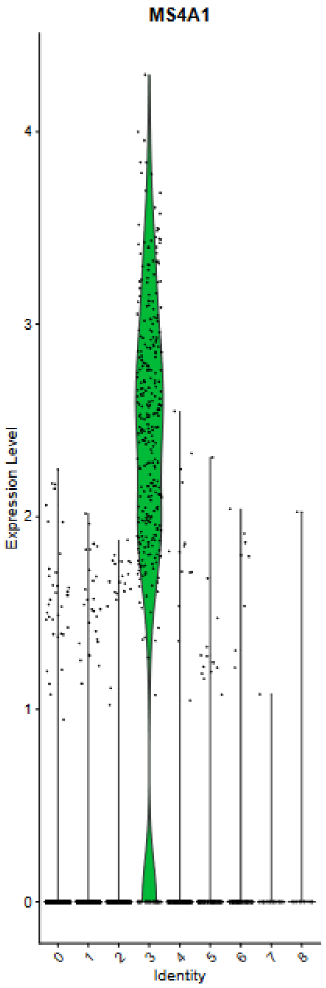
Selected Files: integration_plot.pdf

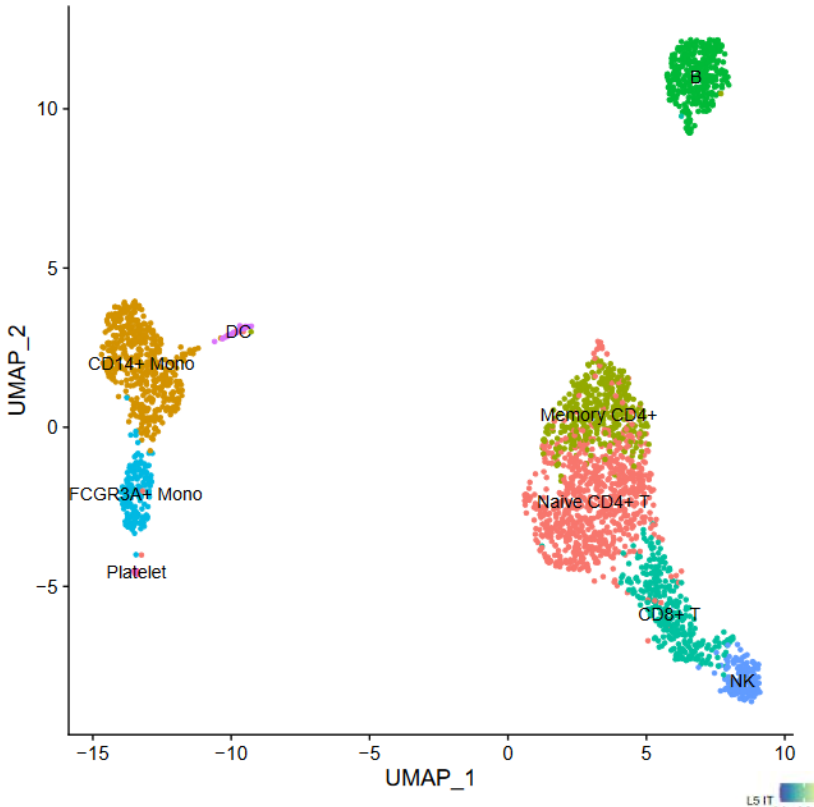
Chipster visualizations

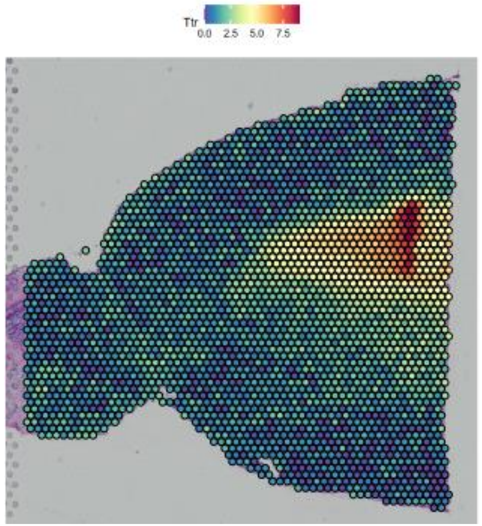


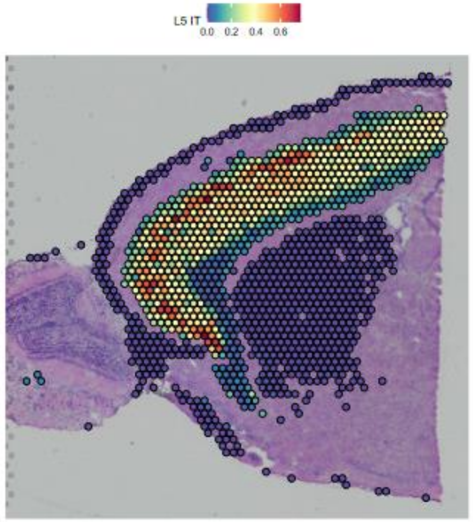












Options for importing data to Chipster

- 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

Analysis sessions

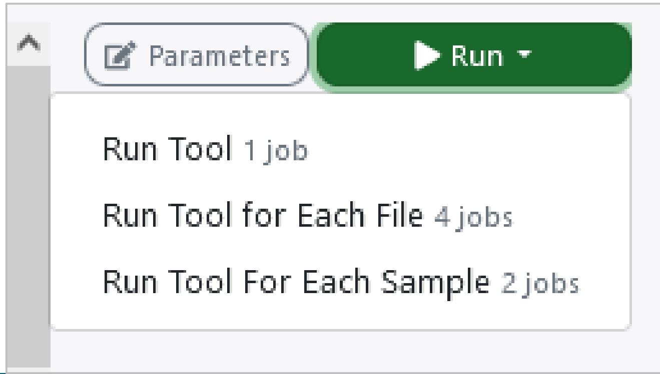
- Your analysis is saved automatically in the cloud
  - Session includes all the files, their relationships and metadata (what tool and parameters were used to produce each file).
  - Session is a single .zip file.
  - Note that cloud sessions are not stored forever! Remember to download the session 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
  - Close Chipster
  - Open Chipster later and the results will be there

Running many analysis jobs at the same time

- You can have many analysis jobs running at the same time
  - No need to wait that one finishes before starting a new one

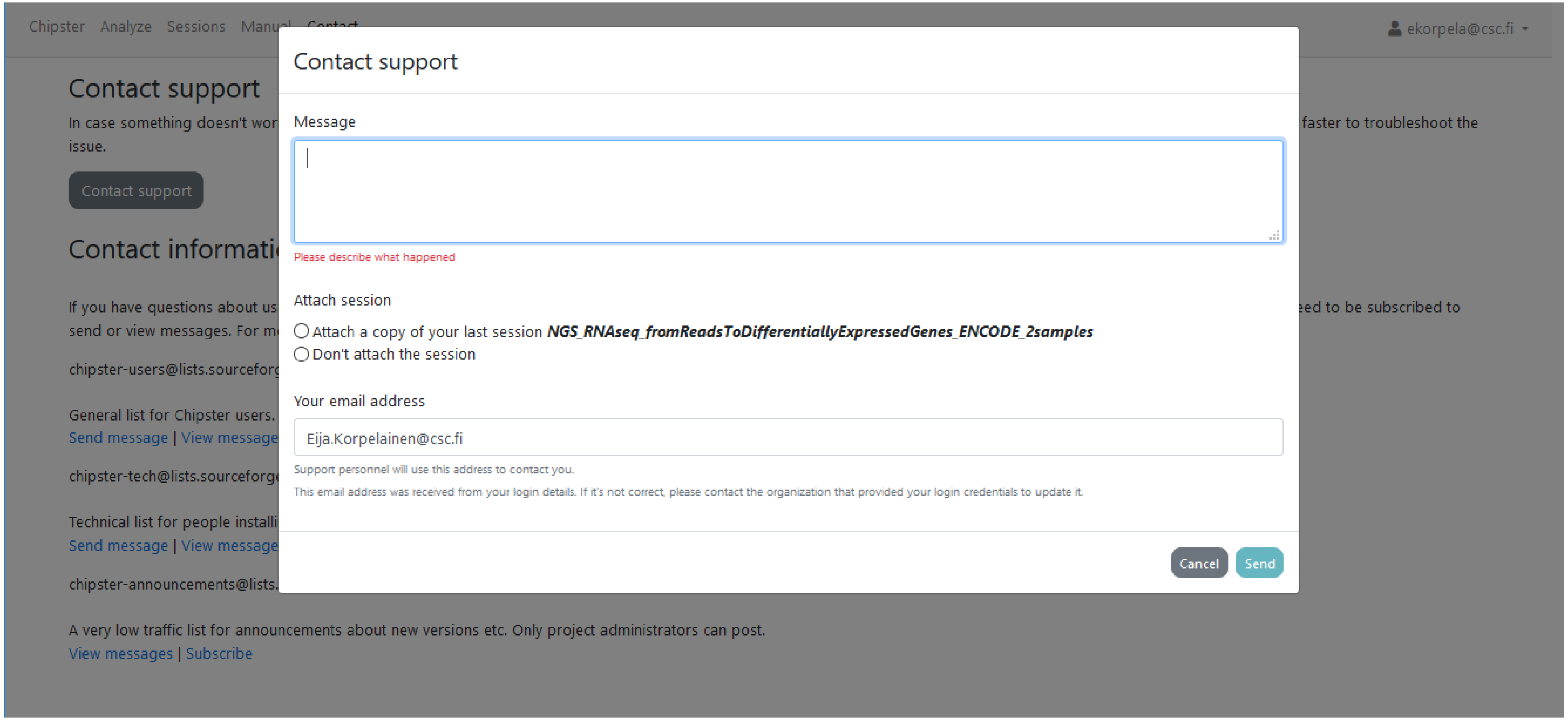
Run button gives several options:

- Run tool
  - Runs the selected analysis tool once
- Run tool for each file
  - Runs the selected analysis tool for each of the input files individually
- Run tool for each <u>sample</u>
  - If you have grouped paired end FASTQ files to samples using the Define samples –option, you can run the selected analysis tool for the input files in a sample specific manner.



Problems? Send us a support request

-request includes the error message and link to analysis session (optional)



Contact support

In case something doesn't wor faster to troubleshoot the issue.

Contact informati

If you have questions about us eed to be subscribed to send or view messages. For m

chipster-users@lists.sourceforg

General list for Chipster users.

Send message | View message

chipster-tech@lists.sourceforge

Technical list for people installi

Send message | View message

chipster-announcements@lists.

A very low traffic list for announcements about new versions etc. Only project administrators can post.

View messages | Subscribe

Contact support

Message

Please describe what happened

Attach session

○ Attach a copy of your last session ***NGS_RNAseq_fromReadsToDifferentiallyExpressedGenes_ENCODE_2samples***

○ Don't attach the session

Your email address

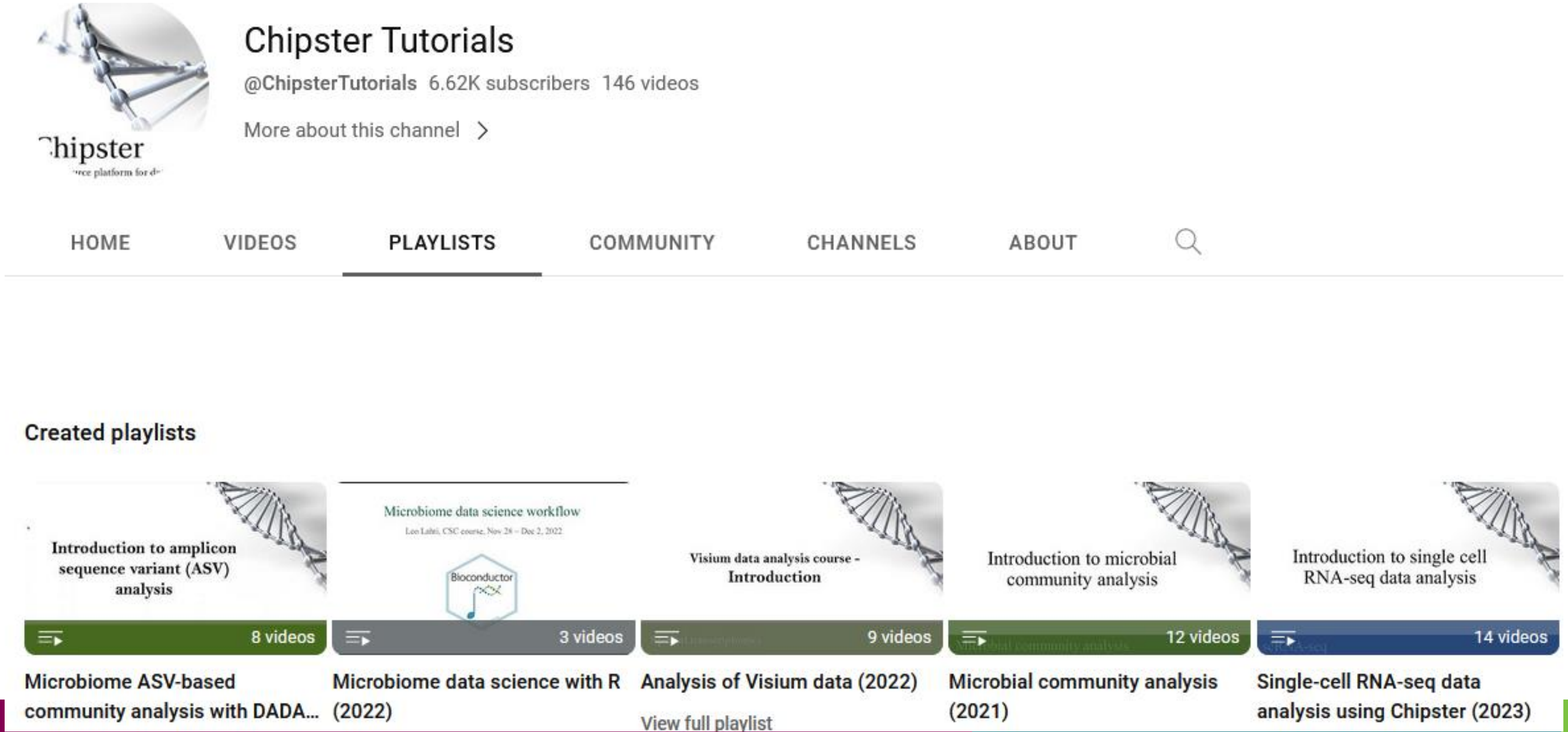
Eija.Korpelainen@csc.fi

Support personnel will use this address to contact you.

This email address was received from your login details. If it's not correct, please contact the organization that provided your login credentials to update it.

More info

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



Chipster Tutorials

@ChipsterTutorials 6.62K subscribers 146 videos

Created playlists

Introduction to amplicon sequence variant (ASV) analysis — 8 videos
Microbiome ASV-based community analysis with DADA...

Microbiome data science workflow — 3 videos
Microbiome data science with R (2022)

Visium data analysis course - Introduction — 9 videos
Analysis of Visium data (2022)
View full playlist

Introduction to microbial community analysis — 12 videos
Microbial community analysis (2021)

Introduction to single cell RNA-seq data analysis — 14 videos
Single-cell RNA-seq data analysis using Chipster (2023)