

Bioinformatics data analysis using Chipster



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

You will learn



- What Chipster is
- How the user interface works
- How to import data
- How to store and share your analysis
- How to speed up your analysis
 - run the same analysis step for all the samples simultaneously
- How to get help
- Where to find training materials

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/>



Chipster

Open source platform for data analysis



- Home
- Getting access
- Manual
- Tutorial videos
- Course material
- Cite
- Contact

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.



Launch Chipster

Training:

- 4.-5.3.2025 [Single-cell RNA-seq data analysis](#)
- 1.-2.4.2025 [Analysis of bulk RNA-seq data](#)
- 8.-9.4.2025 [Microbial community analysis](#)
- 15.5.2025 [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 introduction video](#)
- ASV-based microbial community analysis using DADA2: [Tutorial videos](#)
- [Instructions for moving data from Puhti to Chipster](#)
- [Video on how to convert tables to Chipster format and create phenodata file](#)

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

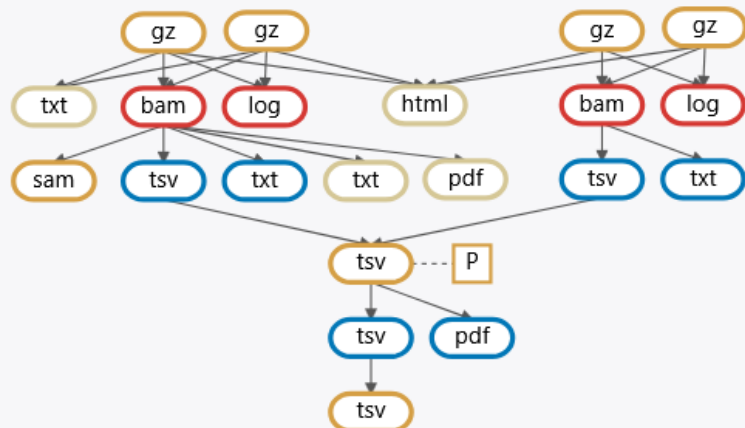


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ekorpela@csc.fi

Workflow List

Add file



Tools

Toolset

NGS

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



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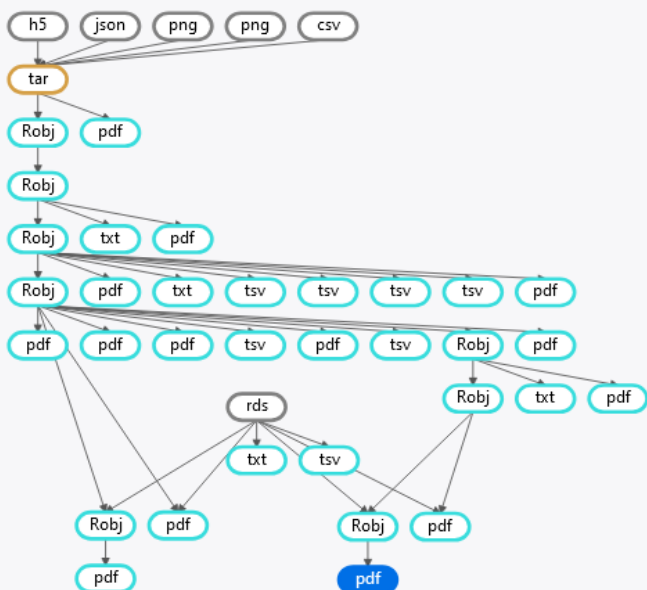
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Files

Workflow List

Find file

Add file



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- Microbial amplicon data preprocessing for OTU
- Microbial amplicon data analyses
- CNA-seq

Tool

- Seurat v5 -Setup and QC
- Seurat v5 -Filter spots
- Seurat v5 -Identify top expressed genes
- Seurat v5 -Normalization and PCA
- Seurat v5 -Combine multiple samples, normalization and PCA
- Seurat v5 -Clustering
- Seurat v5 -Visualize gene expression
- Seurat v5 -Visualize clusters
- Seurat v5 -Identify spatially variable genes based on clusters
- Seurat v5 -Identify spatially variable genes without pre-annotation
- Seurat v5 -Subset out anatomical regions based on clusters
- Seurat v5 -Integration with scRNA-seq data**
- Seurat v5 -Visualize cell types after integration with scRNA-seq data

Parameters

Run

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 ...

PDF

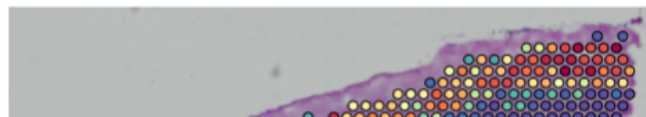
Open in New Tab

Details

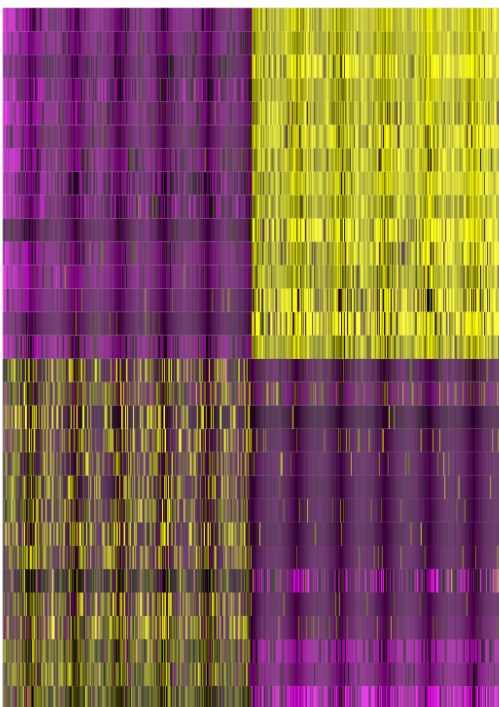
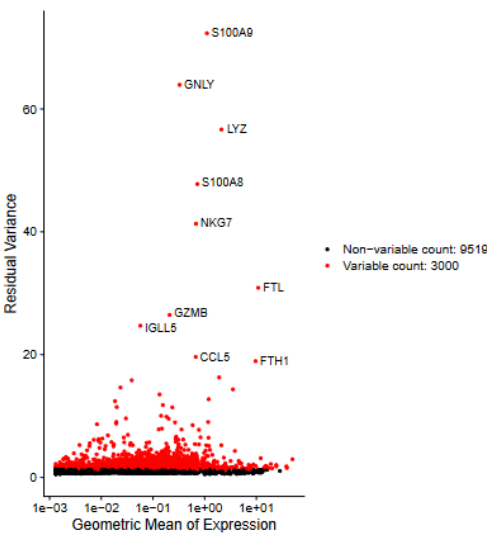
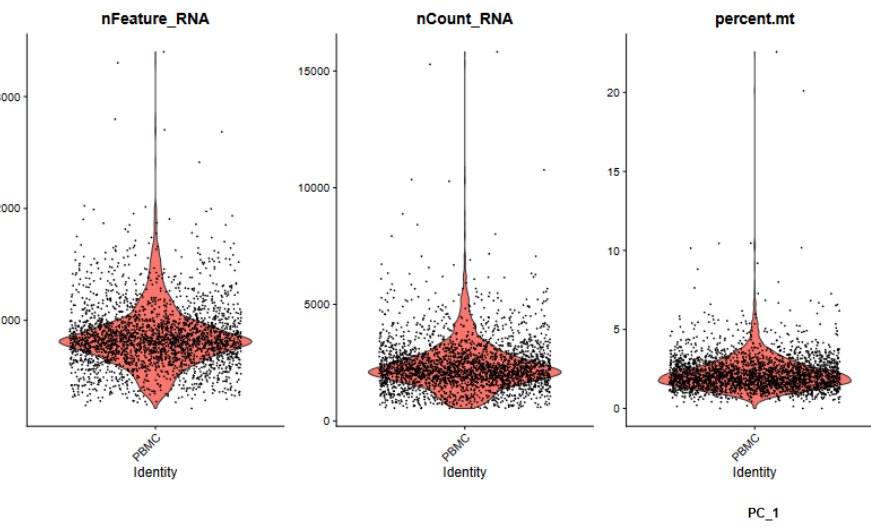


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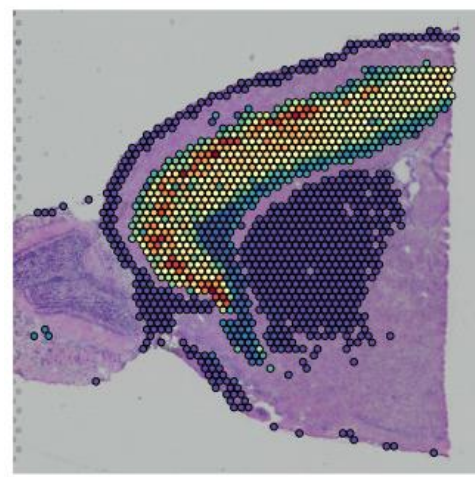
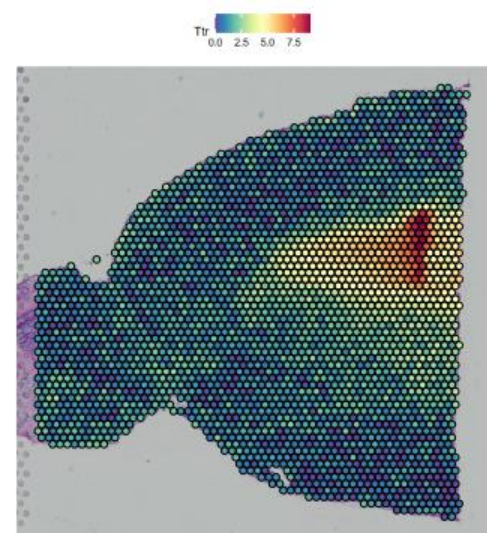
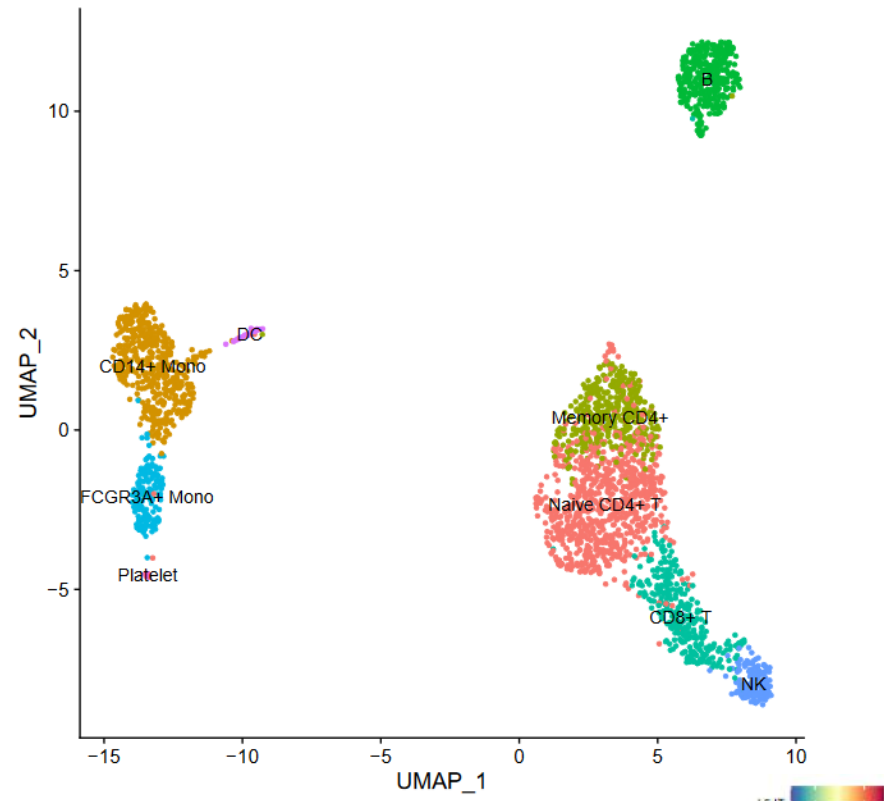
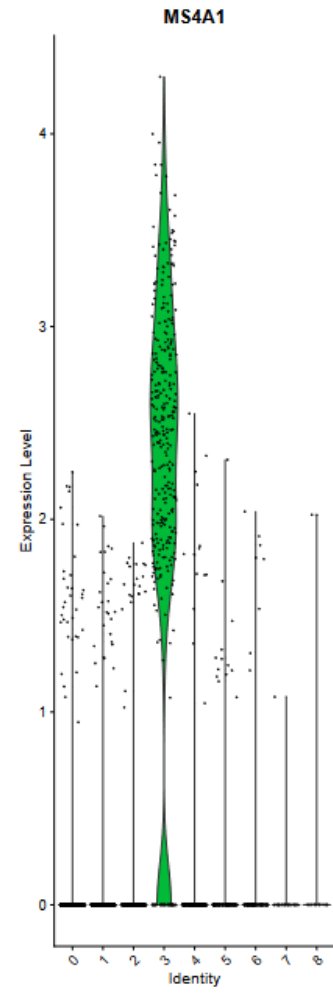
L2/3 IT 0.0 0.2 0.4 0.6 0.8



Chipster visualizations



GST3
TYROBP
S100A9
PTL
LST1
FCN1
AIF1
LYZ
FTH1
S100A8
TYMP
FCER1G
CFD
LGALS2
LGALS1
CCL5
TRAF3IP3
AQP3
GIMAP5
STK17A
CD247
CTSW
CD27
ACAP1
B2M
CD2
IL7R
LTB
IL32
MALAT1



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

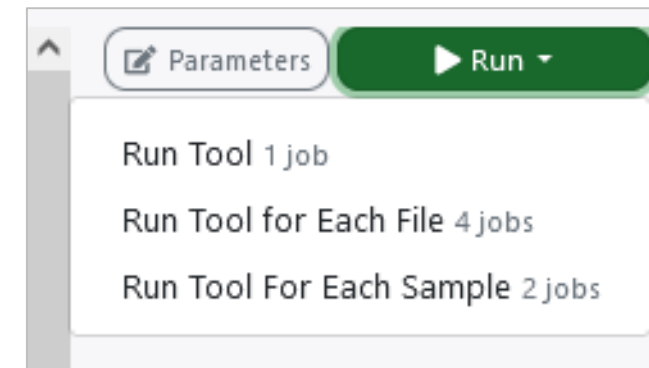
Running many analysis jobs at the same time



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

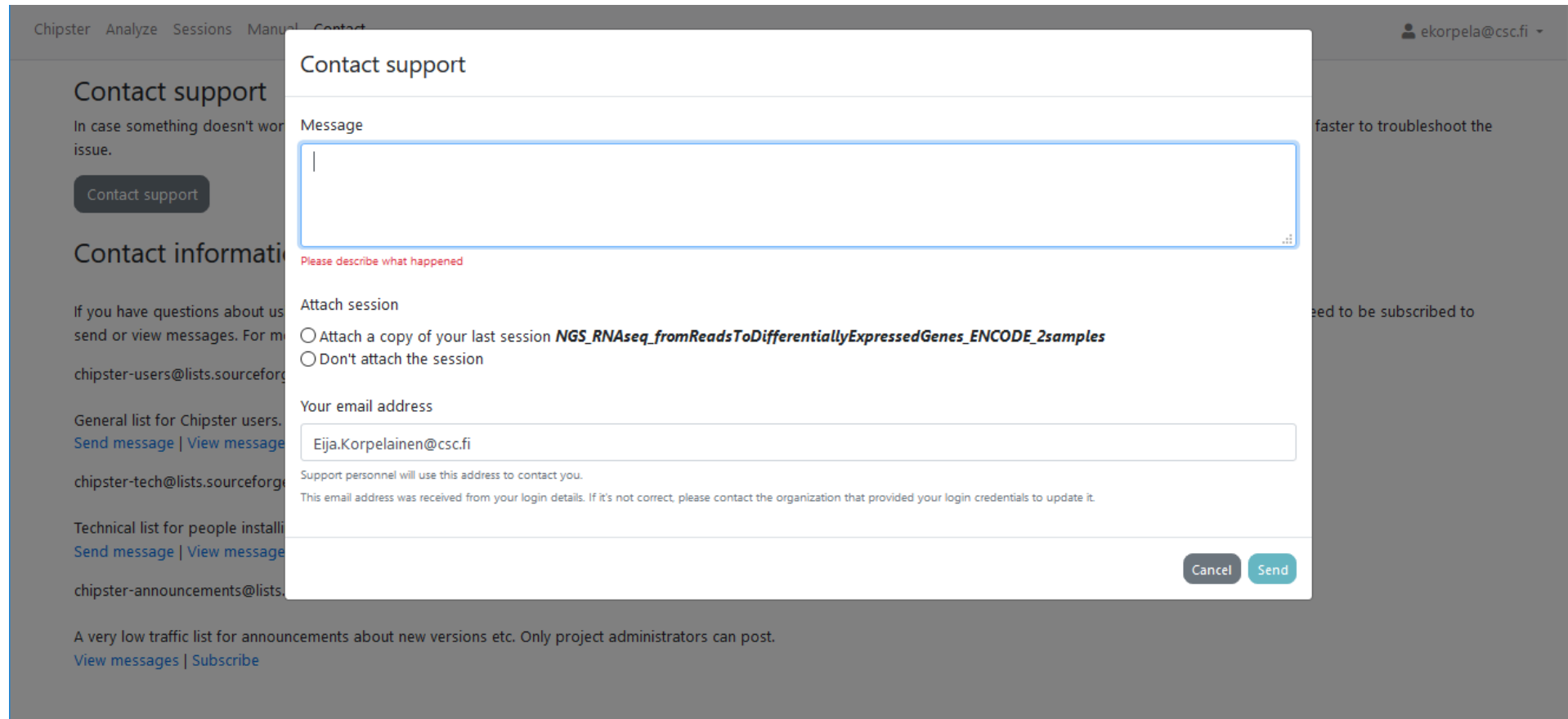
Run button gives several options:

- 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 sample
 - 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)



The screenshot shows a web application interface with a 'Contact support' modal form. The background is a dark grey sidebar with navigation links: 'Chipster', 'Analyze', 'Sessions', 'Manual', and 'Contact'. The main content area is also dark grey. The modal form is white and has a title 'Contact support'. It contains a 'Message' text area with a placeholder '|', a 'Please describe what happened' hint, an 'Attach session' section with two radio buttons, and a 'Your email address' text field with the value 'Eija.Korpelainen@csc.fi'. At the bottom right of the modal are 'Cancel' and 'Send' buttons. The background sidebar has a 'Contact support' button and several email lists with 'Send message' and 'View message' links. The top right of the sidebar shows a user profile 'ekorpela@csc.fi'.

Chipster Analyze Sessions Manual Contact

ekorpela@csc.fi

Contact support

In case something doesn't work, please send us a support request. We will try to help you faster to troubleshoot the issue.

Contact support

Contact information

If you have questions about using Chipster, you can send or view messages. For more information, see the [Chipster user guide](#).

chipster-users@lists.sourceforge.net
General list for Chipster users.
[Send message](#) | [View message](#)

chipster-tech@lists.sourceforge.net
Technical list for people installing Chipster.
[Send message](#) | [View message](#)

chipster-announcements@lists.sourceforge.net
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

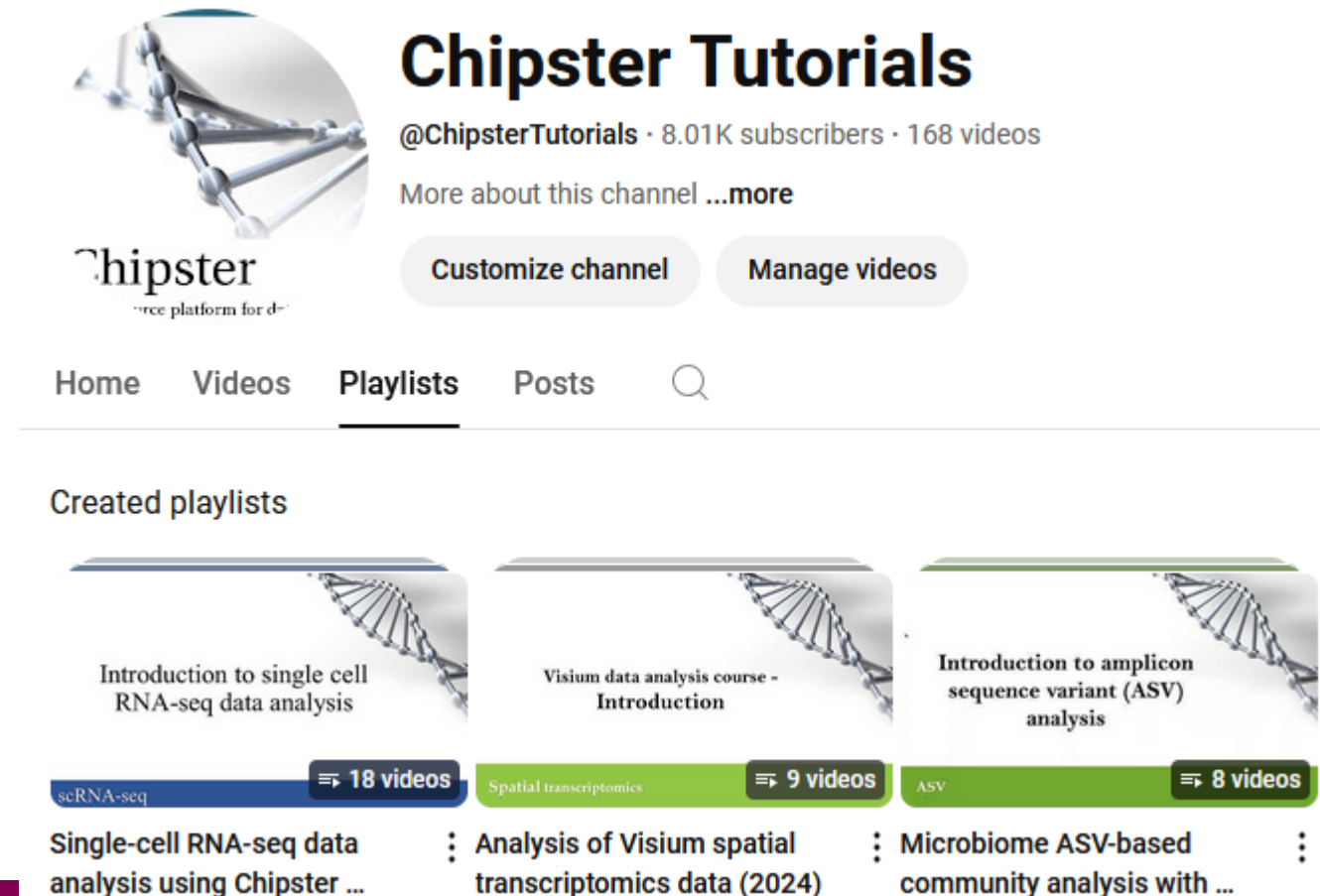
Eija.Korpelainen@csc.fi

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.

Cancel Send

More info

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



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Created playlists

Playlist Title	Video Count	Thumbnail Description
scRNA-seq	18 videos	Introduction to single cell RNA-seq data analysis
Spatial transcriptomics	9 videos	Visium data analysis course - Introduction
ASV	8 videos	Introduction to amplicon sequence variant (ASV) analysis

Single-cell RNA-seq data analysis using Chipster ... Analysis of Visium spatial transcriptomics data (2024) Microbiome ASV-based community analysis with ...