Pathogen genome analysis with PathogenWatch

Upload data to owncloud

Version: June 2025

World Health Organization

Utrecht University

AALFA

ULB UNIVERSITÉ LIBRE DE BRUXELLES

IPSN International Pathogen Surveillance Network

Launch 20 May 2023

Introduction

Pathogenwatch (https://pathogen.watch/) is a web-based tool for genomic surveillance that enables users to upload and analyse their own genome data. Pathogenwatch performs a series of species-specific analytics including MLST, identification of resistance and virulence loci, replicon typing and genome clustering. MLST Sequence typing is available for over 100 species using schemes from PubMLST, Pasteur, and Enterobase. Users can create interactive visualisations of phylogenetic trees make with genome collections of publicly available genomes and including their own uploaded genomes data.

Uploaded data (both sequence data and metadata) can be shared with Pathogenwatch through custom made collections. However, these collections are only per species, and contain only the assembled genomes.
For IPSN, we will use a shared owncloud drive, where all sequence data (pod5 files, fastq files, fasta files) can be uploaded and can be assessed by all partners.

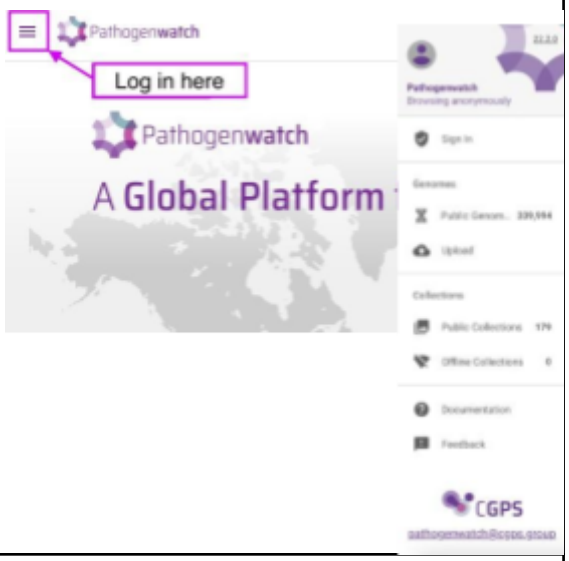
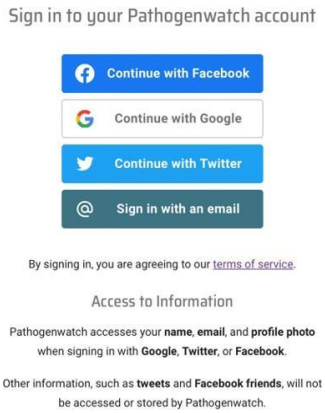
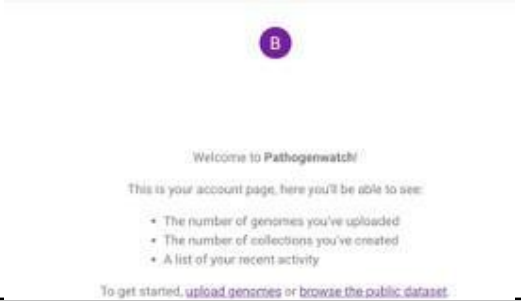
Manual to upload genomic data to Pathogenwatch

For the IPSN project, we made a gmail account, to make sure that we can share the genomes between ULB-UU-DRC:

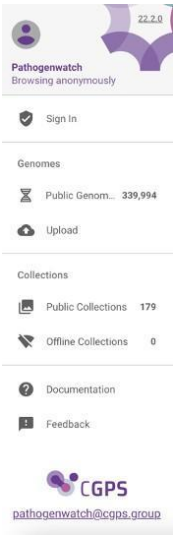
Emailadress: ipsn.drc@gmail.com

Password: ipsn.drc.nanopore

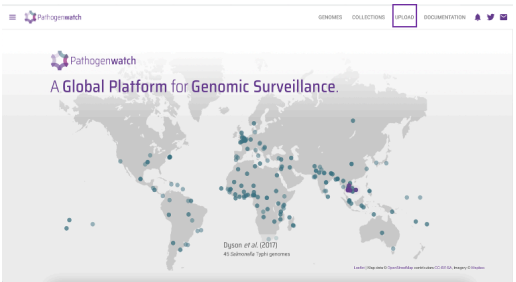
Create an PathogenWatch account

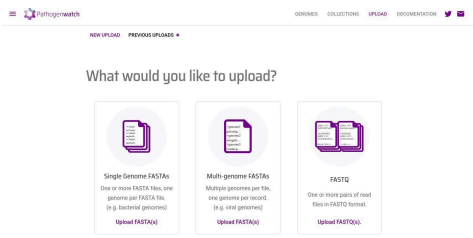
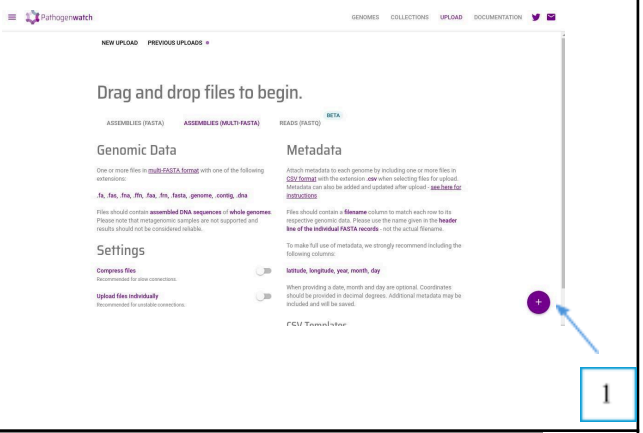
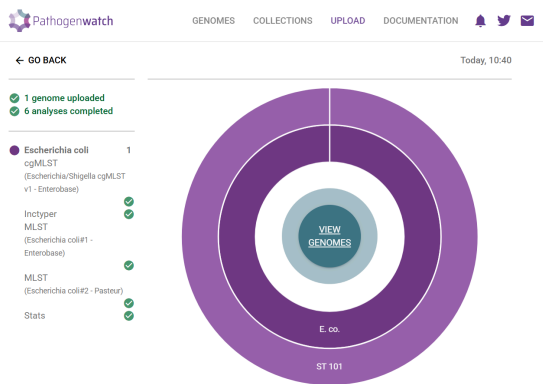
Open PathogenWatch on your browser https://pathogen.watch/ Click on “Sign In” by clicking on the icon in the upper left corner of the page. Note: it is possible to set your metadata private, see https://cgps.gitbook.io/pathogenwatch/how-to-use-pathogenwatch/private-metadata	
Click: “ Sign in with an email” and use emailadress ipsn.drc@gmail.com Login to gmail to get link for login Gmail login: Email address: ipsn.drc@gmail.com Password: ipsn.drc.nanopore	
View My Account page Now that you are logged in, you will see your Account page where you can manage your genomes, collections and account settings.	

Navigating PathogenWatch

Navigate the site - Click the menu icon The main menu bar can be accessed by clicking on the menu con on the upper left corner of the page.	
The menu allows you to navigate the site. There are four key pages: - Genomes - Collections - Upload - Documentation More information about navigating the site: https://cgps.gitbook.io/pathogenwatch	

Importing data

Navigate to the “upload” page: On the home screen, click on “Upload” in the upper right corner.	

Select the file type to upload Click the “Upload” button Click on “Single Genome FASTAs”	
Drag and drop files to begin 1. Click the “+” button to select genome files to upload (fasta files) 2. Click the “+” button to select meta file to upload (csv-file) – see below this table how to make this table	
Processing screen and viewing results Depending on the species of the genome, Pathogenwatch will give the following results: - Species - AMR (not for every species) - Core summary (not every species) - cgMLST - Inctyper (not for every species) - MLST If you click the "View Genomes" button, you will be directed to the results page of all your uploaded genomes.	

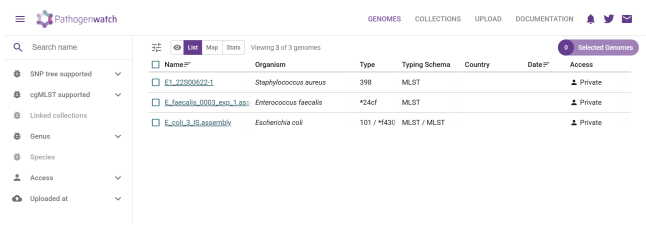
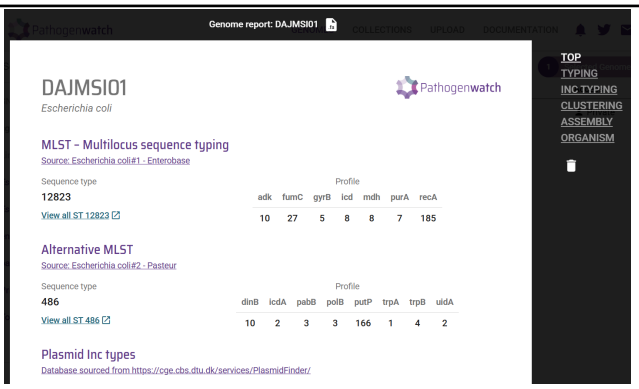
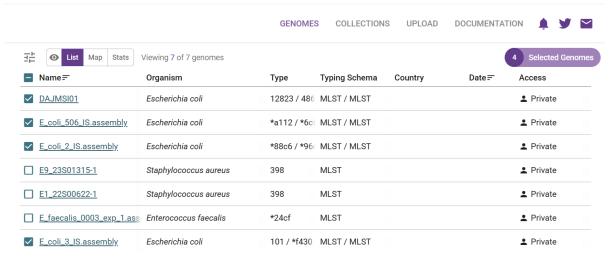
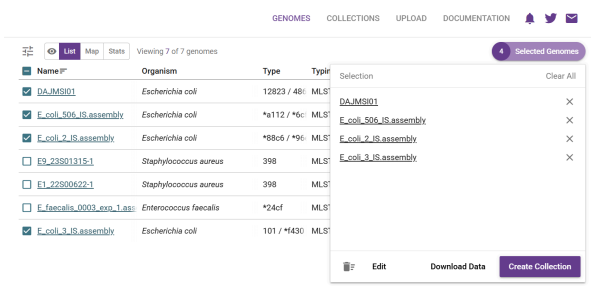
Make csv-file with metadata

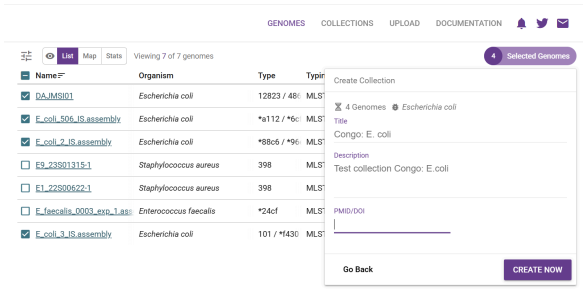
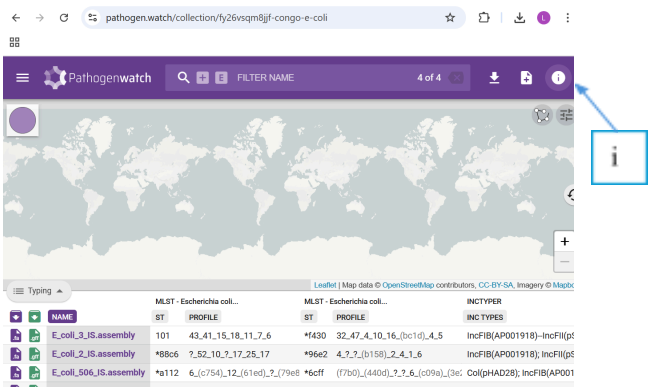
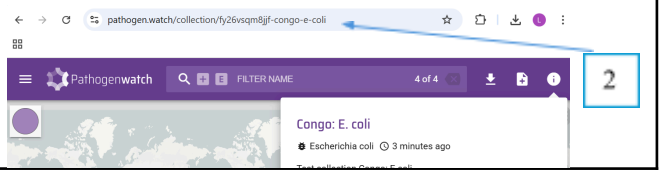
Content of file:	
Displayname (name of fasta) (required):	Example01
Year (optional):	2025
Month (optional):	5
Day (optional):	22
Country:Location (optional):	Congo:Bukavu
Latitude (optional):	2.5123

Longitude (optional): 28.8480
Strain (original strain name) (optional): MiniLab01
Source (optional): Blood

Example of csv-file with metadata:
Displayname,Year,Month,Day,Country,Latitude,Longitude,Strain,Source
Example01,2025,5,22,Congo:Bukavu,2.5123,28.8480,MiniLab01,blood

Viewing genomes and make a collection to share

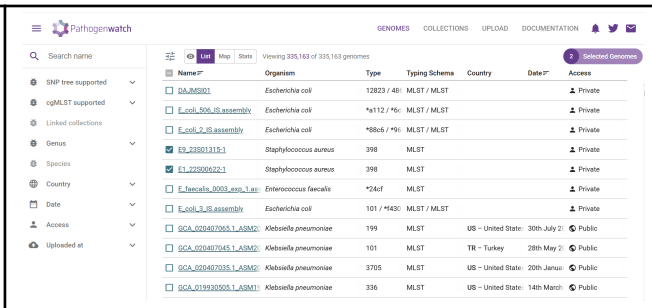
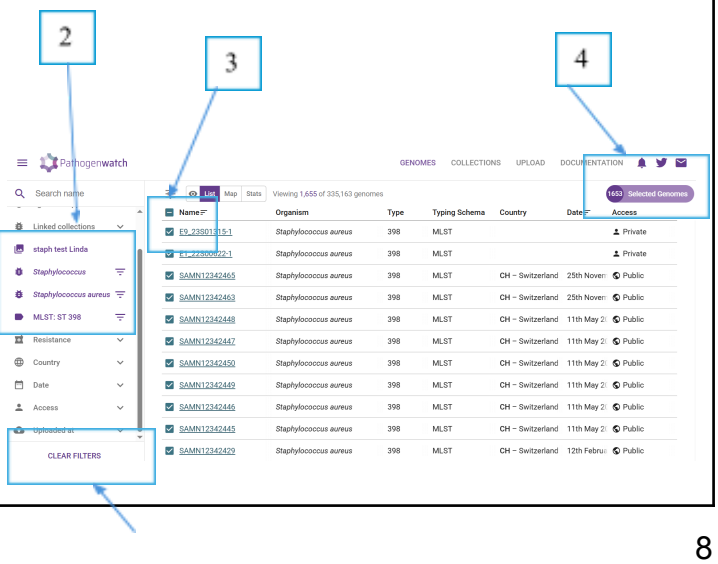
View your uploaded genomes The uploaded assemblies are presented in the "view Genomes" page	
You can click the names of the uploaded genomes. This will show you the "genome report", a detailed report of PathogenWatch analysis of the assembled genome.	
To make a collection; select the genomes (of the same species) and click on "selected genomes"	
Click on "create collection"	

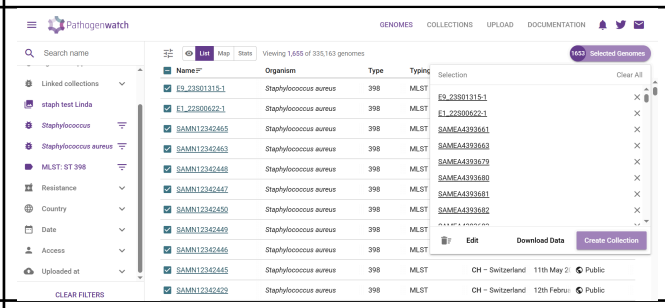
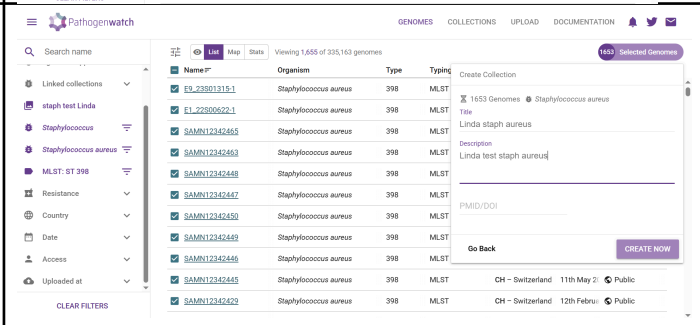
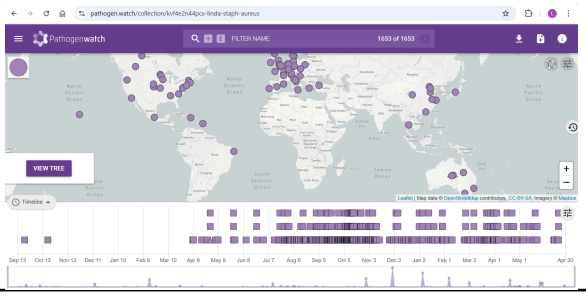
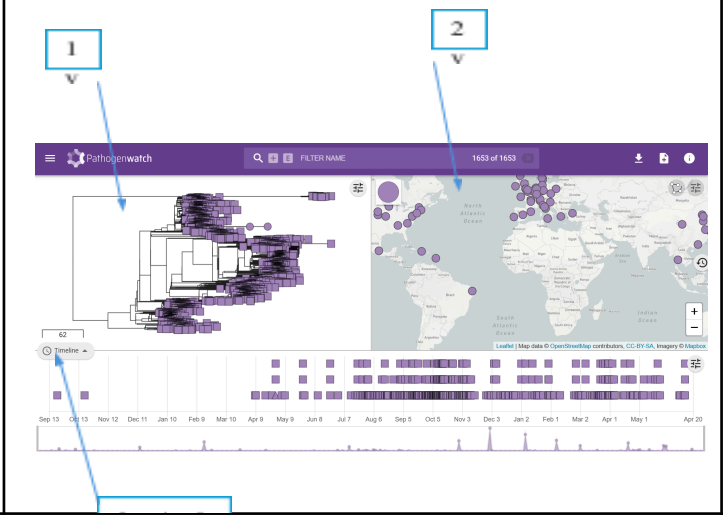
Fill in Title and description for this collection and create “create now” PMID/DOI is optional	
To share the collection, click on “i” button in the upper right corner	
Default setting is that the access level of the collection is “Private”. 1. Click on “Shared” to make the collection available for sharing.	

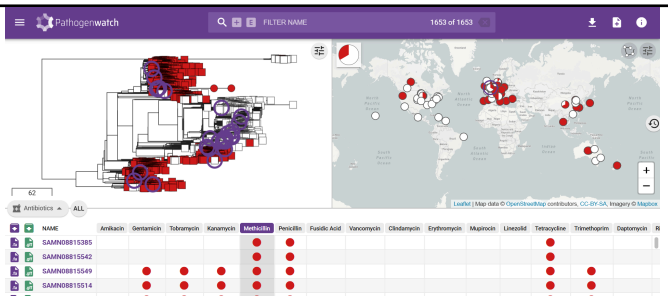
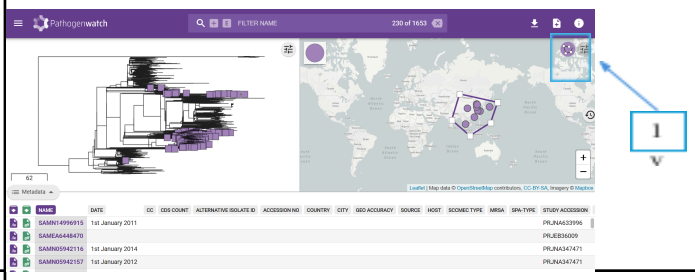
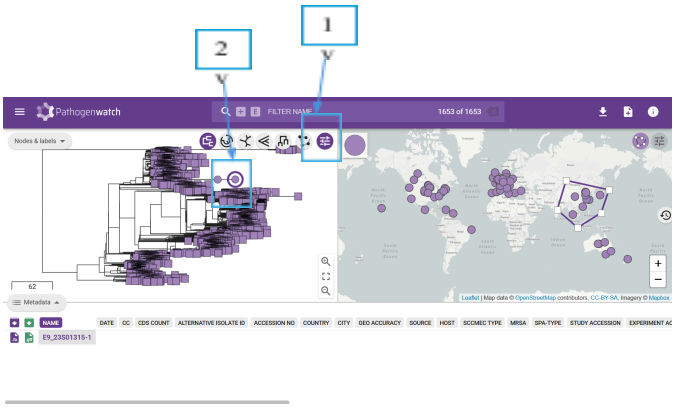
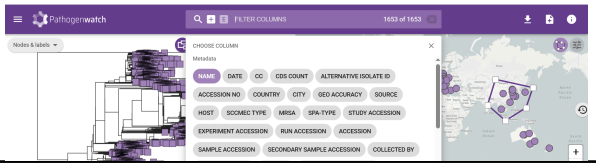
2. To share this collection; copy URL of collection in browser	
Note: Only genomes of same species can be included in a collection. If genomes of multiple species are uploaded, make multiple collections with these genomes to share	

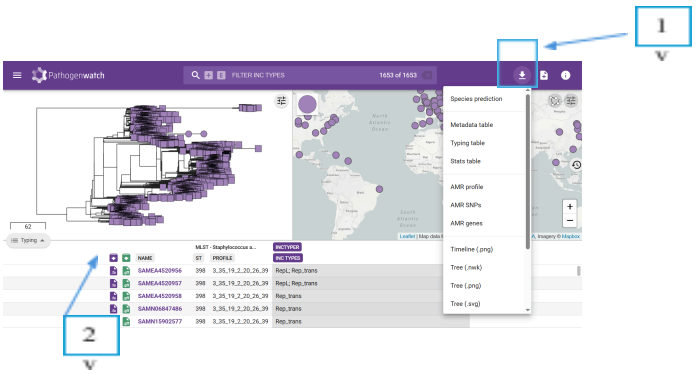
Create a tree with your genome and publicly available genomes

Note: only a selection of species can be used to build trees. Unfortunately, it is not possible to build a tree with *E. coli*.
In this example, we will use *Staphylococcus aureus*

Go to the page with the list of your uploaded genome(s) and select the genome that you want to include in the tree Select only genomes of similar species/MLST STs. For different species/STs; build different trees	
1. Click on “CLEAR FILTERS” at the bottom left corner. 2. Filter the publicly available genomes of Pathogenwatch from the left sidebar. Filter the genomes with the analysis results of your genome. Next is an example: • Genus – Staphylococcus • Species – Staphylococcus aureus • MLST – ST398 3. Click on the tick that selects	

all genomes and then click on “Selected Genomes”. 4. You can see that the number of genomes has now increased.	
Create a collection with your genome(s) and the publicly available selected genomes by clicking on “Selected genomes” in the upper right corner and select “Create collection”	
Name your collection as follows: - Title - Description - A short description of the collection, perhaps to explain to other people what it is for. - PMID/DOI (optional) The PubMed or DOI identifier if it is linked to a publication. Click "Create Now" and you will be taken to the “Collection View”.	
If you click “view tree”, a tree will be calculated using a neighbour-joining method	
Locate the five interactive components: 1. A phylogenetic tree. 2. A global map showing the locations of genomes that have geospatial metadata. 3. A metadata display area that includes the user-supplied data, calculated typing assignments such as MLST, and antimicrobial resistance predictions.	

4. A query bar that allows the selection or finding of assemblies by searching the metadata fields. 5. A timeline showing the collection dates of assemblies that have temporal metadata.	
In the “Antibiotics” window, you can select a specific antibiotic. Circles in the map will be colored present/absent (red/white) genotype or resistant/sensitive (red/white) phenotype. The circle in the top left shows the overall ratio for the selected resistance phenotype or genotype	
With the group selection tool (1), you can draw a line around a set of points to select. These are then highlighted in the “Tree View” and “Metadata Table”.	
1. Click on this icon to see all different trees, zoom function etc. 2. You can click on leaves and nodes and they are selected with a purple halo. Selected assemblies are highlighted in the “Map View” also with a purple halo and shown exclusively in the “Metadata Tables”. Tip: If you right click on the tree, you can export the tree, labels etc.	
The “Filter Bar” allows you to select assemblies according to their attributes in the “Metadata Tables”, including by typing assignments or antimicrobial resistance.	

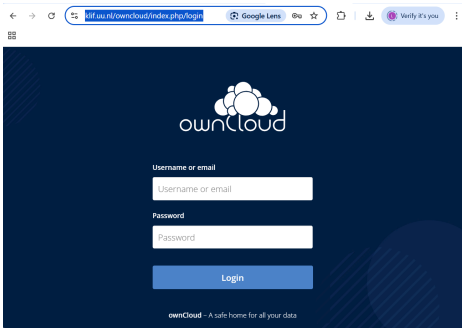
You can filter on multiple columns by clicking on the '+' symbol.	
Download tree and files 1. In the upper right corner, you will find the download button, where you can download metadata tables, profiles and tree files. 2. To download the fasta and/or gff files, select the files in the metadata window.	

Upload sequence data to Owncloud

All sequence data (pod5 files, raw read fastq files, assembled fasta files) can be shared through the following owncloud page:

Webpage: https://klif.uu.nl/owncloud/index.php/login

Username: ipsn.drc@gmail.com
Password: ipsn.drc.nanopore

Navigate to Owncloud page: https://klif.uu.nl/owncloud/index.php/login	
Login: Username: ipsn.drc@gmail.com Password: ipsn.drc.nanopore	

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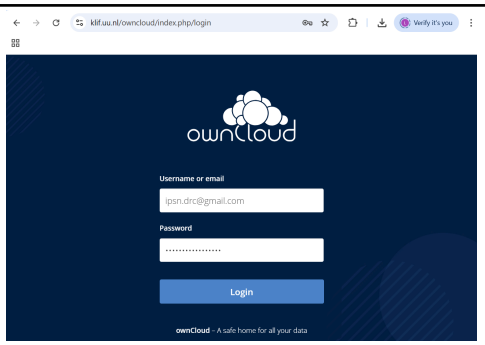
<td> 
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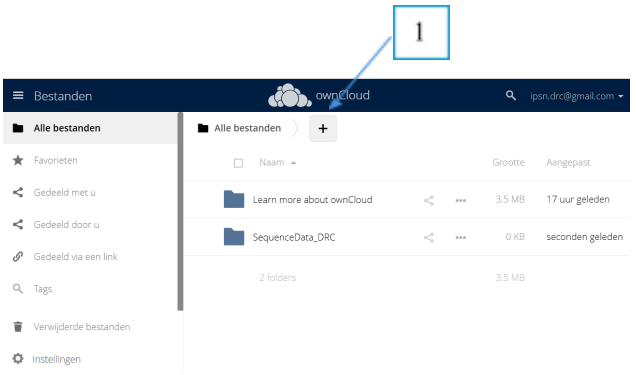
<td>Drag and drop files to upload sequence data to Owncloud

1. Click the “+” button to select files to upload</td>
<td> 
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