UNIVERSITY of TARTU
Tartu Observatory

Framework Partnership Agreement for Copernicus User Uptake

Teaching material about the phytoplankton surface blooms

FP-CUP Activity 2021-2-11 "Tailored downstream applications/products–from Copernicus to coastal and inland water monitoring"

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Abstract

The teaching material includes exercises about retrieving phytoplankton surface bloom information based on remotely sensed Chlorophyll a (Chl a) in large shallow lake L. Peipsi (Estonia/Russia), using the ESTHub satellite data processing portal by the Estonian Land Board and SeNtinel Application Program (SNAP). The main aim is image processing in ESTHUB and in SNAP (9.0.0), applying masks to calculate the bloom area, and using Level 3 processing possibilities for spatio-temporal analyses. A short introduction to the cyanobacterial blooms, major bloom formers in L. Peipsi and common problems due to the surface blooms is given.

Acknowledgements

We are thankful to the ESA Copernicus program and EUMETSAT for satellite data, Estonian Land Board for the ESTHub portal processing possibilities, and Brockmann Consult for the SNAP program.

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Contents

Introduction to the cyanobacterial blooms

Phytoplankton presence in lakes is a natural phenomenon, and phytoplankton forms the basis of a food chain in waterbodies. Lakes and reservoirs are often used as drinking water resources and are relevant for recreation, tourism and irrigation purposes. Problems arise when excess nutrients and warm weather support massive development of cyanobacteria, and this may hinder and prevent normal activities and water body's usage, e.g. when surface scum is reaching to the shoreline, and the presence of toxic blooms may lead to severe drinking water crisis (Backer, 2002, Steffen et al., 2017). A mass of cyanobacteria produces oxygen in the daytime and consumes it during night-time and decay, causing stress for fishes and subsequent fish kills.

The increase of blooms is a particular concern in inland waters (Brooks et al., 2017, Malthus et al., 2019) as the problems with clean freshwater scarcity tend to increase across the globe (WHO, 2022). In the frames of changing climate and rising temperatures, cyanobacterial blooms are increasing in frequency, magnitude and duration on a global scale (Taranu et al., 2015, Huisman et al., 2018, Paerl et al., 2020).

Bloom definition

It is not always easy to distinguish what is meant by the bloom. Generally, a bloom is:

- a rapid and remarkable increase in the concentration of phytoplankton
- development of a level of phytoplankton biomass that is uncharacteristically high for a given water body
- discoloration of waters
- visible scum at the water surface
- an elevated biomass that is above the biomass in the reference state of a given lake, which interferes with the ecosystem services and functioning of this lake.

Ibelings et al. (2016) noted that important is not the presence of cyanobacteria in the community, but the level of their amount for defining a bloom. According to WHO (2021), in the case of cyanobacterial dominance, Chl a concentration > 12 µg/L, is regarded as harmful with a suggestion to raise an alert. For L. Peipsi, this value is too low; thus, for the bloom characterization, a median value for each separate lake part was calculated, and a median value exceeded by a 5 % threshold was chosen to mark the bloom initiation (Table 1). This requires the presence of the long-term dataset, and in case of L. Peipsi, the Chl a measurements started in 1989.

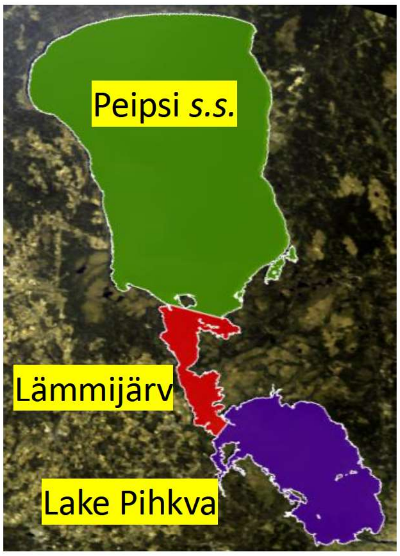
Table 1. Bloom thresholds for various lake parts of L. Peipsi.

Lake part	**Chl a long-term median**	**+ 5%**
Peipsi *s.s.*	17.1 µg/L	18.0 µg/L
Lämmijärv	34.0 µg/L	35.7 µg/L
L. Pihkva	44.4 µg/L	46.6 µg/L

Common bloom formers

The main planktonic widely-distributed toxin-producing bloom-formers include N_2 fixing genera *Dolichospermum* (former *Anabaena)*, *Aphanizomenon*, *Cylindrospermopsis, Nodularia*, the non-N_2 fixing genera *Microcystis* and *Planktothrix* (Paerl & Paul, 2012). Cyanobacteria are capable of very fast replication and rapid vertical movement within the water column, resulting in the formation of dense surface scums (Paerl & Huisman, 2009, Vaičiūtė et al., 2021). Most bloom-forming cyanobacteria contain gas vesicles (aerotopes) which provide buoyancy and allow to form dense surface blooms during quiet weather (Wynne et al., 2013), which, for their patchy nature, is hard to study in the frames of regular monitoring activities. Remote sensing allows to quantify the blooms, find the initiation date, and track the movement of the bloom.

Lake Peipsi – the study area



Lake Peipsi is a large transboundary waterbody (surface area 3555 km^2) shared between Estonia (44%) and Russia (56%). It consists of three parts – northern and largest Peipsi *sensu stricto* (*s.s.*), southern L. Pihkva and their connection Lämmijärv (Figure 1, Table 2). L. Peipsi has 240 inflows; the largest is the Velikaja River (Peipsi, 2008), and the outflow is the Narva River.

Figure 1. The division of L. Peipsi into shapefiles.

Common cyanobacteria, present in L. Peipsi, are visible in Figure 2. Cyanobacterial blooms are a common feature in L. Peipsi, dating back to the first written notes, but the dominant bloom-formers have been changed over the years. At first, *Aphanizomenon* was mentioned, then colonial cyanobacterium *Gloeotrichia echinulata* (a species with mesotrophic preferences (Laugaste et al., 2013)) caused heavy blooms, and during recent years *Dolichospermum lemmermannii* and species of *Microcystis* are more common, causing blue-green water in the shoreline (https://www.terviseamet.ee/et/uudised/peipsi-jarves-vohab-sinivetikas).

Part of the cyanobacterial population is capable of fixing their own nitrogen via heterocysts, depending only on phosphorous and adding extra nitrogen to the water.

Table 2. The basic information about L. Peipsi.

	Peipsi s.s.	Lämmijärv	L. Pihkva
Surface area (km^2)	2,611	236	708
Volume (km^3)	21.79	0.6	2.68
Mean depth (m)	8.3	2.5	3.8
Max depth (m)	12.9	16.3	5.3
Trophic state	Mesotrophic	Eutrophic	Eutrophic

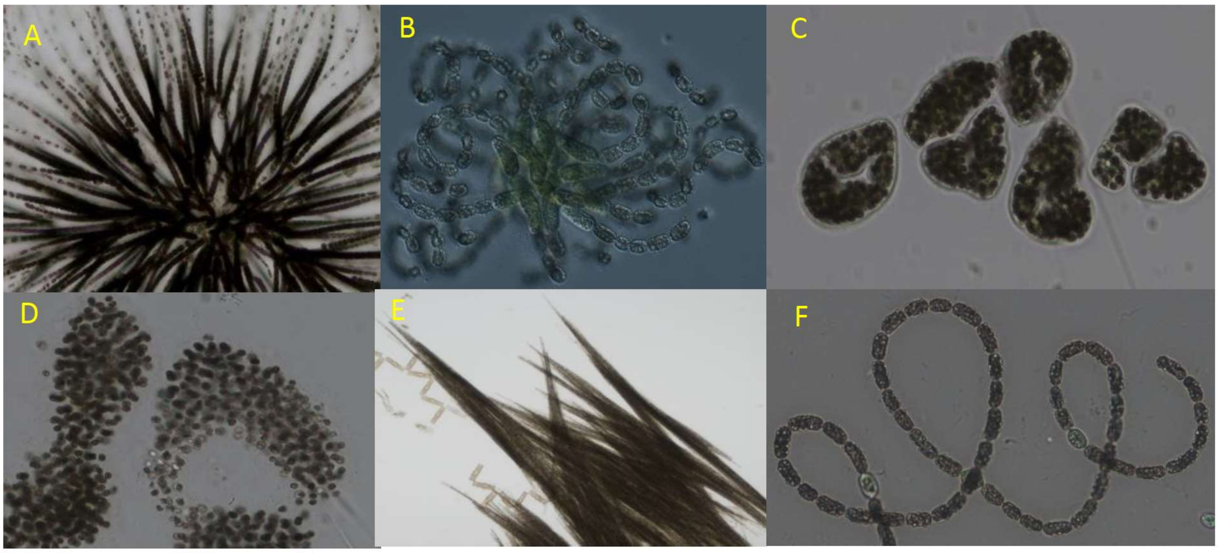


Figure 2. Common cyanobacteria in Lake Peipsi A- *Gloeotrichia echinulata*, B- *Dolichospermum lemmermannii*, C- *Microcystis wesembergii*, D- *Microcystis aeruginosa*, E- *Aphanizomenon* flos-aquae, F-*Dolichospermum* sp. Photos by K. Maileht.

Exercises in this tutorial

1) Calculation of Chl a from a single satellite image, using ESTHub L2 processing, followed by creation of bloom mask with Mask Manager to retrieve the bloom area in SNAP software.
2) Use batch processing in SNAP to retrieve bloom information from multiple images.
3) Use Level 3 binning in ESTHub for spatio-temporal analyses (an average over the selected time period).

Establishment of the ESTHub account (national ID number is needed) – necessary pre-task before the course.

More information: https://geoportaal.maaamet.ee/eng/Spatial-Data/National-Satellite-Data-Centre-ESTHub-p654.html

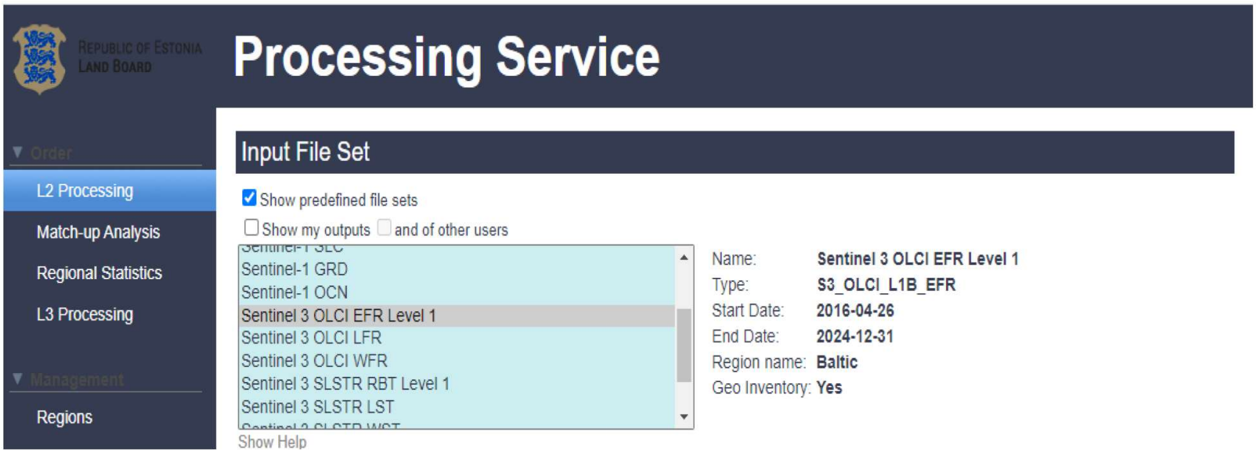
This exercise includes using the ESTHub processing platform (**Login to ESTHub Processing Platform: https://ehcalvalus.maaamet.ee/calest/calvalus.jsp**) and Sentinel Application Platform (SNAP).

ESTHub is a processing platform for Earth Observation images, which is hosted by Estonian Land Board and covers Estonian territory and its surroundings. The **Sentinel Application Platform** (SNAP) 9.0.0. is a program for Earth Observation processing and analysis, downloadable from https://eo4society.esa.int/resources/snap/.

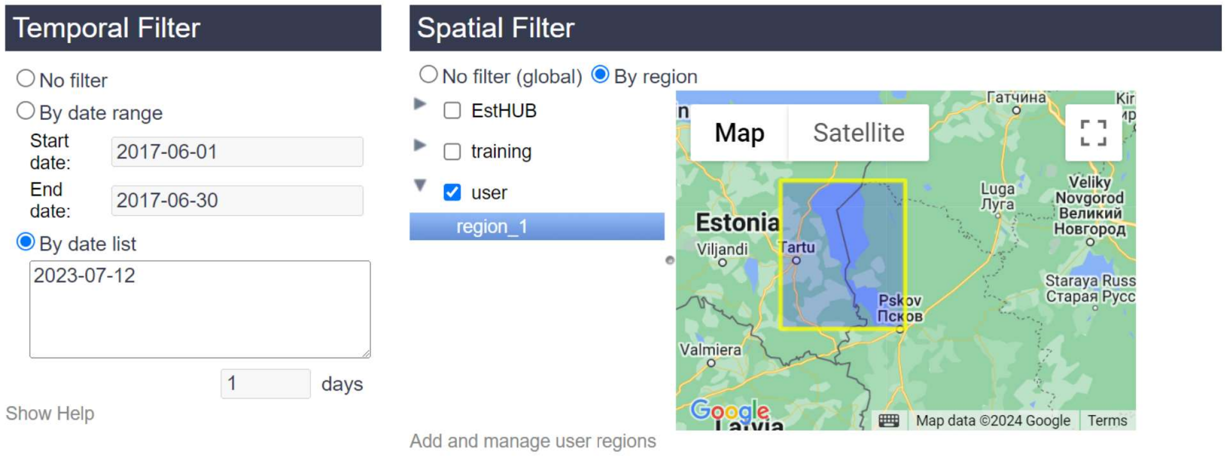
1. Retrieval of the bloom area from 1 selected image

The first exercise is about the usage of Level 1 data and the retrieval of Chlorophyll a concentration via the Maximal Chlorophyll Index and regionally tuned specific coefficients over L. Peipsi, to retrieve lake part specific surface bloom area.

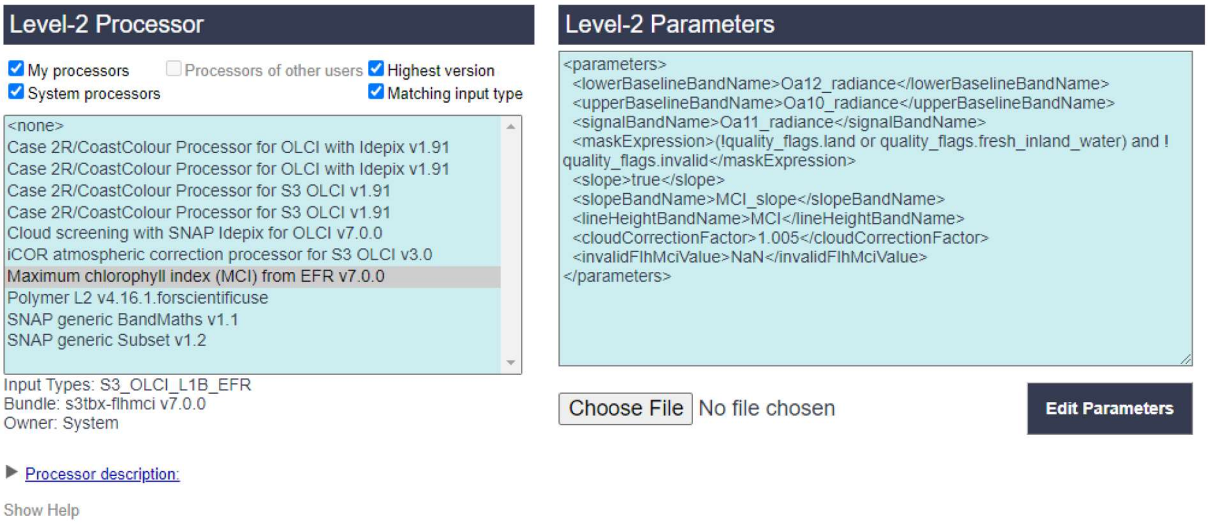
In ESTHub, select **L2 Processing** from the left pane and Sentinel 3 OLCI EFR Level 1 from the **Input File Set.**



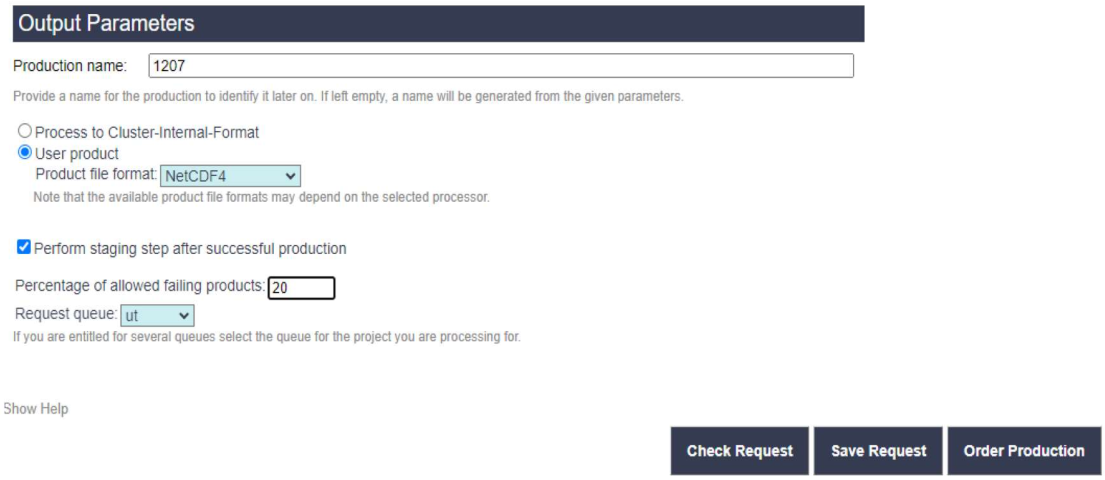
Temporal filter: type the date: 12.07.2023. **Spatial filter** can be either global or more specific. Region can be specified: from **Add and manage user regions**, zoom in to area of interest, draw a new polygon and save it as a new user region. Return to **L2 Processing** and under **Spatial filter**, select the user defined area:



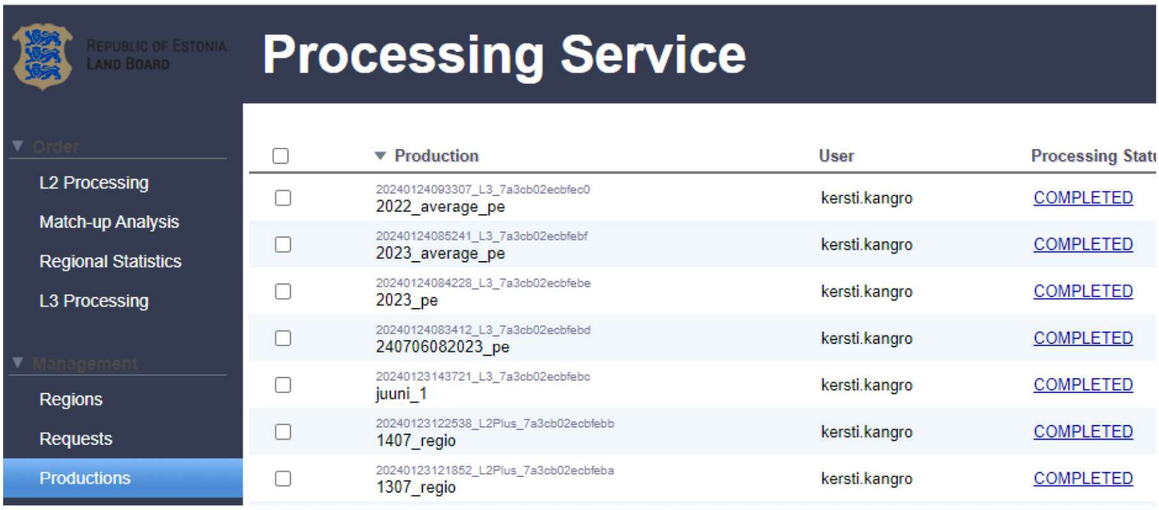
In **Level-2 Processor,** select Maximum chlorophyll index (MCI):

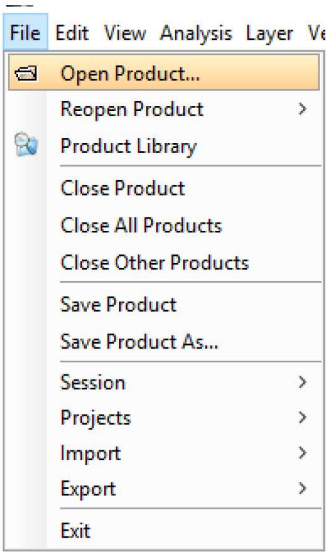


Output Parameters Allow failing products, say the production name, ask the netCDF4 format and allow some extent of failing (20%). Then click **Order Production**.

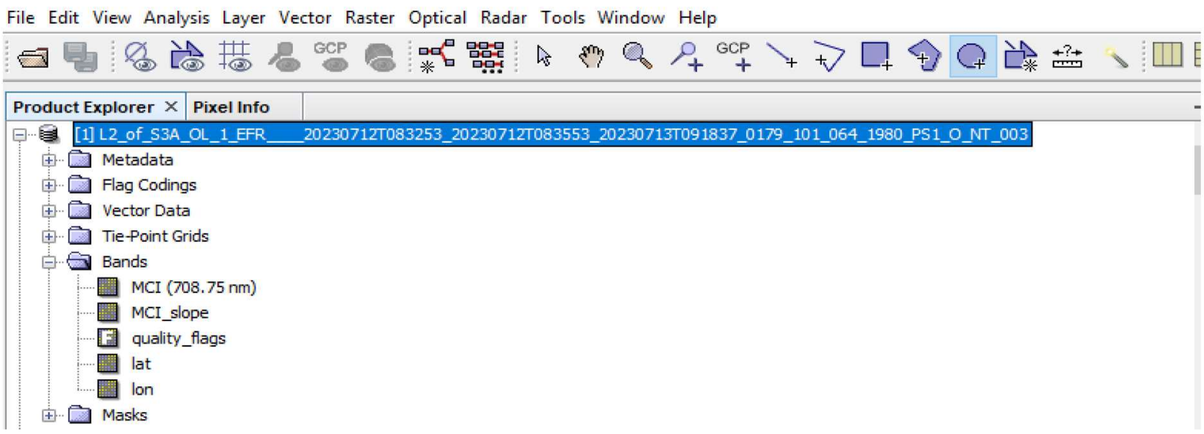


Under **Productions** (on the left pane in ESTHub) is a tab showing the progress in processing (and if there are any errors) and a list of processed files, which can be downloaded after the processing is complete.

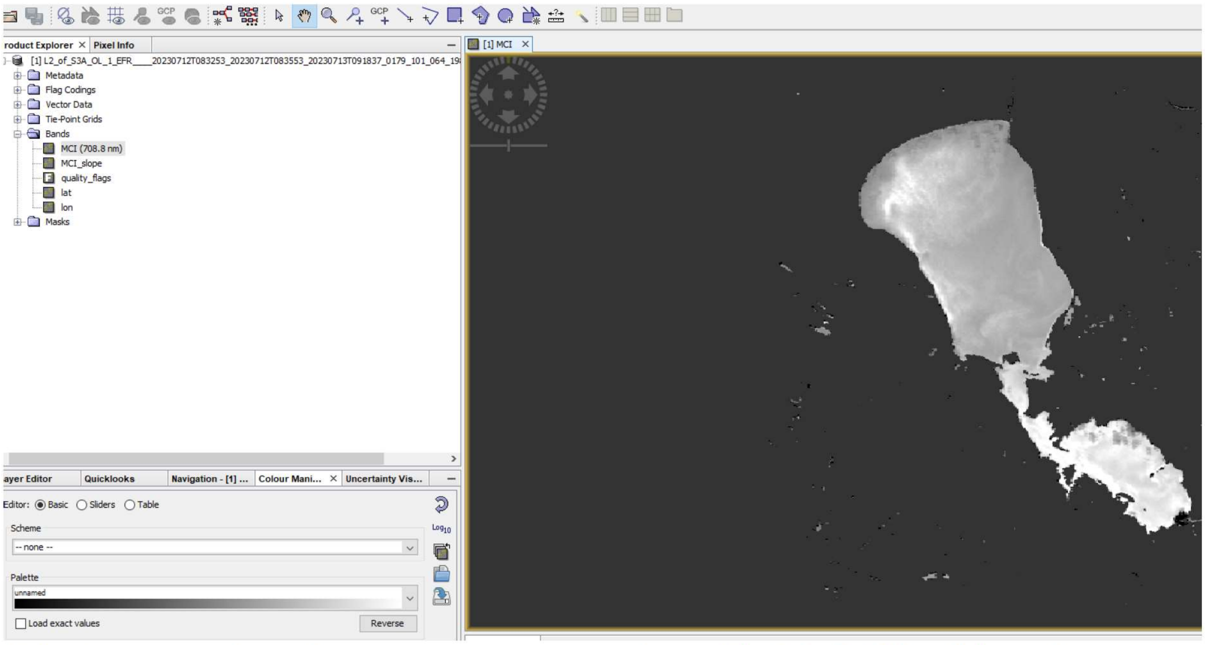




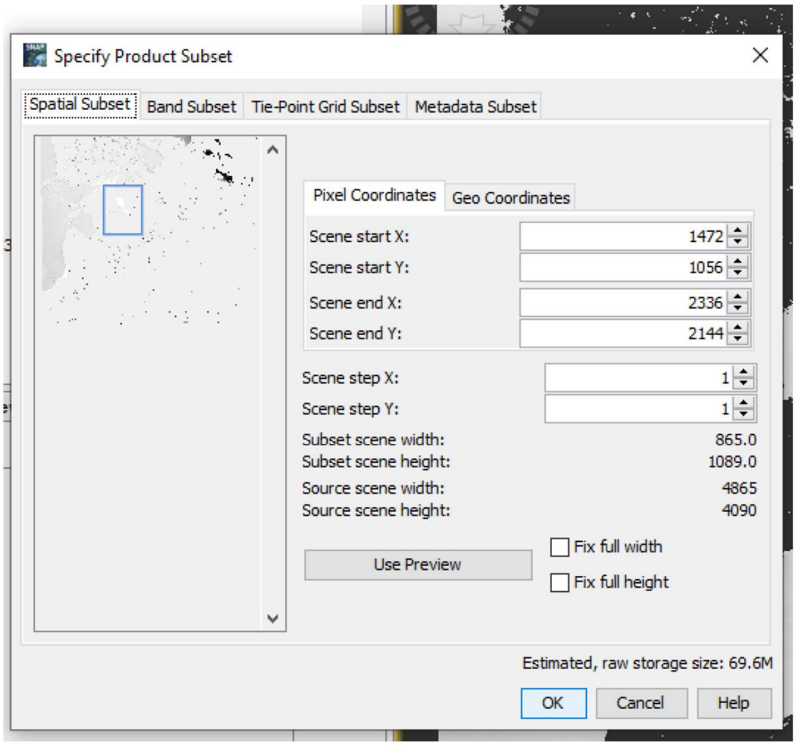
Click on **Download**, download the S3A file with the ending _1980.nc. **The analyses continue in SNAP.** Open SNAP and open the downloaded file (**File** -> Open Product -> L2_of_S3A....nc)



Select **MCI band** (Under **Bands**, click on the +, double-click on MCI (708.8 nm)) and open the image window.

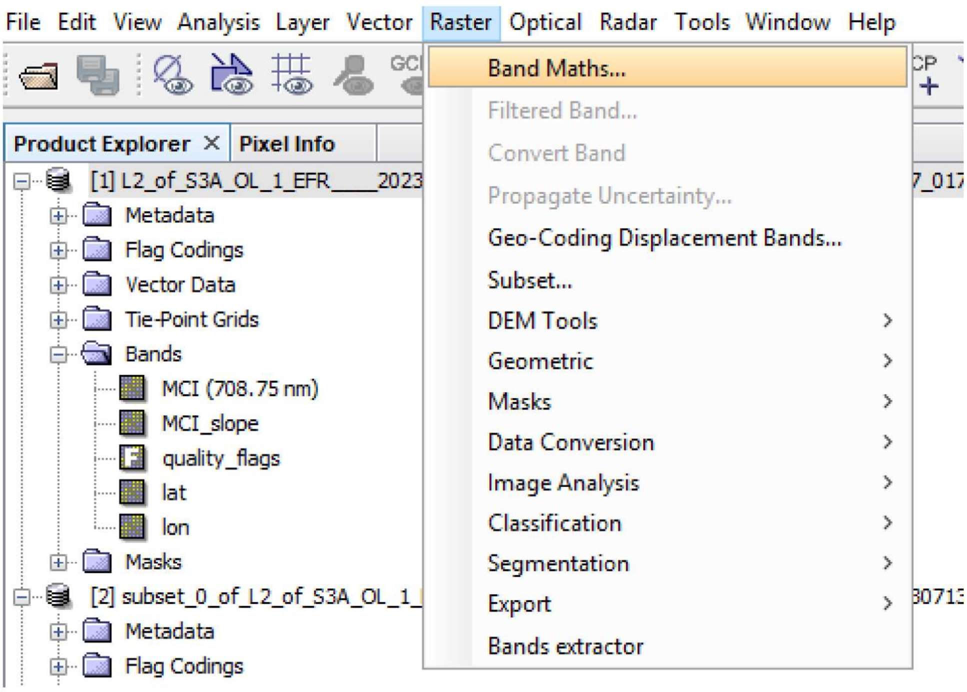


If the image area is too large, you can create a subset with Peipsi: Right-click on the screen and choose “**Spatial subset from View**” and narrow the window with a mouse down to the L. Peipsi, click OK - this reduces the file size and speeds the processing.

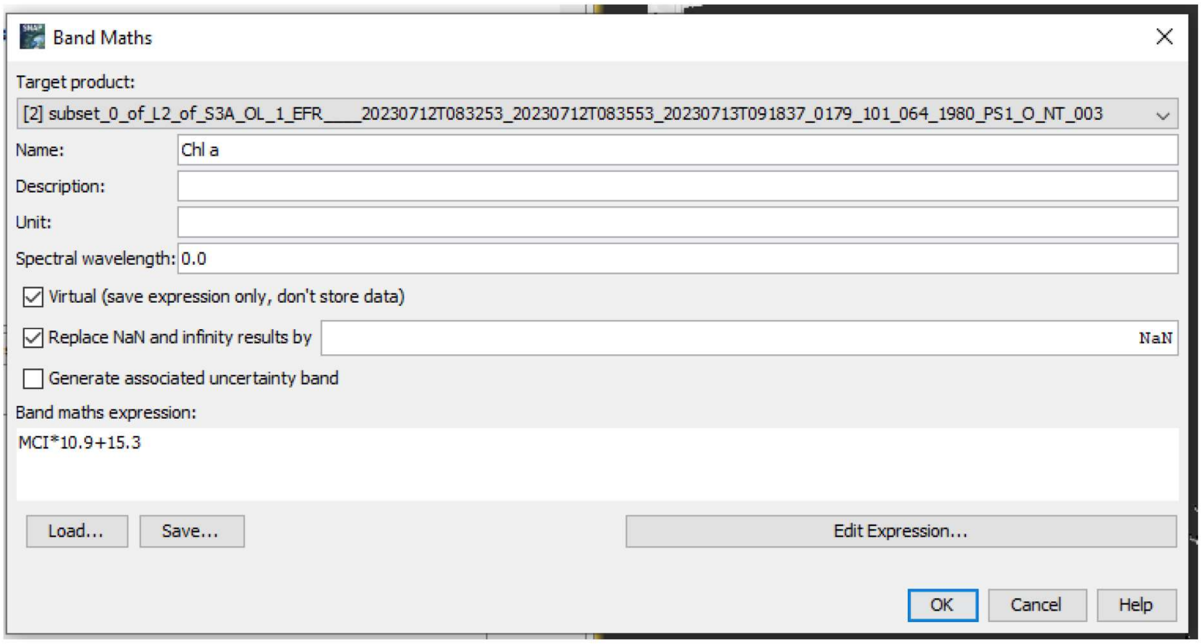


A subset is opened as a new file below the original file. Go to the **subset file (subset_0_of_...)** and open the MCI image window.

Calculate Chl a concentration from MCI (Alikas et al. 2010) using **Raster** ->**Band Maths**:



Raster -> **Band Maths** -> In the opened dialogue box, give a **Name** to the band, e.g., Chl a. **Edit Expression** -> in **Expression** window -> enter the formula. Type in the formula: MCI*10.9+15.3 Click OK.



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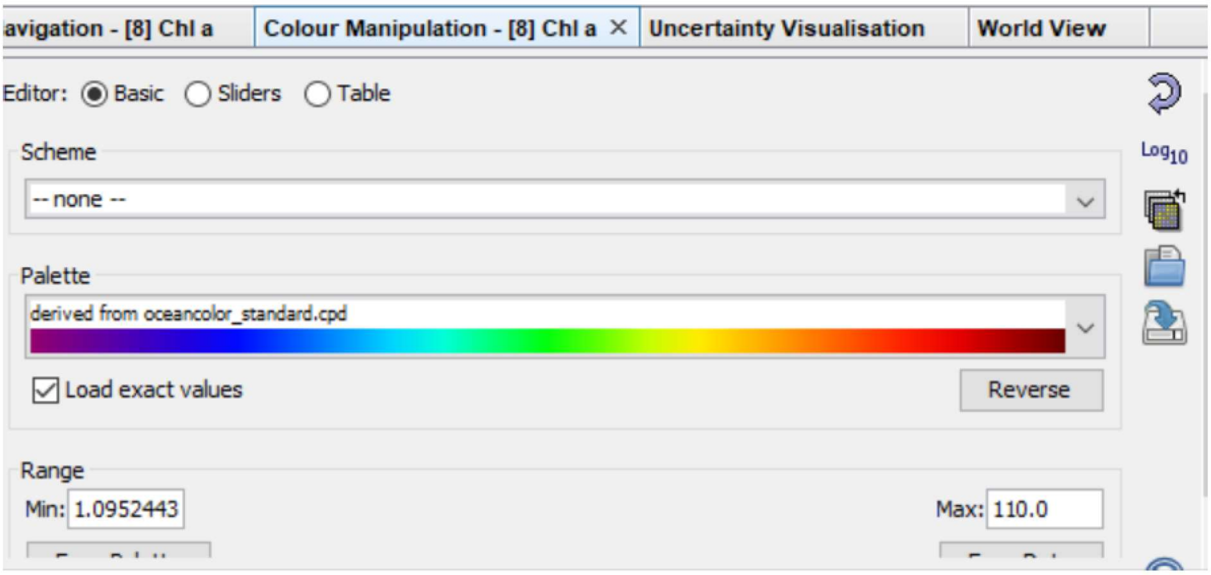
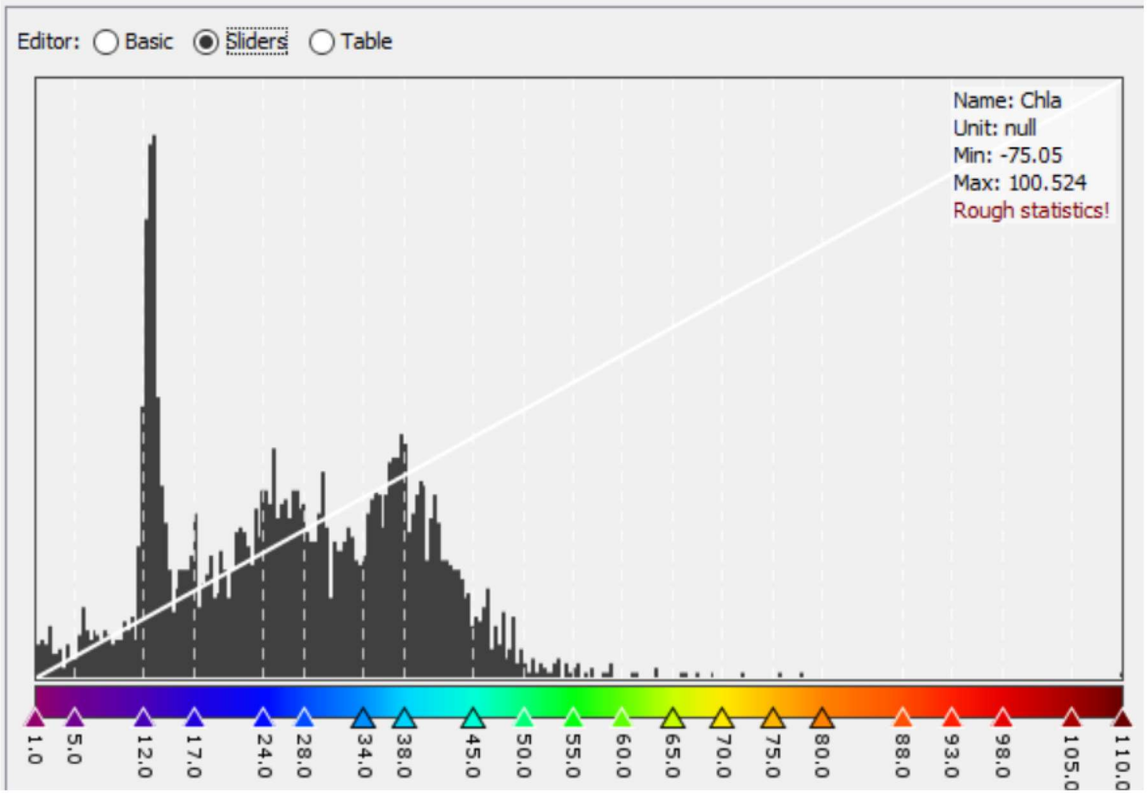
An image of Chl a will appear (if not, click on Chl a band (last in the list under Bands) and Open Image Window).).

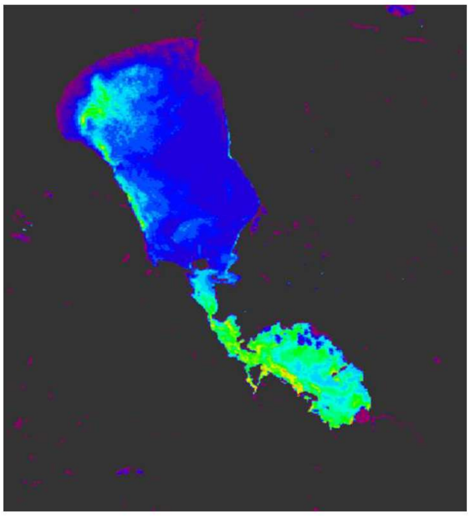
Then use the **Colour Manipulation** window (View-> Tool Windows) to assign colours to Chl a product. Under **Palette,** you can select "oceancolour_standard.cpd". The colouring is continuous. Under „**More options**“, you can also switch to „discrete colours”. The **Range** can be defined either from data or from palette, and the result changes accordingly.



Also, a slider or table view can be used, where values and colours can be changed by double-clicking on them.



The modified colour palette can be saved into a new cpd file. Later, this new colour palette can be chosen from the “Import colour palette” and applied to another image.

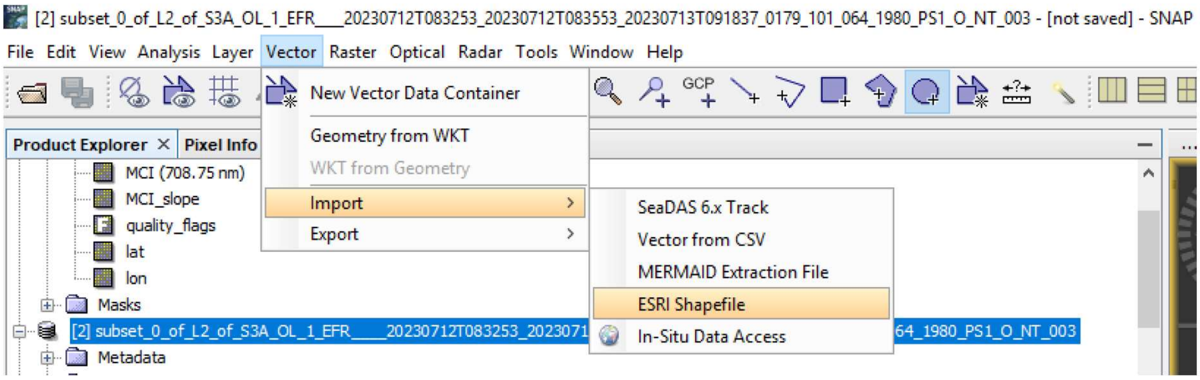


Colour legend can be exported as a File or as an Image. Click on the image and select **<u>Export Colour Legend as Image.</u>** Under **Properties**, colour legend can be modified (header text, orientation, etc.)

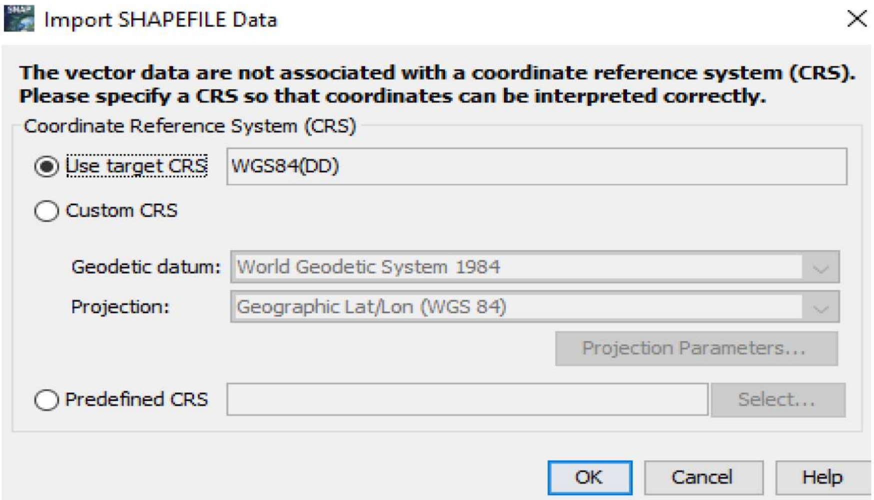
Look at the retrieved Chl a image – where are lower Chl a values? Is Chl a equally distributed in L. Peipsi s.s.? You can use Colour Manipulation tool and adjust the gradient by moving the arrows under the Sliders to focus on different parts in Lake Peipsi.

For the bloom classification:

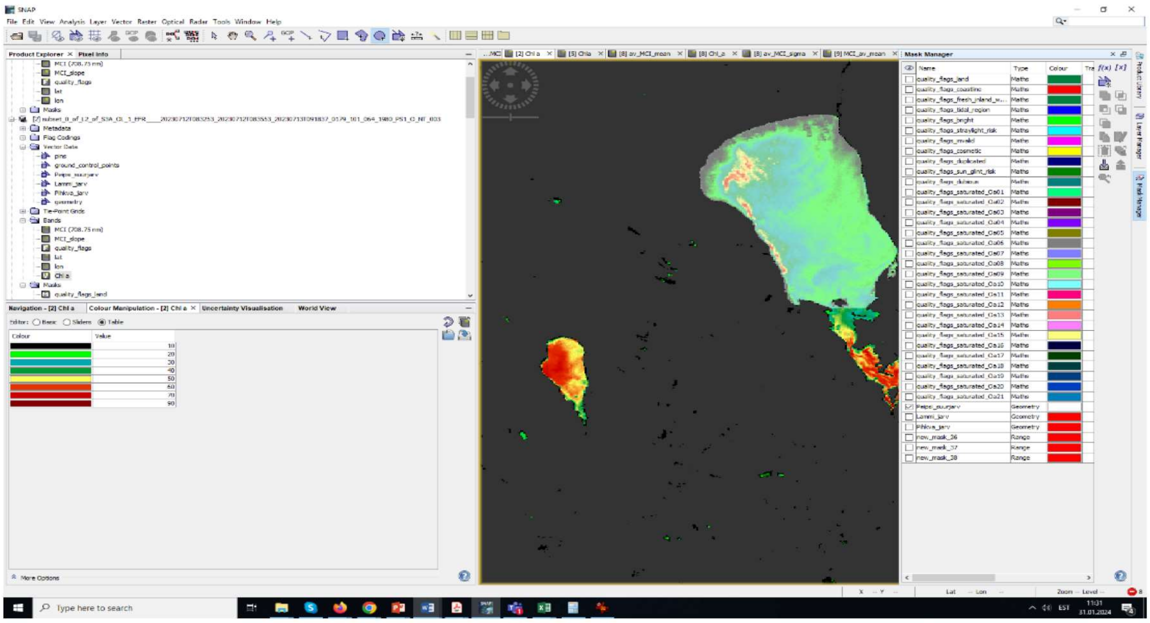
Import the shapefiles for three parts of L. Peipsi (the file name in the Product Explorer window needs to be selected): **<u>Vector-> Import -> ESRI shapefile</u>** (the shapefile folder has to be unzipped) -> select all three shapefiles -> specify the target CRS at WGS84



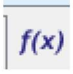
Coordinate Reference System will be asked, the default selection may stay.

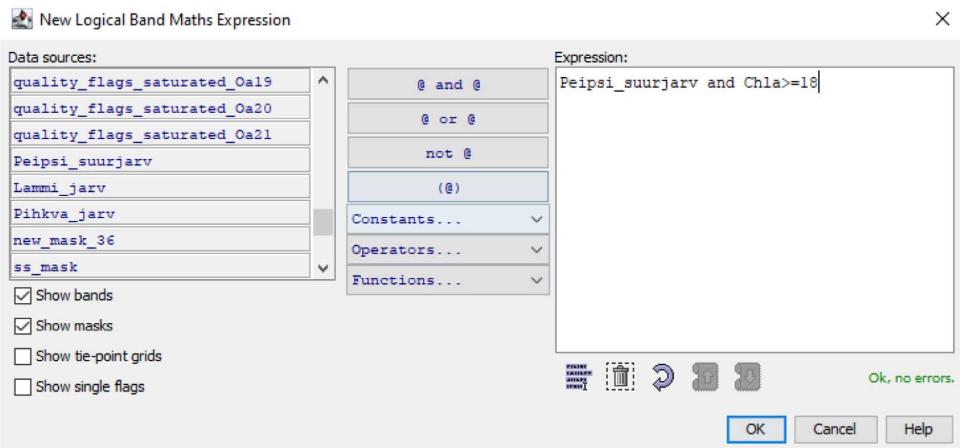


Shapefiles will appear as masks in the **Mask Manager (View-> Tool Windows->Mask Manager).** Its **Type** is Geometry. You can change the name, colour and transparency of the layer. Select a shapefile to make it visible on the image.



For bloom characterization, a new bloom mask according to Chl a thresholds (see Table 1 in the Introduction section) needs to be calculated. First, let's calculate the mask for Peipsi s.s.:

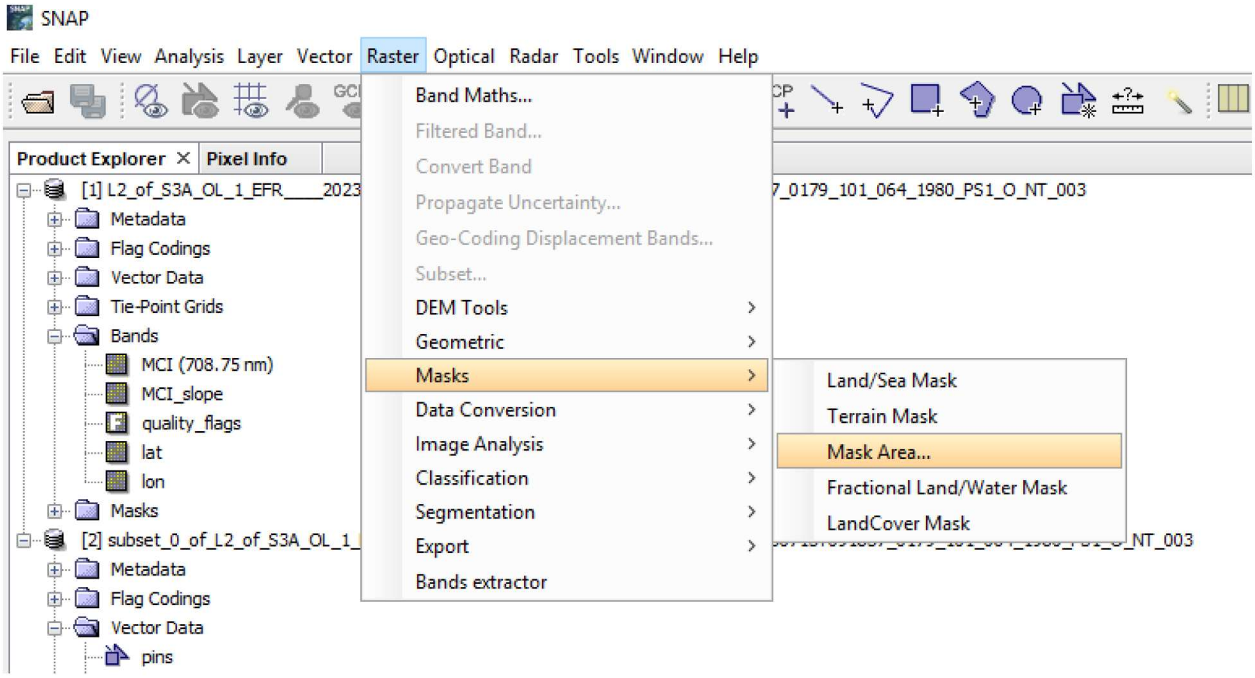
on the **Mask Manager**, click on  to create an expression. Tick on **Show masks** and **Show bands**. Select Peipsi_suurjarv mask, type "and" and select Chla band and add the threshold based on the value from Table 1 for bloom definition.



Give name to new mask. Repeat these steps for Lammijärv and Lake Pihkva with respective thresholds (Table 1). **Compile 3 masked areas: select the new masks for three parts of the lake and then click on**  **to create a union between the masks.**

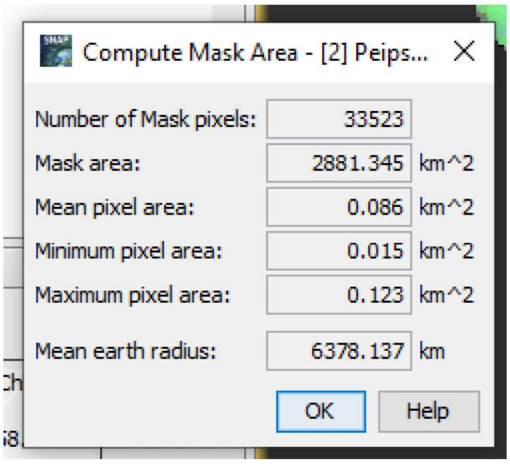
Masks can be exported  and later imported , for later usage. Select the mask by clicking on it. Export the combined bloom masks.

According to the masked area, find out **how large are the bloom areas in all lake parts**?

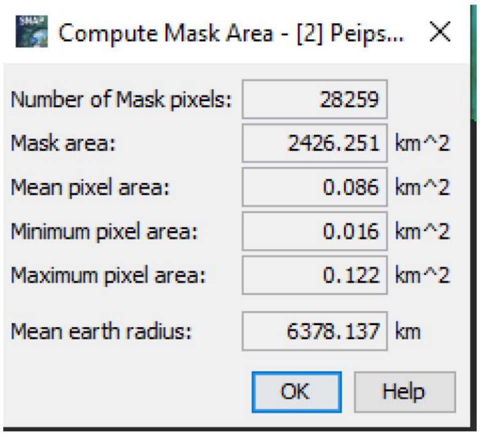


This can be done via **Raster -> Masks -> Mask area**. Select the specific mask from the list and find the surface area in km^2.

Mask size for the Peipsi_suurjarv is 2881.3 km^2.



The surface area for bloom is (geometry mask Peipsi_suurjarv and Chl a ≥ 18 µg/L) 2426 km^2.



How large is the bloom area in a) Lämmijärv; b) Pihkva, c) over the whole lake?

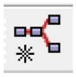
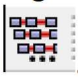
Close the product and save the file.

Optional exercise: do the L2 Processing in ESTHub for the Gulf of Finland area of the same day, calculate Chl a from MCI, apply the colour scheme and look at the visible part of the Gulf of Finland. Can you see the bloom?

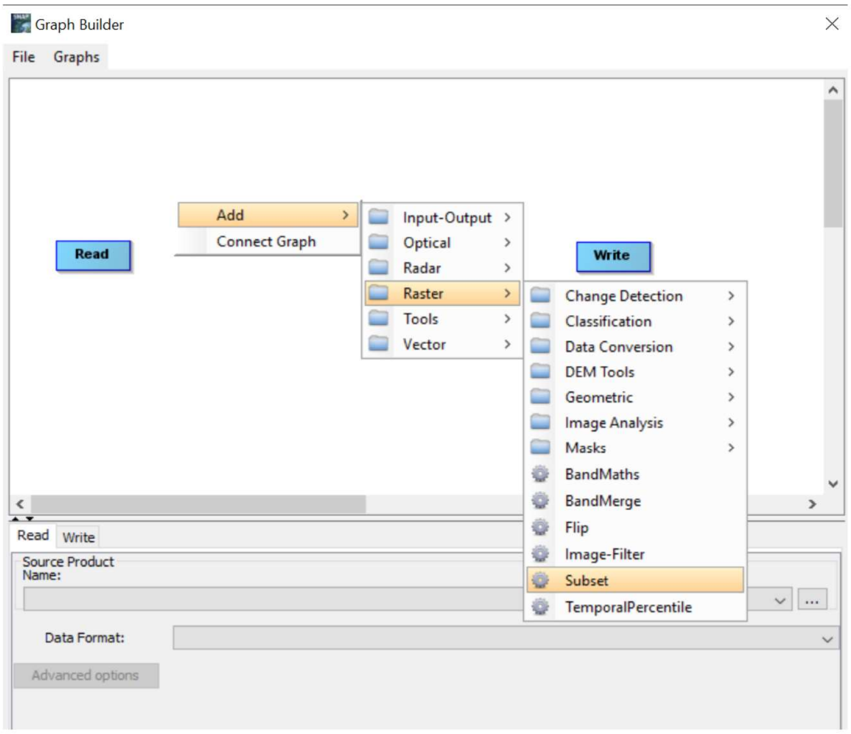
2. Using Graph Builder and Batch Processing Tool in SNAP

This exercise teaches to process several images simultaneously in SNAP, using graph builder and batch processing. Additionally, a possibility to create an average image with a Level 3 Binning opportunity is shown.

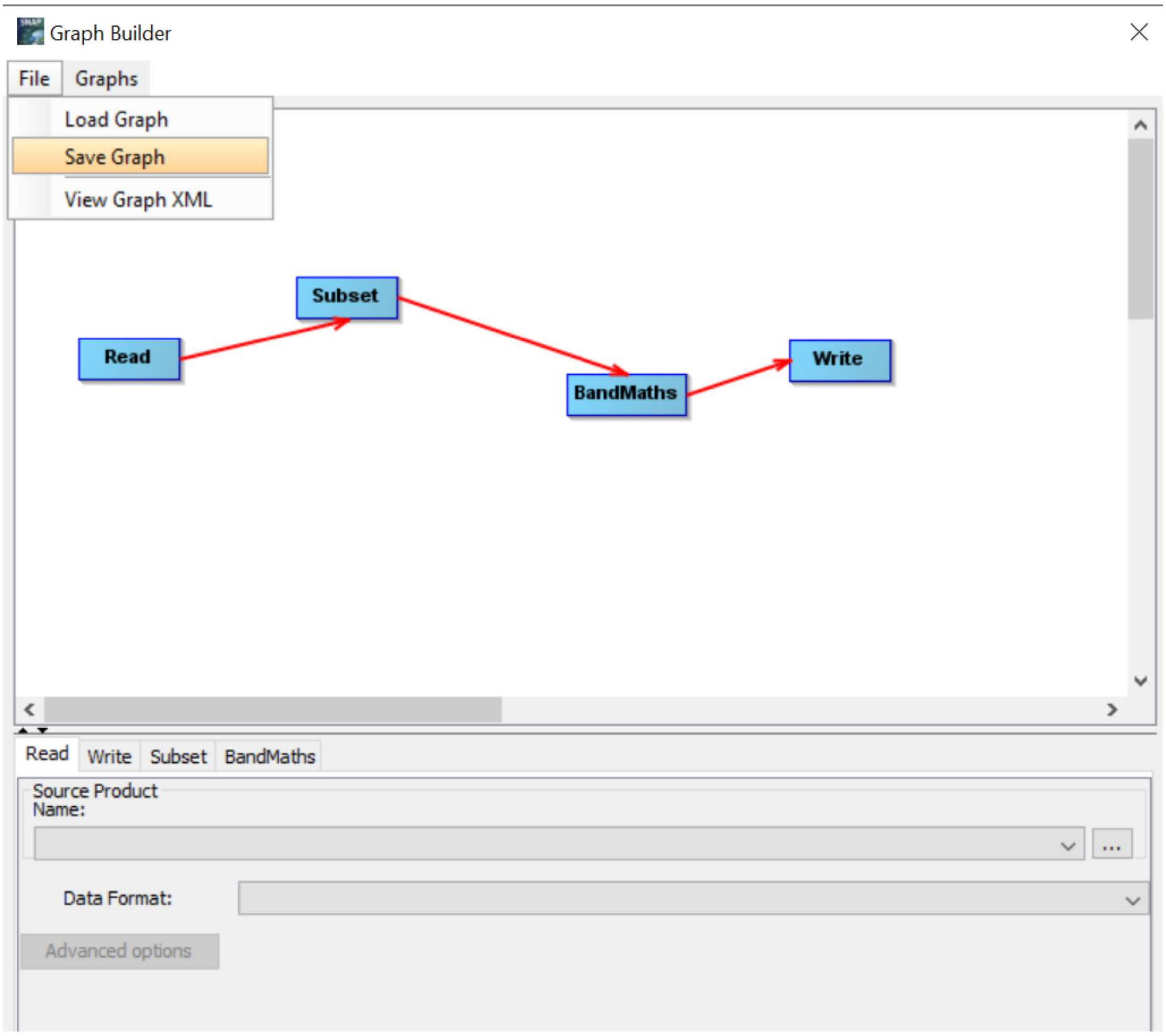
For that, use ESTHub **L2 Processing**, Sentinel 3 OLCI EFR images with MCI according to the instructions from the first exercise for 3 days (e.g. 15th, 16th and 22nd September 2023). Select User -region_1, containing L. Peipsi. Download one S3A image (with the ending code _1980.nc) per date.

In SNAP many images may be processed simultaneously using Graph Builder  and Batch Processing Tool . In the Graph Builder, a sequence of activities can be listed.

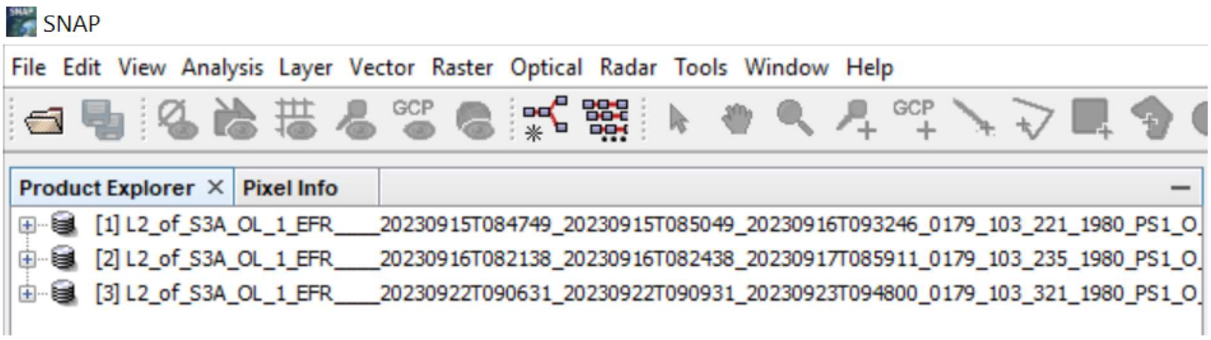
Open SNAP and create a **Graph Builder** scheme for further processing. Right click on the screen and select the processing tool. At first, add the Subset selection (Add-> Raster->Subset) to focus more precisely on L. Peipsi.

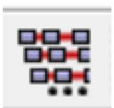


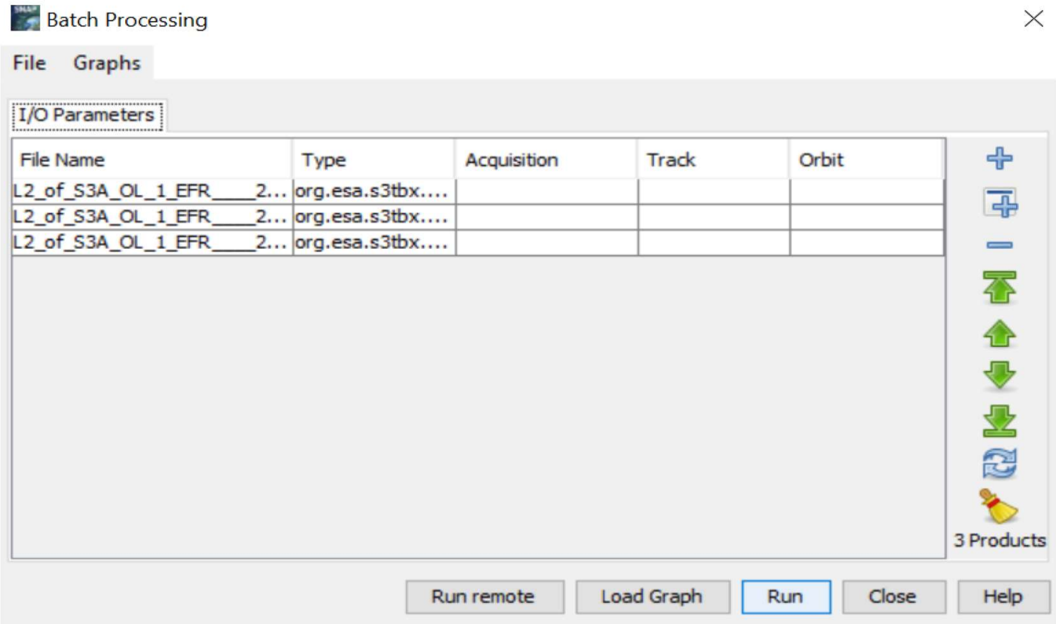
Then add BandMath for the calculation of Chl a (Add-> Raster-> Band Maths). Then right-click and select Connect graph. Connecting arrows will appear. Save the graph, e.g. MyGraph.xml



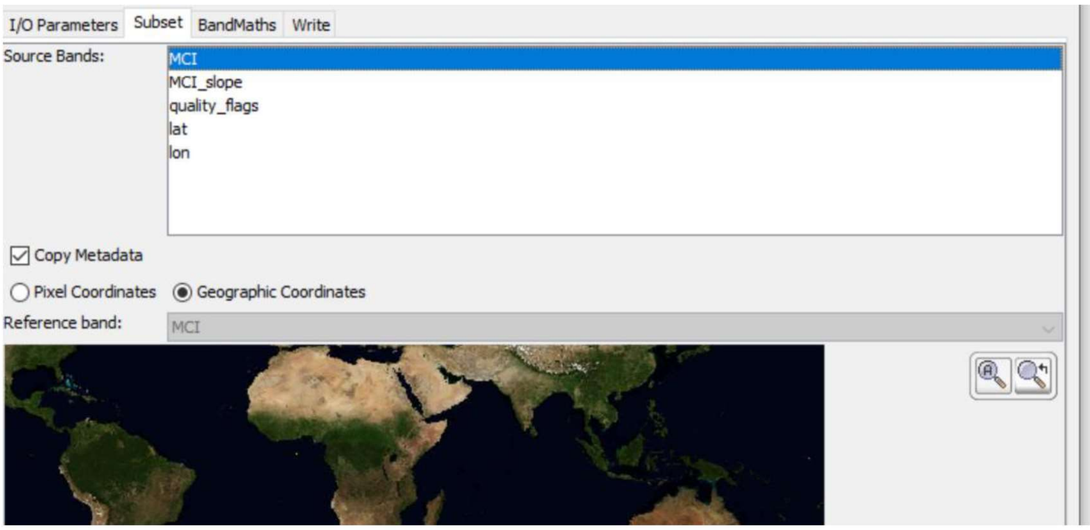
Product Explorer: Open three L2 products from September in SNAP.



Select **Batch processing**.  Use  to load all three files. Load the previously saved graph file from Load Graph.



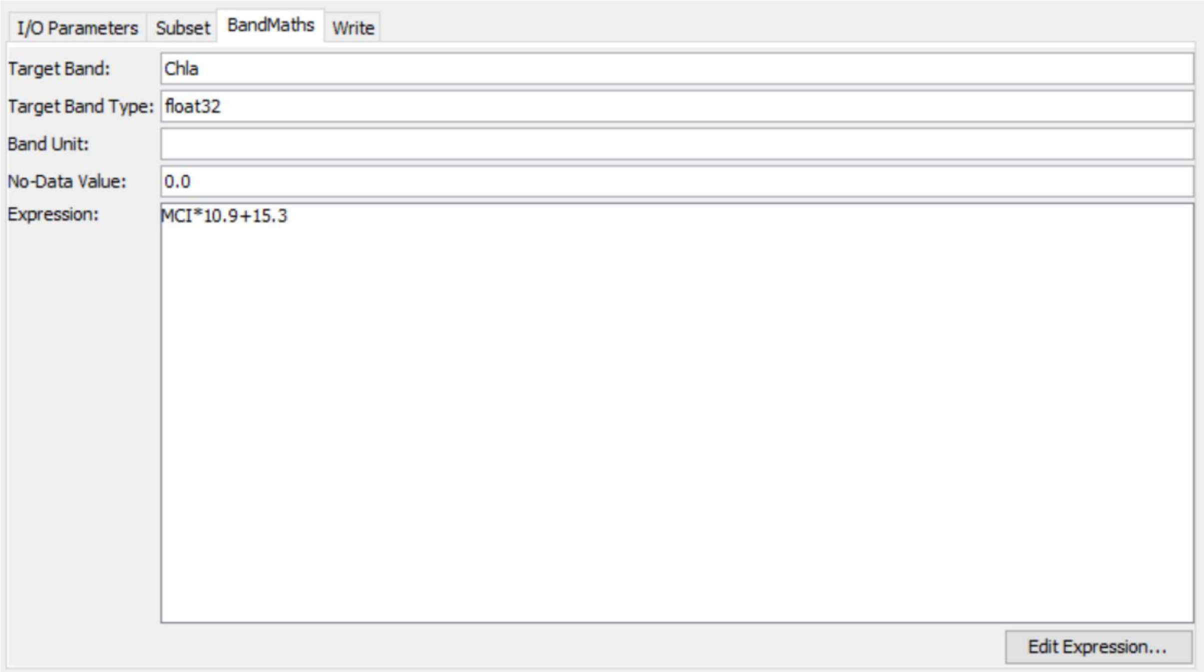
The titles occur besides I/O Parameters, which can be modified. Under **<u>Subset,</u>** select MCI as a source band and select **Geographic Coordinates**.



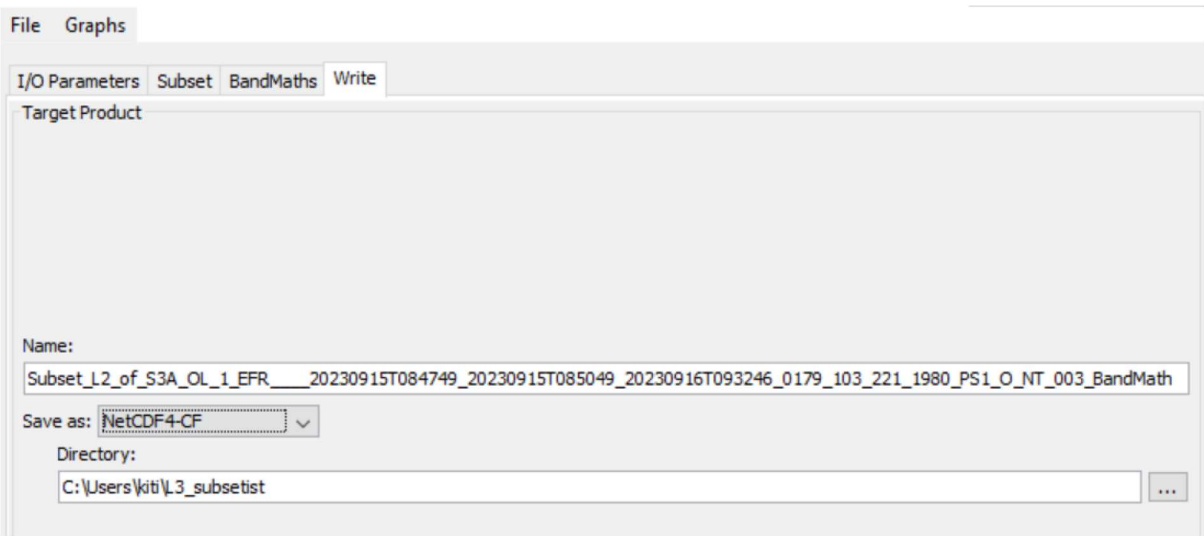
Use  to specify the target area with a mouse inside the red bounding box and click Update. A new polygon will be selected.

A new polygon is specified under Subset with coordinates according to the drawn yellow polygon. As this might take a while, fill in the Band Math section meantime.

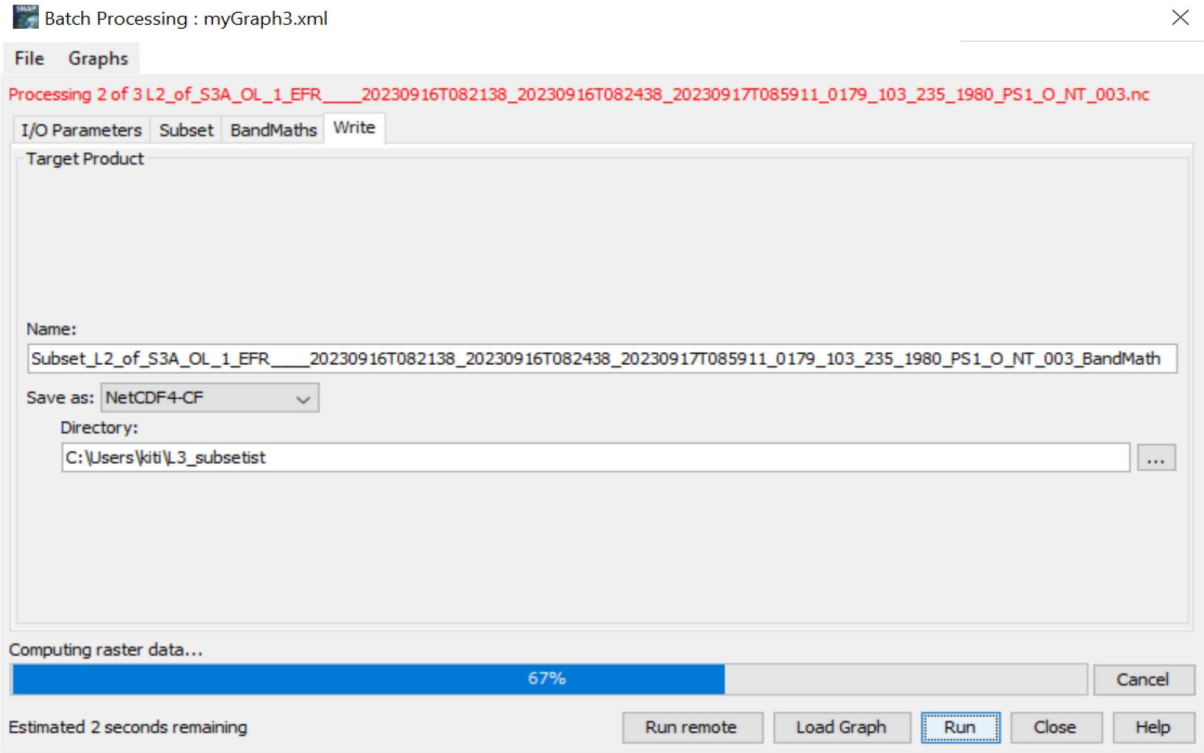
Under **Band Math,** select Target Band: Chl a and add an expression for Chl a calculation.



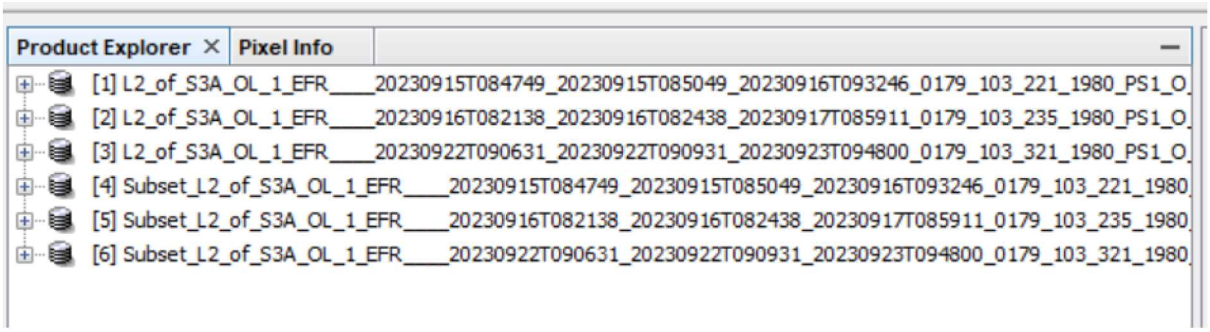
Under the **WRITE** section, specify the folder where products will be generated, and save as a NETCDF4-CF file.



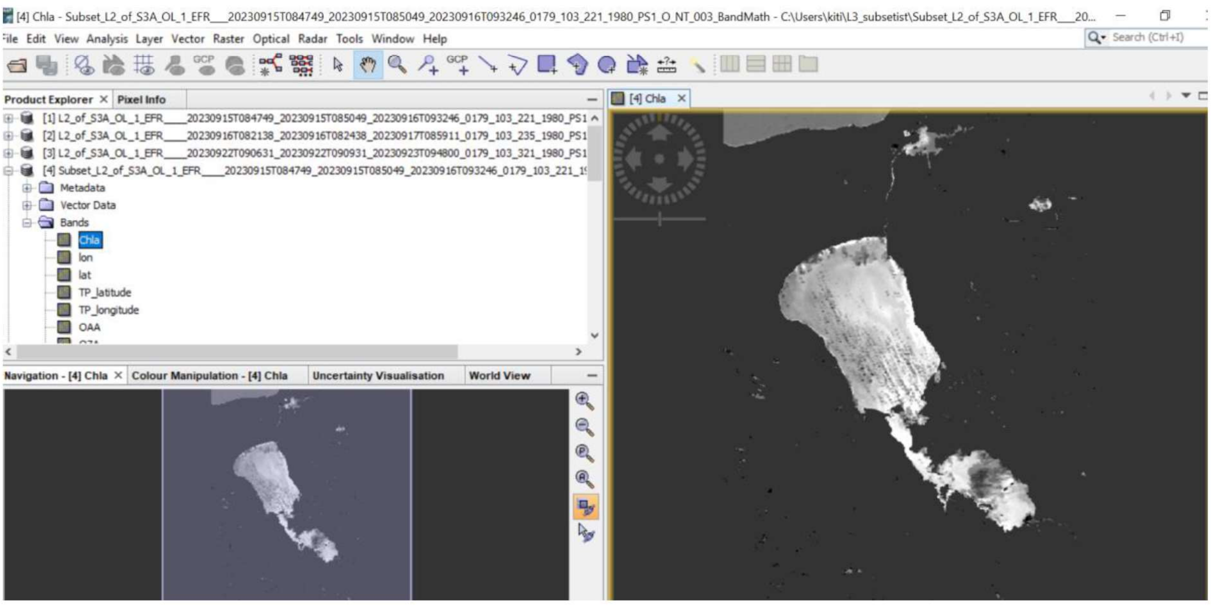
Then hit **RUN**.



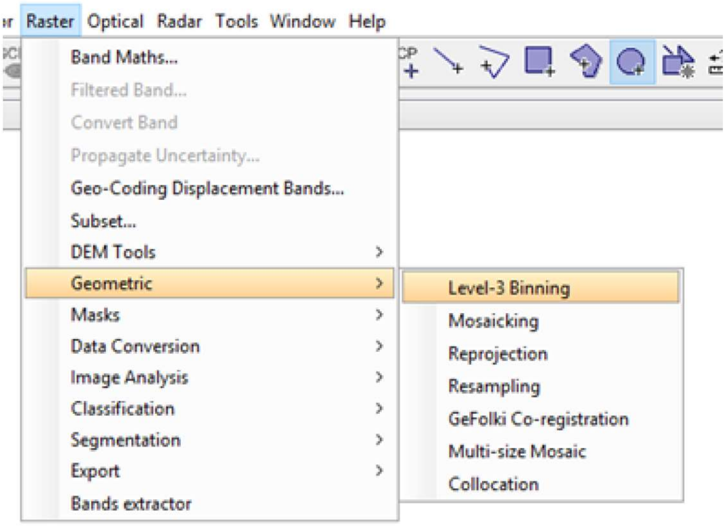
Three new files will be created.



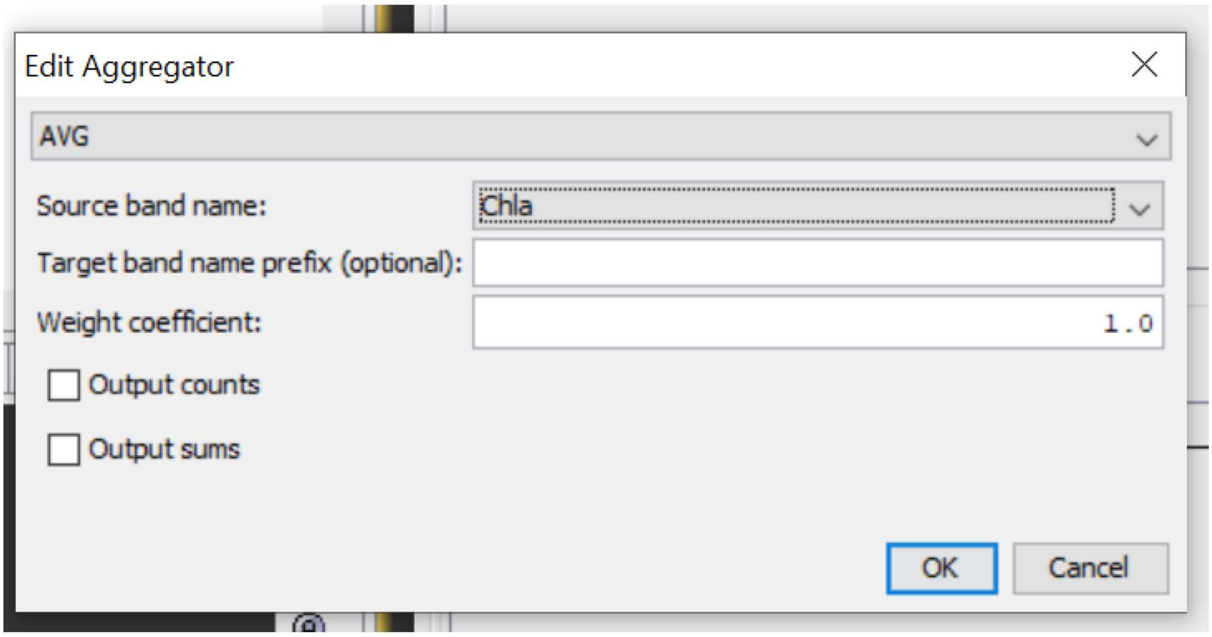
<u>Product explorer</u> Open Chla band in one of the subsets.



Use **L3 binning** (Raster->Geometric -> Level 3 Binning) to find an average Chl a of three September images.



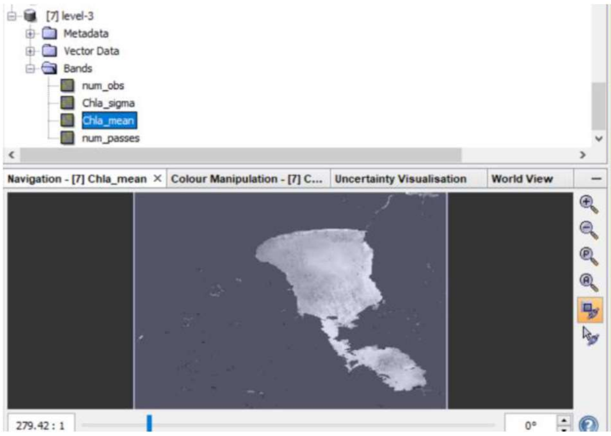
A new window opens. Click on ⊕ , **Add product(s)** and select three subset products -> OK. Under **Configuration** tab, click on ⊕ -> under **Edit Aggregator** select Chla as a **Source band name** and AVG as editing aggregator. Click OK.

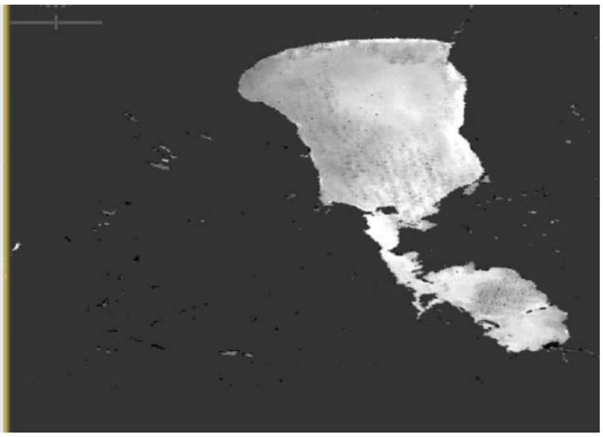


Change **Spatial resolution (km/px)** to 0.3. Click on **RUN**.

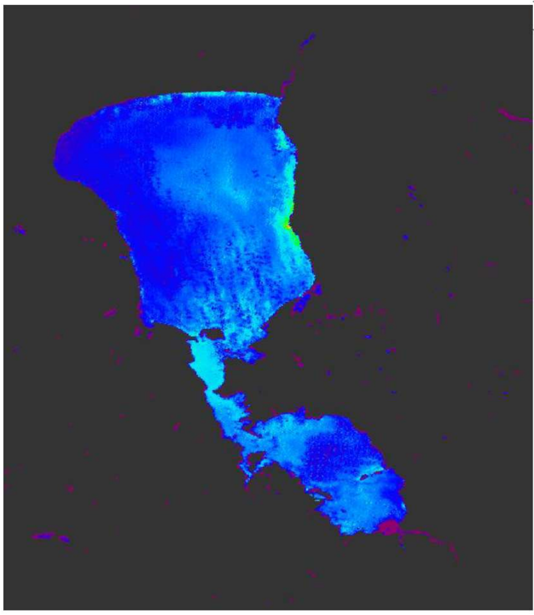
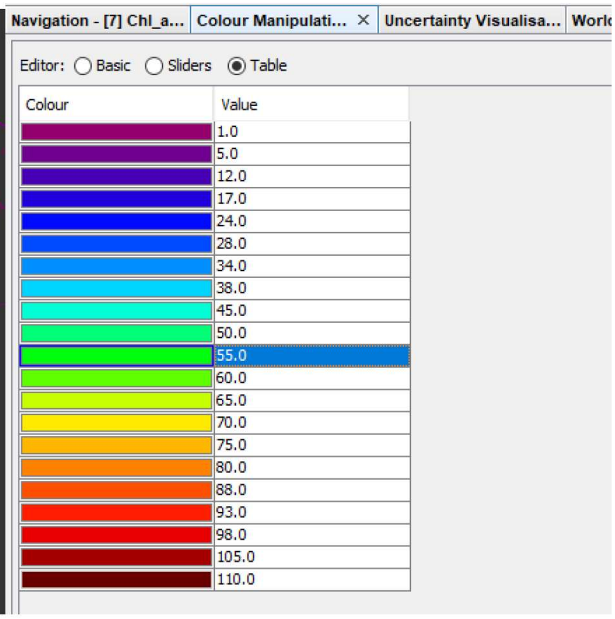
The Level 3 product appears in the **Product Explorer** window on the left. Under Bands, double-click on Chla_mean and the Level 3 image appears on the right side.

Look at the Level 3 image:





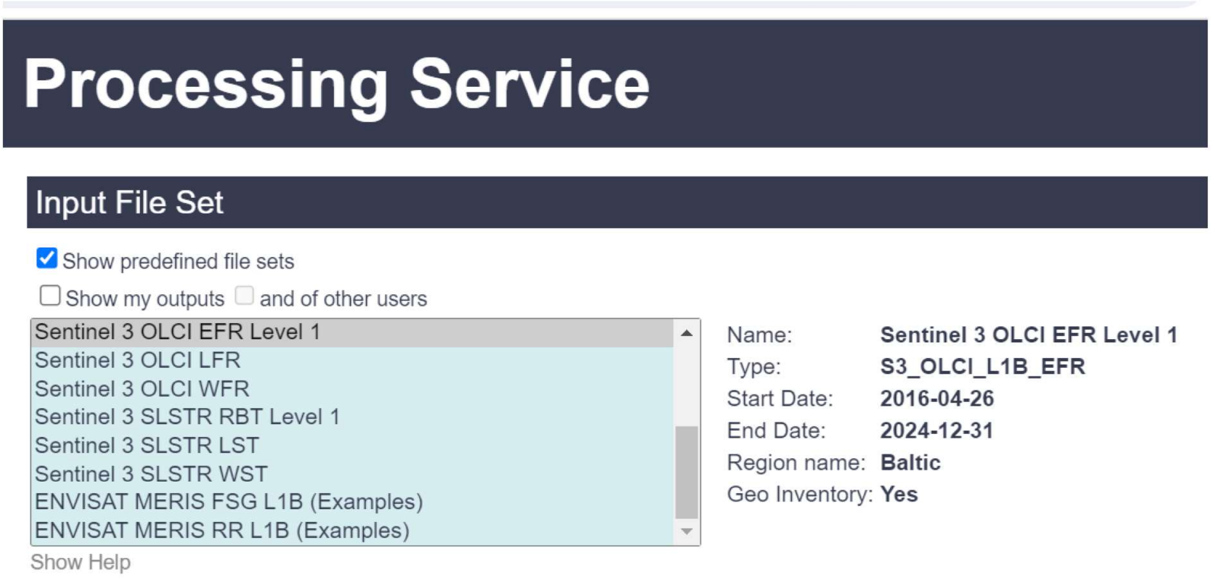
Load the previously created colour scheme file -> select under Range, From Palette, and look at the coloured image.

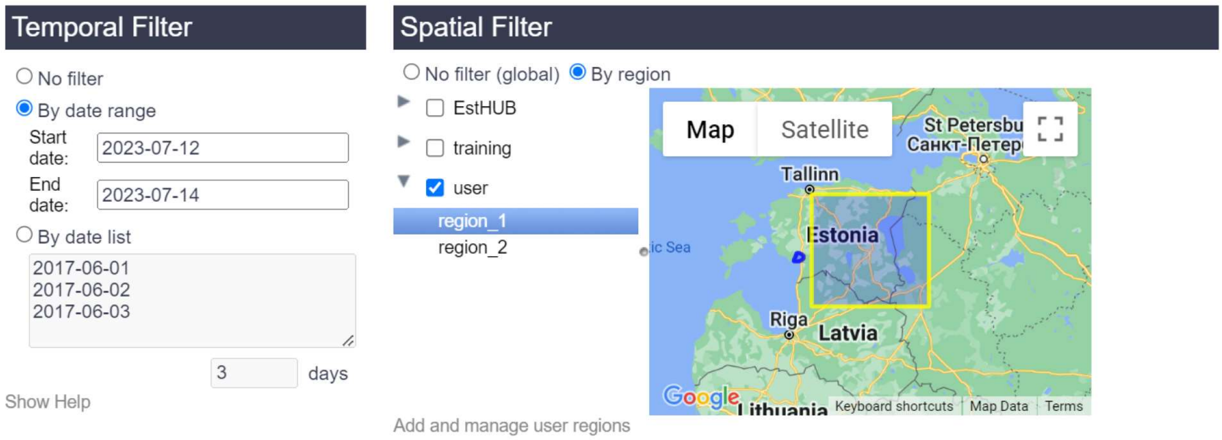



Find out how large was the area with Chl a above 46.6 µg/L in the entire lake Peipsi? (mask Chl a >= 46.6). This is the bloom threshold for L. Pihkva – are higher values present also in other lake parts?

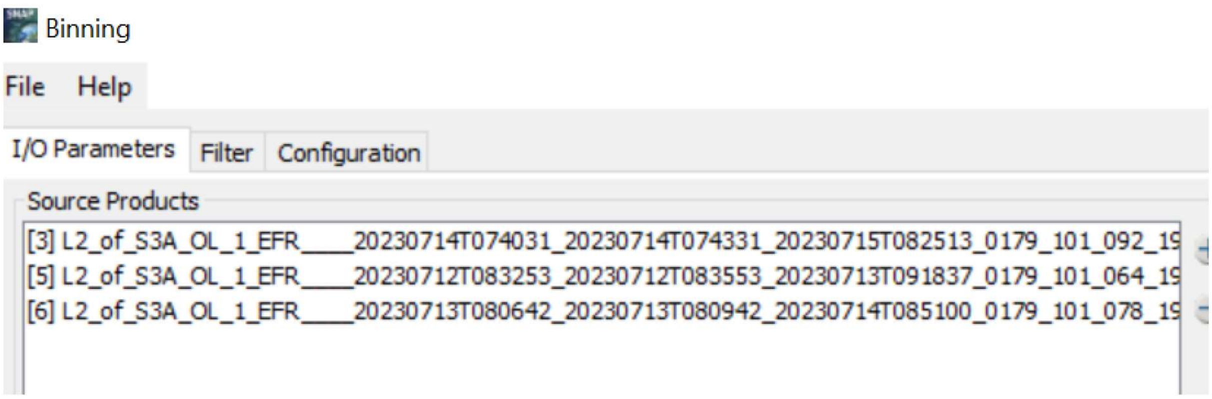
<u>Optional exercise:</u>

Calculate the average Chl a concentration image for L. Peipsi, using SNAP Level 3 binning of three images from July (12^{th}, 13^{th}, 14^{th}) 2023. For that, process 2 additional dates with **L2 processing** according to the scheme from exercise 1. Under **<u>Good-pixel expression</u>**, type in: NOT quality_flags_bright and NOT quality_flags_invalid.

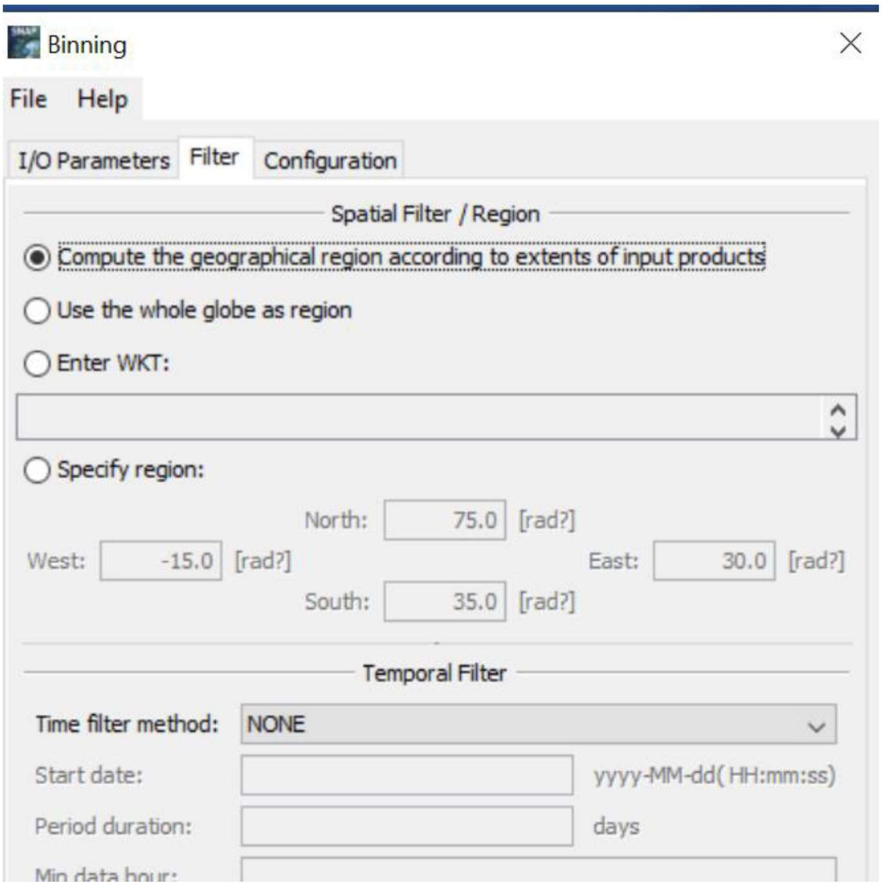




In SNAP, use **<u>L3 Binning</u>** and select 3 products from July, give new name, save them as NETCDF4 in your specified directory.



<u>Binning window</u> Filtering can be done according to coordinates - **<u>Filter</u>** > mark **<u>Specify region</u>** or according to the entire input file.



In this case, **Filter** > mark **Specify region** and add coordinates (North 59.271, West 26.085 South 57.721, East 28.31); under **Configuration**, select +, then AVG from the list and select a source band MCI. Change **Satial resolution** to 0.3 km/px. And click **RUN.**

Target product - A combined L3 product will be generated. Open it, and calculate Chl a using Band Math (Raster->BandMaths) (MCI_mean*10.9+15.3).

Assign a colour palette and look at retrieved average Chl a values: **in which lake part were the lowest values in July?** Were the Chl a values higher or lower in July compared to September in 2023?

3. Using Level 3 processing in ESTHub for retrieving an average value over a time period – a basis for the bloom area calculation

This exercise teaches to create average images over the time period in ESTHUb.

14-day composite images are the basis for bloom estimation (Figure 3).

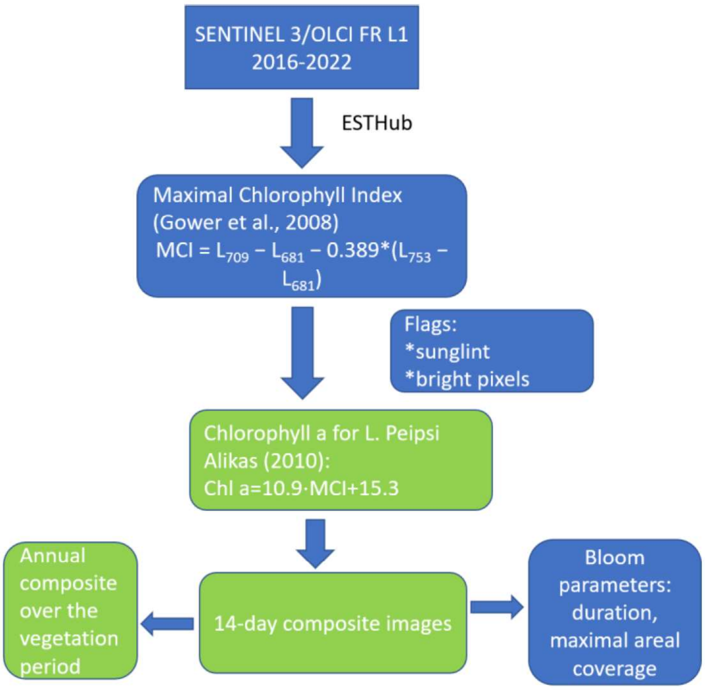
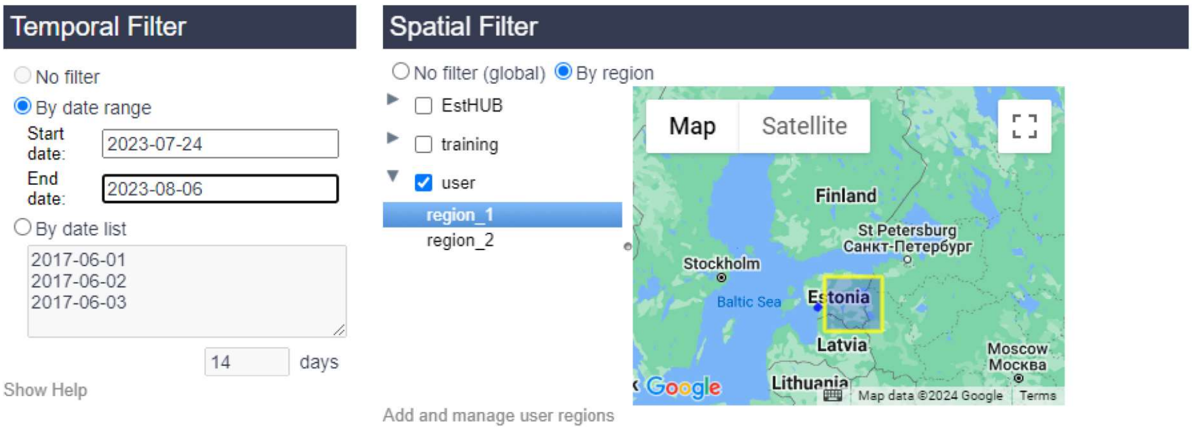


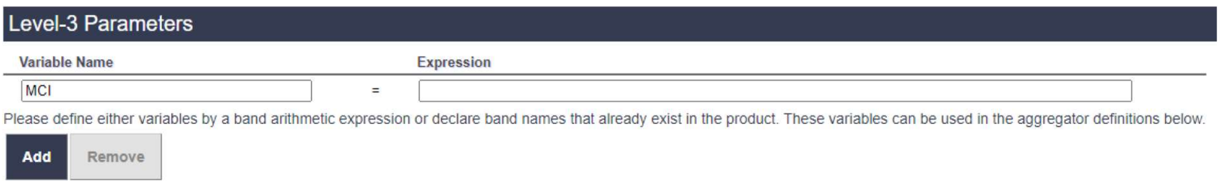
Figure 3. Processing scheme for bloom detection.

In ESTHub, select **L3 processing** and Sentinel 3 OLCI EFR Level 1. Then select the **Temporal Filter** and **By date range insert** 14 days, e.g., 24.07 - 06.08.23. Choose the **Spatial filter** user-defined region 1, which contains Lake Peipsi.

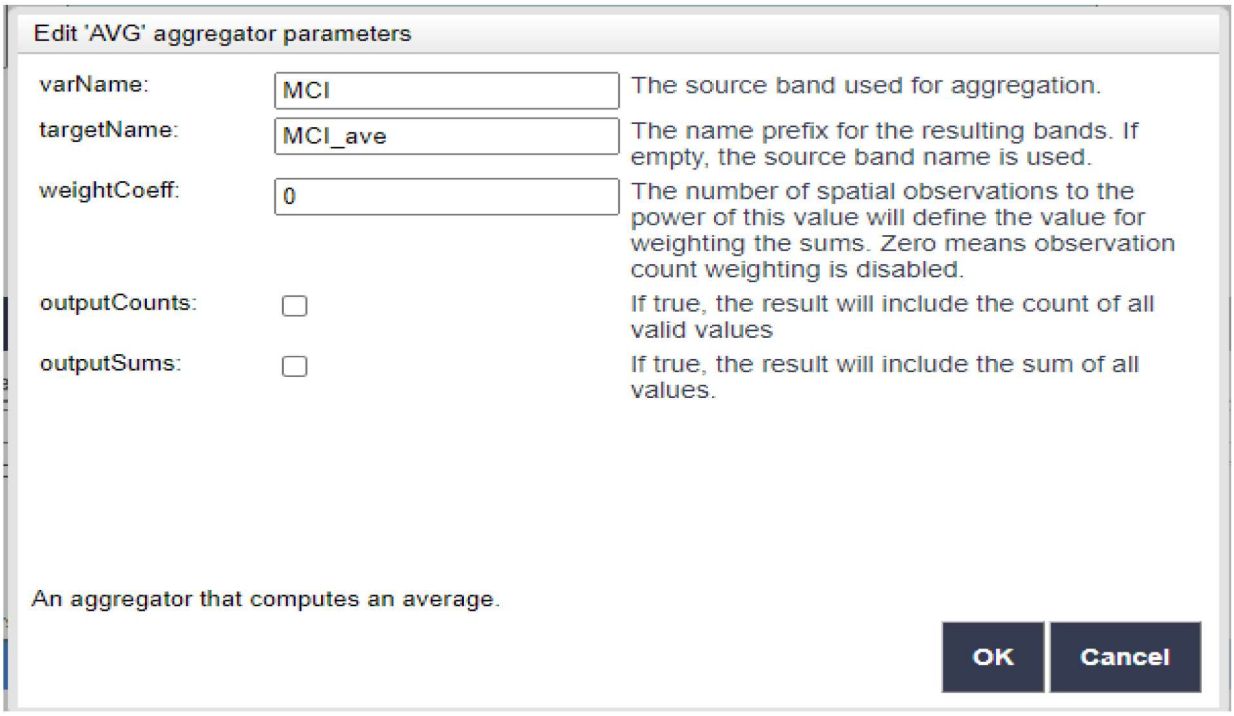


Then, select from **Level-2 Processor** Maximal Chlorophyll Index (MCI) from the list of processors.

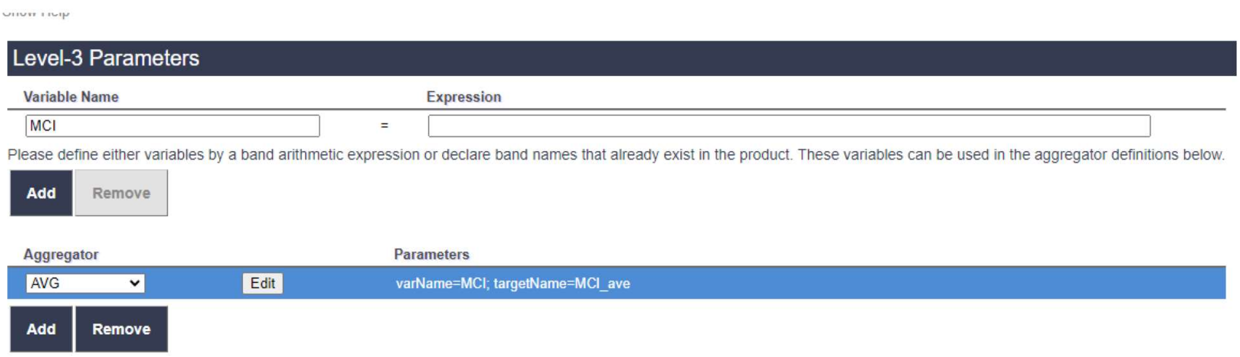
From **Level-3 Parameters**, click on **Add,** type **MCI** on the **Variable Name.**



Aggregator AVG, then click Edit – aggregator parameters, put varName = MCI, targetName MCI_ave; others may be left unchanged. Then click OK.

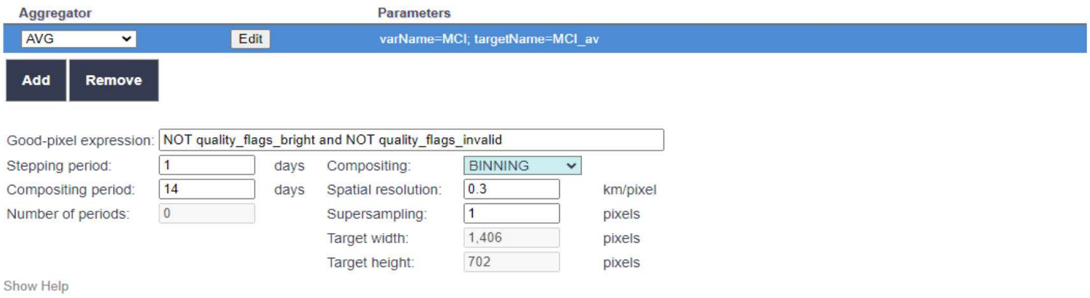


OK, and under Aggregator, the parameter info appears:

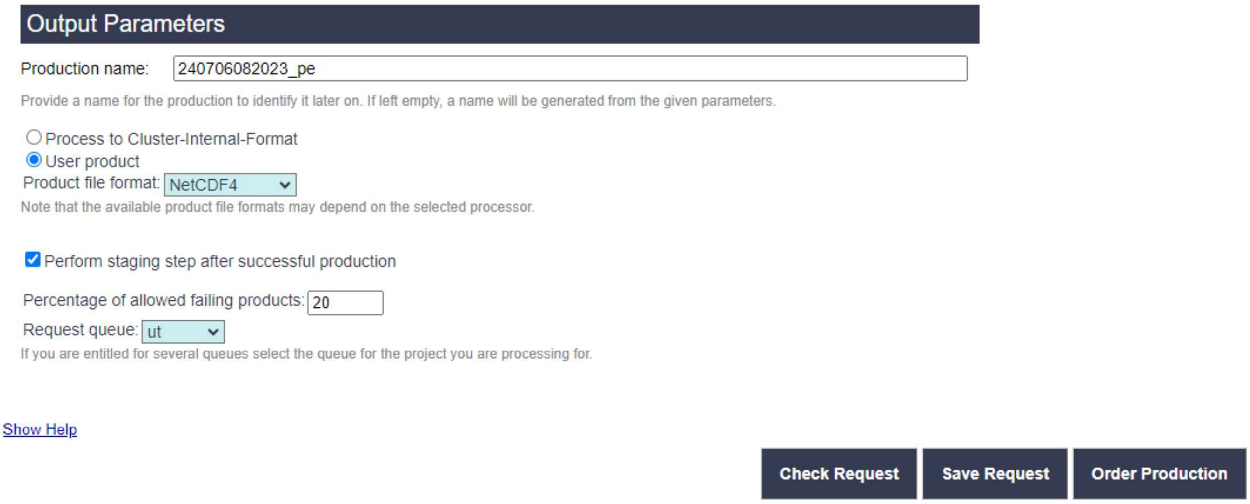


The selected parameters are visible under the Parameters section. Under **Good-pixel expression**, type in: NOT quality_flags_bright and NOT quality_flags_invalid.

Change the stepping period to 1 day and the compositing period to 14 days. Choose Binning as a technique for compositing, and choose the spatial resolution 0.3 (as the pixel for Sentinel 3 is 300x300 m).

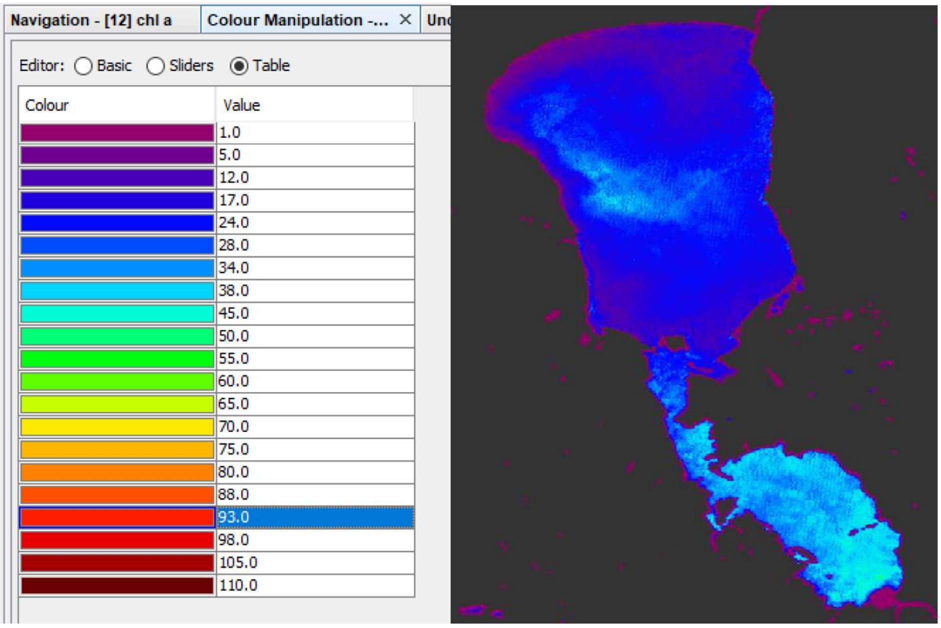


Output parameters: Choose a name for the produced file, change the format to NetCDF4, allow the percentage of failing products (20) and **order the production**.



The processing is visible from **Productions** (in the left pane in EstHub). Download the generated .nc file, unpack it and **open it in SNAP**.

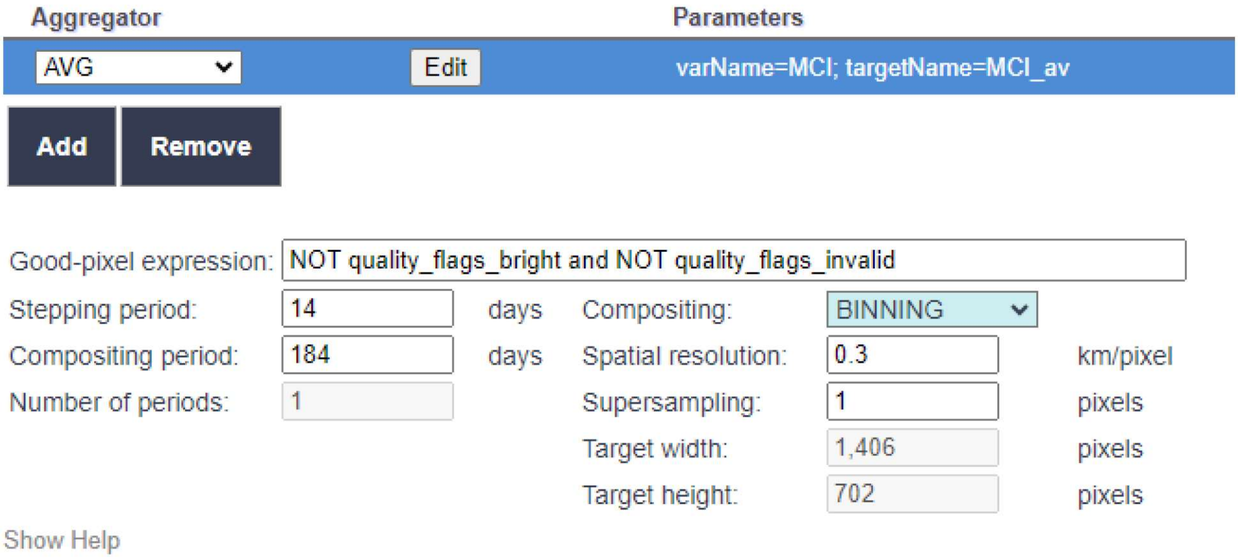
Open an image of MCI_ave_mean. Click on the **Bands**->double-click on MCI_ave_mean -> Image Window opens. Use the **Raster** -> **Band Maths** and calculate Chl a from the band MCI_ave_mean, using Alikas et al. (2010) formula: MCI_ave_mean*10.9+15.3. Use the **Colour Manipulation Scheme** to illustrate Chl a - take the suitable palette (e.g. the one you have previously saved) from  . As a result (if you use the following colour scheme), you will get the following image:



Add the mask with bloom criteria (both, the shapefiles and Chl a threshold masks need to be created again) – how large is the area over the threshold in three lake parts?

Optional exercise. Calculate the average image for the May-October period 2023 and compare it to the average image of the vegetation period 2022.

This calculation can be done using **L3 Processing** in ESTHub, first for 2022 and the second time for 2023. The **time period** for the processing is 01.05-30.10 during both runs; the **stepping period** is 14, and the **compositing period** is 184. Use the files L3_2023-05-01_2023-10-30.nc and L3_2022-05-01_2023-10-30.nc for comparison.



Which year had a larger average bloom area? How big % of the lake was, on average, affected by the blooms?

Additional reading

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