

Plankton Toolbox User's Guide



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Plankton toolbox Users Guide

Table of contents

Introduction.....	3
LifeWatch.....	3
Plankton Toolbox is free software.....	3
Uses for Plankton Toolbox	4
Mac, Windows and Linux	5
Getting the latest version of the software and the user's guide	5
Installing the software.....	5
The Plankton toolbox folder.....	6
Getting help.....	6
Basic concepts	7
Data sets	7
Taxonomic hierarchy	7
Cell volumes and trophic types	7
The user interface.....	7
Welcome	11
Getting started with Plankton counter	12
Plankton counter	13
Sample info.....	15
Counting methods	16
Count sample.....	17
Sample summary.....	18
Dataset manager	18
Data files – Text(*.txt)	19
Dataset screening.....	22
Select datasets.....	22
Check structure	23
Check code list and samples.....	23
Check column values	24
Plot parameters.....	24
Dataset reports.....	25
Dataset analysis.....	25

Select dataset(s)	25
Clean up.....	26
Aggregate/complement data	26
Filter.....	27
Predefined graphs	27
Generic graphs.....	28
Statistics.....	29
Exports.....	29
Managing counting lists.....	30
Managing general species lists	30
Important lists	30
Getting started on Mac	31
Technical information for developers	37
Acknowledgements	37
References.....	37

Introduction

Plankton form the base of the food web in most aquatic ecosystems. There is a need to estimate the biomass, abundance and the biodiversity of plankton organisms. Eutrophication, climate change, invasive species and harmful algal blooms are some of the reasons to monitor plankton. Microscope based methods are currently the standard in several monitoring programs including HELCOM-COMBINE, for the Baltic Sea, and OSPAR-JAMP, for North Eastern Atlantic Ocean covering the area between the Azores and the Arctic Ocean. Phyto- and zooplankton samples are collected using e.g. water sampling devices, hoses or nets. Data have been collected for decades and large data sets are available e.g. at international and national data centres. To work with the data in a consistent way may be difficult without the right tools.

The Plankton Toolbox is a free tool for aquatic scientists, and others, working with phyto- and zooplankton data. It is available for MacOS and Windows. Plankton Toolbox makes it relatively easy for non-programmers to work with large data sets on the diversity, abundance, biovolume and carbon content of plankton efficiently. The software is useful for working with datasets emanating from quantitative and qualitative analyses of phytoplankton and zooplankton. Phytoplankton, including harmful algae, are enumerated and identified in numerous ways; see e.g. Karlson et al. (2010). One of the most popular quantitative methods is water sampling, preservation of the sample and subsequent microscope analysis using the sedimentation chamber method (Utermöhl, 1958; Edler and Elbrächter 2010). The method produce data on the biodiversity of plankton. The cell volume of the taxa is also often included to facilitate the calculation of biomass. Plankton toolbox offers a work flow for calculating biovolume of organisms based on Olenina et al. (2006) and also carbon content based on the algorithms by Menden-Deuer and Lessard (2000).

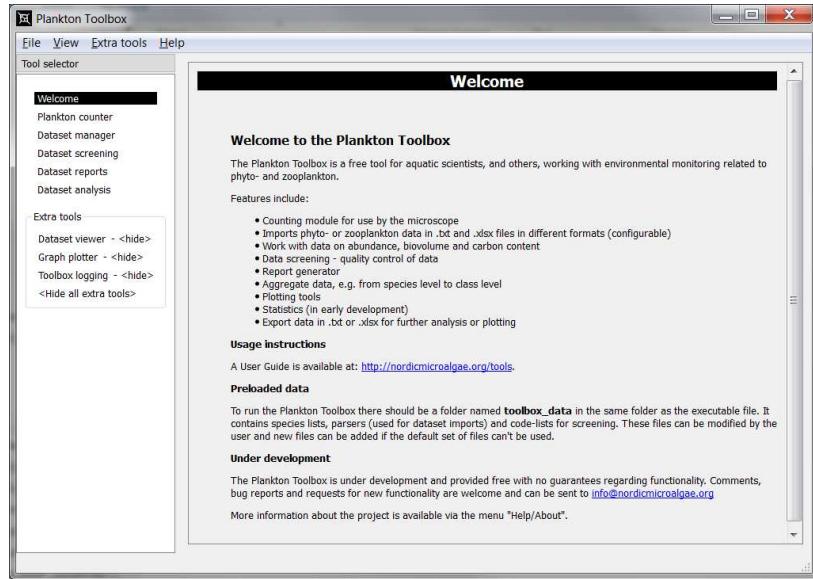
LifeWatch

The development of the Plankton Toolbox is part of the Swedish LifeWatch project funded by the Swedish Research Council Vetenskapsrådet. LifeWatch is also a European Union programme on sharing biodiversity data across Europe.

Plankton Toolbox is free software

Plankton Toolbox is free software and comes with ABSOLUTELY NO WARRANTY.

Uses for Plankton Toolbox



The software Plankton Toolbox has many features, here follows the main ones:

1. The **Plankton counter** provides
 - a. A tool for the microscopist analysing (counting) plankton samples in a consistent way.
 - b. A graphical user interface designed for counting samples using a computer by the microscope. If you prefer pen and paper by the microscope you may find the Plankton counter module useful anyhow.
 - c. A way to record metadata such as sampling data, station name etc.
 - d. A way to store templates with some metadata pre entered, e.g. when samples from different dates from a certain station are analysed
 - e. A way to work with lists of organisms
 - i. The HELCOM-PEG list
 - ii. The Nordic Marine Phytoplankton group list
 - iii. A zooplankton list (ZEN – in development)
 - iv. A list of your own choice
 - v. User defined subsets of lists mentioned above
 - f. Information on traits such as trophic type, cell volume, harmfulness etc.
 - g. Easy calculations of cell abundance and biomass based on concentrated volume, counted area, sedimentation chamber size etc.
 - h. A data format for storing results together with metadata and methods used
 - i. A way to save the results as a report
2. With the **Data set manager** you can :
 - a. Select results from the Plankton counter module
 - b. Import data sets in various formats, e.g. data sets downloaded from data centres.
 - i. Text files
 - ii. Microsoft Excel (.xlsx) files
 - c. Combine different data sets
3. With **Data set screening** you can:
 - a. Carry out some quality control of the data, e.g.
 - i. Screen your data
 - ii. Make plots of the raw data
4. With **Data set reports** you can:

- a. Select what data you want to include in the report
 - i. Export data in various ways, e.g. in special formats
- 5. With **Data set analysis** you can
 - a. Clean up your data, e.g.
 - i. to remove some data in your data set
 - 1. to select a certain species
 - 2. to select a time period
 - 3. to select a station
 - 4. to select a depth interval
 - b. Aggregate/complement your data
 - i. If a sample has been counted at a high level of detail, e.g. at the size group level, you may want to aggregate to a higher taxonomic level, e.g. species, order or class level. Also non-taxonomic plankton groupings may be used.
 - ii. Add zeroes – when combining data from several sampling occasions it is often useful to add zeroes for taxa that have not been observed
 - c. Plot your results
 - d. Calculate statistics

Mac, Windows and Linux

Plankton Toolbox is available for Mac and Windows. A Linux version will be made available upon request. The software has been tested extensively on Windows 7 and to a smaller degree on MacOS 10.11.1, El Capitan. The user's guide provides examples, i.e. screen shots, from Windows 7 and Mac.

Getting the latest version of the software and the user's guide

The software and the user's guide may be downloaded from <http://nordicmicroalgae.org/tools>

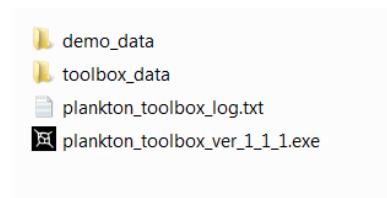
Installing the software

Download the zip file. Unpack it and place it in a convenient place on your computer. It should also be possible to run the software on a server or on a virtual machine.

Windows

Place the whole folder with the software and supplied subfolders and files e.g. on the C: drive or the D: drive if you have multiple partitions on your hard drive.

Start the software by double clicking on the black and white icon.



In some computing environments you need to be a local administrator of your computer to be allowed to install or run software. Check with your IT-department if this is needed.

Mac

The instructions below are preliminary but should work for most users.

After unzipping the folder downloaded from <http://nordicmicroalgae.org/tools> you need to do the following:

1. Place the whole folder with the software and supplied subfolders and files in the logged in user's folder, e.g. in Peter, if you are logged in as Peter on your Mac. The folder icon looks like a small house.
2. This will start the window for terminal on the Mac. A few seconds later Plankton Toolbox starts. The terminal window will run in the background. The information shown in the terminal window is not of importance for the user of Plankton Toolbox.

For further instructions and screen prints concerning Mac, go to page 36.

The Plankton toolbox folder

In the same folder as the software two other folders reside:

toolbox_data
demo_data

toolbox_data

This folder must not be moved or deleted. Settings for and results from Plankton counter, essential species lists etc. reside in the folder. Read more about this in the section on taxonomic lists near the end of the user's guide.

demo_data

Example datasets with plankton data downloaded from the Swedish Oceanographic Data Centre (<http://sharkweb.smhi.se>) is found in this folder.

Getting help

The user's guide is at present the only help system for Plankton Toolbox. The user community is encouraged to use the forum at <http://nordicmicroalgae.org/forum> to post questions and answers and to suggest improvements for the software. Also use the e-mail address info@nordicmicroalgae.org for questions.

Basic concepts

Data sets

Plankton Toolbox treats data as datasets. A data set may contain results from one or several samples. Datasets may be combined, e.g. when working in the *Data manager* and *Dataset analysis*.

Taxonomic hierarchy

One of the features of Plankton Toolbox is the ability to aggregate data to different taxonomic levels, e.g. to class level. This requires a taxonomic tree, i.e. a hierarchy. There are two different taxonomic hierarchies supplied with the package. You may also create your own hierarchy. The hierarchies are user selectable, i.e. the user can use a tree of his or her own choice.

1. The taxonomic hierarchy used in Nordic Microalgae, <http://nordicmicroalgae.org>. This is based on AlgaeBase, <http://algaebase.org> (Guiry and Guiry 2015).
2. The taxonomic hierarchy used in the HELCOM-PEG list.

Cell volumes and trophic types

Another feature of Plankton Toolbox is the ability to work with biovolumes of phytoplankton. A list of cell volumes for phytoplankton taxa from the Baltic Sea region based on Olenina et al. (2006) is supplied with Plankton Toolbox. This list is updated yearly by the HELCOM Phytoplankton Expert Group and is available for download at www.ices.dk. The list also includes information on the trophic type of the organisms, e.g. autotrophic, mixotrophic or heterotrophic. The term not specified (NS) is used for cells that have an unknown trophic type. In addition to the standardised lists support for lists handling synonyms and user defined lists is part of Plankton Toolbox. Calculation of carbon content is part of Plankton Toolbox. The equations used for phytoplankton were developed by Menden-Deuer and Lessard (2000).

The user interface

The user interface consists of one or a few window panes. There is a main window pane and window panes called Extra Tools. You may show and hide window panes as you please. If you have a large computer monitor you may choose to have all open. It is also possible to tear off window panes and place them on the same or on another computer monitor. The Extra Tools may easily be moved around by clicking and dragging them. They may float in front of the toolbox, or placed where one wishes, far right or below the work space.

The Extra Tools

Toolbox logging

In this text file activities are logged and errors reported. Keep the window open when importing new data sets to note problems with species names etc.

Dataset viewer

You can see the original data, the filtered data or choose to not see any data for increased speed.

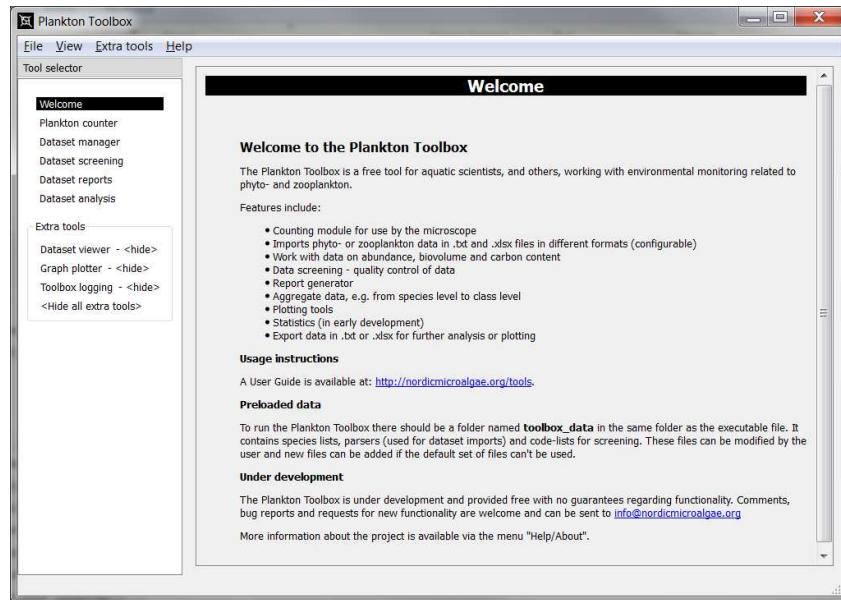
Data may be exported through the clipboard and pasted into other software such as a text editor or Microsoft Excel.

Data may be exported using the save function as text files or xlsx files.

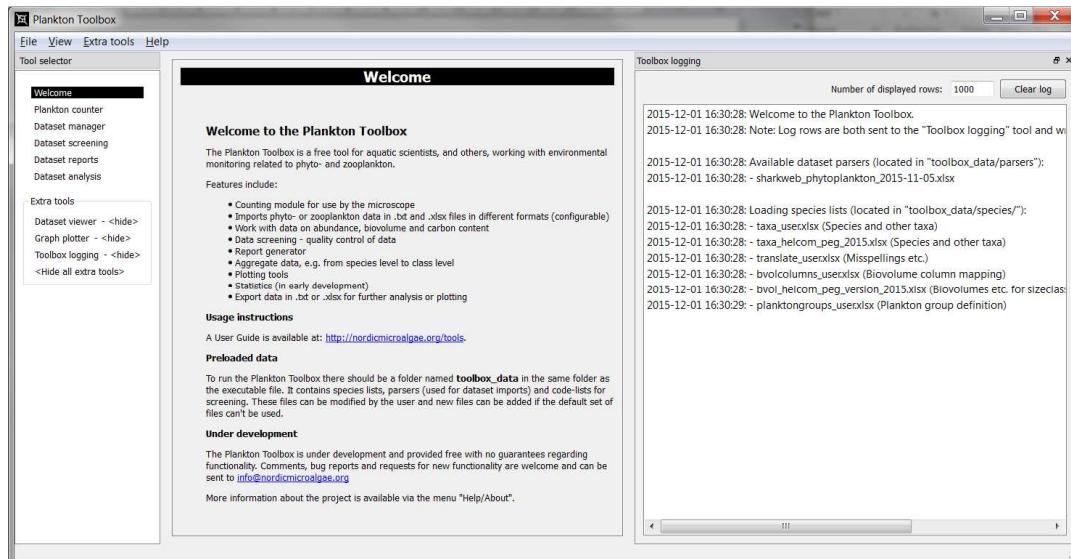
Graph plotter

In this window pane new plots are shown. Plots may be exported in various formats, e.g. jpg and png.

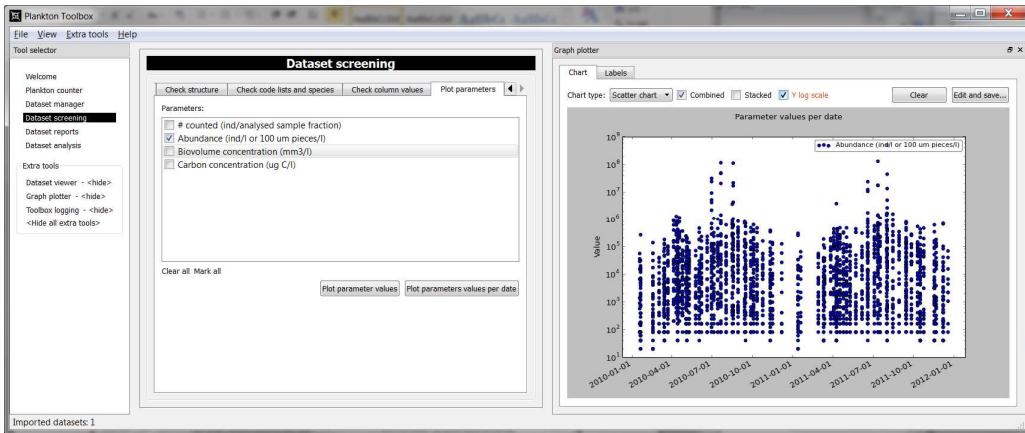
Here follows some examples of how you may configure the user interface.



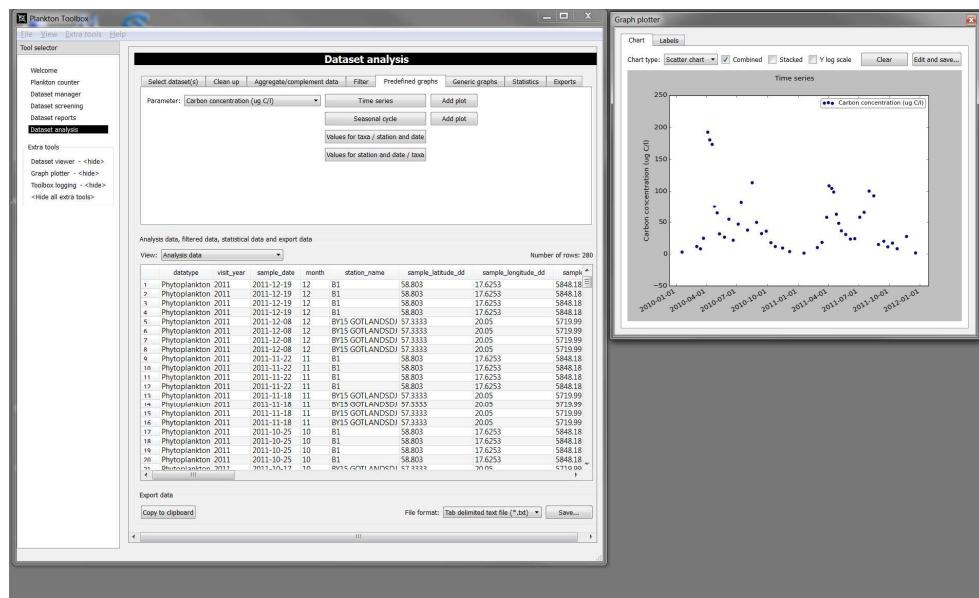
Main window only



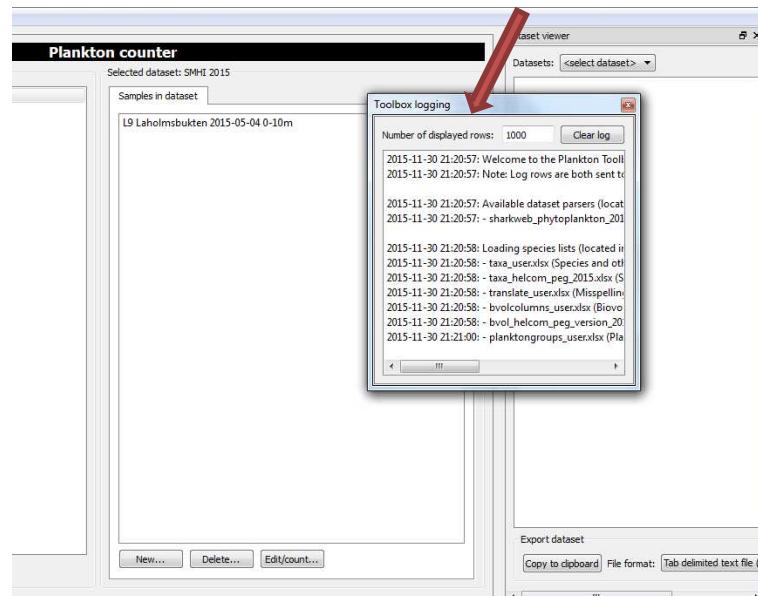
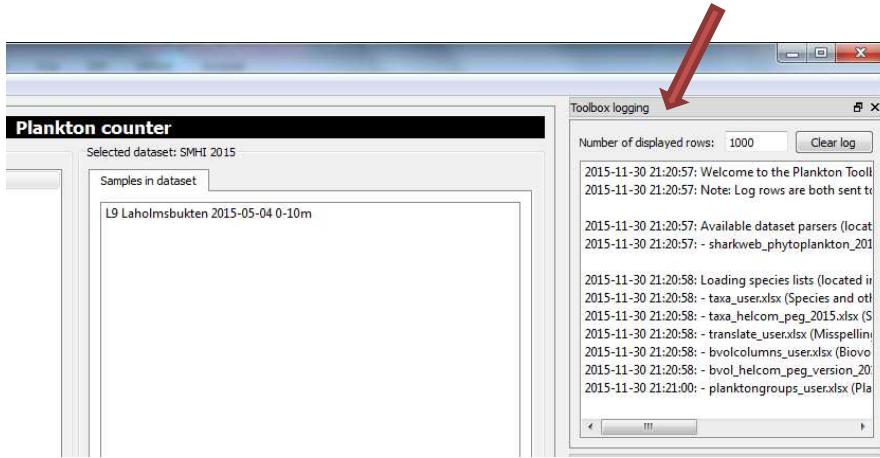
Main window pane with window pane *Toolbox logging* open



Main window with window pane *Graph plotter* open



Main window pane with *Graph plotter* in a separate window.

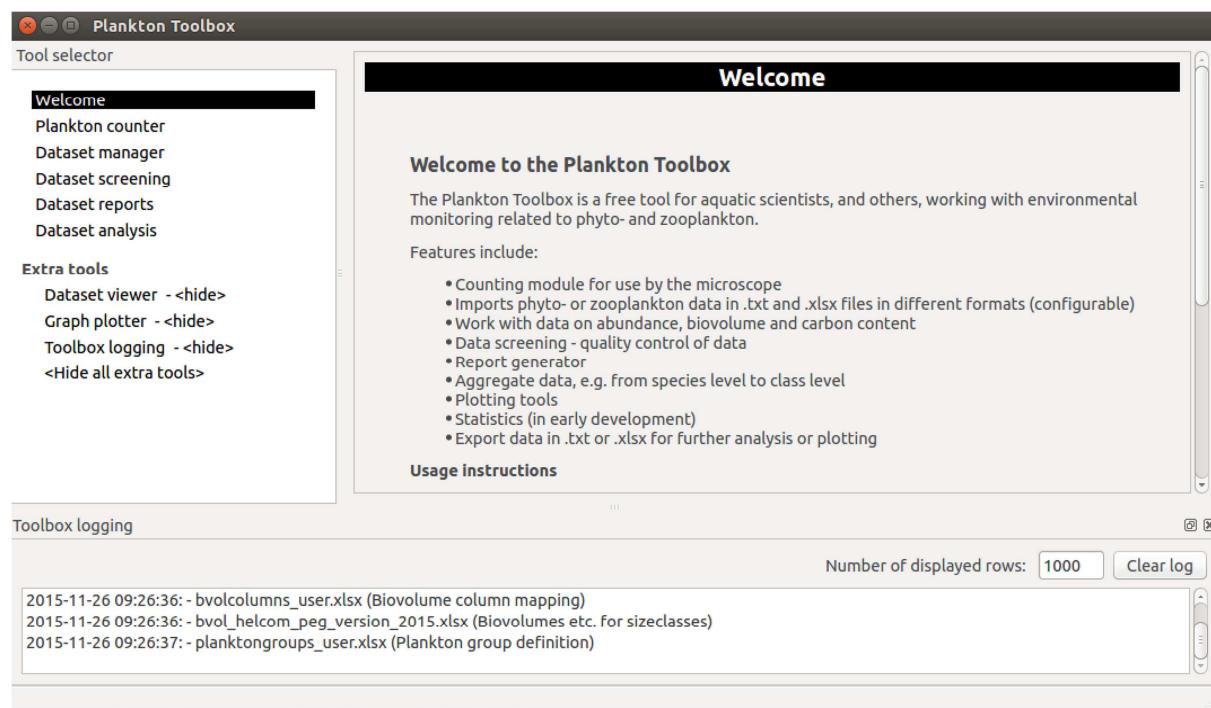


Tearing off the *Toolbox logging* window pane to a separate window



Docking the *Toolbox logging* window pane below the main window pane.

Welcome



The Plankton Toolbox welcome page. Text and links will guide you to useful information.

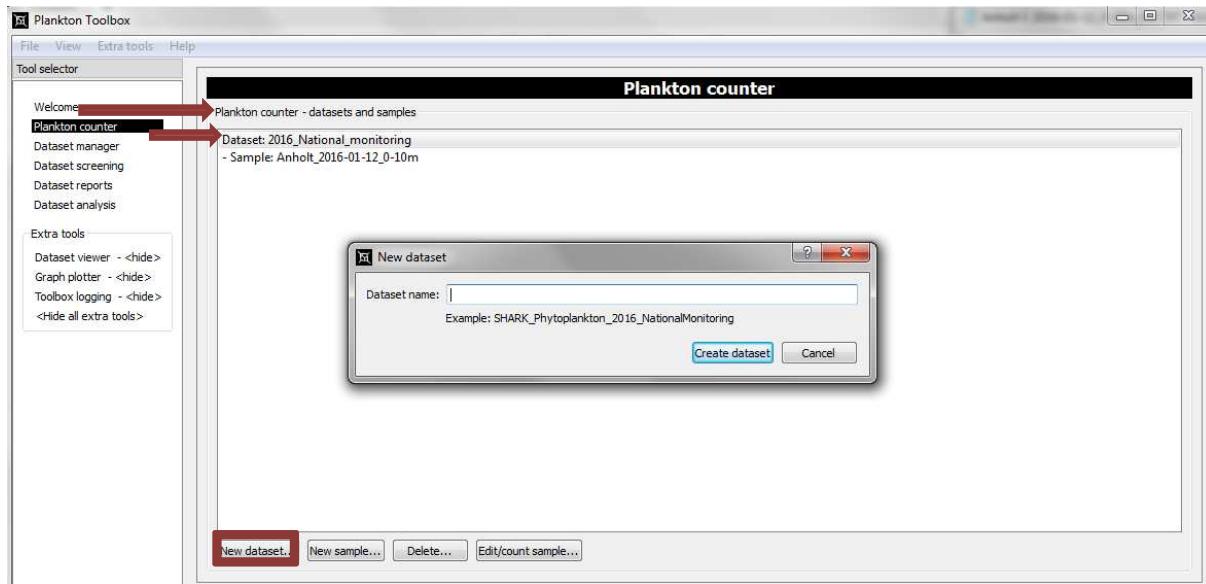
Getting started with Plankton counter

To get started counting a plankton sample you need the following information:

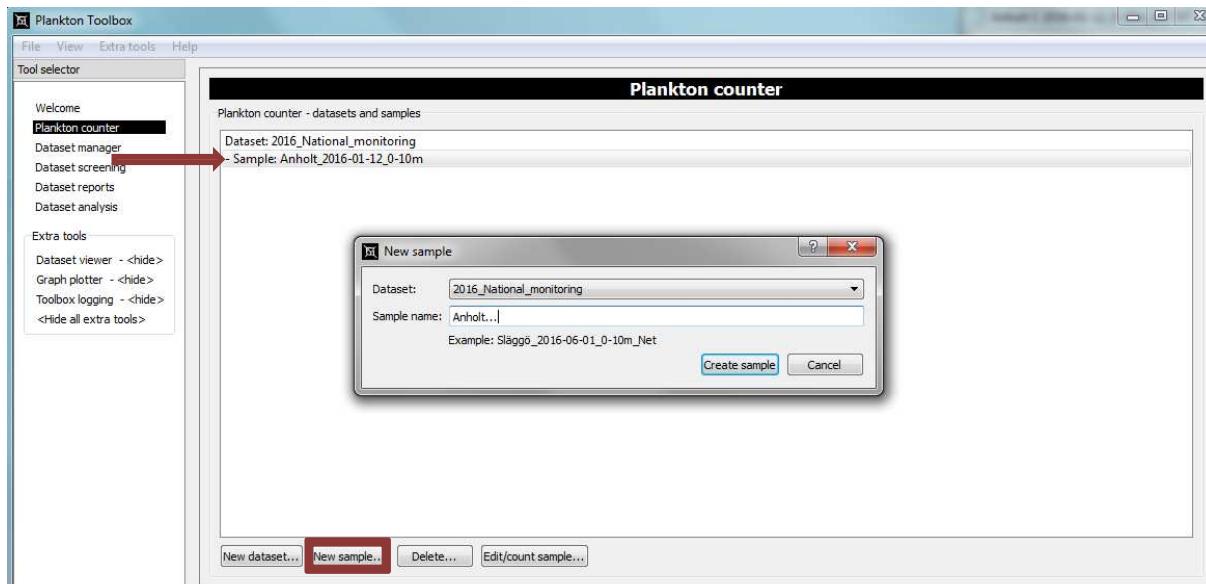
1. Meta data about the sample, where it was collected, when, how it was preserved etc.
 - a. You may want to save the data as a *template sample*
2. A list of taxa that you expect to find in the sample, A useful list for the Baltic Sea area is provided (see managing species lists for details)
3. Information on your counting device e.g.
 - a. Volume of sedimentation chamber or filtered volume, e.g. 20 mL
 - b. The diameter of sedimentation chamber or filtered area, e.g. 26 mm
4. Information on your microscope. You may need to use a stage micrometer (a small ruler) to check the diameter of the field of view in your microscope at a certain magnification. The information may look like this:
 - i. 5x objective xx mm
 - ii. 10x objective yy mm
 - iii. 20x objective zz mm
 - iv. 40x objective åå mm
 - v. 100x objective ää mm
5. Information on sample volume and the volume of preservative added is needed to calculate the dilution of the sample that is a result of adding preservative.
6. The next thing to do is to set up a *method* that suits your work. You may want to set up methods for different magnifications and for different counting styles. Some examples:
 - a. 5x whole chamber
 - b. 10x whole chamber
 - c. 20x transect counting (=counting diameters)
 - d. 40x transect counting (=counting diameters)
 - e. 100x field of view counting (useful for counting autotrophic picoplankton in the fluorescence microscope)
7. Start counting!

Plankton counter

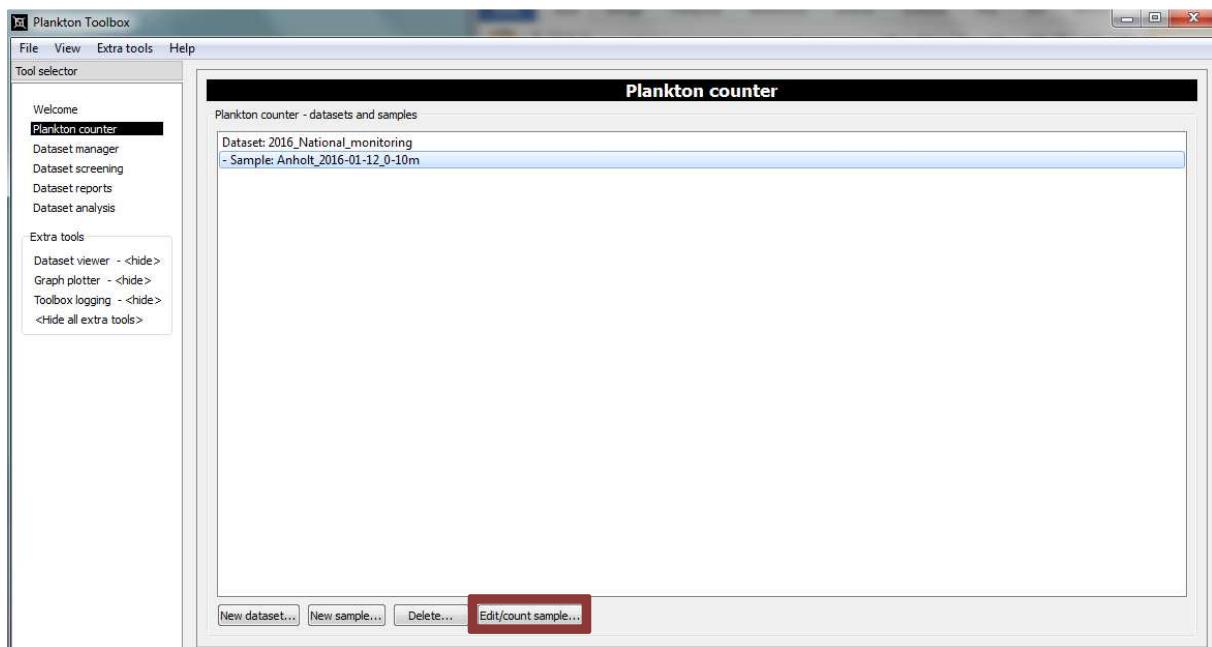
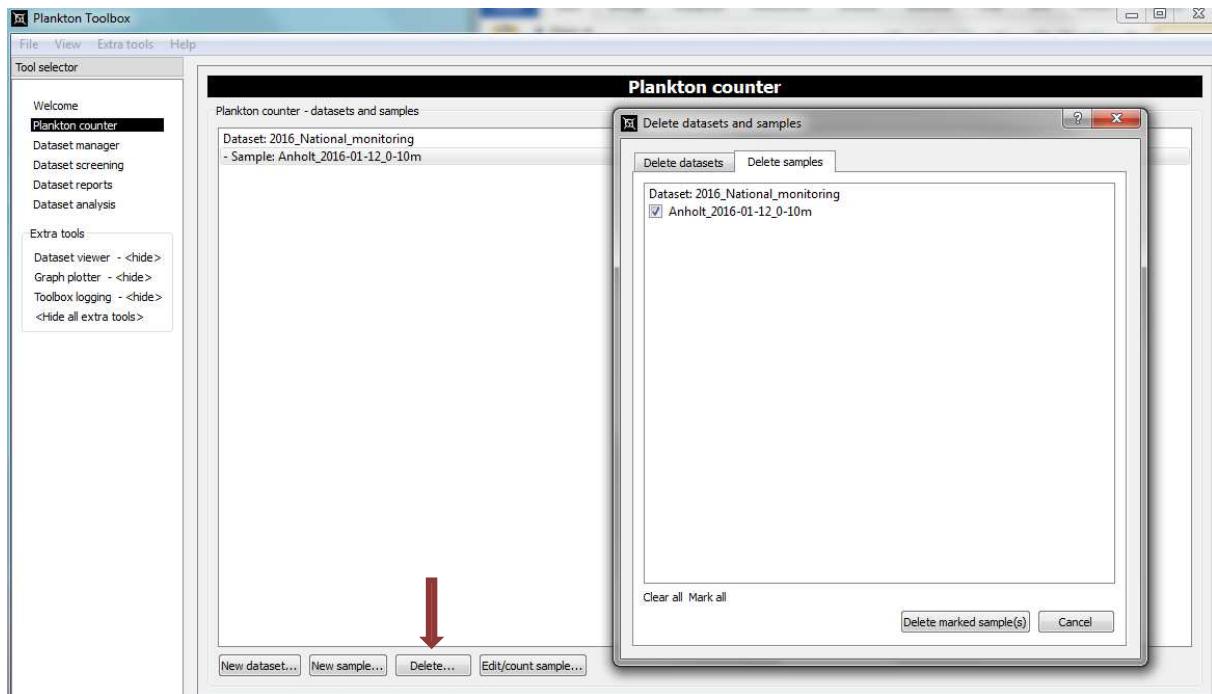
The plankton counter is a tool for counting zooplankton or phytoplankton samples. The module enables you to record your results while analysing.



Choose one of the existing Plankton counter datasets or create a new one by clicking **New dataset...** and naming the dataset. In the dataset several samples may be added (new samples are added by **New sample...**), so if you have a program for a whole year, you may add all stations, dates and depths analysed.



Delete incorrect or unwanted samples or datasets:



To enter an existing or new count, click the Edit/count button or double click the selected dataset.

Sample info

Dataset : 2016_National_monitoring Sample: Anholt_2016-01-12_0-10m

Sampling

Sample name: Anholt_2016-01-12_0-10m

Sample id:

Sampling: Year: 2016 Month: 01 Day: 12 Sampling time (UTC): hh:mm

ICES metadata: Year: 2016 Country code: 34 Platform code: 01 Series:

Project: BAS

Station name: Anholt E

Latitude, degree: 56 minute: 39.99 Longitude, degree: 12 minute: 7.0

Latitude, decimal: 56.6666 Longitude, decimal: 12.1167

Sampler type code: HOS (Hose)

Sample min depth (m): 0 Sample max depth (m): 10 Water depth (m): 55

Sampled volume (L): 6 →

Net sampling

Net type code:

Sampler area (m²): Mesh size (µm): Wire angle (deg): Tow length (m):

Analysis

Analysis laboratory: SMHI

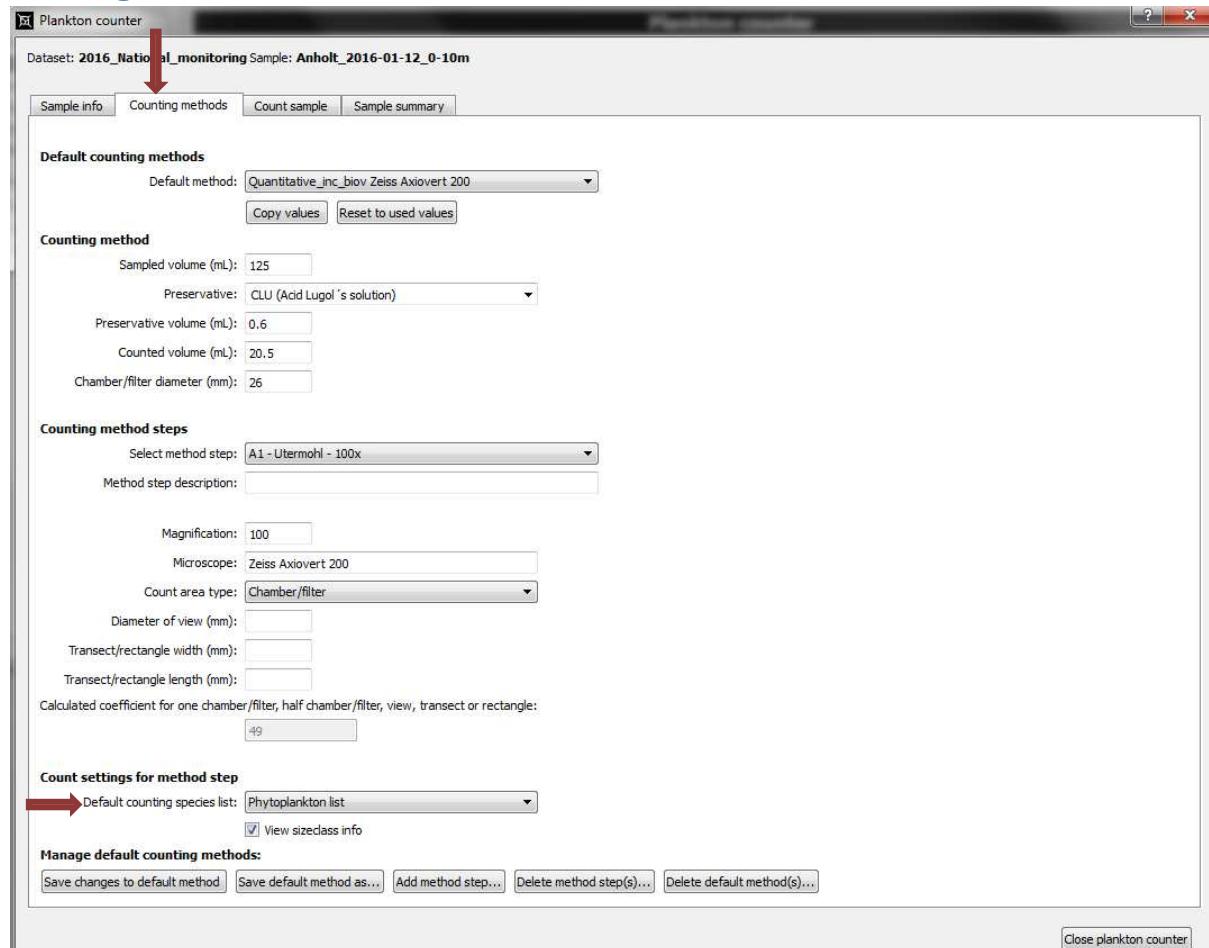
Analysis, Year: 2016 Month: 09 Day: 13

Analysed by: Marie Johansen

Comments: Chamber 20-9

Fill in all relevant info about this sample. If you have a template already, just click [Copy from sample...](#) and find the template from an earlier count/sample. The information is automatically saved and you can proceed to Counting methods. Sampled volume is the volume actually sampled with the hose. This volume is not used when calculating, it is only sampling information.

Counting methods



Fill in/choose the relevant info. Choose “Default method”, default lists are found/saved in the folder named counting_methods. Click **Copy values** to get the values from the chosen default method. If you are in the middle of a count and accidentally change some values, click **Reset to used values** and your values are back.

Existing defaults may be changed by clicking **Save changes to default method** and new defaults may be added by clicking **Save default method as...**. Choose species list for the count (Default counting species list), mark the “view sizeclass info” if this is an analysis including biovolumes. All cells may be filled in with information of your own choice, also the drop down menu.

Count sample

The screenshot shows the 'Plankton counter' application window. The 'Count sample' tab is active. In the center, there's a 'Summary' section with a table of counted species. To the right is a 'Species lists' panel containing a large table of species with columns for scientific name, size class, cells, trophic type, and size info. A red arrow points from the 'Count sample' tab to the 'Species lists' panel.

Scientific name	Size class	Cells	Trophic type	Size info
Alexandrium [3]: 5	1	1	MX	Range: 28-32, L1: 30, D1: 21, D2: 15
Dinophysis acuminata	2	1	MX	Range: 33-37, L1: 35, D1: 25, D2: 1...
Ceratium fusus [2]: 4	3	1	MX	Range: 38-42, L1: 40, D1: 39, D2: 20
Coscinodiscus concinnus [1]: 3	4	1	MX	Range: 43-47, L1: 45, D1: 32, D2: 2...
Dinophysis acuminata [3]: 4	5	1	MX	Range: 48-52, L1: 50, D1: 36, D2: 25
Dinophysis acuminata [4]: 2	6	1	MX	Range: 53-57, L1: 55, D1: 40, D2: 2...
Dinophysis acuta	1	1	MX	Range: 55-57, L1: 56, D1: 41, D2: 28
Dinophysis acuta	2	1	MX	Range: 58-60, L1: 59, D1: 43, D2: 2...
Dinophysis acuta	3	1	MX	Range: 61-65, L1: 63, D1: 46, D2: 2...
614 Dinophysis acuta	4	1	MX	Range: 75, L1: 75, D1: 55, D2: 75
Dinophysis acuta	5	1	MX	Range: 85, L1: 85, D1: 62, D2: 42.5
Dinophysis dens	1	1	MX	Range: 45-50, L1: 48, D1: 28, D2: 1...
Dinophysis norvegica	1	1	MX	Range: 49-50, L1: 45, D1: 31, D2: 2...
Dinophysis norvegica	2	1	MX	Range: 50-60, L1: 55, D1: 37, D2: 2...
Dinophysis norvegica	3	1	MX	Range: 60-70, L1: 65, D1: 44, D2: 3...
Dinophysis norvegica	4	1	MX	Range: 70-80, L1: 75, D1: 51, D2: 3...
Dinophysis odiosa	1	1	HT	Range: 40-70, L1: 55, D1: 36, D2: 2...
Dinophysis tripos	1	1	MX	Range: 75, L1: 75, D1: 40, D2: 24
Dinophysis	1	1	MX	Range: 15-20, L1: 18, D1: 12.6, D2:...
Dinophysis	2	1	MX	Range: 20-25, L1: 23, D1: 16.1, D2:...
Dinophysis	3	1	MX	Range: 25-30, L1: 28, D1: 19.6, D2:...
Dinophysis	4	1	MX	Range: 30-40, L1: 35, D1: 24.5, D2:...
Dinophysis	5	1	MX	Range: 40-45, L1: 43, D1: 30.1, D2:...
Dinophysis	6	1	MX	Range: 45-50, L1: 48, D1: 33.6, D2:...
Dinophysis	7	1	MX	Range: 50-60, L1: 55, D1: 38.5, D2:...
1261 Dinophyceae	1	1	AU	Range: <10, D1: 10
1262 Dinophyceae	2	1	AU	Range: 10-15, D1: 12.5
1263 Dinophyceae	3	1	AU	Range: 15-20, D1: 17.5
1264 Dinophyceae	4	1	AU	Range: 20-25, D1: 22.5
1265 Dinophyceae	5	1	AU	Range: 25-30, D1: 27.5
1266 Dinophyceae	6	1	AU	Range: 40, D1: 40
1267 Dinophyceae	7	1	AU	Range: 40-45, D1: 45

Now you can start your count. Select species list. Find the species you want to count in the species list (right column). Count by clicking the space bar or by marking the buttons on the screen. The species you count end up in the left column, where you can mark species already in the existing count. You can also save the left hand list as a template for later counts. If you want to create a counting species list before you start, you can create a .txt-file and save it in the following folder:

Plankton Toolbox -> toolbox_data\plankton_counter\config\counting_species_lists

Sample summary

Dataset: 2016_National_monitoring Sample: Anholt_2016-01-22_0-10m

scientific_full_name	taxon_class	scientific_name	trophic_type	size_class	unit_type	counted_units	coefficient	abundance_units/l	volume_ml/m3	carbon_ugc/m3	volume_um3/unit	carbon_pg/unit	variable_comment	species_flag_c
1 Alexandrium	Dinophyceae	Alexandrium	AU	3	cell	5	49	245.0	4.066	485.6	16000.0	1982.0		
2 Ceratium fusus	Dinophyceae	Ceratium fusus	AU	2	cell	4	49	196.0	4.66	544.3	23770.0	2777.0		
3 Coscinodiscus concinnus	Bacillariophyceae	Coscinodiscus concinnus	AU	1	cell	3	49	147.0	158.3	3303.0	1077000.0	22470.0		
4 Dinophysis acuminata	Dinophyceae	Dinophysis acuminata	MX	3	cell	4	49	196.0	2.38	289.7	12140.0	1478.0		
5 Dinophysis acuta	Dinophyceae	Dinophysis acuta	MX	4	cell	2	49	98.0	7.933	860.0	80950.0	8776.0		

Export sample (.xlsx)... Save edited changes Close plankton counter

In the sample summary you get an overview of your count. If you detect mistakes you may change species or delete entire posts. Click [Export sample \(.xlsx\)...](#) and save your results wherever suitable.

Dataset manager

The Plankton Toolbox offers a dataset manager where you can import data from different sources to manipulate in several ways.

File View Extra tools Help

Tool selector

- Welcome
- Plankton counter
- Dataset manager**
- Dataset screening
- Dataset reports
- Dataset analysis
- Extra tools
 - Dataset viewer - <hide>
 - Graph plotter - <hide>
 - Toolbox logging - <hide>
 - <Hide all extra tools>

Dataset manager

Import datasets/datafiles

Predefined formats Plankton counter datasets Parsers - Text file (*.txt) Parsers - Excel files (*.xlsx)

Select parser: sharkweb_phytoplankton_2015-11-05.xlsx

Select import column: SHARKweb (internal names)

Select export column: Export (internal names)

Import dataset(s)...

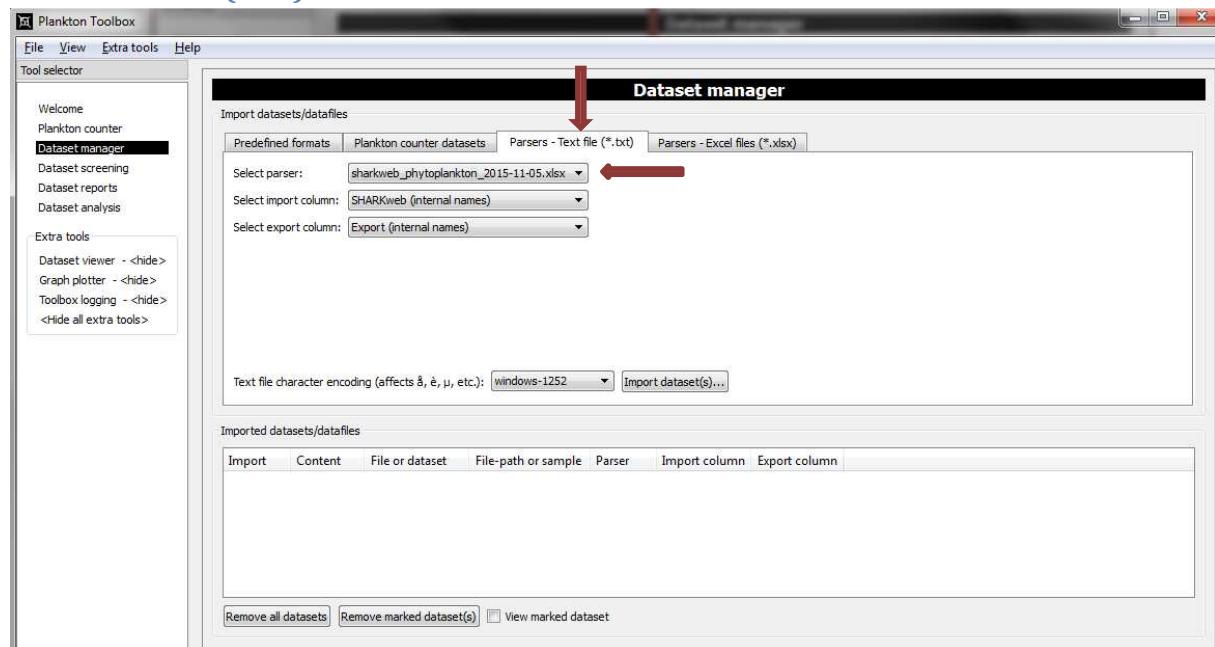
Imported datasets/datafiles

Import Content File or dataset File-path or sample Parser Import column Export column

Remove all datasets Remove marked dataset(s) View marked dataset

Plankton Toolbox imports data in text (txt) and Microsoft Excel (xlsx) files in different formats. Since data formatting differs depending on the source of the data, importing formats are configurable by the user through parsers. A useful function is that data from different sources, in different formats, can be combined by importing multiple files. The data can then be exported as one consistent dataset in txt or xlsx format by the user.

Data files - Text(*.txt)



To work with text- or Excel files you may need a custom-made parser which SMHI can help you with. In the text files tab you can for instance manage data downloaded from the Sharkweb, <http://www.smhi.se/klimatdata/oceanografi/havsmiljodata/marina-miljovervakningsdata>, unfortunately only available in Swedish.

When downloading from the Sharkweb, make sure you choose “internt namn” (internal name), then click “sök” (search).

RESULTAT PROVER OCH MÄTVÄRDEN (Rad 1 till 2000 av 14542 visas) [Nästa sida](#)

	datatype	visit_year	visit_date	station_name	reported_station_name	water_depth_m	latitude_dm	longitude_dm	location_id	lat
1	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
2	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
3	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
4	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
5	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
6	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
7	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
8	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
9	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
10	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.
11	Phytoplankton	2014	2014-12-09	SLÄGGÖ	SLÄGGÖ	62	58 15.4980	11 25.9980	N58.2583 E11.4333	58.

[Rensa resultat](#)**DIVERSE**

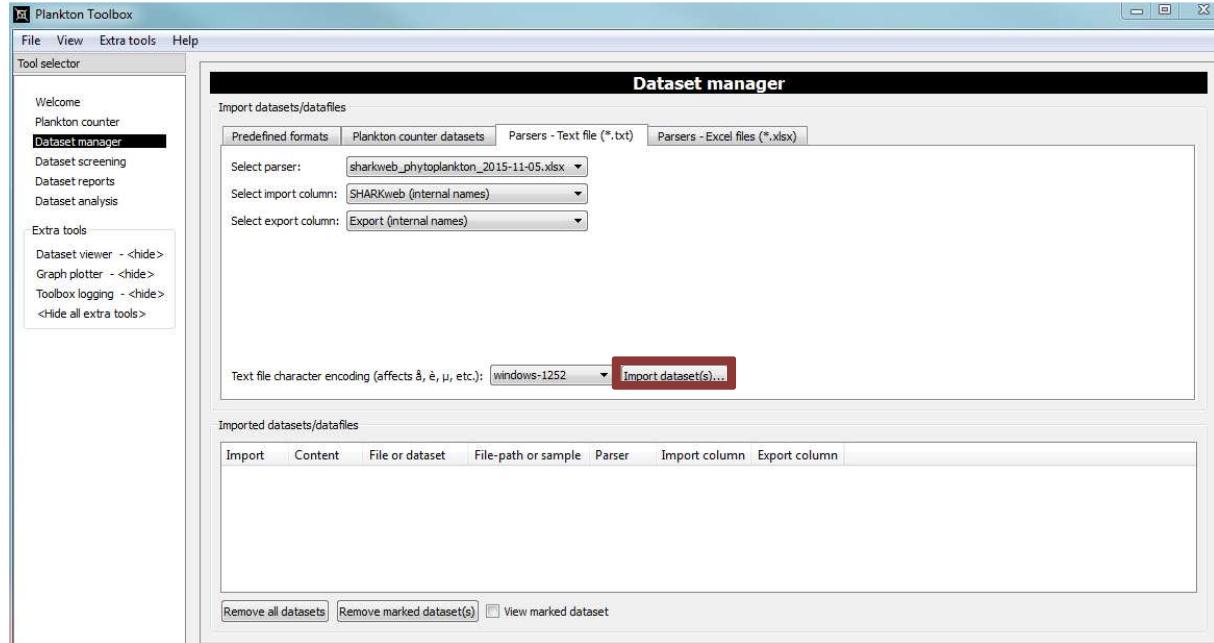
Ladda ner data Allmänna inställningar

Decimal/fält-avgränsare: Punkt/tabb ✓ Radbrytning: Windows ✓ Teckenkodning: Windows-1252 ✓

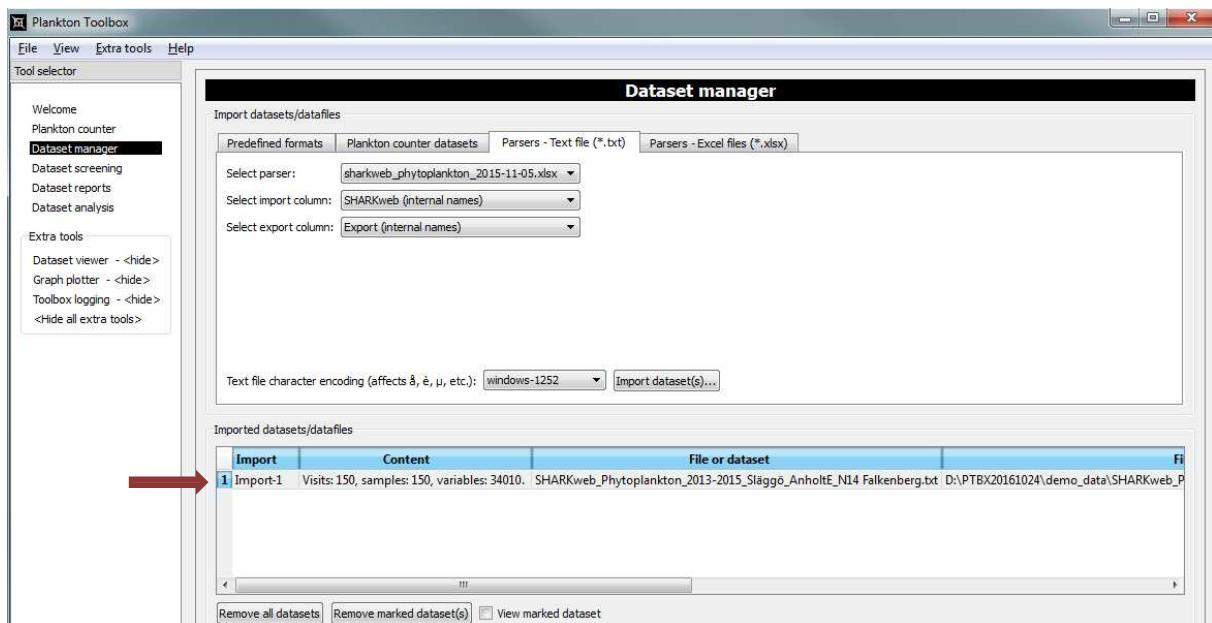
Villkor för nerladdning Jag accepterar villkoren

[Ladda ner data](#)

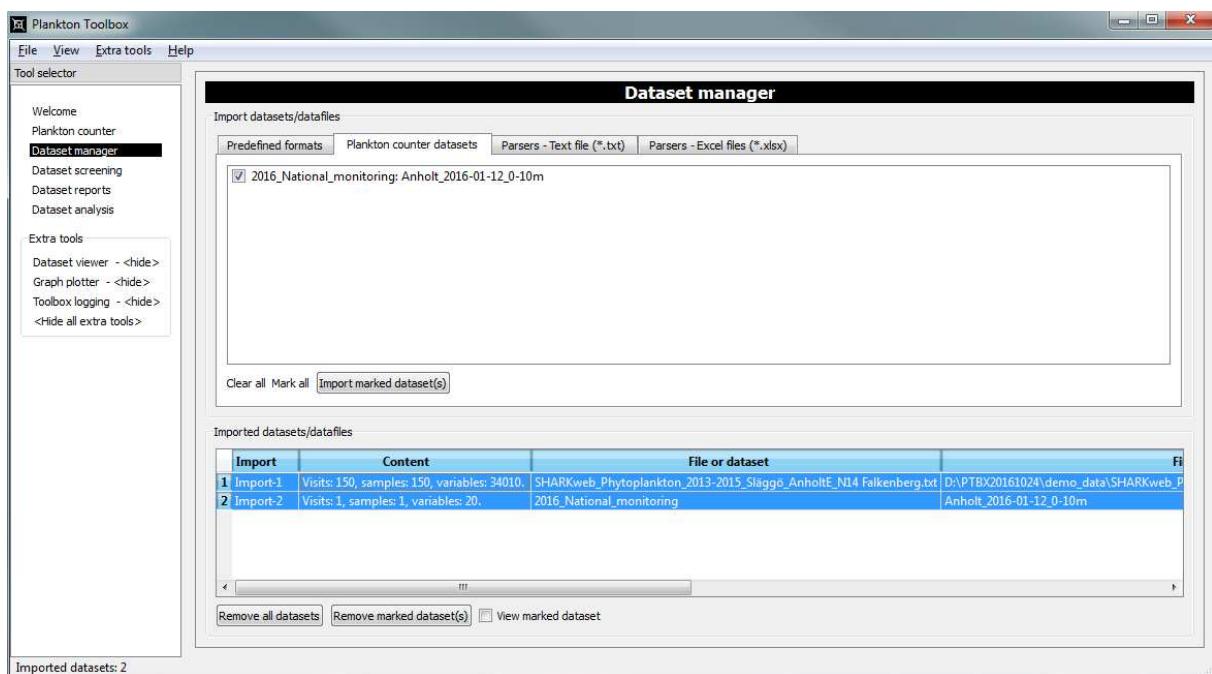
The results will appear, accept the downloading terms (jag accepterar villkoren), and click “ladda ner data” (download). Now your data is ready for the data manager.



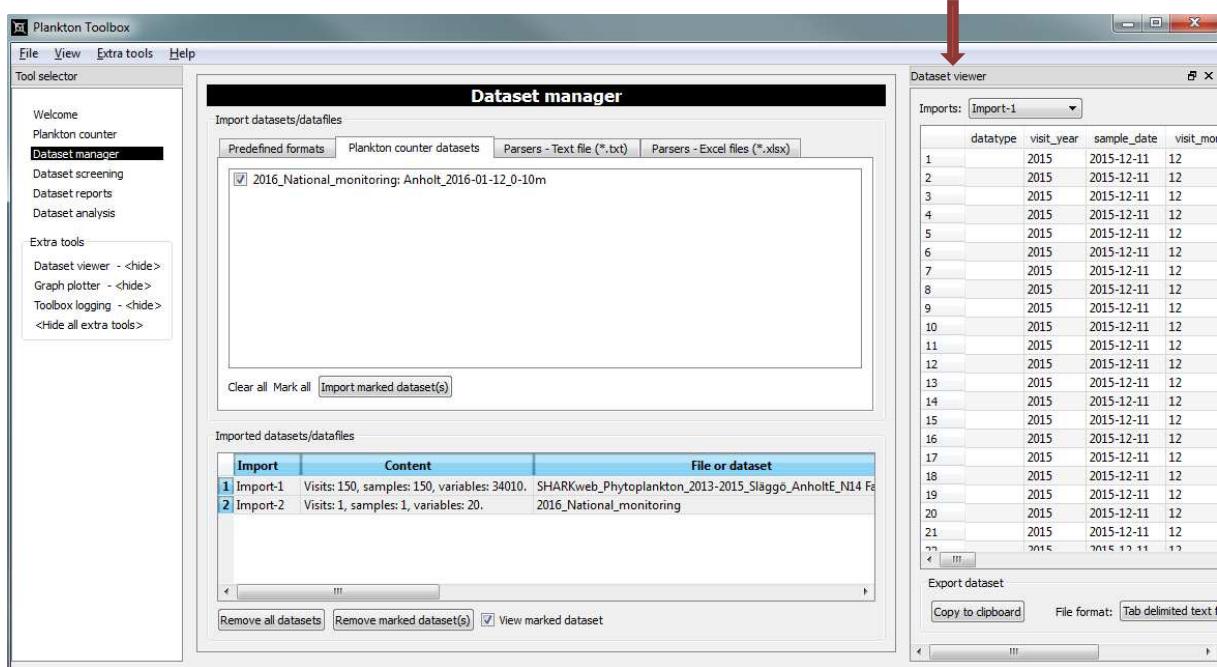
Click the import dataset(s) to browse for the data file(s) that you want to work with.



You may add files with other formats, for example from the plankton counter:



Mark the data file and if you want a quick look, tick “view marked dataset”, then a window with the data will appear:

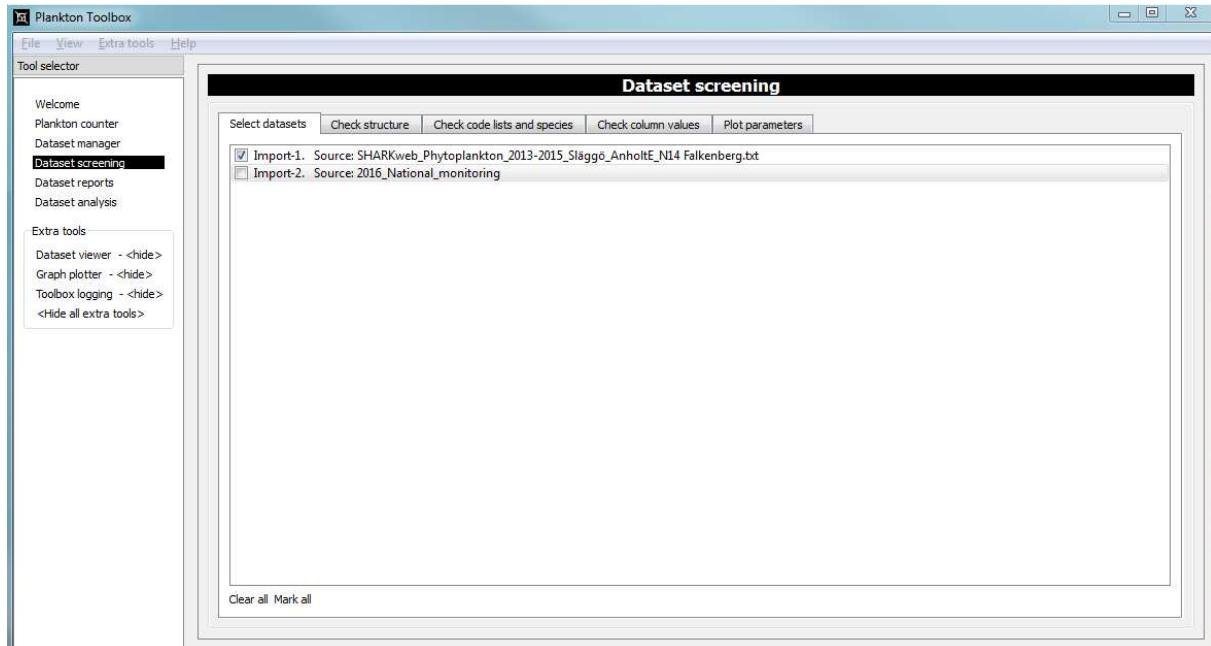


In the viewer, the data shows up, if it is satisfying already, choose file format and save. To hide the viewer, click <hide> in the Extra tools or just click the x in the upper right corner. For further analysis, go to Dataset analysis.

Dataset screening

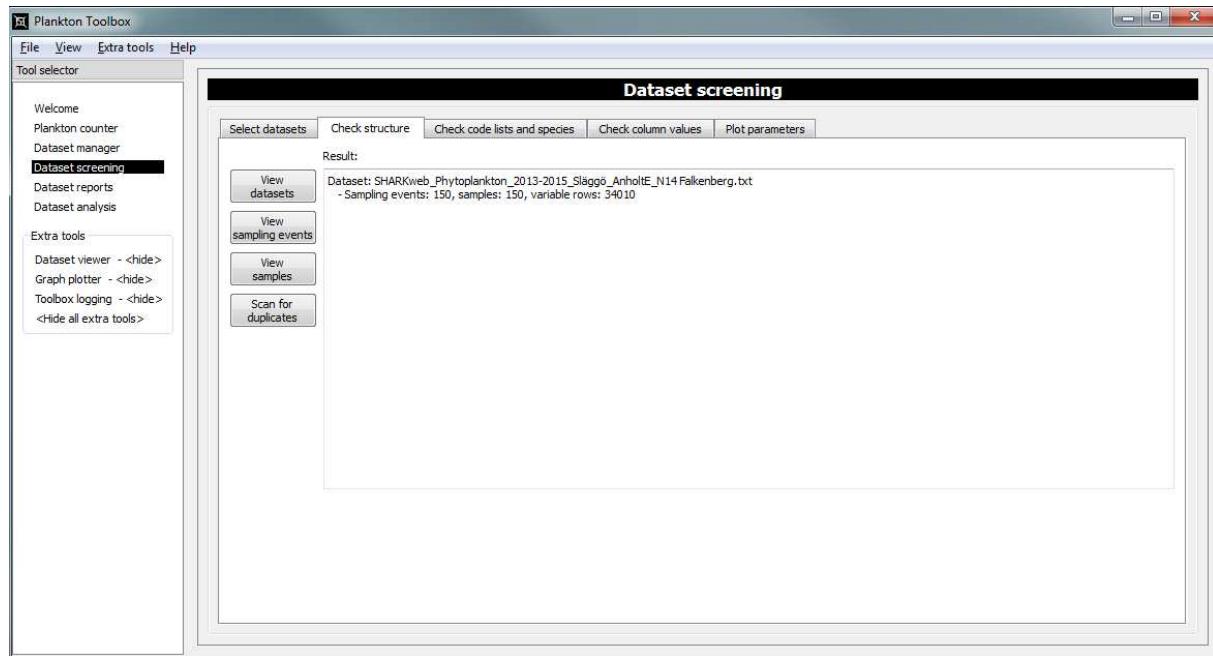
When the data has been imported the raw data can be screened in different ways to check for duplicate data, look for unrealistic dates, positions etc. There are also plotting tools to visualize the raw data.

Select datasets



The dataset(s) imported in the data manager can be screened here, mark the one(s) to be screened.

Check structure



Check the data structure and also get a quality check by clicking

View samples

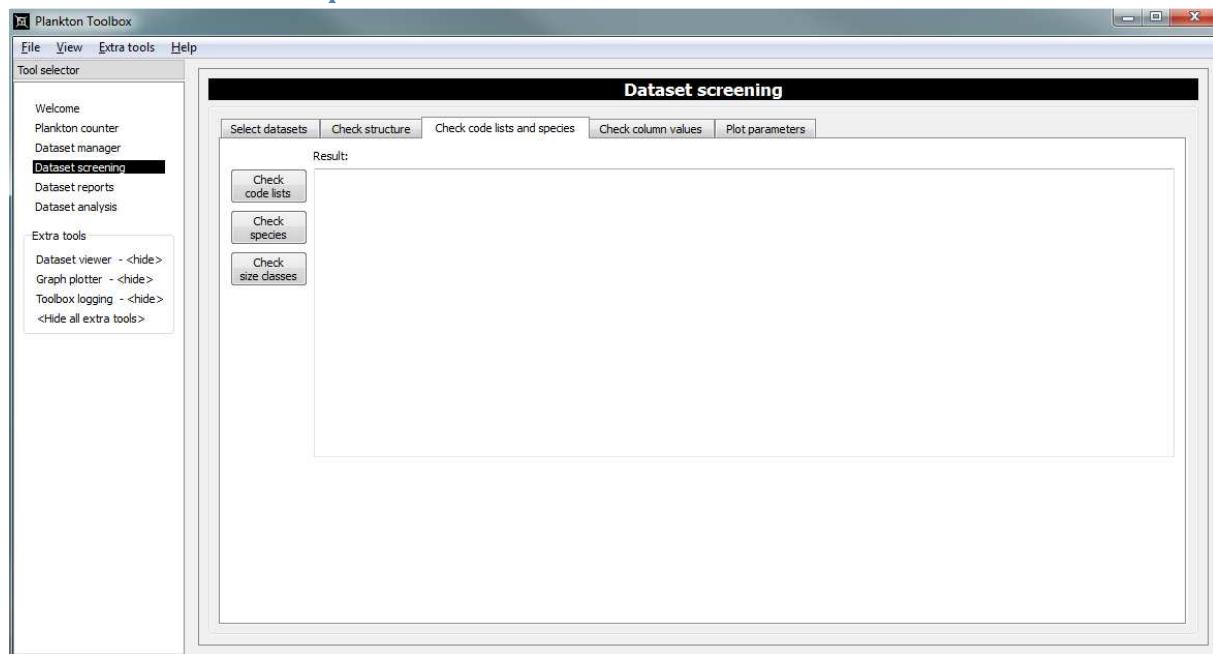
and

Scan for duplicates

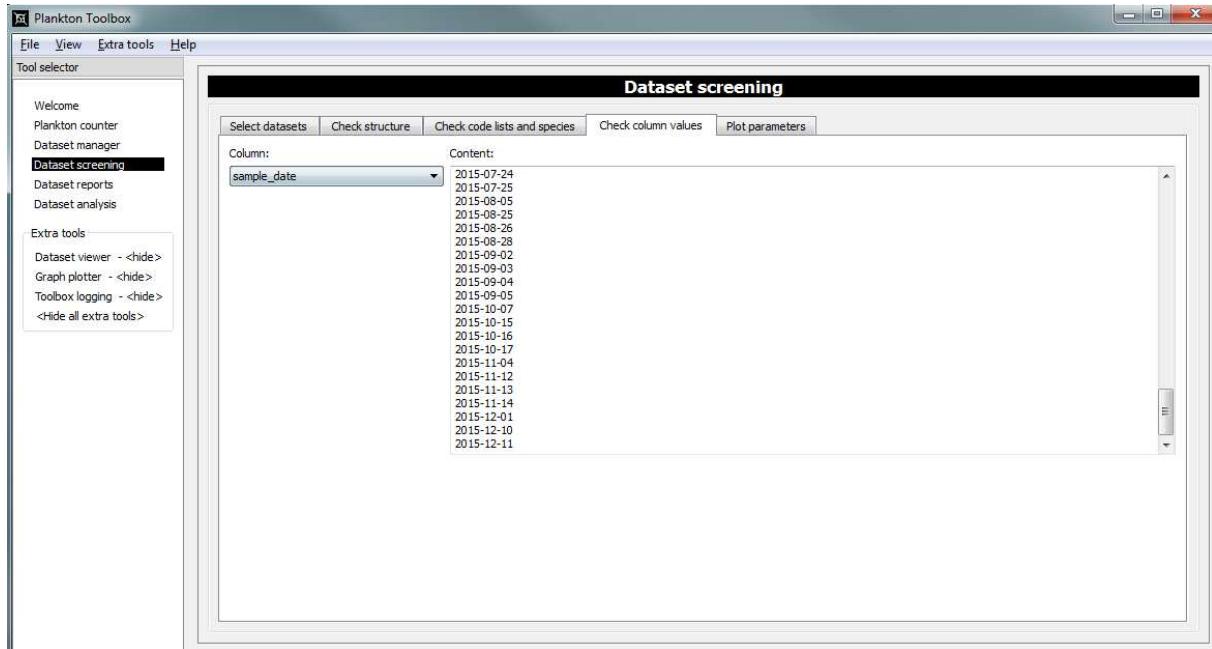
View datasets

View sampling events

Check code list and samples

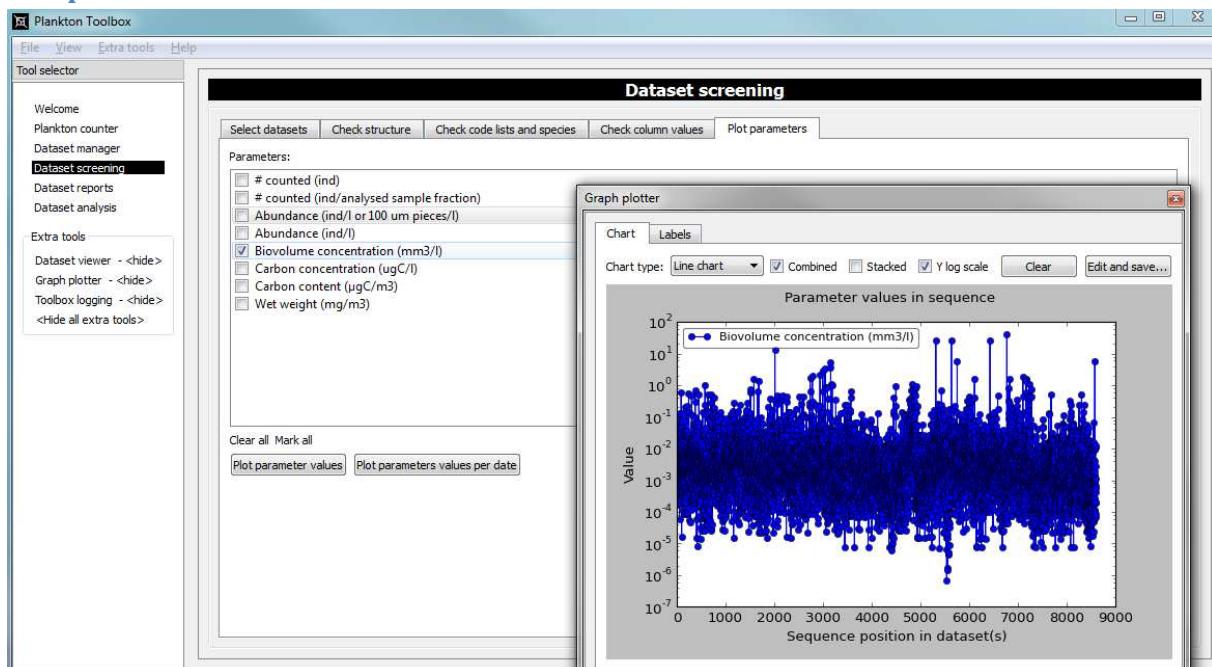


Check column values



Each column may be marked in the drop down menu and checked.

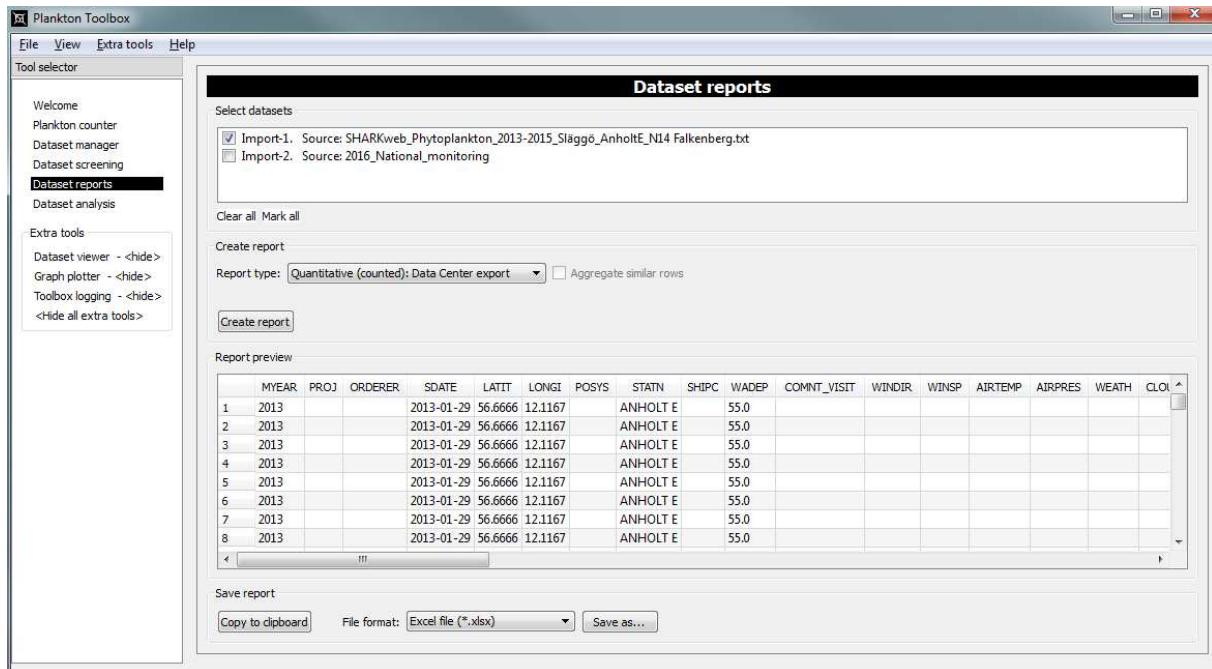
Plot parameters



Mark the parameter(s) you want to plot and click either [Plot parameter values](#) or

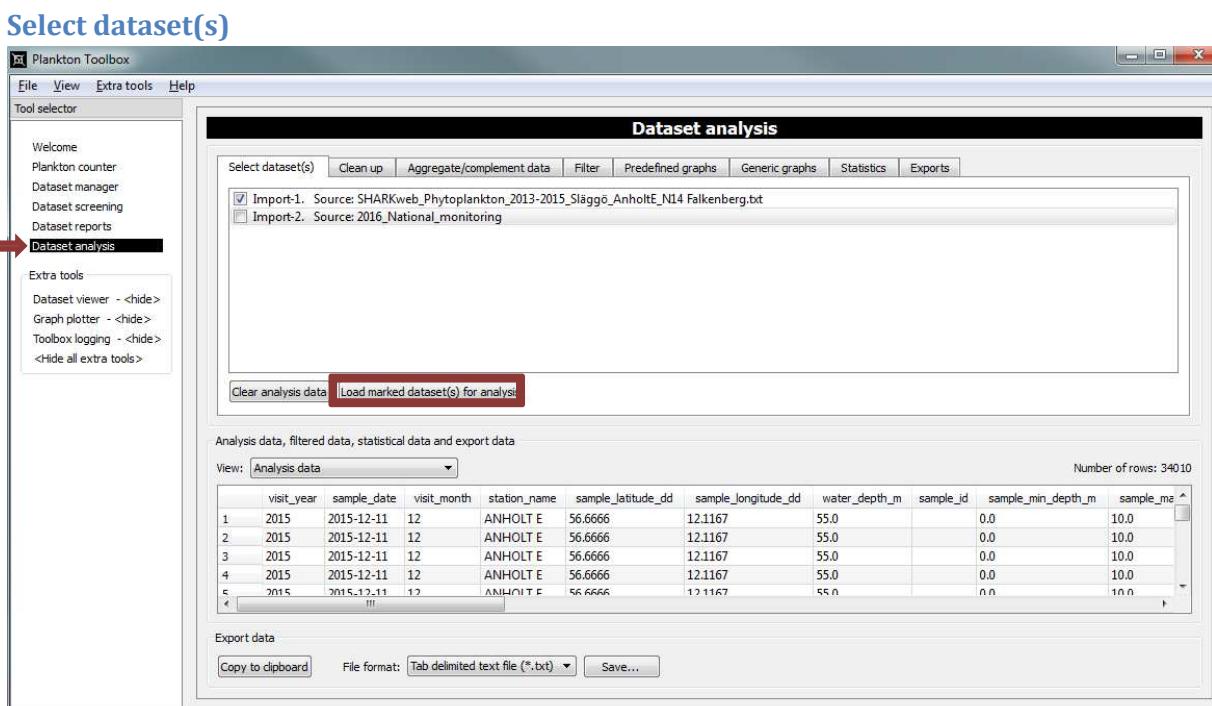
[Plot parameters values per date](#)

Dataset reports



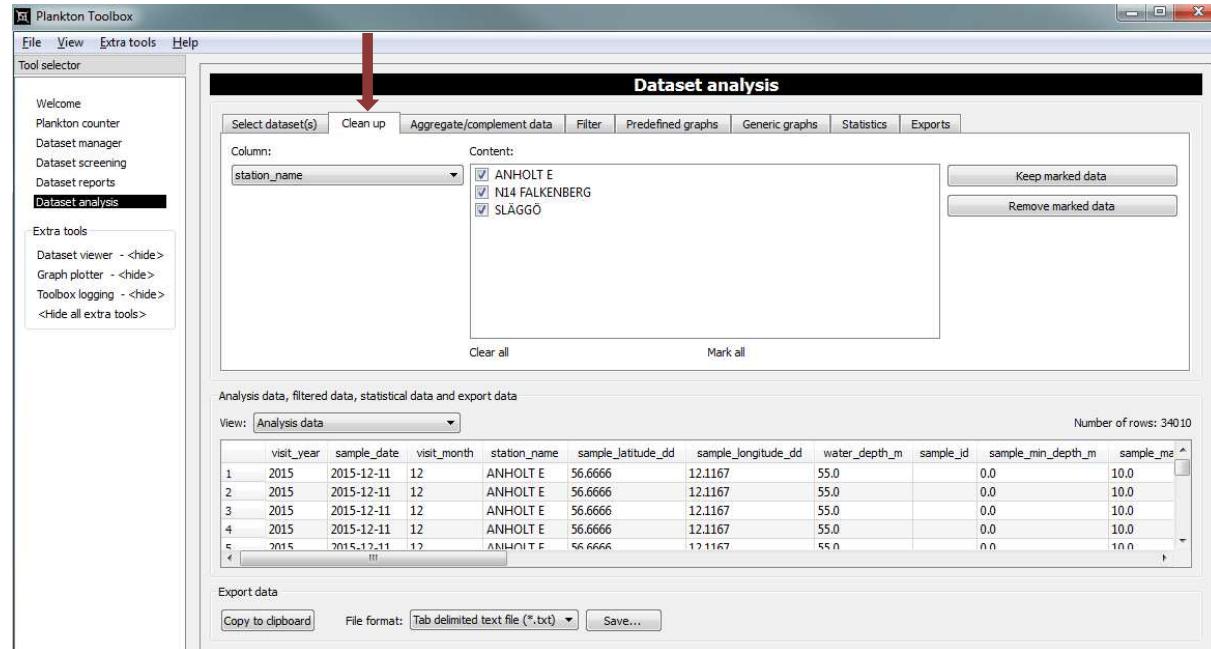
A handy way to format a dataset into a data report for delivery, for instance for data host reporting format.

Dataset analysis



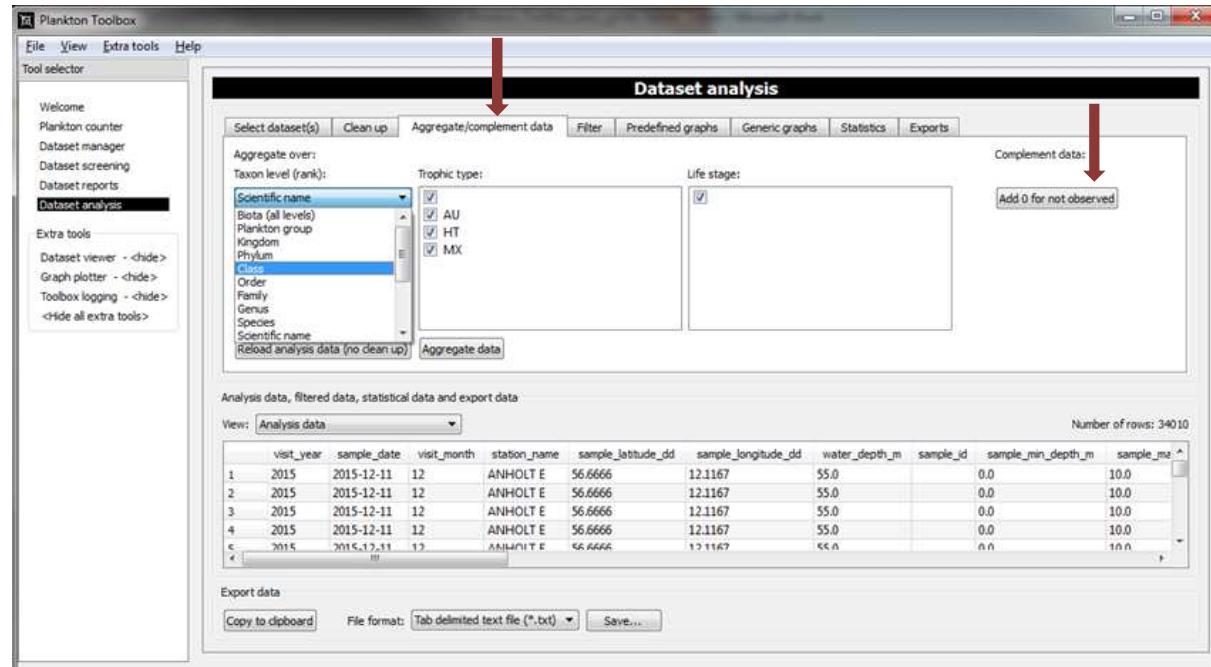
To analyse data, click Load marked dataset(s) for analysis, and the data will appear in the lower window. Observe that the data at any time can be saved in two different ways, either by clicking **Copy to clipboard** or **Save...**, remember to choose format.

Clean up



In the “clean up” step you can remove data you do not need, like certain dates, stations, depths, trophic types etc.

Aggregate/complement data



At this step data can be aggregated to different taxonomic levels, e.g. from species level to class level. Here also a function for adding zeros for organisms that are found in some but not all samples, is found. The software looks through all the sampling locations, dates and depths, creates a complete

list of taxa observed in all the samples in the dataset, and adds zeros in abundance for taxa that were not observed in certain samples.

Filter

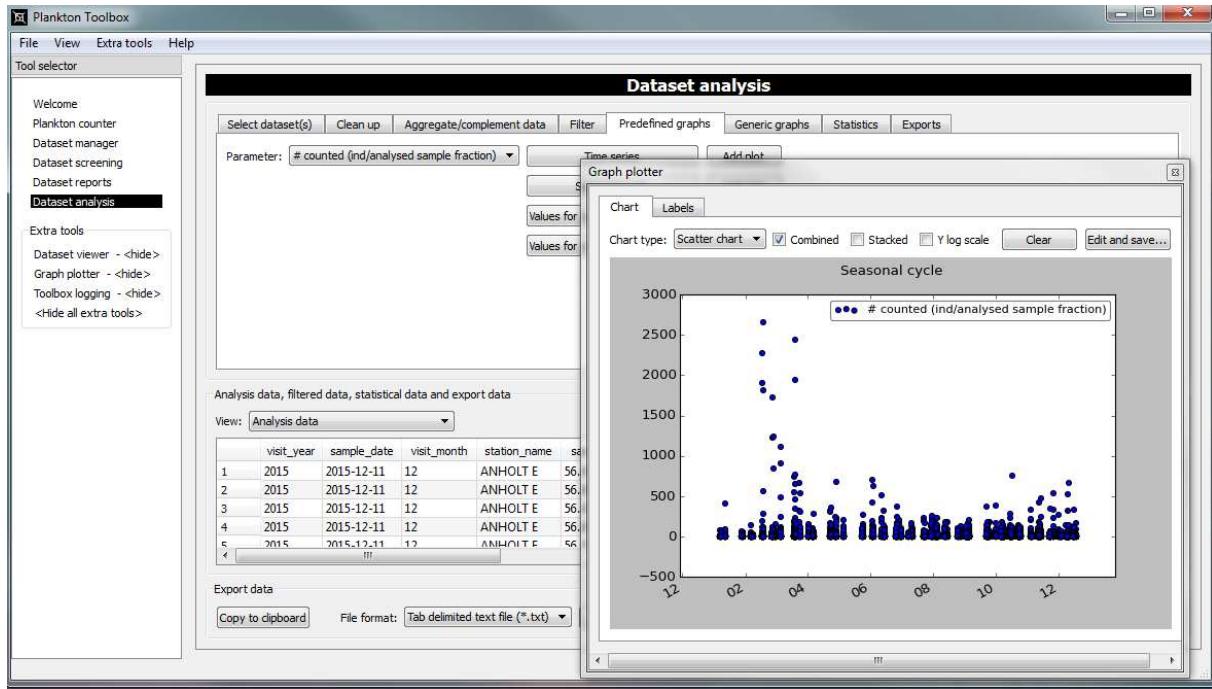
The screenshot shows the 'Dataset analysis' interface. The 'Tool selector' on the left has 'Dataset analysis' selected. The main area has a 'Filter' tab selected. It includes sections for 'Select dataset(s)', 'Clean up', 'Aggregate/complement data', 'Predefined graphs', 'Generic graphs', 'Statistics', and 'Exports'. Below these are dropdowns for 'Date from' (2013-01-08), 'Stations' (ANHOLT E, N14 FALKENBERG, SLÄGGÖ), 'Sampling months' (01-10), 'Sampling events' (ANHOLT E: 2-10), 'Min-max depth' (0.0-10.0), 'Scientific name' (Akashiwo sanguinea, Alexandrium, Amphidinium, Anabaena, Apedinella rana, Anhanzomerus), 'Trophic type' (AU, HT, MX), and 'Life stage'. Buttons for 'Clear all' and 'Mark all' are present. Below this is a table view of 'Analysis data' with 34010 rows. At the bottom are 'Copy to clipboard', 'File format: Tab delimited text file (*.txt)', and 'Save...' buttons.

Here you can filter your data further, for example to exclude certain species or months.

Predefined graphs

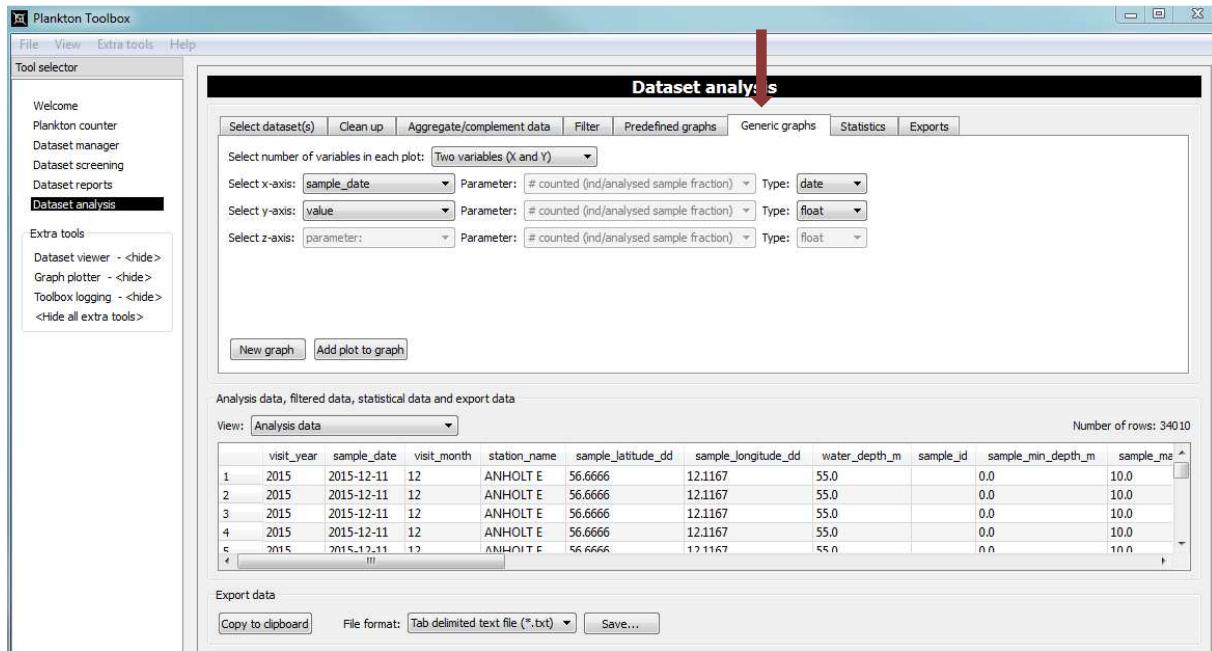
The screenshot shows the 'Dataset analysis' interface. The 'Tool selector' on the left has 'Dataset analysis' selected. The main area has a 'Predefined graphs' tab selected. It includes sections for 'Select dataset(s)', 'Clean up', 'Aggregate/complement data', 'Filter', 'Predefined graphs', 'Generic graphs', 'Statistics', and 'Exports'. Below these are dropdowns for 'Parameter' (# counted (ind/analysed sample fraction)), 'Time series' (Add plot), 'Seasonal cycle' (Add plot), 'Values for taxa / station and date', and 'Values for station and date / taxa'. Below this is a table view of 'Analysis data' with 34010 rows. At the bottom are 'Copy to clipboard', 'File format: Tab delimited text file (*.txt)', and 'Save...' buttons.

A few graphs are available for quality control and such. With the Extra tools in the left margin you can easily view/hide the dataset, graphs or loggings. The current aim of the plotting tools is to give the user the ability to produce fairly simple graphs. For publication quality output it is often necessary to export the data and to use some graphical software package.



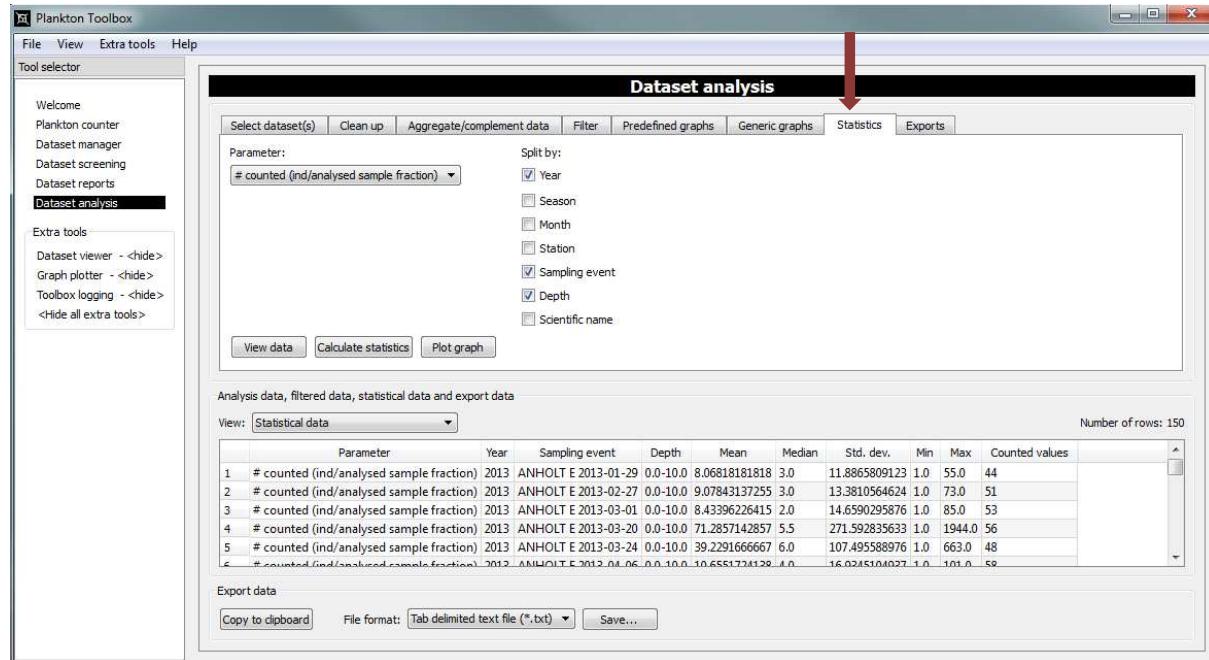
A seasonal cycle is one of the predefined graphs.

Generic graphs



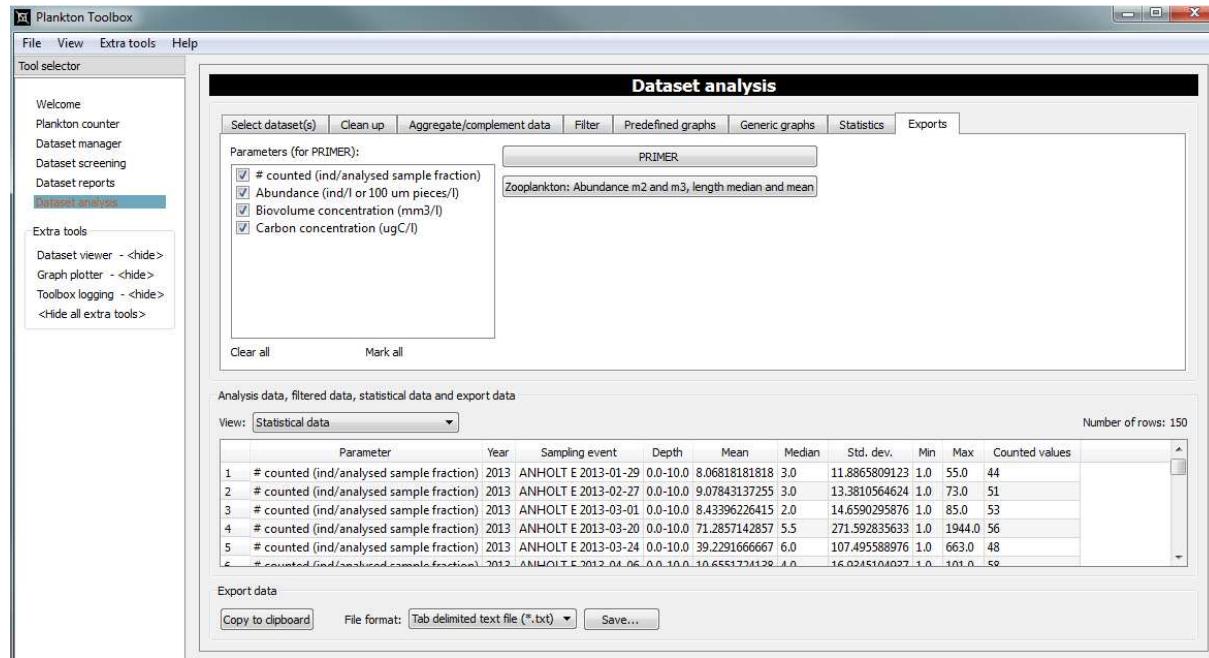
This tab offers more options in generating graphs.

Statistics



Simple statistics may be performed and plotted. This part is planned to be developed further in future releases of the software.

Exports



Arranges the data in for example PRIMER format, a statistical tool specialized for biological data.

At most steps in the data processing data can be copied to the clipboard and pasted into other software running on the computer used. Data may also be exported in txt or xlsx formats for further analyses or plotting using other software.

Managing counting lists

When you count a sample you may click on *Save counting species list as* and save a list of the taxa and size classes you may want to re-use in the future. The counting list will show up in the drop down window to the left in the counting window pane. Keep in mind that the counting lists for counting samples always are subsets of the larger species lists. The subsets are found in the folder:

Plankton Toolbox -> toolbox_data\plankton_counter\config\counting_species_lists

You may change these lists as you please but make sure that you only include taxa and size groups that are found in the general species lists (see separate section on this topic).

Managing general species lists

Plankton Toolbox provides species lists based on the HELCOM-PEG groups lists. You may also use other lists or create your own. Keep in mind that you need to include all organisms found in your sample or your data set in the species lists. Organisms missing in the taxonomic hierarchy will not be included when data is aggregated to different taxonomic levels.

The files with the species list and lists on taxonomic hierarchy are found in the folder Plankton Toolbox -> toolbox_data\species

The lists are imported into Plankton Toolbox when the software is started.

Important lists

1. A list of taxa that you expect to find in the samples you analyze or in the dataset you work with
 - a. The HELCOM-PEG 2016 list is provided. It includes a list of taxa, trophic type, cell shape, cell volume, carbon content per cell etc.
 - b. An amendment to the list focusing on organisms in the Kattegat-Skagerrak may also be included.
 - c. You may add taxa in the file taxa_user.xlsx file. Always include information on taxonomic hierarchy, e.g. rank and the name of the taxon higher in the taxonomic hierarchy.
2. To be able to aggregate data to different taxonomic levels a taxonomic hierarchy is needed
 - a. In the HELCOM-PEG 2016 list the following taxonomic levels are provided:
 - i. Division
 - ii. Class
 - iii. Order
 - iv. Scientific name (most often species)
 - b. In the Nordic Microalgae list (it will be added at a later stage) the following taxonomic levels are provided:
 - i. Biota
 - ii. Phylum
 - iii. Class
 - iv. Order
 - v. Genus
 - vi. Species
 - vii. Subspecies or Variety or Forma
 - c. In the list taxa_user.xlsx you may add new taxa with information on taxonomic hierarchy
3. A list defining synonyms and translations from misspelled to correct names is also provided. The file name is translate_user.xlsx.

Keep in mind that the counting lists always are subsets of the larger general species lists. The subsets are found in the folder:

Plankton Toolbox -> toolbox_data\plankton_counter\config\counting_species_lists.

Plankton Toolbox

Getting started on Mac

The first time you run Plankton Toolbox on a Mac you need to change some settings. Fortunately you need to carry out the process only once.

This tutorial applies to MacOS X 10.11.1, El Capitan. In general it is applicable also to other versions of MacOS.

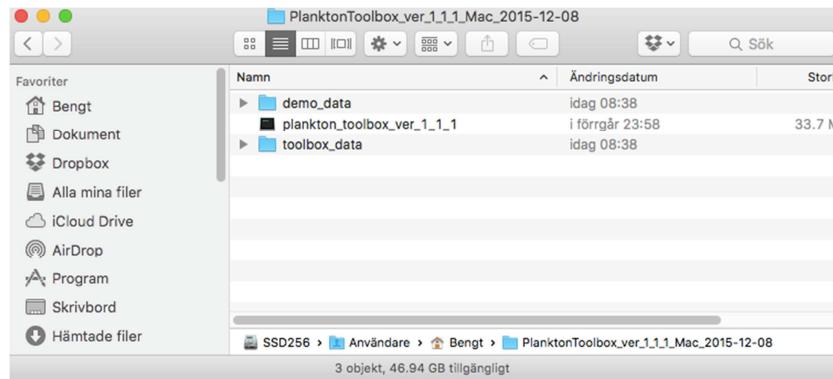
Download the zip archive with the software and accompanying files from:

<http://nordicmicroalgae.org/tools>

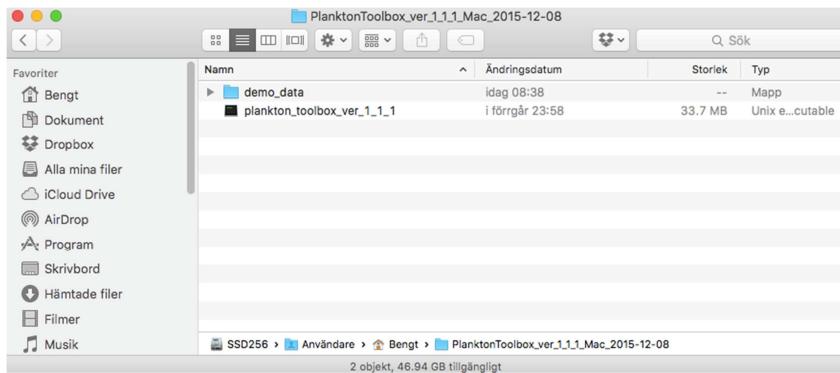
Unpack the archive, e.g.

PlanktonToolbox_ver_1_1_1_Mac_2015-12-08.zip

Move the whole folder to the users folder on your Mac, i.e. the folder with a small house as a symbol. The folder probably has a name like *Peter* if you are logged in as Peter.



Move the folder *toolbox_data* up one level to “Peter”



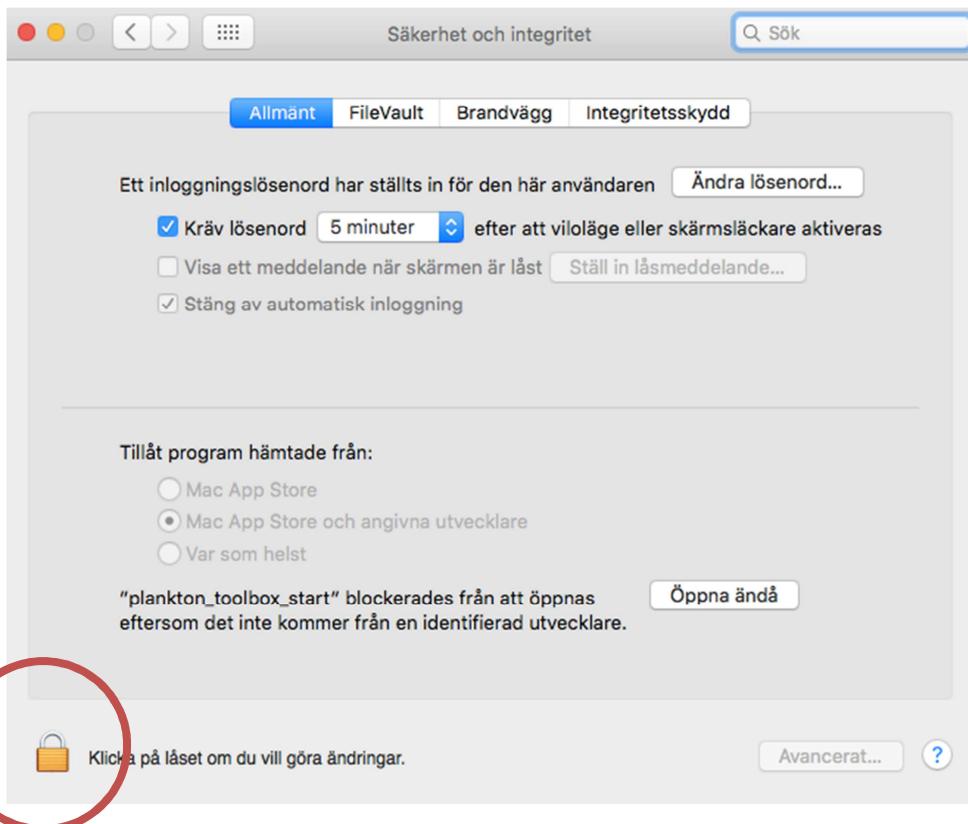
Open the folder and double click on plankton_toolbox_ver_1_1_1 to start the software



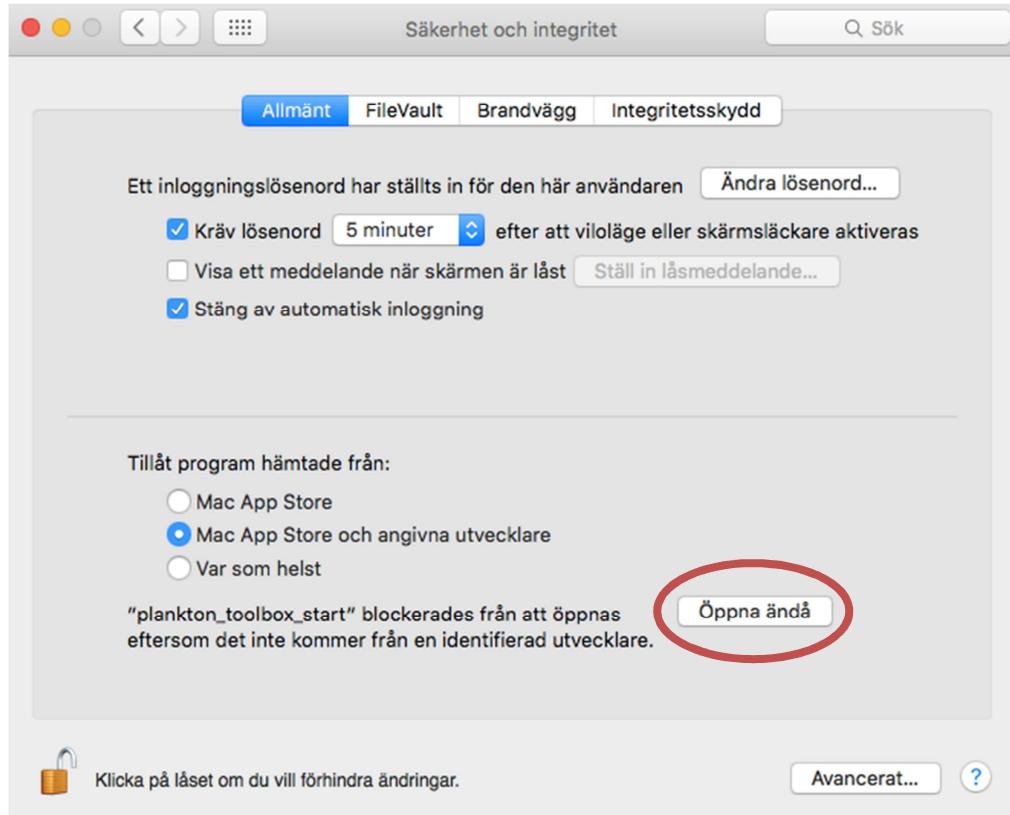
You will probably see the message above.



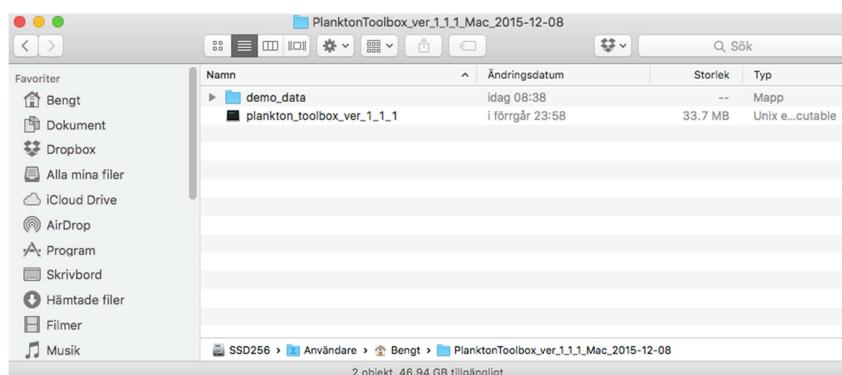
Go to Settings on your Mac and click on Security and integrity.



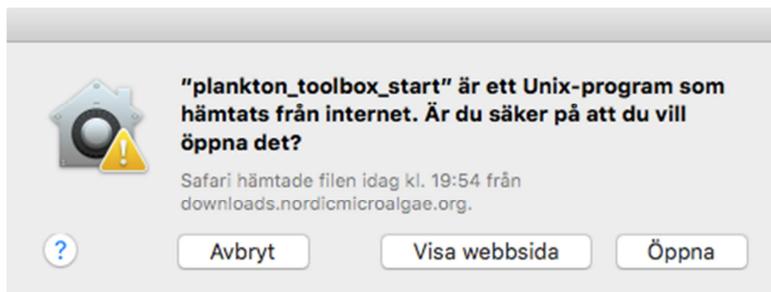
Unlock to be able to make changes



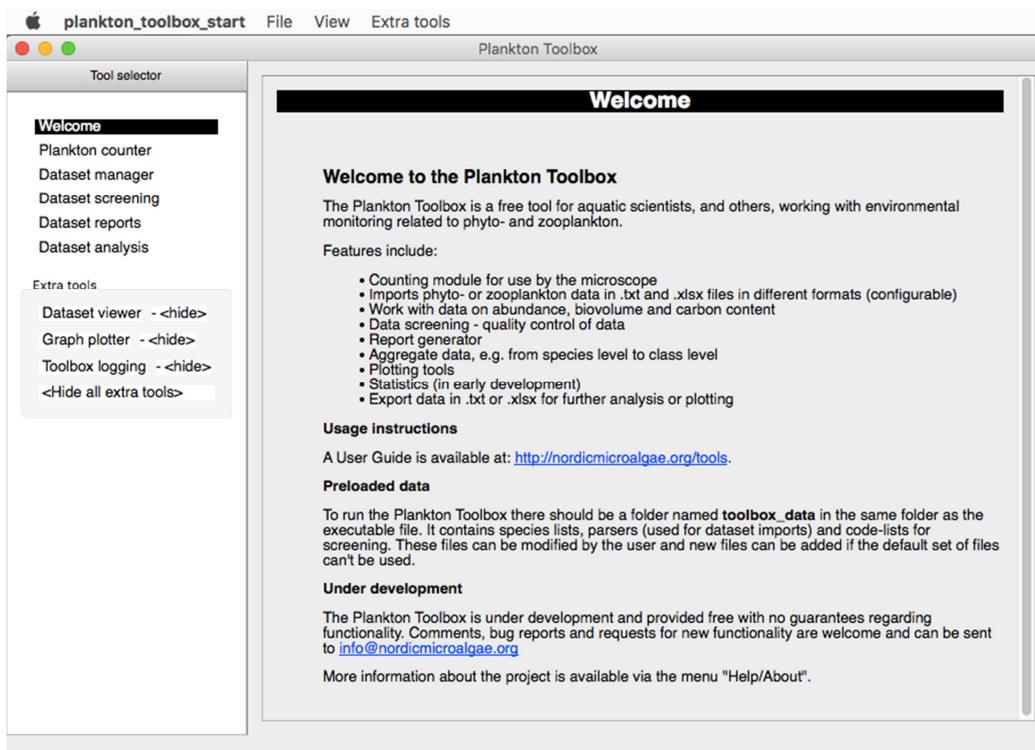
Click on *Open anyway*



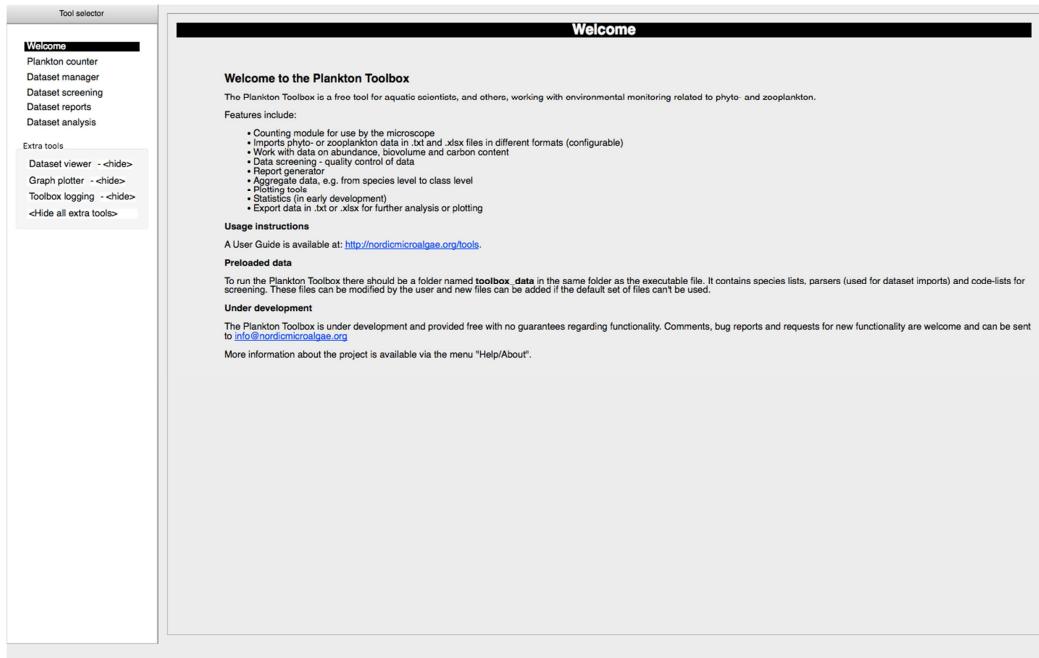
Go back to the folder where Plankton toolbox resides and double click on plankton_toolbox again.



The last warning message. Click on *Open*.



The software is running. You may choose to run Plankton Toolbox in full screen mode. Just click on the green button in the upper left part of the window.



Plankton Toolbox running in full screen mode.

```
Bengt — plankton_toolbox_start — plankton_toolbox_start • plankton_toolbox_start — 80x24
Last login: Mon Dec  7 20:04:48 on ttys000
/Users/Bengt/PlanktonToolbox_ver_1_1_1_Mac_2015-11-07/plankton_toolbox_start ; e
xit;
Bengt-MacBook-Air:~ Bengt$ /Users/Bengt/PlanktonToolbox_ver_1_1_1_Mac_2015-11-0
7/plankton_toolbox_start ; exit;
QPixmap::scaled:Pixmap is a null pixmap
QPixmap::scaled:Pixmap is a null pixmap
QPixmap::scaled:Pixmap is a null pixmap
```

The Window for the Mac Terminal will be running in the background. The information shown in the Terminal window is not of relevance for the user of Plankton Toolbox.

```

Bengt — plankton_toolbox_start — 80x24
Last login: Mon Dec  7 20:04:48 on ttys000
/Users/Bengt/PlanktonToolbox_ver_1_1_1_Mac_2015-11-07/plankton_toolbox_start ; e
xit;
Bengts-MacBook-Air:~ Bengt$ /Users/Bengt/PlanktonToolbox_ver_1_1_1_Mac_2015-11-0
7/plankton_toolbox_start ; exit;
QPixmap::scaled:Pixmap is a null pixmap
logout
Saving session...
...copying shared history...
...saving history...truncating history files...
...completed.

[Processen slutförd]

```

You may want to quit the Mac Terminal after you have quit Plankton Toolbox.

Technical information for developers

The software Plankton Toolbox was developed by Arnold Andreasson using open source software, i.e. Python version 2.7. The code is free as defined by the MIT-license, the Open Source Initiative, <http://opensource.org/licenses/mit-license.php>.

The code is available at <http://code.google.com/p/planktontoolbox/> (a move to GitHub is planned) A version control system for keeping track of different versions of the code is used.

Acknowledgements

The development of Plankton Toolbox was supported by the Swedish Research Council through the Swedish LifeWatch project. The effort by phytoplankton specialists who tested the software and suggested improvements is much appreciated.

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<http://helcom.fi/Lists/Publications/BSEP106.pdf> (7 October 2015).

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www.smhi.se



www.svenskalifewatch.se/en/



www.lifewatch.eu