

The MorFishJ User Manual

MorFishJ v0.0.1

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Introduction

Status of the manual

Hi there! This manual is a work-in-progress.

MorFishJ is an open-source software package for traditional morphometric analysis of fish from side view images in ImageJ. With **MorFishJ** you can collect morphological trait data from fish images in a standardised and reproducible way through a semi-automated procedure, which accelerates data collection and increases data accuracy by reducing user bias.

Motivation

While advances in modern morphometrics (landmarks configuration and outline analysis) have increasingly facilitated data acquisition and analysis, traditional morphometrics has not kept pace. Collection of traditional morphometric data from fish images is generally slow and not reproducible. A typical workflow in ImageJ is:

1. Open an image.
2. Adjust the image if necessary (or do this beforehand with another software).
3. Draw reference lines to help with trait measurement (Optional).
4. Measure traits one by one.
5. Save results.
6. Close the image (losing track of the work done).
7. Open the next image and repeat the procedure.

Additionally, traits are often defined and measured differently by different researchers as a standardised protocol does not exist yet, making it impractical to merge data obtained from multiple studies.

The MorFishJ package

MorFishJ allows users to perform a complete morphometric characterisation in a limited time while recording and storing all steps, and saving results in a ready-to-use format suitable for statistical analysis with multiple software. Analyses of large photographic databases are facilitated by allowing users to stop and restart their analyses without losing progress.

About this manual

This manual is a step-by-step user guide to MorFishJ. It explains best practices for project organisation, walks through each implemented analysis, and provides detailed explanations and examples for specific steps.

1 Installation

[ImageJ](#) is an open source image processing program commonly used by researchers to extract morphometric data from fish images. As such, [MorFishJ](#) has been developed as an extension of this software and it can be used in both ImageJ 1.x and Fiji (ImageJ2) distribution.

Therefore, the installation of ImageJ (<https://imagej.nih.gov/ij/download.html>) or Fiji (<https://imagej.net/software/fiji/downloads>) is required before installing [MorFishJ](#).

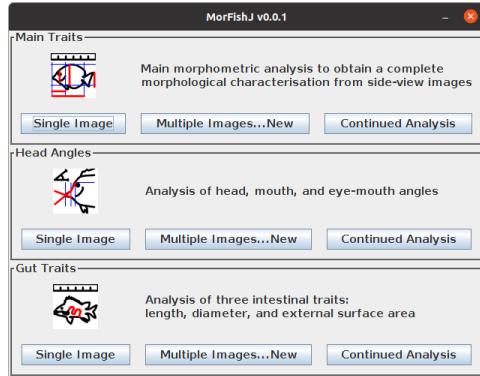
Warning

[MorFishJ](#) depends on [ImageJ 1.53e](#), thus, if ImageJ/Fiji was previously installed, first check the current ImageJ version below the toolbar. If it is older than 1.53e, to update ImageJ click **Help -> Update ImageJ...**, choose the latest version and click OK. Then ImageJ/Fiji must be restarted.

Once ImageJ/Fiji is installed/updated, proceed with installing [MorFishJ](#) following these steps:

1. Download [MorFishJ](#):
 - for people familiar with GitHub: clone or download the entire [GitHub repository](#);
 - for people not familiar with GitHub: [click here](#) to go to the project's main page on GitHub, click on the green button **Code**, then click on **Download ZIP**, thus extract the content.
2. Copy the [MorFishJ v0.0.1](#) folder in the `ImageJ/plugins/` or `Fiji.app/plugins/` directory.

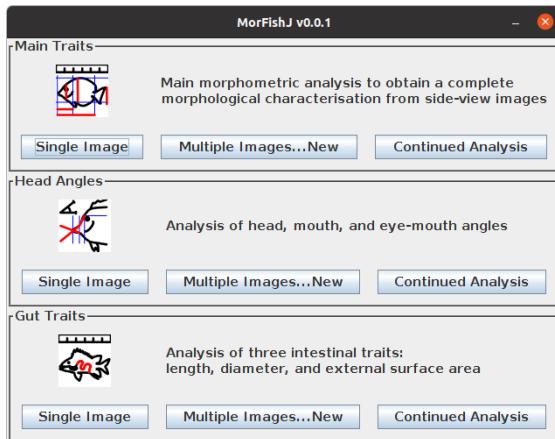
Now MorFishJ is installed. Open ImageJ/FIJI and click **Plugins** → **MorFishJ v0.0.1** → **MorFishJ GUI**. The following GUI appears in the upper left corner of the screen.



💡 Tip

In Fiji the Plugins menu is often crowded, thus it may be easier to use the **Search** field under the toolbar to find and start MorFishJ.

2 GUI



The GUI of MorFishJ provides a simple and direct access to all the morphometric analyses. Each analysis can be started by clicking on the appropriate button.

2.1 Morphometric analyses

Three morphometric analyses are currently available in MorFishJ:



Main Traits

The workhorse of MorFishJ. Performs a complete morphometric analysis measuring 22 traits that cover all body parts visible from side view images, excluding dorsal, pelvic, and anal fins.



Head Angles

It allows to measure three head angles related to vision and feeding (Brandl and Bellwood 2013; Bellwood et al. 2014; Brandl, Robbins, and Bellwood 2015).



Gut Traits

It allows to measure three intestinal traits related to fish diet (Ghilardi et al. 2021).

2.2 Single and multiple image analysis

Each analysis has three different buttons:

- **Single Image:** to analyse only one image (may be useful for beginners to get used to each step before analysing the entire image database).
- **Multiple Images...New:** to start a new analysis of an image database.
- **Continued Analysis:** to continue analysing an image database from where it was last left.

2.2.1 Single Image

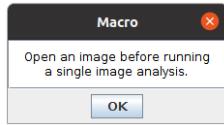


Warning

An image must be opened before starting a single image analysis.

Clicking on the **Single Image** button of the desired analysis before opening an image will display the following message.

To open an image click on **File -> Open...** or use the shortcut **Ctrl+O** or drag the image over the ImageJ GUI.



Once the image is opened click on the **Single Image** button of the desired analysis. The image is duplicated and all the following steps will be performed on the duplicated image to avoid any unwanted modification of the raw image. The **ROI Manager** window is automatically opened and the first dialog box appears, to either set the scale or adjust the image, depending on the type of analysis selected.

The steps required to perform the selected analysis are explained in the following chapters.

2.2.2 Multiple Images

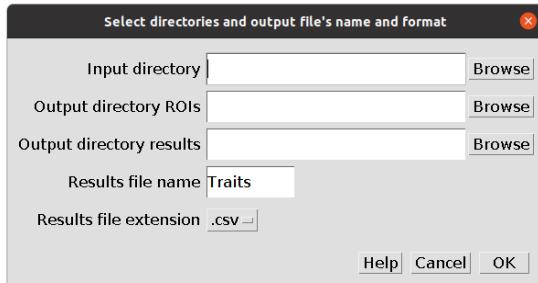
New analysis

Before starting to analyse an image database the new project should have a clear folder structure. **MorFishJ** does not require a fixed folder structure, but only an input directory where the raw images are stored and two output directories, one to save the ROIs and one to save the results and log files (although the same output directory could be used for all outputs). Therefore, you can set your own folder structure. However, it is advisable that each project has its own directory with the following structure.

```
./ProjectName/
  raw_images
    img1.JPG
    img2.JPG
    img3.JPG
    ...
  results
  ROIs
```

There are three subdirectories: one containing the raw images, one to save the ROIs and processed images, and one to save the results and log files.

To start a new analysis click on the **Multiple Images...New** button of the desired analysis. The following dialog box appears.



Use the **Browse** button to add the path to the input directory where the raw images are stored, and the output directories where the ROIs and results will be saved. Alternatively, it is possible to drag the directories over the dialog box. By default the results file will be named **Traits** and will be saved in **.csv** format, but it is possible to change both the name and the extension, which can be changed to **.txt** through the drop-down list.

Once all the fields are completed click **OK**. Two files are created in the selected directory for the results:

- a log file with the name **TraitLog** followed by the date of creation in **dd_mm_yyyy** format and including all the metadata required to restore the project.
- a results file with the selected name and extension. Results are appended to this file at the completion of the analysis of each image.

! Important

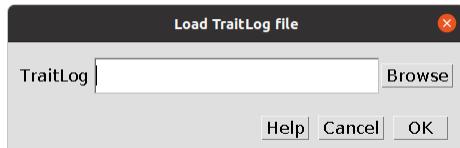
Do not edit the **TraitLog** file by hand and do not change its directory!

The first image in the input directory is automatically opened and duplicated. All the following steps will be performed on the duplicated image to avoid any unwanted modification of the raw image. The **ROI Manager** window is automatically opened and the first dialog box appears, to either set the scale or adjust the image, depending on the type of analysis selected.

The steps required to perform the selected analysis are explained in the following chapters.

Continued analysis

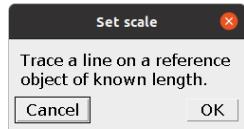
To continue a project from where it was last left, click on the **Continued Analysis** button of the desired analysis. The following dialog box appears.



Use the **Browse** button or drag the file over the dialog box to add the path to the **TraitLog** file of the project. Thus click **OK**. The project is restored and can be continued from the next image. The new results will be appended to the existing results file.

3 Set scale

Two analyses, **Main Traits** and **Gut Traits**, require to set the scale for the image. This is the first step of both analyses. The following dialog box appears.

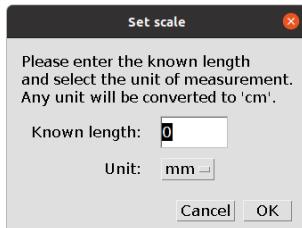


Trace a straight line on a reference object and click **OK**.

Tip

The reference object can also be the fish itself if its length (standard, fork, or total) is known. In this case trace a line over the fish to select the appropriate length.

The following dialog box appears.



Enter the known length of the traced line and select the unit from the drop-down list. Three options are available (*mm*, *cm*, and *inch*), but any unit will then be converted to *cm*. Thus all linear measurements will be saved in *cm* and areas in *cm*².

The traced line will be stored in the ROI Manager as **px.cm** and then saved with all other ROIs. A column **px.cm** will also

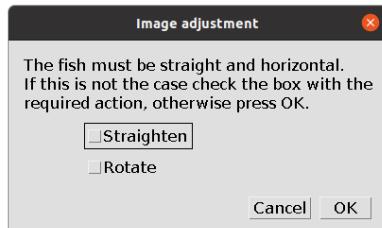
be included in the results file indicating the scale of the images in pixels/cm.

 Warning

At the moment it is not possible to run the **Main Traits** and **Gut Traits** analyses on images without a reference object or known fish length as setting the scale is required. However, in the upcoming update setting the scale will become optional and all images can be analysed.

4 Straighten and rotate

Two analyses, **Main Traits** and **Head Angles**, require the fish to be in a straight and horizontal position. For such analyses the software allows to adjust the image if required. For the **Main Traits** analysis this is the second step, after setting the scale (as described in Chapter 3), whereas for the **Head Angles** analysis it is the first step. The following dialog box appears.



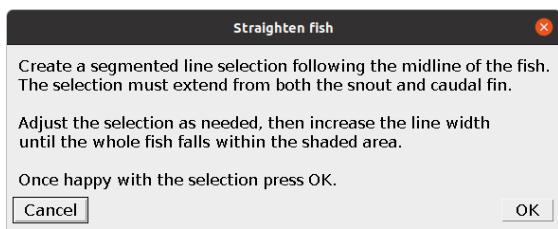
It allows to select one of two options:

- **Straighten:** to straighten the fish if it is in a bent position.
- **Rotate:** to rotate the image and set the fish in an horizontal position.

Therefore, if the fish is not straight and horizontal, select the appropriate option and click **OK**. Otherwise, click **OK** without selecting any option and continue.

Straighten

When the fish is bent, select **Straighten** and click **OK**. The following dialog box appears together with the **Line Width** window.



Follow the instructions given in the dialog box, create a segmented line selection, adjust the width and click **OK**. The fish will be straightened and in an horizontal position. The following figure shows an example of fish straightening.

4.0.0.1 Before



4.0.0.2 After



💡 Tip

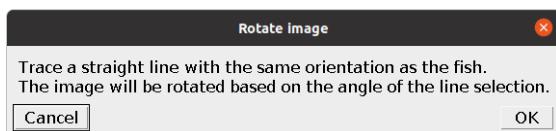
Selecting **Spline fit** within the **Line Width** window can improve the selection and straightening of the fish.

⚠️ Warning

If the fish is overly bent, straightening can lead to deformation of the body which affects the measurement of the traits. Use this option with care.

Rotate

When the fish is straight but not horizontal, select **Rotate** and click **OK**. The following dialog box appears.

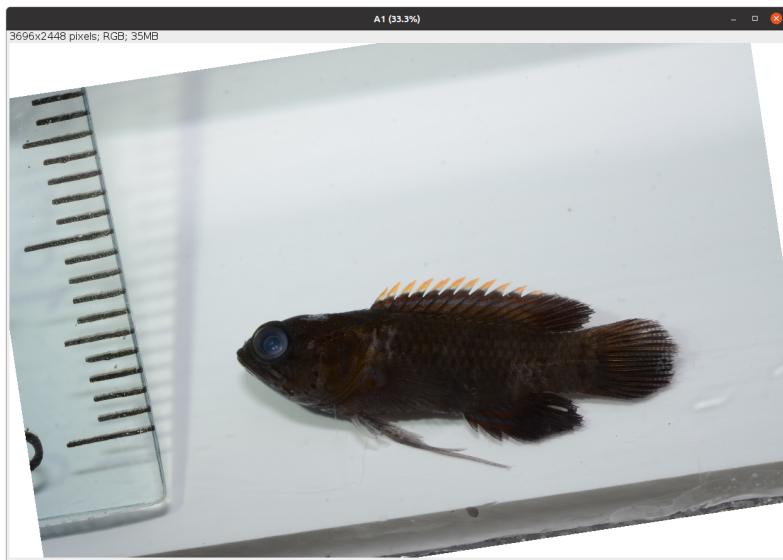


Follow the instructions given in the dialog box, trace a line and click **OK**. The image will be rotated and, if the line was placed well, the fish will be in an horizontal position. The following figure shows an example of image rotation.

4.0.0.1 Before



4.0.0.2 After



5 Main Traits

The **Main Traits** analysis is the workhorse of MorFishJ as it performs a complete morphometric characterisation of fishes. It requires the user input to trace the outline of the body and pectoral fin, and to position some reference lines (Table 5.1) and landmark points. The coordinates of these lines and points allow to extract 22 morphometric measurements described in Table 5.2.

5.1 Analysis

Once the steps described in Section 2.2 are completed the screen will be populated with a number of windows:

- the ImageJ/Fiji main window
- the MorFishJ GUI
- a fish image (this is a duplicate of the raw image to prevent any modification)
- the ROI manager
- the **Set scale** dialog

While the majority of the analysis is automated, there are a number of steps that require the user input:

1. Set the scale for the image as described in Chapter 3.
2. Adjust the image if necessary as described in Chapter 4.
3. The following dialog allows to select the orientation of the fish (i.e., whether the fish is facing left or right) from a drop-down list. This step is important for the correct automatic placement of some reference lines and points.

Table 5.1: Reference lines traced on fish images to aid the measurement of morphometric parameters (Table 5.2)

Reference line	Description	User input
A	Vertical line at the narrowest point of the caudal peduncle	Yes
B	Horizontal line touching the highest edge of the body (excluding fins)	No
C	Horizontal line touching the lowest edge of the body (excluding fins)	No
D	Vertical line touching the most anterior tip of the body	No
E	Vertical line touching the most posterior tip of the caudal fin	No
F	Horizontal line touching the highest edge of the caudal fin	No
G	Horizontal line touching the lowest edge of the caudal fin	No
H	Vertical line at the base of the caudal fin (end of the vertebral column or posterior edge of the hypural plate). Parrotfishes (Labridae: Scarini) are an exception and the line should be placed between the last and second to last scale lying along the midline (FishBase)	Yes
I	Vertical line touching the posterior margin of the operculum	Yes
J	Horizontal line cutting the eye in halves	Yes
K	Vertical line cutting the eye in halves	Yes
L	Vertical line at the pectoral fin insertion	Yes

Table 5.2: Morphometric parameters taken on fish images

Code	Trait	Description	Reference
TL	Total length	Length from the most anterior point of the body (D) to the most posterior point (E) (excluding the caudal filaments)	FishBase
SL	Standard length	Length from most anterior point of the body (D) to the base of the caudal fin (H)	FishBase
MBd	Maximum body depth	Body depth at the deepest part of the body (excluding fins). Measured as the vertical distance between B and C	Bellwood et al. (2014)
Hl	Head length	Horizontal distance from most anterior tip of the head (D) to the posterior margin of the operculum (I)	Barnett, Bellwood, and Hoey (2006)
Hd	Head depth	Head depth measured at the vertical of the orbit centroid along K	Villéger et al. (2010)
Ed	Eye diameter	Internal diameter of the orbit measured along J	Bellwood et al. (2014)
Eh	Eye position	Vertical distance from the orbit centroid (J × K) to the bottom of the body (K × C)	Toussaint et al. (2016)
Snl	Snout length	Horizontal distance from the anterior margin of the orbit to the tip of the snout (D)	Barnett, Bellwood, and Hoey (2006)
POC	Posterior of orbit centroid	Horizontal distance from the orbit centroid (J × K) to the posterior margin of the operculum (J × I)	Bellwood et al. (2014)
AO	Anterior of orbit	Horizontal distance from the anterior margin of the orbit	Bellwood et al. (2014)



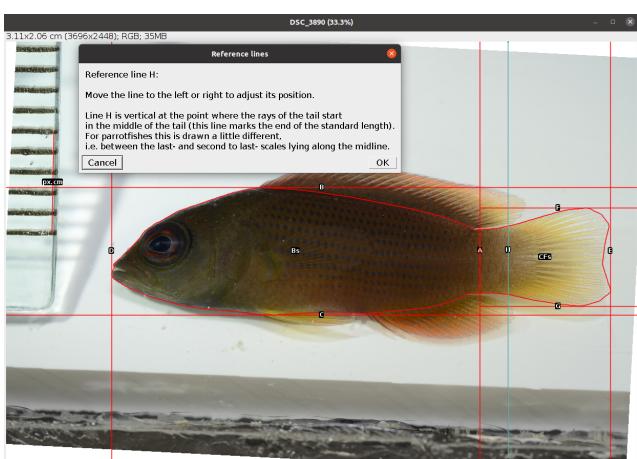
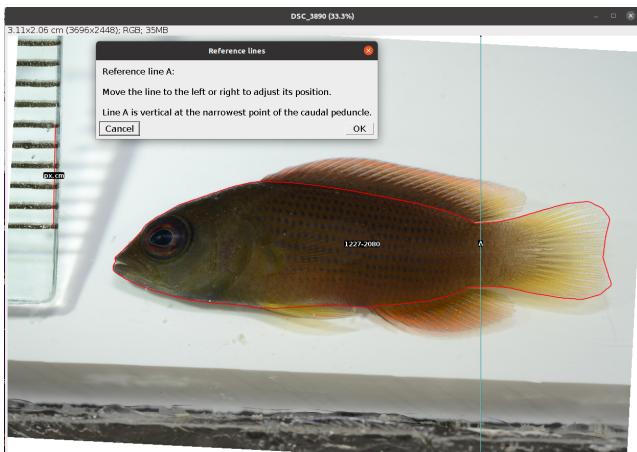
4. Select the fish outline following the instruction in the dialog. Trace a polygon around the body and caudal fin, excluding the dorsal, pelvic, and anal fins as in the example below. Also avoid including any portion of pectoral fin protruding from the body area. Once the selection is completed it can be adjusted as needed.

 Tip

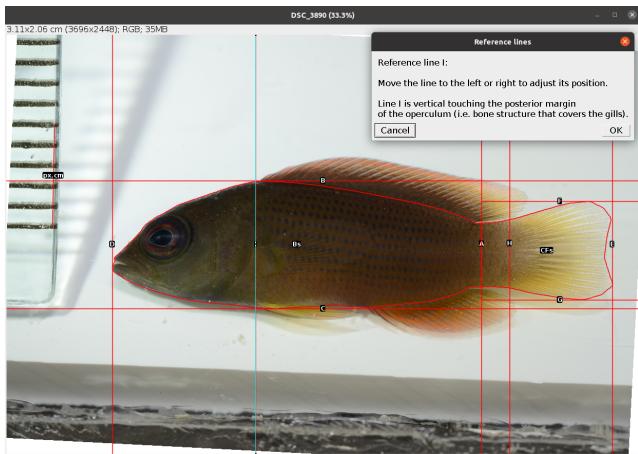
The points that define the selection can be moved. To add a new point to the selection press **Shift** and click on an existing point. To remove one point press **Alt** and click on the point. See [Polygon Selection Tool](#).



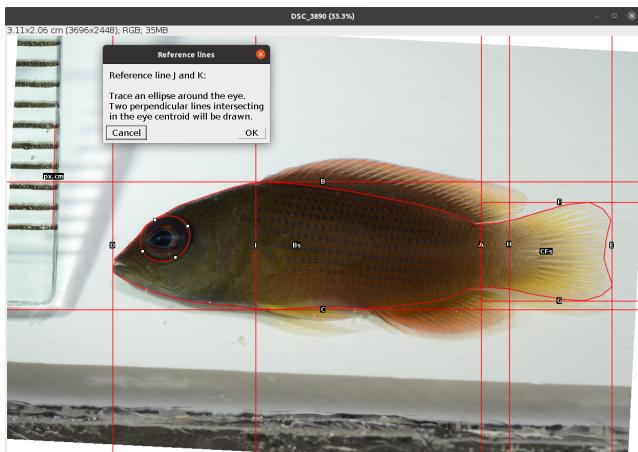
5. Position reference line A at the narrowest point of the caudal peduncle. After clicking **OK** several automatic steps will split the outline in two, the body area (Bs) and caudal fin area (CFs), and add reference lines B-G.
6. Position reference line H at the base of the caudal fin to mark the end of the standard length.



7. Position reference line I at the posterior margin of the operculum.

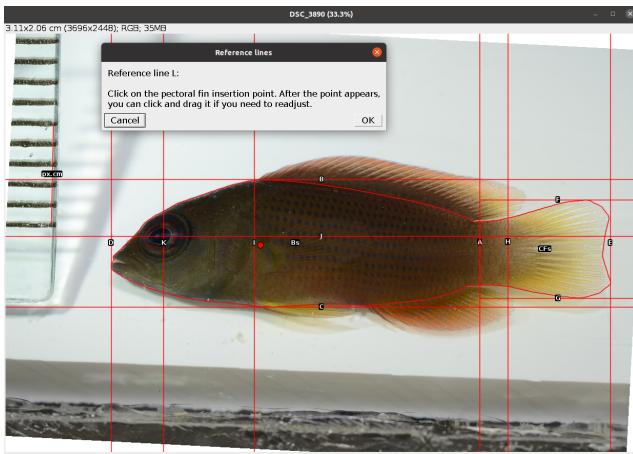


8. Trace an ellipse around the eye as in the example below (see [Elliptical Selection Tool](#) for specific instructions on how to use this tool). After clicking OK two new reference lines (J-K) are drawn perpendicular intersecting at the eye centroid.

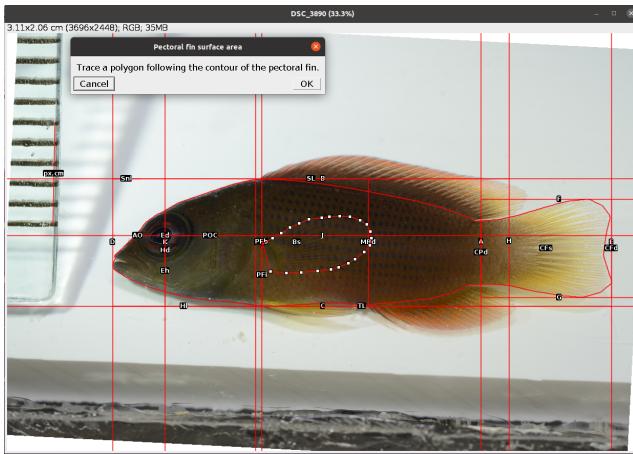


9. Place a point at the insertion of the pectoral fin as in the example below.

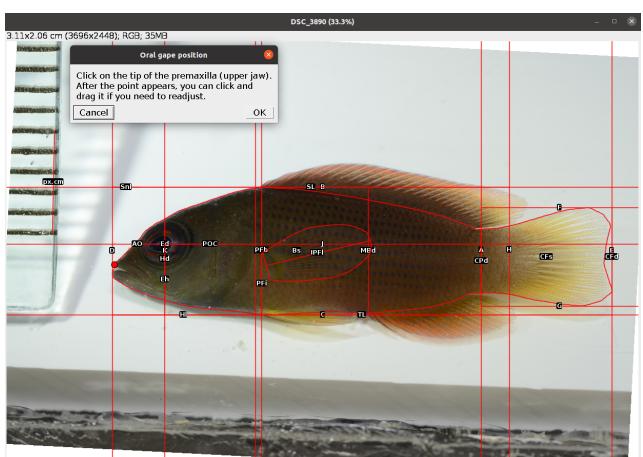
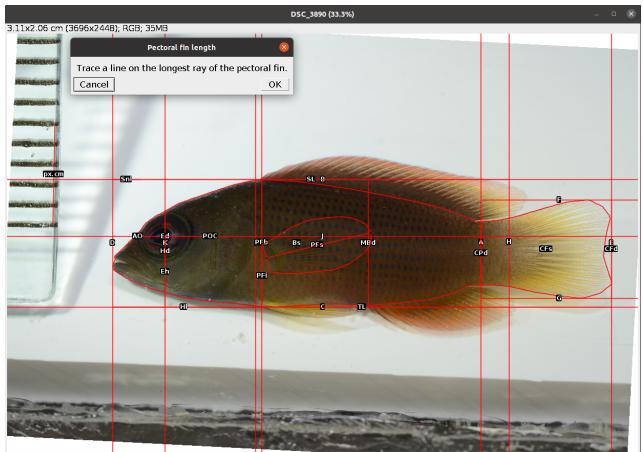
After clicking OK reference line L appears passing through the selected point and 14 new traits are drawn and added to the ROI manager together with all reference lines.



10. Select the outline of the pectoral fin as in the example below. After clicking OK this is saved in the ROI manager as PFs.

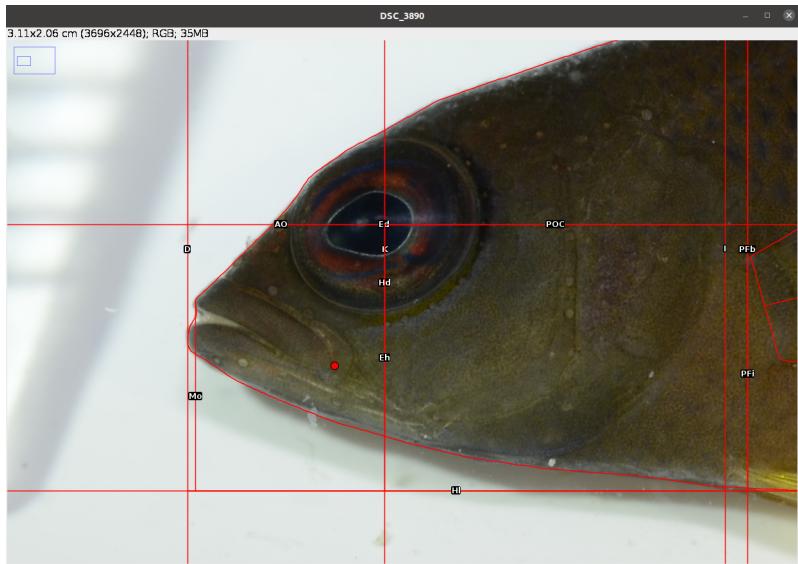


11. Trace a line on the longest ray of the pectoral fin. After clicking OK this is saved in the ROI manager as PFl.
12. Place a point on the tip of the premaxilla (upper jaw) as in the example below. After clicking OK a new trait (Mo) is drawn and saved in the ROI manager.
13. Place a point on the corner of the mouth. The point should be placed at the intersection between the maxilla



and the mandible, not where the flesh of the upper and lower jaw meet! See the example below.

5.1.0.1 Correct

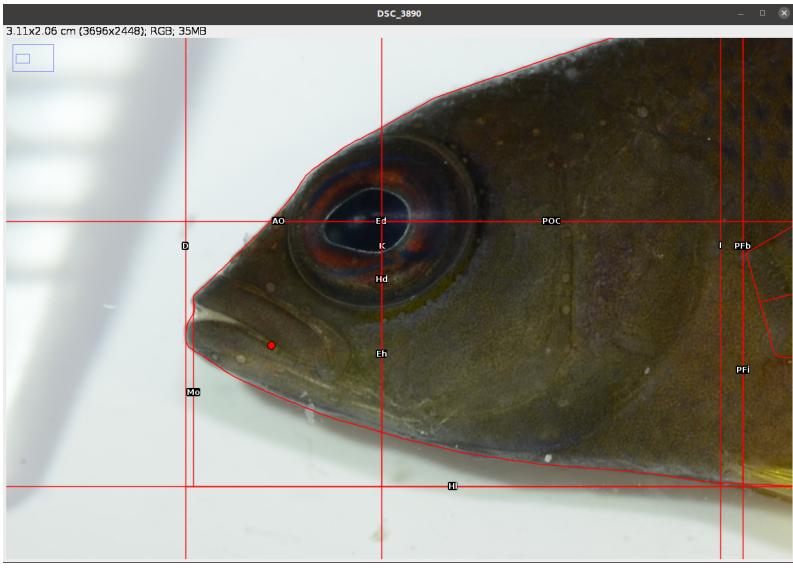


5.1.0.2 Incorrect

After clicking **OK** the last three traits are drawn and saved in the ROI manager.

The analysis of the image is completed. In case of single image analysis a window named **Traits** containing all the results appears. This can be saved by clicking on **File -> Save As....**. All ROIs in the ROI manager can also be saved as a zip file by clicking on **More >>> -> Save....**. In case of multiple image analysis a new raw will be added to the results file, the ROIs are saved in their directory, where also the rotated or straightened images are saved as .jpg files. The current image is closed and the next is opened. Repeat steps 1-13 for all images.

It is possible to stop and restart the analyses (see Section 2.2) without losing progress. Everything done until the last completed image is saved, thus, if the analysis is stopped before



completing an image, only the steps performed on that image are lost.

5.2 Results

The results file/table contains one row for each image and 25 columns. The first column, `image_id`, is the name of the image without extension. The second column, `px.cm`, is the scale of the image in pixels/cm. The columns 3-24 are the morphometric measurements described in Table 5.2. Currently, all linear measurements are in centimetres and all areas in squared centimetres. The last column, `time`, is the time spent to analyse the image (steps 1-13) in seconds.

References

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