



## **PAPARA(ZZ)I™ 2.8 - User Manual**

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## PAPARA(ZZ)I

*Program for Annotation of Photographs and Rapid Analysis (of Zillions and Zillions) of Images*

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PAPARA(ZZ)I is available at:

**<https://papara-zz-i.github.io>**

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## Chapter 1 Installing and Starting PAPARA(ZZ)I™

PAPARA(ZZ)I™ is an open-source and stand-alone program that runs under 64-bit Windows, Mac OS X and Linux operating systems. Alternatively, PAPARA(ZZ)I can also be run directly from MATLAB (versions R2010a to R2015b), by running the *PAPARA(ZZ)I.m* script from the main command window.

**Important:** *although the PAPARA(ZZ)I installer is virus free, antivirus programs sometimes block its execution. If this is the case, de-activate the antivirus before running the installer.*

### 1.1 Windows systems

To start the installation, run (double-click) one the installer files and follow the instructions:

- *PAPARA(ZZ)I\_vX.X\_web.exe*: this package file installs PAPARA(ZZ)I and downloads the MATLAB Runtime from the internet (if not already installed).
- *PAPARA(ZZ)I\_vX.X\_mcr.exe*: this package file includes both PAPARA(ZZ)I and the MATLAB Runtime (use this option if an internet connection is not available).

**IMPORTANT remark for computers protected with Avast! Antivirus (and with possibly other antivirus programs):**

*Avast Antivirus automatically blocks **without notifying the user** any executable program that is unknown by the Avast file reputation database, such as PAPARA(ZZ)I. Therefore, to install and run PAPARA(ZZ)I on computers protected with AVAST Antivirus, we recommend to deactivate the antivirus before running the installer file or the program. The antivirus can be reactivated as soon as PAPARA(ZZ)I has started. If you do not wish to turn off the Avast Antivirus at all, you can alternatively uncheck the 'Enable reputation services' and 'Enable DeepScreen' boxes in the settings of AVAST Antivirus before running PAPARA(ZZ)I. We think that the antivirus warning is caused by PAPARA(ZZ)I's ability to connect to the WoRMS register online.*

### 1.2 Mac OS X systems

To start the installation, run (double-click) one the installer files and follow the instructions:

- *PAPARA(ZZ)I\_vX.X\_web.app*: this package file installs PAPARA(ZZ)I and downloads the MATLAB Runtime from the internet (if not already installed).
- *PAPARAZZI\_vX.X\_mcr.app*: this package file includes both PAPARA(ZZ)I and the MATLAB Runtime (use this option if an internet connection is not available).

Once the installation is finished, open a command terminal (in *Applications* → *Utilities* → *Terminal*), type the following command and press [Enter]:

```
../../Applications/PAPARAZZI/application/run_PAPARAZZI.sh ../../Applications/MATLAB/MATLAB_Runtime/v90
```

PAPARA(ZZ)I will start within a few seconds to a few minutes (depending on the computer speed and on whether PAPARA(ZZ)I is started for the first time).

*Remark: the command above is only valid if PAPARA(ZZ)I and the MATLAB Runtime are installed in their respective default installation folders. If not, amend the folder paths in the command above to point to the correct directories.*

### 1.3 Linux systems

To start the installation, run one the installer files by typing the following command in a terminal: **./PAPARAZZI\_vX.X\_web.install** (where X.X is the version number). Wait a moment (it may take several minutes) and follow the instructions that appear on the screen.

There are two types of installers:

- *PAPARAZZI\_vX.X\_web.install*: this package file installs PAPARA(ZZ)I and downloads the MATLAB Runtime from the internet (if not already installed).
- *PAPARAZZI\_vX.X\_mcr.install*: this package file includes both PAPARA(ZZ)I and the MATLAB Runtime (use this option if an internet connection is not available).

*Remark: running the installer in Linux may require 'root' permissions; this is done with the following commands:*

- *in most Linux distributions: **sudo ./PAPARAZZI\_vX.X\_web.install**,*
- *in Debian (if sudo is not installed): **su root ./PAPARAZZI\_vX.X\_web.install**.*

Once the installation is finished, open a command terminal, type the following command and press [Enter]:

```
./usr/PAPARAZZI/application/run_PAPARAZZI.sh /usr/local/MATLAB/MATLAB_Runtime/v90
```

PAPARA(ZZ)I will start within a few seconds to a few minutes (depending on the computer speed and on whether PAPARA(ZZ)I is started for the first time).

*Remark: the command above is only valid if PAPARA(ZZ)I and the MATLAB Runtime are installed in their respective default installation folders. If not, amend the folder paths in the command above to point to the correct directories.*

*Remark: running PAPARA(ZZ)I does normally not require the 'root' permissions. However, PAPARA(ZZ)I requires writing access to the folder that contains the images.*

## Chapter 2 Getting started

### 2.1 Annotator's username

Upon starting, PAPARA(ZZ)I prompts the user for a *username* and for the path to the folder that contains the images (*image folder*). The username is only used by the program to differentiate annotations made by the different users.

PAPARA(ZZ)I only displays the annotations that were previously made under the current username. Annotations made by other users are not visible. To view and export annotations from other users, simply restart PAPARA(ZZ)I and choose a different username.



Figure 1: Welcome screen of PAPARA(ZZ)I prompting the user for a username.

### 2.2 List of keywords

A list of keywords must be loaded before any annotation can be made (unless connected to WoRMS). The list of keywords is a simple text file with one keyword per line. Keywords can be organised into groups separated by empty lines. Group titles (i.e. non-selectable keywords) can be defined by inserting a “\_” character before and after the keyword (example: *\_Group Title\_*).

### 2.3 Connect to WoRMS

PAPARA(ZZ)I can connect to and query the World Register of Marine Species (WoRMS) in order to use standardised taxa names. To do so, select the “Connect to WoRMS” option from the drop-down menu at the top of the left panel. If the connection is successful, a list of taxa appears in the left panel. It is possible to navigate through the register from this list:

- Double-click on one taxa to display the children of the selected taxa.
- Select the “Higher rank” button to display the parent taxa.

- Select the “More results...” button to return more results in case the list of taxa is too long (it is only possible to query the register for a limited amount of taxa).
- Select the “WoRMS Taxon search” button to display additional search options. Once the desired taxon has been found, double-click on it to display it in the list in the left panel.

*Remark: this option requires an access to the internet.*

## Chapter 3 Direct Image Analysis

### 3.1 Add an annotation

Select the desired keyword on the left panel and select the desired location in the image. A yellow circle appears.

*Remark: application can be closed anytime. All annotations are saved automatically.*

### 3.2 Select an annotation and display associated keyword

To select an annotation, simply do LEFT-CLICK on the annotation circle. The associated keyword is displayed in the info bar. The annotation can be de-selected in the same way.

### 3.3 Modify an annotation

To modify the keyword associated to an annotation, do SHIFT + LEFT-CLICK on the annotation and select a new keyword on the left panel.

### 3.4 Delete an annotation

To delete an annotation, select it first (LEFT-CLICK), then do RIGHT-CLICK on it. The annotation circle disappears from the image and the annotation is deleted from the files. This action cannot be undone.

*Remark: any associated size measurement is also deleted. However the measurement line will not disappear from the image until the image is refreshed.*





### 3.5.2 *Modify size measurements*

To modify a size measurement, simply draw a new one (the previous measurement will be automatically removed).

### 3.5.3 *Measure the orientation of a feature*

Lengths measurements are *directional* in that they can be used to measure the direction angle of the measured features. For this reason, when making a length measurement, it is important to select first the front end (e.g. fish head) of the selected feature, and second the rear end (e.g. fish tail) of the selected feature. When the length measurement is completed, a dot appears at one end of the measurement line to indicate the front of the feature.

The orientation of the size measurements is used to compute the angle of direction of the features in relation to the upper side of the image. Resulting angles are available in the data export files.

*Remark: angles measurements are of interest when combined with the heading information of the camera in order to calculate the direction of each feature in relation to the North.*

## 3.6 Image scale

To add a scale bar, select the “Draw scale” button in the left panel. Then select the start and end points of the scale bar on the image. The length of the scale bar must be provided in metres.

The scale bar is used by the program to assess the size of the image area, to compute densities of marked features, and to scale the annotated features for which size measurements exist (see 3.5).

To modify a scale bar, simply draw a new one (the previous scale bar will be automatically removed). The scale bar can be fully removed by deleting the corresponding file:

*image folder\username\_scale\imagename.txt*

## 3.7 Maximum display scale (aka. maximum zoom)

It is possible to set a limit to the display scale, i.e. to set a maximum zoom level that the user cannot exceed when zooming in on the image. This option is designed to ensure that all images of the dataset are analysed with the same level of details. It also ensures that analyses are consistent between different users, in that they can all work with the same level of details.

The value of the display scale limit is the ratio between the distance on the screen and a corresponding distance on the scene represented in the image. In other words, a display scale of  $A:B$  means that  $A$  centimetres on the display represent  $B$  centimetres on the image. In order for the program to compute the correct display scale, it is important to adjust the screen resolution in pixels per inch (PPI). If unknown, the screen PPI is can be calculated with the


following formula:

$$PPI = \frac{\sqrt{vpxl^2 + hpxl^2}}{D}$$

The variables *hpxl* and *vpxl* are the horizontal and vertical resolutions of the monitor (in *pixels*), and *D* is the length of the monitor diagonal (in *inches*). The values for *hpxl* and *vpxl* can be found in the display settings of the operating system, and the value for *D* can either be measured with a ruler directly on the monitor or found in the technical specifications of the monitor.

*Remark: the image scale bar must have been defined for this function to work. If it has not, then the display scale is not constrained. Therefore, it is good practice to draw the image scale bar before starting the analysis of an image.*

### 3.8 Image Usable Area



In some cases, the corners of an image are too dark or too fuzzy to permit reliable analysis. In order to exclude those areas of the image from the analysis, it is possible to define a “usable area”: select the  button and draw a rectangle on the image. A separate summary file will be automatically created during the data export to summarize the annotations presents in the usable area.

To modify the usable area, simply draw a new one (the previous one will be automatically removed). The usable area can be fully removed by deleting the corresponding file:

*image folder\username\_rectangle\imagename.txt*

*Remark: if you modify the usable area during a gridded/random point analysis (Chapter 4), it is recommended to reload the image (**Refresh** button) after drawing the rectangle. This will re-generate the gridded/random points within the limits of the rectangle.*

### 3.9 Flagging an image as unusable

Unusable images (e.g. bad quality) can be flagged as unusable and ignored during the data export. To do so, simply select the  button. All existing annotations will disappear from the image and a large black cross will appear instead. This action can be undone by de-selecting the  button.

*Remark: this action is fully reversible and the previously existing annotations, scale bar, usable area or size measurements are not deleted by this action.*

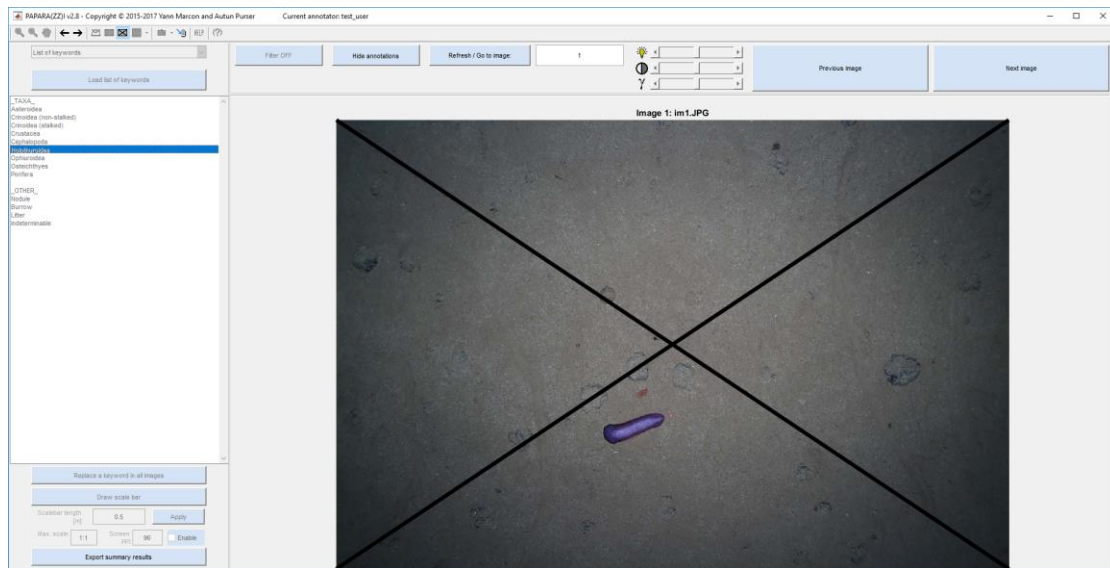



Figure 3: Image flagged as unusable. The annotation interface is greyed out.

## Chapter 4 Gridded/Random Point Analysis

PAPARA(ZZ)I offers the possibility to conduct systematic analysis of images using either gridded points or randomly distributed points. To use this functionality, select the desired option in the drop-down menu associated to the  button. Depending on the selected option, a gridded or randomly distributed point array will be automatically generated. This functionality can be turned off by de-selecting the button again.

*Remark: this option can take a few seconds if the amount of points is large.*

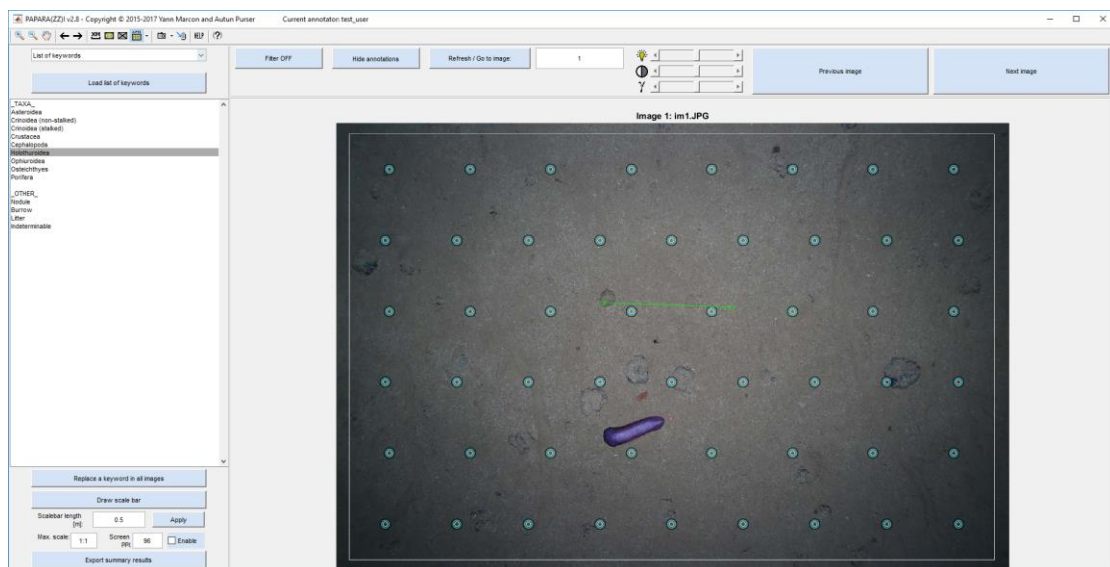


Figure 4: Gridded generated points. The number of points can be defined by the user. Points are automatically distributed evenly across the user-defined usable area (white rectangle).

## 4.1 Annotating a generated point

First select the desired point, and then select the relevant keywords from the left panel. The point appearance will turn to a single blue circle.

Generated points support multi-annotations, i.e. it is possible to create several annotations for a same generated point. To do so, simply select as many keywords in the list as necessary while the point is selected. To disable the annotation mode for the point, deselect it.

*Remark: every mouse click on the list of keyword will add an annotation to the selected point; therefore, make sure to deselect the points once they are adequately annotated.*

## 4.2 Working with multi-annotation points

Activating and editing the different annotations that are contained within a multi-annotation point is done as follow: first select the point (LEFT-CLICK). Then, once the point is selected, do SHIFT + LEFT-CLICK on it in order to display (and to activate) the next annotation. Repeat the last step until the desired annotation is displayed. The active annotation can be edited (e.g. size measurements, reset) in the same way as for single annotated points.

*Remark: changes made to the active annotation do not affect the other annotations associated to the same point.*

## 4.3 Reset the keyword associated to a generated point

To reset the keyword associated to a generated point, select it first (LEFT-CLICK), then do RIGHT-CLICK on it. The annotation circle will be set back to its default appearance and the associated keyword is set back to 'empty'. This action cannot be undone.

First select the desired point, and then select the relevant keyword from the left panel. The point appearance will turn to a single blue circle.

*Remark: size measurements can also be associated to generated points.*

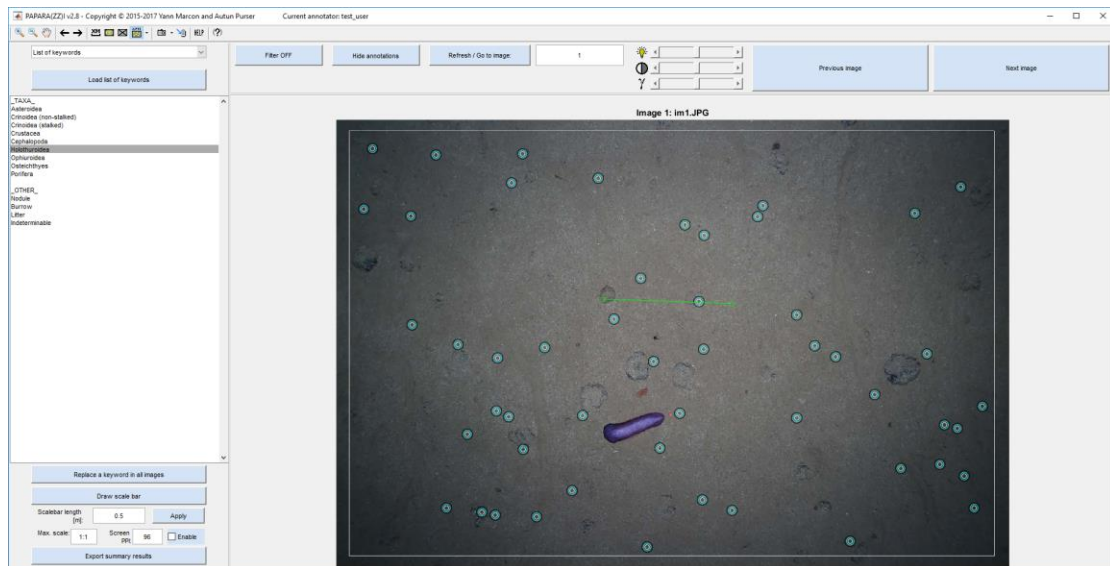


Figure 5: Randomly generated points. The number of points can be defined by the user. The points are constrained to the user-defined usable area (white rectangle).

## Chapter 5 Other options

### 5.1 Randomising the image order

It is possible to randomise the order of the images before starting the analysis. For instance, the quality of analysis may change along the course of the analysis, as the user gets more familiar with the dataset and more 'trained' for the feature classification. Randomising the image order may help reduce such analysis bias.

Randomising the image order is done at the start of the program: a dialog box prompts the user to ask whether the image order should be randomised. If so, a random order is generated and saved in the following file: *image folder\username\_annotations\randomlist.txt*.

This file is automatically loaded each time the same user re-opens the same project. If the user wishes to reset the original image order or to compute a different random image order, this can be done simply by deleting this file and restarting PAPARA(ZZ)I.

### 5.2 Changing the mouse pointer

If desired, the mouse pointer can be changed to a clearer one. To do so, simply do RIGHT-CLICK on an empty area of the image. The pointer will change. Repeat this procedure to change the pointer back to its original shape.

### 5.3 Brightness, contrast and gamma correction

The brightness, contrast and gamma correction of the images can be adjusted using the sliders

located in the upper panel in order to facilitate the analysis of images of poor quality. Adjustments in brightness, contrast and gamma corrections are only for display and are not maintained from an image to the next.

*Remark: adjustments of gamma correction may be slow for high-resolution images.*

## 5.4 Hiding / showing annotations

Use the "Hide annotations / Show annotations" toggle button to disable or enable the display of the annotations on the image. Hiding the annotations will also hide the size measurement bars.

## 5.5 Flip through image regions

When zooming in on an image, it is possible to flip through the different regions of the image. This is useful in order not to miss any region when the zoom function is used during the analysis. To flip through the different regions of the current image, use the arrow buttons (← and →).

## 5.6 Annotations filter


A filter can be used when navigating through the series of images in order to restrict the display of annotations to a set of selected features only. To do so, simply select the "Filter" button and select at least one keyword (CTRL + LEFT-CLICK to select several keywords). Turning the filter on modifies the behaviour of the navigation buttons (arrow buttons) in such a way that only images containing one or more selected features are displayed. The filter acts only on the display level. The filter does not delete any annotation and it does not affect the behaviour of the data export.

*Remark: filter works only if keyword list has been loaded.*

## 5.7 Batch replace keywords


Select the "Replace a keyword in all images" button in the left panel to modify a certain keyword in all annotated images. This function is useful to rename features that may have been erroneously annotated in the set of images.

## 5.8 Export of annotated images

Annotated images can be exported and saved as image files at any time by selecting the  button in the toolbar. The drop-down menu associated to this button gives the possibility to choose between several file formats (\*.jpeg, \*.tiff, \*.eps).

*Remark: the Encapsulated PostScript (EPS) format allows the annotation symbols to be edited in a vector graphics editor (Adobe Illustrator, CorelDraw, etc.).*

## 5.9 Export of analysis results

Exporting the analysis results can be done anytime by pressing the “Export summary results” button in the left panel or the  button in the toolbar. A set of summary files is then automatically created in the following folder: *image folder\data-export\*.

- *username\_WholeImage\_Abundances.txt*: this file summarises all annotations for all images (except images that are flagged as unusable). It also provides basic statistics based on the existing size measurements.
- *username\_UsableArea\_Abundances.txt*: this file summarises all annotations that are contained in the usable area of the images (except images that are flagged as unusable). If an image does not have a defined “usable area”, then the entire image area is used in the calculations. This file also provides basic statistics based on the existing size measurements.
- *username\_WholeImage\_Angles.txt*: this file summarises the orientation and direction of all size measurements for all images (except images that are flagged as unusable).
- *username\_UsableArea\_Angles.txt*: this file summarises the orientation and direction of all size measurements that are contained in the usable area of the images (except images that are flagged as unusable). If an image does not have a defined “usable area”, then the entire image area is used in the calculations.
- *username\_WholeImage\_SizeDistribution\_Keyword/ID.txt*: this file lists all the size measurements (and related direction angles) that have been made for a particular keyword. There is one file per keyword (i.e. per taxa). These files can be used for size distribution analyses.
- *username\_UsableArea\_SizeDistribution\_Keyword/ID.txt*: this file lists all the size measurements (and related direction angles) that have been made for a particular keyword within the usable area (measurements made on images that are flagged as unusable are ignored). If an image does not have a defined “usable area”, then the entire image area is considered. These files can be used for size distribution analyses.
- *username\_Legend.txt*: this is a legend file that describes the full label for every keyword ID used in the filenames.

The data export only exports results from the currently selected image analysis mode (*direct analysis* or *gridded/random generated points*). To export results of a different analysis mode, simply select the desired mode and press the “Export results” button again.

*Remark: angle measurements are provided in degrees in relation to the upper side of the images (positive angles are in clockwise direction).*



## 5.10 Lens distortion compensation

In some cases, distortion effects associated with camera lenses may affect the accuracy of the length and area measurements on the image (e.g. fisheye lens). It is possible to compensate for the effect of lens distortion by providing the camera intrinsic parameters and the lens distortion coefficients.

The lens distortion compensation is applied to all length measurements (e.g. length of scale bar, size measurements), area calculations (e.g. image area, usable area) and angle calculations. Therefore, it indirectly affects the calculated density values. Lens distortion compensation is applied during the data export.

### 5.10.1 Importing camera intrinsic parameters and lens distortion coefficients

Camera intrinsic parameters and lens distortion coefficients must all be provided in the file:

*image folder\camera\_intrinsics.pap*

The file is comma separated and is structured as follow:

| Line # | File content   |
|--------|--|
| 1      | default,OpticalCentreX,2880,OpticalCentreY,1920,FocalMM,24,SensorWidthMM,36,SensorHeightMM,24,SensorWidthPXL,5760,SensorHeightPXL,3840,SkewCoeff,0,k1,-0.1,k2,0,k3,0,p1,0,p2,0       |
| 2+     | Image_name,OpticalCentreX,2880,OpticalCentreY,1920,FocalMM,24,SensorWidthMM,36,SensorHeightMM,24,SensorWidthPXL,5760,SensorHeightPXL,3840,SkewCoeff,0,k1,0.1,k2,-0.05,k3,0,p1,0,p2,0 |

### 5.10.2 Instructions for the camera\_intrinsic.pap file:

- The *camera\_intrinsic.pap* file is not compulsory.
- The default camera parameters (line 1) are applied to all images, except those for which image-specific camera parameters have been individually specified (line 2+).
- The default camera parameters are mandatory unless image-specific camera parameters are provided for every image. **PAPARA(ZZ)I may stop working if this condition is not satisfied.**
- Image-specific parameters must be provided in individual lines, each starting with the relevant image filename.
- The 'default' line *must* occur before all image-specific lines or the default settings will override some of the image-specific camera parameters.
- All lines starting with something else than 'default' or a valid image filename are ignored.

*Remark: the camera intrinsic parameters and distortion coefficients can be changed at any time. The lens distortion compensation is applied only during the data export and it does not affect any of the raw images, annotations, scales, size measurements, etc.*



### 5.10.3 Parameters description

Camera intrinsic parameters:

- Optical centre [pixels]: *OpticalCentreX*, *OpticalCentreY*
- Lens focal length [mm]: *FocalMM*
- Size of the camera sensor [mm]: *SensorWidthMM*, *SensorHeightMM*
- Size of the camera sensor [pixels]: *SensorWidthPXL*, *SensorHeightPXL*
- Skew coefficient: *SkewCoeff*

Lens distortion parameters:

- Radial distortion coefficients: *k1*, *k2*, *k3*
- Tangential distortion coefficients: *p1*, *p2*

### 5.10.4 Lens distortion correction

The radial and tangential corrections are done using the Brown–Conrady distortion model:

Radial distortion: 
$$x_{\text{distorted}} = x + x(k_1 * r^2 + k_2 * r^4 + k_3 * r^6)$$

$$y_{\text{distorted}} = y + y(k_1 * r^2 + k_2 * r^4 + k_3 * r^6)$$

Tangential distortion: 
$$x_{\text{distorted}} = x + [ 2 * p_1 * x * y + p_2 * (r^2 + 2 * x^2) ]$$

$$y_{\text{distorted}} = y + [ p_1 * (r^2 + 2 * y^2) + 2 * p_2 * x * y ]$$

with  $r^2 = (x^2 + y^2)$ .