

NOT TO BE CITED. A manual by Jose A. Fernandes based on manuals written by Philippe Grosjean and Kevin Denis: <u>http://www.sciviews.org/zooimage/</u> Note: It is a specific manual that only uses some of the functionality of ZooImage. For more information consult ZooImage manuals and website.

12. Zooplankton Tutorial using an Spread Sheet

12.2.1. Introduction

In this tutorial, an example of 10 zooplankton images is used to show you the process of image treatment done by the software. These colour images are acquired from scanner colour connected to a computer. They proceed from specialists of Azti Tecnalia, and they were selected from a series of sample realized across the Bay of Biscay. This data set, provided with ZooImage, allows you to test the software. Because all photographs are not succeeded, the data set presents a gap in the name of images (the seventh photography is missed). The software can take this sinning in consideration during the importation of images (see below). For all this process a Spread Sheet is going to be used for introducing metadata to make more easy and comfortable the process to technicians. In this example a excel file is used, but it can be used any other kind of Spread Sheet.

12.2.2. Resumed advices

- 1. Give names like p-0001.jpg to your samples instead of p-1.jpg. There is some automatic renamers out there. Be carefull with missing stations.
- 2. Remove from spread sheet stations where there is no image.
- 3. Use the current date format (yyyy-mm-dd): 2005-12-22.
- 4. Use "." notation for decimal number.
- 5. Do not change order or names of colums in the excel file.
- 6. Random forest can not have empty folders in the training set, neither only one item. It should hava at least two.

12.2.2. Scanning images

An advice: Give names like p-0001.jpg to your samples instead of p-1.jpg.

12.2.1. Getting ready with the spread sheet

Use the spread sheet of the example has a template, feel free to change or adapt it to your necessities. For your consideration:



- 1. In the spread sheet there will be fields that have values directly; you just time the correct one for your samples.
- 2. Or the field can be a calculated one, this is to save time; most of times, instead of modifying that field, you should modify the fields that is the source for the calculated value.
- 3. The order of columns should not be altered, you can add more columns at the end, but do not change the existing ones, or ZooImage could not work properly and you will not be able to know why (working on improving this).
- 4. The name of columns should not be changed or ZooImage will not work properly. The names are case sensitive.
- 5. Be careful with dates format, it have to be yyyy-mm-dd. But be careful sometimes excel shows that format, but if you go to the field, you can see in the top that is storing it with another representation.
- 6. Preferably use "." notation, instead of "," for decimal amounts. We are working in doing this indifferent.
- 7. SubPart should have at least four digits of decimal precision.
- 8. VolIni should have at least three digits of decimal precision

12.2.2. Import images

Prepare an empty directory on your hard disk (let's say, C:\Spread-Sheet, but you can freely choose another partition or directory name).

Change the active directory there, using the Options \rightarrow Change active dir... menu and select that directory.



Select Options \rightarrow Change active dir...in the menu





Select the directory you just created



Your directory is now the active one, as you can see in the assistant status bar.

Copy the "SpreadSheet-example" in this directory that can be downloaded from the ZooImage WebSite.



You should have something like this: FALTA CAMBIAR IMAGEN

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🕀 🧰 ZooImage-example		4	3

Exporting the table from Microsoft Excel

Open ZooImage-template.xls into Microsoft Excel. This file is already complete for our ten example images, but you can then see how it should look. It can be used has guide to put your own data.

	A	В	С	D	Е	F	G	Н	1	J	К	L	M	N 🗖
1	Sample	Image	Cam	Туре	Stn	<u>Date</u>	<u>Fecha</u>	<u>LAT_PV</u>	LONG_PV	T³S	<u>Vollni</u>	<u>vol probeta</u>	vol alicuota	SubPart
2	BIO.1998-5-18.P0001+A	0001	BIO	А	p-1	1998-05-18	18-5-98	432850	25107	16.6	8.1207	216	6	0.02777777
3	BIO.1998-5-18.P0002+A	0002	BIO	А	p-2	1998-05-18	18-5-98	433151	25167	17.0	9.0731	232	6	0.02586208
4	BIO.1998-5-18.P0003+A	0003	BIO	A	p-3	1998-05-18	18-5-98	433448	25168	16.2	8.3525	234	6	0.02564102
5	BIO.1998-5-18.P0004+A	0004	BIO	А	p4	1998-05-18	18-5-98	433751	25177	15.6	9.0250	202	6	0.0297029;
6	BIO.1998-5-18.P0005+A	0005	BIO	A	p-5	1998-05-18	18-5-98	434055	25185	15.6	8.9633	206	6	0.02912621
7	BIO.1998-5-18.P0006+A	0006	BIO	А	p-6	1998-05-18	18-5-98	434352	25191	16.0	9.1961	222	6	0.02702702
8	BIO.1998-5-18.P0007+A	0007	BIO	А	p-7	1998-05-18	18-5-98	434651	25195	15.5	9.0371	222	6	0.02702702
9	BIO.1998-5-18.P0008+A	0008	BIO	А	p-8	1998-05-18	18-5-98	434951	25201	15.7	9.5010	220	6	0.02727272
10	BIO.1998-5-18.P0009+A	0009	BIO	А	p.9	1998-05-18	18-5-98	435258	25201	15.3	9.9051	224	6	0.02678571
11	BIO.1998-5-18.P0010+A	0010	BIO	A	p-10	1998-05-18	18-5-98	435549	25205	15.1	9.3791	220	6	0.02727272
12														

In our example, we have ten samples and ten images, one image for each sample (in a realworld application, you will have, of course, much more samples and many more images per sample



to process... but the mechanism remains essentially the same). You must create a table with the first column having the following headers: 'Sample', 'Image', 'Campain', 'Type', 'Stn' and 'Date'. This fields must exist with that name and in that order. VollIni and SubPart must exist too, with that name, but can be in any order. 'Sample' is the name of the different samples. 'Image' is the list of sequences of the images to use for each sample. All the other columns are calibrations and quantitative determinations of the. You can add new column like here with "LAT_PV", this new column will be automatically considered by the software during importation. BUT NEVER CHANGE ORDER OR NAME OF FIELDS IN BLUE. AND NEVER CHANGE NAME OF FIELDS IN ORANGE. In addition, this fields always need to have data.

Once this table is compiled, save it in plain text format. Select File \rightarrow save as... menu entry.

N	licrosoft Excel - ZooImage-template.txt										_ 8 ×
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9	BIO.1998-5-18.P0008+A 0008 BIO A	p-8	1998-05-18	18-5-98	434951	25201	15.7	9.5010	220	6	0.02727272
10	BIO.1998-5-18.P0009+A 0009 BIO A	p.9	1998-05-18	18-5-98	435258	25201	15.3	9.9051	224	6	0.02678571
11	BIO.1998-5-18.P0010+A 0010 BIO A	p-10	1998-05-18	18-5-98	435549	25205	15.1	9.3791	220	6	0.02727272

In the Save as dialog box, change the type to 'Text (Tab delimited) (*.txt)'. MAKE SURE THERE IS NO EMPTY LINES AT THE END OF THE FILE.



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A couple of warning messages will be displayed, but you can ignore them (just click 'OK' and 'Yes', respectively).

At the end, you should have a file ZooImage-template.txt file created in the same directory as your original ZooImage-template.xls file. **Close Excel** (this is very important, otherwise, any other program cannot access the file you just created!). It is possible that you have to replace the existing .txt file by the new.

Proceeding the table to import images and built the metadata files: first importation method

Whether you created your table with Microsoft Excel or OpenOffice Calc, you should end up with something similar to this, when opened in a plain text editor.



11.

Jose Antonio Fernandes My research: http://www.sc.ehu.es/ccwbayes/members/jafernandes/ AZTI - Tecnalia / Unidad de Investigación Marina Herrera kaia portualdea z/g 20110 Pasaia (Gipuzkoa) Tel: +34 943 004 800 (Ext.848) - Fax: +34 943 004 801 e-mail: jfernandes@pas.azti.es www.azti.es ; www.tecnalia.info

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BIO.1998-5-	18.P0005+	A 0005	BIO	A	p-5	1998-05-18	18
BIO.1998-5-	18.P0006+	A 0006	BIO	A	p-6	1998-05-18	18
BIO.1998-5-	18.P0007+	A 0007	BIO	A	p-7	1998-05-18	18
BIO.1998-5-	18.P0008+	A 0008	BIO	A	p-8	1998-05-18	18
BIO.1998-5-	18.P0009+	A 0009	BIO	A	p-9	1998-05-18	18
BIO.1998-5-	18.P0010+	A 0010	BIO	A	p-10	1998-05-18	18

This file, together with the ImportTemplate.zie file, located in the same directory, will tell to ZooImage how to compile instructions to import your images. We present just bellow the content of the ImportTemplate.zie file for our example images.

ImportTemplate.zie has various parameters: [Table to do]

[Image]:	Various parameters	of the image	acquisition	system (in our case,	a scanner).
	1	0	1	~		

[Import]: *FilenamePattern=Phyto_<4>.jpg* : Name of the file with 4 descriptives numbers.

FractionPattern=: Fraction digitized of the sample.

Convert= Software used to convert the raw image into an other readable format.

FileExt= Extension name of the file format.

FileConv= Convention parameters to use to transform the other formar into a jpg format.

Return= Parameters of the program to convert he raw data in an other format.

FileExt2=jpg : Final format.

Nmin=5 : Minimum number of picture for each sample (default value).

Nmax=5 : Maximum number of picture for each sample (default value).

[Fraction]: Code=A or B :Size fraction of the sample (i.e : A= -50 μ m, B= +50 μ m).



[Calibration]: *PixelSize* : Size of the pixel. *PixelUnit* : µm in our case.

[Subsample]: *SubPart=NA* :Subsampling part.

SubMethod= Subsampling method.

CellPart=????

Replicates=1 : Number of replicate or name of replicat???.

VolIni= number of cubic meter filtred by the net.

VolPrec=Precision of the net sample.

ImportTemplate.zie	
🗾 Eile Edit Search Project View Format Column Macro Advanced <u>W</u> indow <u>H</u> elp	_ 8 ×
211	-
[Image]	
Author= AZTI - Tecnalia - Unidad de Investigación Marina	
ImageType=trans 8bits color 600dpi	
Hardware=hp Scanjet 8200	
Software=Digital Imaging	
[Import]	
FilenamePattern=p-<4>.jpg	
FractionPattern=	
SubsamplePattern=	
Convert=	
Return=	
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[Fraction]	
Code=A	
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SubMethod=volumetrv	
CellPart=1.00	
Replicates=1	
VolIni=	
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Now click on the second button on the toolbar, the one with the following icon:





Or select Analyze \rightarrow Import images... in the menu.

🚏 ZooImage1 assistant												
Anal	yze Objec	s Apps	Functions	Utilities H	lelp							
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ZooImage shows a 'Select data to import...' dialog box. First change type files of type field

to 'Table and importTemplate.zie (*.txt)'.

Select data to in	nport						?	×
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Then, select the table you just saved from Excel or OpenOffice Calc:

ZooImage processes the table, converts the images and automatically creates the associated metadata files (look at the activity printed in the 'R Console' window):



R Console File Edit Misc Packages Help ZooImage ٠ Loading required package: utils Loading required package: tcltk Loading Tcl/Tk interface ... done Loading required package: tcltk2 Loading required package: svMisc Loading required package: svWidgets Loading required package: svDialogs Creating .zie file... ... ok! Reading Filemap... Checking all lines in the .zie file for raw images... ... OK! Processing all lines in the .zie file (import images and make .zim files)... ...OK! -- Done! --> -€

At the end of the process, a log file is displayed with a detail of the operations done, and possibly, explicit error messages in case of missing or wrong images for instance:



R ZooImage1 log	
File Edit	
=== ZooImage1 log started 2007-05-23 01:11:49 ===	1
Creating .zie file	
Creating .zie file	
Reading Filemap OK!	
Checking all lines in the .zie file for raw images OK!	
Processing all lines in the .zie file (import images and make .zim files)	· 📃
Writing .zim file for sample 'BIO.1998-5-18.PO001+A'	
Processing image 'p-0001.jpg	
Writing .zim file for sample 'BIO.1998-5-18.PO002+A'	
Processing image 'p-0002.jpg	
Writing .zim file for sample 'BIO.1998-5-18.PO003+A'	
Processing image 'p-0003.jpg	
Writing .zim file for sample 'BIO.1998-5-18.PO004+A'	
Processing image 'p-0004.jpg	
Writing .zim file for sample 'BIO.1998-5-18.PUUU5+A'	
Processing image 'p-0005.jpg	
Writing .zim file for sample 'BIO.1998-5-18.PUUU6+A'	
Processing image 'p-0006.jpg	
Writing .zim file for sample "Bio.1996-5-16.P000/+A"	
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Flocessing mage p-oolo.jpg	
OK, no error found,	
	► //.

This is the typical way of working for ZooImage: the program is made to process in batch many images. You can leave the program unattended because it will give an informative message about problems encountered. Also, for most complex tasks, a first quick pass is programmed to check if all files and data are there, so that you can let it work during the night once this first pass is successful. Then, most of the time, the program can recover from an error and will simply process the following files without interruption.

At this stage, you have imported all your images into ZooImage. Here is what you have :



🚞 Spread-Sheet			_ 🗆 🗵								
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ImportTemplate.zie	1 KB	ZooImage Erratum	25/01/2007 18:10								
📃 ZooImage-template.txt	2 KB	Documento de texto	22/05/2007 20:57								
ZooImage-template.xls	27 KB	Microsoft Excel Wor	22/05/2007 20:56								
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BIO.1998-5-18.P0003+A.zim	1 KB	ZooImage Metadata	23/05/2007 1:12								
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BIO.1998-5-18.P0010+A.zim	1 KB	ZooImage Metadata	23/05/2007 1:12								

You can see that your images have disappeared from your directory. Instead place, you have PIEx-01+A.zim and PIEx-02+A.zim files, together with the new re-named images as .tif or .jpg, depending on the original source.

For the next step, it is necessary to have .jpg formatted images on this directory, specially if we want to process images in colour. In this case, we have to rename the images changing the extension from ".tif" to ".jpg".

At the end, we should have (depending on the version of *Zooimage* this could appear slightly changed):

- .txt file
- . xls file
- .zim files
- .jpg files (or .tif)
- "_raw" and "_work" subdirectories:
 - Original images (.tif) (renamed, depending on version)



.zie: Original template and template plus data

Depending on the process and Zooimage version, the "_raw" or the "_work"

directory is used during processing.

BI0.1998-5-18.P0001+A.zim

<pre>[Image] Author= AZTI - Tecnalia - Unidad de Investigación Marina ImageType=trans &bits color 600dpi Hardware=hp Scanjet 8200 Software=Digital Imaging [Import] FilenamePattern=p-<4>.jpg FractionPattern= SubsamplePattern= Convert= Return= FileExt= FileConv= FileExt2=jpg Nmin=5 Nmax=5 [Fraction] Code=A Min=-1 Max=-1 [Subsample] SubPart=0.027777778 SubMethod=volumetry CellPart=1.00 Replicates=1 VolIni=8.1207 VolPrec= CellPart=1</pre>	No.	🖉 <u>F</u> ile	Edit	<u>S</u> earch	Project	<u>V</u> iew	Forma <u>t</u>	Column	Macro	<u>A</u> dvanced	<u>W</u> indow	He
<pre>[Image] Author= AZTI - Tecnalia - Unidad de Investigación Marina ImageType=trans 8bits color 600dpi Hardware=hp Scanjet 8200 Software=Digital Imaging [Import] FilenamePattern=p-<4>.jpg FractionPattern= SubsamplePattern= Convert= Return= FileExt= FileConv= FileExt= FileConv= FileExt2=jpg Nmin=5 Nmax=5 [Fraction] Code=A Min=-1 Max=-1 [Subsample] SubPart=0.027777778 SubMethod=volumetry CellPart=1.00 Replicates=1 VolIni=8.1207 VolPrec= CellPart=1</pre>	Z	I1										
<pre>Author= AZTI - Tecnalia - Unidad de Investigación Marina ImageType=trans 8bits color 600dpi Hardware=hp Scanjet 8200 Software=Digital Imaging [Import] FilenamePattern=p-<4>.jpg FractionPattern= SubsamplePattern= Convert= Return= FileExt= FileConv= FileExt= FileConv= FileExt2=jpg Nmin=5 Nmax=5 [Fraction] Code=A Min=-1 Max=-1 [Subsample] SubPart=0.027777778 SubMethod=volumetry CellPart=1.00 Replicates=1 VolIni=8.1207 VolPrec= CellPart=1</pre>	[Imag	e]									
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Replicates=1 VolIni=8.1207 VolPrec= CellPart=1	c	ellP	art=	1.00								
VolIni=8.1207 VolPrec= CellPart=1	R	epli	cate	s=1								
VolPrec= CellPart=1	۱v	olIn	i=8.	1207								
CellPart=1	۱v	olPr	ec=									
	C	ellP	art=	1								

These are the ZooImage Metadata files that give all the information required to further process the images. You have also two subdirectories: _raw and _work.



🚞 _raw			
Archivo Edición Ver Favorito	os Herramientas	Ayuda	A
🔾 Atrás 🝷 🕥 – 🏂 🔎	Búsqueda 🔀	Carpetas 🛛 🕼 🎲	X 🍤 💷 -
Dirección 🛅 C:\Spread-Sheet_rav	V		💌 🄁 Ir
Nombre 🔺	Tamaño	Тіро	Fecha de modificación
Import_ZooImage-template.zie	2 KB	ZooImage Erratum	23/05/2007 1:11
p-0001.jpg	801 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0002.jpg	539 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0003.jpg	450 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0004.jpg	593 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0005.jpg	582 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0006.jpg	467 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0007.jpg	363 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0008.jpg	405 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0009.jpg	551 KB	ACDSee JPEG Image	23/05/2007 1:12
p-0010.jpg	447 KB	ACDSee JPEG Image	23/05/2007 1:12

An Import_ZooImage-template.zie file was also compiled and created. It can be used instead of the Table + ImportTemplate.zie files to tell to ZooImage how to reimport those images.

12.2.3. Process images

To process your images, use the menu entry Analyze \rightarrow Process images..., the shortcut Ctrl+J, or click on the third button in the toolbar.

🕆 ZooImage1 assistant											
Analyze	Objects	Apps Fund	ctions	Utilities Help	ı.						
lõ		Proce		Jes	2			<i>I</i>	6	Ê	٢
Ready - C	:/Spread-9	Sheet									

Then, a dialogue is displayed to advertise you to close R in case of computer with low Ram memory.



ZooImage1 picture processing		×
	Once images are acquired and imported into ZooImage1 (they have correct associated metadata), they must be processed. To do so, start 'ImageJ' (just click 'OK') and select the method for your images in 'Plugins -> ZooImage1'. For very large images, or on computers with limited RAM memory, it is advised to close all other programs. Check the option below to close R in this case.	imported into ZooImage1 metadata), they must be ed. st click 'OK') and select n 'Plugins -> ZooImage1'. n computers with limited close all other programs. o close R in this case.
ОК	ancel Help	

For our images, we have to select the Scanner Color plugin.

🛓 ImageJ			
File Edit Image Process Analyze	Plugins Window	Help	
	Macros	•	1 🎢 🔪
Angle tool	Shortcuts	•	
-	Utilities	•	
	New		
	Edit		
	Compile and Run		
	Analvze	•	
	Color	•	
	Demos	•	
	FIT	•	
	Filters	•	
	Graphics	•	
	Input-Output	•	
	Macros	•	
	Stacks	•	
	ZooPhytolmage	Þ	Macrophoto Gray16
			Microscope Color
			Scanner Color
			Scanner Gray16

The plugin first asks you to select a .zim file. Do not select on image file here. The zim



files and <u>renamed jpg images</u> must be in the same directory. Depending the version of ZooImage, the files might not be moved automatically and have to be done manually. It is recommended to move .jpg files to the directory where are the zim files, in this case the root <u>'C:\Spread-Sheet'</u>.

Open a .zim file			<u>? ×</u>
Look in:	😋 Spread-Sheet	- E	🕂 🎟 -
History Desktop My Documents	 _raw _work BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A BIO.1998-5-18.P0002+A.1 BIO.1998-5-18.P0002+A BIO.1998-5-18.P0003+A.1 BIO.1998-5-18.P0003+A BIO.1998-5-18.P0004+A.1 BIO.1998-5-18.P0004+A.1 BIO.1998-5-18.P0004+A.1 BIO.1998-5-18.P0004+A.1 BIO.1998-5-18.P0004+A.1 	 BIO.1998-5-18.P0005+A BIO.1998-5-18.P0006+A.1 BIO.1998-5-18.P0006+A BIO.1998-5-18.P0007+A.1 BIO.1998-5-18.P0007+A BIO.1998-5-18.P0008+A.1 BIO.1998-5-18.P0008+A BIO.1998-5-18.P0009+A.1 BIO.1998-5-18.P0009+A BIO.1998-5-18.P0009+A BIO.1998-5-18.P0009+A BIO.1998-5-18.P0010+A BIO.1998-5-18.P0010+A 	ImportTemplate ZooImage-template CooImage-template
My Computer	▼ File name: Files of type: All Files (*.*)		 ● ●

The reasons why you have to select the .zim file instead of the corresponding image are:

- We are sure you have metadata associated with the image(s),
- As explained here above, you could have several images for the same sample/fraction. The plugin will process **all** images associated with the selected .zim file, not only one. In the example, we have only one image for each .zim file.

You then have a dialogue box with parameterization of your process:



🛓 ZooImage1 Image F	Processor X
Selected item: BIO	.1998-5-18.P0001+A.zim
🔽 Process all item	ns in this directory?
Read from directory:	
Parameters set:	wide spectrum [0.25 - 20] 💌
Calibration set:	Eosin
🗖 Zip images	
🔽 Analyze particle:	S
🔽 Make vignettes	
🔽 (Sharpen vignett	es)
🗌 Show outlined o	bjects
	OK Cancel

- You can **process all items in this directory** (all images that have associated .zim files), or only that one [*keep this checked now*].
- You can optionally **read images from a different directory**. This function is useful if you saved your large images on DVDs or external disks. You just have to copy the small associated .zim files in your process directory and you point to the directory that contains the images on your DVD [*leave this blank now*].
- Analyze particles: Option that allows you to do the measurements on the particles after processing the images [*leave this option checked now*].
- Make vignettes: Option that allows you to extract small images for each identified object, called 'vignettes' in PhytoImage's terminology [*leave this option checked now*].
- Sharpen vignettes: Option that allows you to apply a "sharpen" filter on the pictures in the vignettes. This often enhances the quality of the vignettes, but is not necessary for some kinds of pictures [*leave this option checked now*].
- Show **outlined objects: Option that allows you to** display a composite image with the detected object outlines superposed to the grayscale image. This is a very useful diagnostic to determine if segmentation and detection of the objects was correct [*So, leave this option*]



checked now].

The show outlined objects option works only for the last picture processed. So, either uncheck process all items in this directory, or be prepared to wait for the last picture to get this diagnostic image! You should zoom in the image (Image \rightarrow Zoom \rightarrow 100% entry menu) and pan it by selecting the hand button and dragging the image content in the window to best see the result.

When you start the process by clicking OK on the dialog box, ImageJ do the following work:

- It opens a Log window and reports its activity in it.
- It opens each image in turn, process it, and possibly measure particles and extract vignettes. You can follow the process on the screen. Note that a scale bar is added in the top-right corner of each vignette for convenience.
- It possibly displays the outlined objects of last picture if it was requested. Also, the last table of measurements is left open for inspection.

🛓 In	nageJ				_	- 🗆 🗵	🛓 Lo	g				- 🗆 🗵
File	File Edit Image Process Analyze Plugins Window Help					File	Edit Font					
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		_			_	_	10/1	O file(s) cor	rectly prod	essed in 24	4 min	
118 Q	(1_OUT (25%) 5v79 41 mm (2810v1876): 8-hit f	OMB					Меа	n time per s	uccessful	y processe	d file: 147	sec
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			¢	9				Ó				
		*						7				
	:						1. 5					
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🛓 R	esults											_ 🗆 🗵
File	Edit Font											
	Label	Area	Mean	StdDev	Mode	Min	Мах	X	Y	XM	YM	Perit
63	BIO.1998-5-18.P0010+A.1	0.0824	148.1522	17.6396	152	116	175	14.2698	66.2989	14.2698	66.2973	1.12
64	BIO.1998-5-18.P0010+A.1	0.1487	153.9880	13.2605	173	128	175	78.5071	66.5685	78.5070	66.5680	1.76
65	BIO.1998-5-18.P0010+A.1	0.0914	143.7059	18.5325	156	107	174	46.7352	67.2395	46.7340	67.2397	1.19
66	BIO.1998-5-18.P0010+A.1	0.1451	171.6914	3.0604	169	164	177	118.7249	68.1876	118.7253	68.1844	3.14
67	BIO.1998-5-18.P0010+A.1	1.5033	91.5387	37.0581	62	59	175	18.1855	68.1128	18.1861	68.1054	6.05
68	BIO.1998-5-18.P0010+A.1	0.0502	152.8929	11.1864	155	134	170	29.9696	67.9185	29.9699	67.9190	0.87
69	BIO.1998-5-18.P0010+A.1	0.0484	162.9259	7.7108	169	150	174	118.5875	69.6540	118.5879	69.6540	0.76
70	BIO.1998-5-18.P0010+A.1	0.0573	162.5000	8.2188	152	149	175	53.8610	69.9040	53.8606	69.9045	0.93
71	BIO.1998-5-18.P0010+A.1	0.1541	170.9070	3.2417	174	165	178	118.6392	71.1159	118.6392	71.1165	2.66
72	BIO.1998-5-18.P0010+A.1	0.0645	162.7778	7.5710	162	147	175	72.7500	71.3166	72.7508	71.3150	0.98 🗸
•												۱



IF ANY PROBLEM APPEARS DURING THIS PROCESS:

<u>If the process failed somewhere</u> look if your images are of the right type, if they are not too big for the RAM memory allocated and if the correct plug-in, parameters set and calibration set where selected. Look at the log file and the images produced in the _work directory to help you track the problem.

If you receive a message with "out of memory" then you must download the last version of ImageJ, actually the one that corrects this "leaking problem" is the beta version, not the last official one. In addition, the memory available to ImageJ can be increased. It is not recommendable to reserve more than 2/3 of Ram available. Select in the menu Edit \rightarrow Options \rightarrow Memory...:





The plug-ins created several files in your _work subdirectory for each processed image:

🗁 _work								
Archivo Edición Ver Favoritos He	Archivo Edición Ver Favoritos Herramientas Ayuda							
😋 Atrás 🔹 🕥 🗸 🏂 🔎 Búsqueda 🛛 🍋 Carpetas 🛛 🕼 🎲 🗙 🌱 💷 -								
Dirección 🛅 C:\Spread-Sheet3_work_wo	vrk							
Nombre 🔺	Tamaño	Tipo	Fecha de modificación					
BIO.1998-5-18.P0001+A.1_dat1.zim	53 KB	ZooImage Metadata	23/05/2007 2:50					
BIO.1998-5-18.P0001+A.1_msk1.gif	24 KB	ACDSee GIF Image	23/05/2007 2:50					
001+A.1_out1.gif	30 KB	ACDSee GIF Image	23/05/2007 2:50					
📴 BIO.1998-5-18.P0001+A.1_vis1.gif	328 KB	ACDSee GIF Image	23/05/2007 2:50					
BIO.1998-5-18.P0002+A.1_dat1.zim	49 KB	ZooImage Metadata	23/05/2007 2:53					
1998-5-18.P0002+A.1_msk1.gif	22 KB	ACDSee GIF Image	23/05/2007 2:53					
002+A.1_out1.gif	25 KB	ACDSee GIF Image	23/05/2007 2:53					
1998-5-18.P0002+A.1_vis1.gif	191 KB	ACDSee GIF Image	23/05/2007 2:53					

In this work directory, are created several images and file:

BIO.1998-5-18.P0001+A.1_dat1.zim: Iinitial raw image renamed during importation.

BIO.1998-5-18.P0001+A.1_msk1.gif: Binary image with the mask used to detect the silhouette of the particles.

BIO.1998-5-18.P0001+A.1_out1.gif: Image with the outline and labels of all particles that are retained after applying a minsize/maxsize filter.

BIO.1998-5-18.P0001+A.1_vis1.gif: 'Visual' image (used to make vignettes for visual identification of the particle by taxonomists).

BIO.1998-5-18.P0001+A.1_dat1.zim: _dat1.zim files associated for each image with all metadata and measurements associated with the image(s).



🏀 BIO	.1998-5-18.P0001+A.1_dat1.zim	- Sc1			_ 8 ×
File E	dit Search View Tools Options	Language Buffers Help			
	🗲 🖬 😡 🚑 🕹 🛍 🖻 🗡	< ြ က Q 🚭			
File Nm Nm	Ext2=jpg in=5 iax=5				_
= [Fr	action]				
Coi Mir Ma	de=A h=-1 x=-1				
← <mark>[Su</mark> Sul Cel Rep Vol Vol Cel	ubsample] bPart=0.027777778 bMethod=volumetry lIPart=1.00 olicates=1 Ini=8.1207 IPrec= IIPart=1				
← [Pr Vei Mir Ma Cal Pro Sta Reo Blu Gre Thi	ocess] rsion=1.0-0 thod=wide spectrum [0.25 - isize=0.25 xSize=20.0 libration=Eosin ocessPixSize=0.04233 ocessPixSize=0.04233 ocessPixUnit=mm aining=haematoxilyn dCoef=0.1 eCoef=0.9 eenCoef=0.8 reshold=125	- 20]			
(Da 1 2 3 4 5 6 7	ata] em	Label BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1 BIO.1998-5-18.P0001+A.1	Area 0.1021 0.0520 0.0753 0.5053 0.0502 0.1451 0.0555	Mean 168.8772 145.8276 154.4286 118.4007 144.6429 139.3704 152.7419	StdC 4.91 22.2 14.0 28.2 20.2 22.5 18.1
•					•





The four images in the _work subdirectory for each initial image after processing them. From left to right and top to bottom: the original image, the mask, the outline and the visual.



🗁 BIO.1998-5-18.P0001							
Archivo Edición Ver Favoritos I	Herramienta	as Ayuda					
🔇 Atrás 👻 🕥 🗸 🏂 🔎 Búsqueda 🦻 Carpetas 🛛 🕼 🎲 🗙 🌱 💷 🗸							
Dirección 🛅 C:\Spread-Sheet3_work\B	IO.1998-5-	18.P0001					
Nombre 🔺	Tamaño	Тіро	Fecha de modificación				
1.jpg BIO.1998-5-18.P0001+A.1_1.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:50				
1998-5-18.P0001+A.1_2.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:50				
1998-5-18.P0001+A.1_3.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:50				
1998-5-18.P0001+A.1_4.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:50				
1998-5-18.P0001+A.1_5.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				
10.1998-5-18.P0001+A.1_6.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				
10.1998-5-18.P0001+A.1_7.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				
10.1998-5-18.P0001+A.1_8.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				
1998-5-18.P0001+A.1_9.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				
10.jpg 🔤 BIO.1998-5-18.P0001+A.1_10.jpg	1 KB	ACDSee JPEG Image	23/05/2007 2:51				

The program also creates an additional subdirectory for each sample. It places a copy of all the related _dat1.zim files (metadata + measurements on all particles) and a series of xxxx_yy.jpg files called 'vignettes', that are small-pictures of each particle with a scale added at the top right of it.

Once the image processing is done, you can close ImageJ and return to ZooImage.



12.2.4. Create ZID files

To finalize your images import/process, you must now build .zid files. In the PhytoImage1 assistant, use the menu entry Analyze \rightarrow Make .zid files..., the shortcut Ctrl+Z, or click on the fourth button in the toolbar.





You have now to create the **.zid files**. These are special *ZooImage/PhytoImage Data* files that contain all you need for the rest of the analysis, but saves as much disk space as possible.

Now, click on the fourth button in the PhytoImage1 assistant:

ZooImage1 data processing	×
	You should have processed all your images now. The next step is to finalize the .zid files (ZooImage Data files). There will be one data file per sample and it is all you need for the next part of your work Once this step succeed, you can free disk space by: 1) Transferring all raw images (or .zip files in the _raw subdirectory) to DVDs (Apps -> CD-DVD burner). 2) Safely delete the whole _work subdirectory (possibly after verification of the process of the images). 3) Remove also .zim files after making a backup. At the end, you should have only .zid files remaining in your working directory. Click 'OK' to proceed (select working directory) ✓ Update also comments of _raw/[images].zip files.
ОК	Cancel Help

By clicking OK, you compute .zid files for your processed samples. The option **update also comments of _raw/[images].zip files** add .zim data as comments to zipped image files (if you selected that option in the process). [*Since we did not zipped images, we should uncheck that option now and click OK*]. You are prompted for a directory where treated data are located. Select "Spread-Sheet" (C:\Spread-Sheet):



Buscar carpeta	? ×
Please choose a directory, then select OK.	
C:\Spread-Sheet_work	
_work	
Plantilla Spread-Sheet work work BIO.1998-5-18.P0001 BIO.1998-5-18.P0002 BIO.1998-5-18.P0003 BIO.1998-5-18.P0004	
Aceptar Cance	elar

ZooImage calculates .zid files and issues a report at the end of the process. For convenience, it first carries out the verification of files just created. Stay in front of the computer during checking. **Make sure there is no error reported once the compression is done.**



R ZooImage1 log		_ _ _ ×
File Edit		
=== ZooImage1 log started 200	D7-05-23 11:29:01 ===	<u> </u>
Verification BIO.1998-5-18.P0001 - OK BIO.1998-5-18.P0002 - OK BIO.1998-5-18.P0003 - OK BIO.1998-5-18.P0004 - OK BIO.1998-5-18.P0005 - OK BIO.1998-5-18.P0006 - OK		
BIO.1998-5-18.P0007 - OK BIO.1998-5-18.P0008 - OK	R ZooImage1 log	-OX
BIO.1998-5-18.P0010 - OK BIO.1998-5-18.P0010 - OK		
OK, no error found	Done, no file to update!	
Compression BIO.1998-5-18.P0001 - OK		
BIO.1998-5-18.PO002 - OK BIO.1998-5-18.PO003 - OK		
BIO.1998-5-18.P0004 - OK BIO.1998-5-18.P0005 - OK		
BIO.1998-5-18.P0006 - OK		
BIO.1998-5-18.P0008 - OK BIO.1998-5-18.P0008 - OK		
BIO.1998-5-18.P0009 - OK BIO.1998-5-18.P0010 - OK		
OK, no error found		<u>_</u>
<u> </u>		► //.

Cleaning the hard disk at the end of the process.

In other tutorials there is a cleaning process explained, but because this is a specific process based in the practices at Azti, here will be no cleaning process. Instead we recommend to copy everything to an external disk for future work. And have a second one has backup. This copies can be unattended using Cobian Free Software. Cobian permits to do syncronization of folders, schedule backups and deals well with long names.

FALTA TUTORIAL COBIAN.

Note that .zid files are a special kind of zipped archives that contain all PhytoImage needs to work with one sample: the _dat1.zim files, all the vignettes, and a dat1.Rdata (compilation of all the data in R format). You can, thus, inspect .zid files easily with programs like WinZip, for instance:



🖼 Filzip - BIO.1998-5-18.P0001.zid											
File Edit Actions Options Extras Help											
New Open - Add Extract	Delete View Encrypt	KV It About Exit									
Folders X	Filename Type	Size	Packed	Ratio	Date / Time	▲					
<u> </u>	🚾 BIO.1998-5-18.P000 JPEG Ima	1,238	1,041	16%	23/05/2007 2	2:51					
12	🚾 BIO.1998-5-18.P000 JPEG Ima	723	542	25%	23/05/2007 2	2:51					
🖃 🕎 BIO.1998-5-18.P0001.zid	🚾 BIO.1998-5-18.P000 JPEG Ima	1,162	1,004	14%	23/05/2007 2	2:51					
BIO.1998-5-18.P0001	🚾 BIO.1998-5-18.P000 JPEG Ima	733	551	25%	23/05/2007 2	2:51					
	BIO.1998-5-18.P0001+A.1_dat1.zim.	53,362	21,319	60%	23/05/2007 2	2:50					
	BIO.1998-5-18.P000 RDATA U	27,352	27,009	1%	23/05/2007 1	1:29 📕					
	•										
C:\Spread-Sheet\BIO.1998-5-18.P00	01.zid 0 entry(ies) selected, 0	КЬ									

12.2.5 Manually classifying vignettes

In order to train the computer to (semi)-automatically recognize phytoplankton taxa on the basis of images measurements done in PhytoImage, you have to make a manual training set. Unfortunately, the 'PhytoImage-example' training does not have enough particles to make a valid training set. If you have access to the IFREMER report and the associated training set, you can follow instructions in SpainBioman tutorial to make a phytoplankton training set with these data. Otherwise, you can switch to the SpainBioman tutorial (**Chapter 12.1**), the principle remains exactly the same for phytoplankton in PhytoImage.

12.2.6. Make training set

To make the training set, use the menu entry Analyze \rightarrow Make training set..., the shortcut Ctrl+M, or click on the fifth button in the toolbar.

Transferred Transferred	nage1 as	ssistant								- IX
Analyze	Objects	Apps Fur	ictions Ut	ilities Help	0					
lo		2		÷2	2		<i>I</i>	6	Ŷ	٢
Ready - C	:/Archivos	de program	a/ZooImag	e/bin/R/R-z	Make trail	ning set				

We are going to choose the option of Another config... to use a specification of classes adjusted to Bay of Biscay. It can be modified later if necessary.

There is a predefined file between the templates that have to be selected:



Select a .zic file.							? ×
Buscar en	: 🔂 Spread	Sheet		•	G 💋 🛛	• 🔝 🕈	
Documentos recientes Escritorio Mis documentos Mi PC	in _raw work Bioman.z	ic					
Mis sitios de red	Nombre:	Bioman.zic				•	Abrir
	Tipo:	Zoolmage Cl	assification Scł	neme (*.zic)		•	Cancelar

After that the folder where to place the training set have to be selected:

Buscar carpeta	? ×
Please choose a directory, then select OK.	
C:\Spread-Sheet	
Spread-Sheet	
dotnetnuke	
🕀 🛅 hitzekinjolasten	
🗄 💼 Inetpub	
⊡ idk-1_5_0-doc	
PlantillasZooImage	
📄 🗁 Spread-Sheet	
raw	
work	
Spread-Sheet2	<u>ل</u> تے .
	•
Aceptar Cance	lar

And give a name to the folder, by defect _train:



Question			
Subdirectory w	here to creat	te the training set:	
,		--- - --	
_train			
	ок	Cancel	

And finally select the Zid files with the vignettes that are going to be used for make the training set, in our case we will have preselected the most interesting ones doing an visual inspection of the original .jpg:

Select one or se	veral Zid files	<u>?</u> ×
Buscar en:	: 🔁 Spread-Sheet 📃 🕓 🤣 🔛 -	
	Craw Cwork BIO.1998-5-18.P0001.zid	
Escritorio	BIO.1998-5-18.P0002.zid BIO.1998-5-18.P0003.zid BIO.1998-5-18.P0004.zid BIO.1998-5-18.P0004.zid	
	BIO.1998-5-18.P0006.zid BIO.1998-5-18.P0007.zid BIO.1998-5-18.P0007.zid BIO.1998-5-18.P0008.zid	
MIS documentos	PBIO.1998-5-18.P0009.zid PBIO.1998-5-18.P0010.zid	
Mi PC		
Mis sitios de red	Nombre:	orir
	Tipo: Zoolmage data files (*.zid) Can	celar

Because in this example there is only 10 images, all will be selected, after the process look at log files to see if all were processed successfully:



R ZooImage1 log	_ D ×
File Edit	
=== ZooImage1 log started 2007-05-23 17:54:33 ===	1
Extracting data C:\Spread-Sheet\BIO.1998-5-18.P0010.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0001.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0002.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0004.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0005.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0006.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0007.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0008.zid - data C:\Spread-Sheet\BIO.1998-5-18.P0008.zid - data	
Extracting vignettes	
C:\Spread-Sheet\BIO.1998-5-18.P0010.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0001.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0002.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0004.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0004.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0005.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0006.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0007.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0008.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0008.zid - vignettes C:\Spread-Sheet\BIO.1998-5-18.P0009.zid - vignettes	
Making directories C:/Spread-Sheet/_train/_/_unused_ C:/Spread-Sheet/_train/_/badfocus C:/Spread-Sheet/_train/_/badimage	•

The XnView will open to be able to arrange the different particles in their class. Just move the particle or vignette to the corresponding folder, do click on the image and without leaving the button drag the image to the appropriate folder:





To revise the particles classified, click in the folder of the class:





If you want to make a new class, you only have to make a folder for it:





Once you have finish, just close XnView. You can reopen it if you did not finish executing:

C:\Archivos de programa\ZooImage\bin\XnView\ xnview.exe

12.2.7 Reading training set

In order to do a classifier the training set data must be read, use the menu entry Analyze \rightarrow Read training set..., the shortcut Ctrl+T, or click on the sixth button in the toolbar.

Tool 🕐	nage1 as	ssistant									- I X
Analyze	Objects	Apps Fur	nctions U	tilities Help							
16		2		Ê	2			3	61	Ê	٢
Ready - C	:/Spread-9	5heet				Read traini	ng set				

Select the folder where training set was previously created:





Give a name to the object that will be created in R:

Question	
Name for the ZITrain object:	
ZItrain	
OK Cancel	

After loading, statistics of the ZooPlankton classes are shown:



R Console				
File Edit Misc Packages	Help ZooImage			
Classification sta	ats:			
artifact 72 Copepoda_small 46 Zooplankton_round 15	Copepod_medium 152 Decapoda_larvae 3 Zooplankton_small 85	Copepoda_large 129 Euphausid_like 9	copepoda_multiple 8 marine_snow 13	
Proportions per c	lass:			
artifact 13.5338346 Copepoda_small 8.6466165 Zooplankton_round 2.8195489	Copepod_medium 28.5714286 Decapoda_larvae 0.5639098 Zooplankton_small 15.9774436	Copepoda_large 24.2481203 Euphausid_like 1.6917293	copepoda_multiple 1.5037594 marine_snow 2.4436090	
4				▶ //

12.2.8 Make classifier

Now a classifier can be created, use the menu entry Analyze \rightarrow Make classifier..., the shortcut Ctrl+C, or click on the seveth button in the toolbar.

Transistant											
Analyze	Objects	Apps Fu	inctions U	tilities Help							
lõ	3	2		£	2	Make classifier		6	Ŷ	٢	
Ready - C:/Spread-Sheet											

Then the type of classifier must be specified. For different problems one can be better than other. I recommend to choose Random Forest or k-nearest neighbour:



ZooImage1 make classifier	×
	This is a simplified version of the classifiers where you just need to select one algorithm. Warning! Many algorithms have parameters to be fine-tuned before efficient use and this must be done for each specific data set! Here, only default parameters that have proven efficient with plankton are applied automatically. Some methods already work pretty well that way.
	Learn using an algorithm:
	🔿 linear discriminant analysis
Ca.	C recursive partitioning (tree)
\sim	C k-nearest neighbour
	C learning vector quantization
	C neural network
	🖸 random forest
ок	Cancel Help

12.2.9 Analyse Classifier

ZooImage have this utility to see a confusion matrix to evaluate how 'good' is the classifier. An additional tool is being developed. use the menu entry Analyze \rightarrow Make classifier..., the shortcut Ctrl+C, or click on the seveth button in the toolbar.

Transistant												<u> </u>
Analyze	Analyze Objects Apps Functions Utilities Help											
lo		2		Ð	2			3		6	Ŷ	٢
Ready - C:/Spread-Sheet Analyze classifier												

The confusion matrix helps to evaluate the classifier. If the error is big or there is a lot of confusion, the training set must be done. The diagonal are the instances well classified:



R Console		
File Edit Misc Packages Help ZooImage		
Manual training set data collected in	n 'ZItrain'	_
Classification stats:		
artifact Copepod_medium	Copepoda_large copepoda_multiple	
72 152	129 8	
Copepoda small Decapoda larvae	Euphausid like marine snow	
46 3	9 13	
Zooplankton round Zooplankton small		
15 85		
Proportions per class:		
artifact Copepod_medium	Copepoda_large_copepoda_multiple	
13.5338346 28.5714286	24.2481203 1.5037594	
Copepoda_small Decapoda_larvae	Euphausid_like marine_snow	
8.6466165 0.5639098	1.6917293 2.4436090	
Zooplankton_round Zooplankton_small		
2.8195489 15.9774436		
Erro en analyzeClass() : No current c	classifier. Please, make one first!	
>		-
<u>۲</u>		

12.2.10 Edit Samples description

Instead of use this facility, there is an alternative similar to zim files. Open the xls file, and fill the second sheet called ForZis. Some field are generated automatically to save time and to avoid error. Be careful with dates, must be in format yyyy-mm-dd or ZooImage will crash and you will not know why:

M	🔀 Microsoft Excel - ZooImage-template.xls													
	Bile Edit View Insert Format Iools Data Window Help PDF de Adobe													
] D 😅 🖬 🚭 🔃 💞 🐰 🛍 🛍 ∽ - 🍓 Σ ≉ 🛃 🛍 🖓 🗳 Arial 🔹 10 - 🖪 Ζ Ψ ≡ € ‰ +% Ξ -													
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1	Label	Code	SCS	Series	Cruise	Station	Date	Time	TimeZone	Latitude	Longitude Co			
2	BIO.1998-5-18.P00	p-1	BIO	BI01998	BIO	1	1998-05-18	10	10	3.9889	-43.475			
3	BIO.1998-5-18.P00	p-2	BIO	BI01998	BIO	2	1998-05-18	10	10	3.9889	-43.5252			
4	BIO.1998-5-18.P00	р-З	BIO	BI01998	BIO	3	1998-05-18	10	10	3.9889	-43.5747			
5	BIO.1998-5-18.P00	p-4	BIO	BIO1998	BIO	4	1998-05-18	10	10	3.9889	-43.6252			
6	BIO.1998-5-18.P00	p-5	BIO	BI01998	BIO	5	1998-05-18	10	10	3.9889	-43.6758			
7	BIO.1998-5-18.P00	р-6	BIO	BI01998	BIO	6	1998-05-18	10	10	3.9889	-43.7253			
8	BIO.1998-5-18.P00	p-7	BIO	BI01998	BIO	7	1998-05-18	10	10	3.9889	-43.7752			
9	BIO.1998-5-18.P00	р-8	BIO	BIO1998	BIO	8	1998-05-18	10	10	3.9889	-43.8252			
10	BIO.1998-5-18.P00	р-9	BIO	BI01998	BIO	9	1998-05-18	10	10	3.9889	-43.8764			
11	BIO.1998-5-18.P00	p-10	BIO	BIO1998	BIO	10	1998-05-18	10	10	3.9889	-43.9249			
12														



After completion for each sample, you must save it as a save it in plain text format. Select

File \rightarrow save as... menu entry.

	🔀 Microsoft Excel - ZooImage-template.xls											
	Elle Edit View Insert Format Tools Data Window Help PDF de Adobe											
) 🗋 <u>N</u> ew Ctrl+N	X Image: Ima										
i I 🖷	🔁 Open Ctrl+O	Ctrl+0										
	Save As	Loba	4									
		- Labe		D	F	F	G	н	1		K	
1	- 👌 Print Pre <u>v</u> iew	de	SCS	Series	Cruise	Station	Date	Time	TimeZone	Latitude	Longitude	
2	¥		BIO	BIO1998	BIO	1	1998-05-18	10	10	3.9889	-43.475	
3	BIO.1998-5-18.P00 p	-2	BIO	BI01998	BIO	2	1998-05-18	10	10	3.9889	-43.5252	
4	BIO.1998-5-18.P00 p	-3	BIO	BIO1998	BIO	3	1998-05-18	10	10	3.9889	-43.5747	
5	BIO.1998-5-18.P00 p	-4	BIO	BIO1998	BIO	4	1998-05-18	10	10	3.9889	-43.6252	
6	BIO.1998-5-18.P00 p	-5	BIO	BIO1998	BIO	5	1998-05-18	10	10	3.9889	-43.6758	
7	BIO.1998-5-18.P00 p	-6	BIO	BIO1998	BIO	6	1998-05-18	10	10	3.9889	-43.7253	
8	BIO.1998-5-18.P00 p	-7	BIO	BIO1998	BIO	7	1998-05-18	10	10	3.9889	-43.7752	
9	BIO.1998-5-18.P00 p	-8	BIO	BIO1998	BIO	8	1998-05-18	10	10	3.9889	-43.8252	
10	BIO.1998-5-18.P00 p	-9	BIO	BIO1998	BIO	9	1998-05-18	10	10	3.9889	-43.8764	
11	BIO.1998-5-18.P00 p	-10	BIO	BIO1998	BIO	10	1998-05-18	10	10	3.9889	-43.9249	
40												

In the Save as dialog box, change the type to 'Text (Tab delimited) (*.txt)'.

Save As								<u>?</u> ×
Save in:	🛅 PlantillasZ	ooImage	•	← 🗈	$\mathbf{Q}\times$	👛 🎞 🗸	Too <u>l</u> s 👻	
() History	🗐 ZooImage-I	emplate.txt						
Mis documentos								
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<u>(</u>	J File name:	ForZisltxt				•		Save
Mis sitios de red	Save as <u>t</u> ype:	Text (Tab delin	nited) (*.txt)			•		Cancel

Open the text file with notepad or another editor, select all the content (Ctrl + E or Ctrl + A) and copy it (Ctrl + C):



📕 Forž	🕞 ForZis.txt - Bloc de notas											
Archivo	Edición Formato	Ver Ayud	a									
Label	Deshacer	Ctrl+Z	ries	Cruise	Station	Date	Time	TimeZon	e	Latitud	e	Longitude
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BIO.1	Copiar	Ctrl+C	ite 1	BIO	BI01998	BIO	1	1998-05	-18	10	10	3.9889
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-43.6	2 Seleccionar todo	Ctrl+E	in	Fosin		220	10	50	9.02497	7963	1	OBLICUO 2
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-43.7	7518217 4% buffere	· Forma	lin	Fosin		220	10	50	9.03713	3821	1	OBLICUO 2
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43.8	4% buffere	d forma	lin	Eosin		220 15.7	10	50	9.500971 A	3803	1	OBLICUO 2
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віо.1	4% buffere 998-5-18.P001	d forma 0 p	lin -10	Eosin BIO	BI01998	15.3 BIO	10	1998-05	А -18	10	10	3.9889
-43.9	4% buffere	d forma	lin	Eosin		220 15.1	10	50	9.37906 A	391	1	OBLICUO 2

Open the Description.zis that is with the templates file doing doble click on the file:



Description.zis * Sc1				<u>_ 8 ×</u>
File Edit Search View Tools Op	otions Language Buffers Help			
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[Description]				
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Name= Bioman 1998 samp	les			
Objective=	1			
Description=				
Contact= Xabier Irigoven.	Jose Antonio Fernandes S	alvador		
Email= xiriqoien@pas.azti	.es, jfernandes@pas.azti.es	5		
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- [Complec]				
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BIO.1998-5-18.P0002		BIO	BI01998	→BIO —
BIO.1998-5-18.P0003		BIO	BIO1998	→BIO —
BIO.1998-5-18.P0004		BIO	BIO1998	BIO
BIO.1998-5-18.P0005	>p-5	BIO	BIO1998	⇒BIO
BIO.1998-5-18.P0006	→p-6	BIO	>BIO1998	BIO
BIO.1998-5-18.P0007			>BIO1998	BIO
BIO.1998-5-18.P0008	>p-8	BIO	>BIO1998	BIO
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	2	Redo	Ctrl+Y				
-	<u></u>	Cut	Ctrl+X				
	Ic	CODV	Ctrl+C				
	N	Paste	Ctrl+V				
	Ir	Duplicate	Ctrl+D				
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	в	Expand Abbreviation	Ctrl+B	8		AZTI Tecnalia	—→Spain –
		Insert Abbreviation	Ctrl+Shift+R				
=	19	Block Comment or Uncomment	Ctrl+O				
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	BI	D.1998-5-18.P0002	p-2		BIO	BIO1998	BIO
	BI	D.1998-5-18.P0003	р-3		BIO	BIO1998	BIO
	BIC	D.1998-5-18.P0004	p-4		BIO	BIO1998	BIO
	BIC	D.1998-5-18.P0005	p-5		BIO	BIO1998	BIO
	BIC	D.1998-5-18.PUUU6	p-6		BIO	BIO1998	BIO
	BI	J.1998-5-18.PUUU/ C.1000-E_10 D0000	p-7		BIO	BIO1009	BIO
	BI	7 1998-5-18 DAAAA	p-0 n-9		BIO	BIO1998	BIO
	BIC	D.1998-5-18.P0010	n-10		BIO	BI01998	BIO

12.2.11 Process samples



12.2.12 View results



12.2.13 Export results

