



Supplementary file: Step-by-step guide to run MARTA

Automatic quantification of cardiomyocyte dimensions and Connexin 43 lateralization in fluorescence images

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Introduction

MARTA software is designed to process images of cardiac tissue obtained by confocal fluorescence microscopy. The objective of this software is to measure morphological characteristics of cardiomyocytes (CM) and to estimate the amount of CX43 as well as its lateralized proportion from longitudinal cardiac tissue sections. To do this, the software can process a single merged image or multiple separate images (each corresponding to an independent marker).

The steps to run the developed software in 64-bit Windows OS are provided below in <u>video</u> <u>format</u>.



Video Demonstration

Step-by-step explanation

1. Download the program available in the GitHub repository. Select code and Download ZIP (<u>https://github.com/tonibois/MARTA</u>):

P master ▾ P 1 branch ▷ 0 tags		Go to file
tonibois Update README.md		Clone with HTTPS ③ Use SSH Use Git or checkout with SVN using the web URL.
🗅 .gitattributes	Initial commit	https://github.com/tonibois/MARTA.git
🗅 .gitignore	Initial commit	
MARTA_linux	added linux version exe	(남) Open with GitHub Desktop
MARTA_win.exe	added linux version exe	Download ZIP
Parameters_a.png	filename change	yesterday
Parameters_e_default.png	filename change	yesterday
🗅 README.md	Update README.md	10 minutes ago
🗅 a_c1.tif	3rd update	3 days ago
🗅 a_c2.tif	3rd update	3 days ago
🗅 a_c3.tif	3rd update	3 days ago
🗅 e.tif	3rd update	3 days ago

2. Once the ZIP has been downloaded, unzip it into a folder:

				103 110101103 9	lae se requieren.				
	Ŧ	Compressed Folder Tools	MANUAL_USUA	ARIO				- 0	
File Ho	ome Share View	Extract							
Pin to Quick d	Copy Paste Sho	tcut to * to *	Nelete Rename	New tern •	Properties	Select all Select none Invert selection			
_	Clipboard	Organit	ize	New	Open	Select			
$\leftarrow \rightarrow \cdot$	1 A This PC > Des	top > POSTDOC2019_20	120 > SEPTIEMBR	E2020 > MANUAL_USU	ARIO		✓ ð S	earch MANUAL_USUARIO	
		Name	^	Date modified	Type	Size			
📌 Quick a	access	MARTA marte	u tin	9/8/2020 09-47	PM WinRAR 7IP archi	an 80.025 KB			
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Firmar con Aut	itoFirma								
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Open with Win	nRAR								
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Scan with Win	ndows Derender								
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Cut									_
Сору									8::
Create shortcu	ut								
Delete									
Rename									
Properties									

3. Navigate to find the executable file MARTA_v3.exe in the unzipped folder:



To process images, it is important that the images to be processed are located in the same directory as the executable file MARTA_v3.exe. Two test cases have been included in the repository, which correspond to images a and e:

- a
- o a_c1.tif (SERCA)
- o a_c2.tif (CX43)
- a_c3.tif (WGA)
- e
- e.tif (F-Actin + Cx43)
- 4. Double click on the icon corresponding to the executable MARTA_v3.exe. The following screen will appear (default settings configured to process the image "e.tif")

e Automatic Retrieval and Tissue Analysis (N	IARTA)						
C Automatic	 Supervised 						
Add	C Independent						
Input Mask	F Equalize	Evaluate					
Number of images (1 or 3)	1						
File label pattern (no ext)	e	Input extension	.tif	Output extension	.tif		
scaling (units/pixel)	0.114						
Equalized binary threshold	70	Binary threshold for c4	254				
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM	2	Dilation iterations in c1 (CM) 1	
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX)	5	Dilation iterations in c2 (CX) 20	
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT	2	Dilation iterations in c3 (INT) 1	
First Filter minimum area (um**2)	100	Padding scale factor	1				
First Filter minimum perimeter (um)	40						
Second Filter L min (um)	20	Second Filter L max (um)	200				
Second Filter W min (um)	5	Second Filter W max (um)	50				
Second Filter R min	1						
Gamma correction	0.5						
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20				
Small window size (um)	150						
Select CM ID plot	all						
Plot ID numbers	✓ Histograms	Sox Plots	Merge	Binary Channels			
🔽 CM Mask (Ma)	Retrievals overlapped	🔽 Tissue Mask	Plot Individual CMs				
* Parameters for EVALUATION *********							
Minimum Intersection value	50						
Intersection mode (max/ref)	ref						
rameters for Manual Mask Generation	****						
Number of vertices of polygon	8						
X splits	1						
Y splits	1						
			Generate Automatic mask	Generate Manual mask	Exit		
		-					

To help in filling in the values for each of the parameters used by the software, hovering over a blank field provides additional information about the parameter contained in that field:

C Automatic	Supervised			
Add	O Independent			
🔲 Input Mask	Equalize	🗌 Evaluate		
Number of images (1 or 3)	1			
File label pattern (no ext)	e One merged i	nput file (1) or three input files (3)	.tif	Output extension
scaling (units/pixel)	0.114			
Equalized binary threshold	70	Binary threshold for c4	254	
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM)
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX)
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT)
First Filter minimum area (um**2)	100	Padding scale factor	1	
First Filter minimum perimeter (um)	40			
Second Filter L min (um)	20	Second Filter L max (um)	200	
Second Filter W min (um)	5	Second Filter W max (um)	50	
Second Filter R min	1			
Gamma correction	0.5			
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20	
Small window size (um)	150			
Select CM ID plot	all			
Plot ID numbers	✓ Histograms	Box Plots	Merge	Binary Channels
🔽 CM Mask (Ma)	Retrievals overlapped	Tissue Mask	Plot Individual CMs	

AUTOMATIC ANALYSIS OF SINGLE MERGED IMAGE (e)

To process an image in automatic mode using the default settings, select the *Automatic* checkbox:

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Automatic	C Supervised					
Add	C Independent					
Input Mask	✓ Equalize	Evaluate				
Number of images (1 or 3)	1					
File label pattern (no ext)	e	Input extension	tif	Output extension	.tif	
scaling (units/pixel)	0.114					
Equalized binary threshold	100	Binary threshold for c4	254			
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM)	2	Dilation iterations in c1 (CM) 2
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX)	5	Dilation iterations in c2 (CX) 10
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT)	2	Dilation iterations in c3 (INT) 2
First Filter minimum area (um**2)	100	Padding scale factor	1			
First Filter minimum perimeter (um)	40					
Second Filter L min (um)	20	Second Filter L max (um)	200			
Second Filter W min (um)	5	Second Filter W max (um)	50			
Second Filter R min	1					
Gamma correction	0.5					
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20			
Small window size (um)	150					
Select CM ID plot	all					
Plot ID numbers	✓ Histograms	Box Plots	Merge	Binary Channels		
CM Mask (Ma)	Retrievals overlapped	Tissue Mask	Plot Individual CMs			
Parameters for EVALUATION ********						
Minimum Intersection value	50					
Intersection mode (max/ref)	ref					
Parameters for Manual Mask Generation						
Number of vertices of polygon	8					
X splits	1					
Y splits	1					
			Generate Automatic mask	Generate Manual mask	Exit	

Next, press the *Generate Automatic mask* button:

C Adamstin	Constant					
(• Automatic	Supervised					
Add	C Independent					
Input Mask	Equalize	Evaluate				
Number of images (1 or 3)	1					
File label pattern (no ext)	e	Input extension	tif	Output extension .t	tif	
scaling (units/pixel)	0.114					
Equalized binary threshold	100	Binary threshold for c4	254			
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM) 2	2	Dilation iterations in c1 (CM) 2
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX) 5	5	Dilation iterations in c2 (CX) 10
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT) 2	2	Dilation iterations in c3 (INT) 2
First Filter minimum area (um**2)	100	Padding scale factor	1			
First Filter minimum perimeter (um)	40					
Second Filter L min (um)	20	Second Filter L max (um)	200			
Second Filter W min (um)	5	Second Filter W max (um)	50			
Second Filter R min	1					
Gamma correction	0.5					
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20			
Small window size (um)	150					
Select CM ID plot	all					
Plot ID numbers	✓ Histograms	Box Plots	✓ Merge	Binary Channels		
CM Mask (Ma)	Retrievals overlapped	Tissue Mask	Plot Individual CMs			
Parameters for EVALUATION						
Minimum Intersection value	50					
Intersection mode (max/ref)	ref					
Parameters for Manual Mask Generation						
Number of vertices of polygon	8					
X splits	1					
Y splits	1	/				
		C C	Generate Automatic mas	Generate Manual mask	Exit	

In a few seconds (about 16 seconds on an i7 processor), the mask output by the software is generated in a folder created within the same directory. Also, the artificial separation of channels c1 (CM), c2 (CX43) and c3 (Interstitial) corresponding to the e_c1.tif, e_c2.tif, and e_c3.tif images is obtained.



By navigating in this folder generated by the software, the results of the processing in the form of files containing information about each individually detected CM as well as global statistical information from all CM detections can be found.



To get the statistical summary, go to the end of the generated "e_X_paramout.txt" file (where X is a time-dependent character string):

***************************************	***************************************
**************************************	ES ************************************
***************************************	***************************************
RGB mean of input:	33.28
****** RELATIVE PROPORTIONS OF	BIOMARKERS ************************************
Percentage of c2 respect to c3 and c1 (CXEX in %): Percentage of c3 respect to c3 and c1 (INEX in %): Percentage of c1 respect to c3 and c1 (CMEX in %):	0.7 36.41 62.89
*****	***************************************
Intersection between c1 and c3 (%): Tissue area from pixel count (mm2) : ************************************	38.64 0.07936 VSTS ***********************************
Number of detected CMs: Percentage of Cx43 Lateral (%): Average Lenght of CMs found (um): Average Width of CMs (um): Average angle of CMs (degree):	15 14.17+/-18.82 57.83+/-24.58 21.61+/-8.64 -33.01+/-30.4
Total time of execution (s) :	20.64

As an example of the retrieved statistical information when processing image e, , the percentage of lateral CX43 is shown to be 14.7% for a number of detections equal to 15, with an average length of about 58 microns and an average width of 21.6 microns. For information of each CM detection, the user is referred to the $e_X_data.txt$ file. This file can be read as a comma separated file (CSV) using, for instance, *Microsoft Excel* or *LibreOffice*.



AUTOMATIC SUPERVISED ANALYSIS OF SINGLE MERGED IMAGE (e)

The supervised option for this same image "e" is selected by default when the program is run. In any case, it can also be selected in the first row of options at the top right of the screen under the name *Supervised*.

The "*Generate Automatic mask*" button is then pressed again when the *Supervised* option is selected. After doing this, the first detected CM is obtained. The user is asked to decide if he/she wants to save the detection by entering "y" in the dialog. If he/she decides to save the detection accepting that it is a CM, the following will be seen in the screen:



Once "y" has been entered in the dialog window, press OK to continue with the next detection. Only the selected CMs with "y" will be displayed in the final image. However, the data file ($e_X_data.txt$) will still include all CMs with the introduced text assigned to each detection (column "value"). Only CMs saved with the "y" value are displayed in the final image ($X_combined_annotated.tif$ CMs). The CMs folder additionally displays all the detected CMs with the entered "value" being part of their filenames:



MANUAL MASK GENERATION FOR SINGLE MERGED IMAGE (e)

To assess the performance of the automatic method (in supervised or non-supervised mode), a reference mask for the original image "e" is required. The automatic and reference masks should have the same number of pixels and the same dimension. The reference mask can be generated with an external program like GIMP or KRITA's and introduced as an input to the software by enabling the *Input Mask* option. Also, there is the possibility to generate it using MARTA software by clicking the *Manual Mask Generation* button.

The name of the file containing the reference for the image named "e" should be *e_mM* and this should be in the format chosen in the parameter row (common formats are TIFF, PNG and JPG). By default, the input and output images will be in tif format. Therefore, if a manual mask is input, it should be called *e_mM.tif* for this case. The software will already provide this name to the manual output mask.

In the following, the generation of a manual mask using MARTA software is illustrated. First, select the values of the parameters in the bottom part of the screen (see next figure):

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C Automatic	Supervised						
Add	C Independent						
Input Mask	F Equalize	Evaluate					
Number of images (1 or 3)	1						
File label pattern (no ext)	e	Input extension	.tif	Output extension .t	if		
scaling (units/pixel)	0.114						
Equalized binary threshold	70	Binary threshold for c4	254				
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM) 2		Dilation iterations in c1 (CM) 1	
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX) 5		Dilation iterations in c2 (CX) 20	
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT) 2		Dilation iterations in c3 (INT) 1	
First Filter minimum area (um**2)	100	Padding scale factor	1				
First Filter minimum perimeter (um)	40						
Second Filter L min (um)	20	Second Filter L max (um)	200				
Second Filter W min (um)	5	Second Filter W max (um)	50				
Second Filter R min	1						
Gamma correction	0.5						
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20				
Small window size (um)	150						
Select CM ID plot	all						
Plot ID numbers	Histograms	Box Plots	Merge	Binary Channels			
🔽 CM Mask (Ma)	Retrievals overlapped	d 🔽 Tissue Mask	Plot Individual CMs				
******* Parameters for EVALUATION **********							
Minimum Intersection value	50						
Intersection mode (max/ref)	ref						
Parameters for Manual Mask Generation							
Number of vertices of polygon	8						
X splits	1						
Y splits	1						
			Generate Automatic mask	Generate Manual mask	Exit		

By default, an 8-vertex polygon is set to draw the boundary of each CM, but the number of vertices can be any natural number. In this example, the default value of 8 is set. Next, the user should decide in how many parts he/she would like to split the original image to contour each part sequentially. Let's choose values of 3 and 2 for X splits and Y splits, respectively, rather than values of 1 and 1 as in the default case. Next, press the *Manual Mask Generation* button in the screen (with X splits = 3, Y splits = 2 and Number of vertices of the polygon = 8).

Automatic	C Supervised					
(Add	C Independent					
- Add	Tagendent					
I Input Mask	I✓ Equalize	l Evaluate				
Number of images (1 or 3)	1					
File label pattern (no ext)	e	Input extension	.tif	Output extension	tif	
scaling (units/pixel)	0.114					
Equalized binary threshold	70	Binary threshold for c4	254			
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	1	Dilation matrix rank in c1 (CM)	2	Dilation iterations in c1 (CM) 1
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	1	Dilation matrix rank in c2 (CX)	5	Dilation iterations in c2 (CX) 20
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	1	Dilation matrix rank in c3 (INT)	2	Dilation iterations in c3 (INT) 1
First Filter minimum area (um**2)	100	Padding scale factor	1			
First Filter minimum perimeter (um)	40					
Second Filter L min (um)	20	Second Filter L max (um)	200			
Second Filter W min (um)	5	Second Filter W max (um)	50			
Second Filter R min	1					
Gamma correction	0.5					
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20			
Small window size (um)	150					
Select CM ID plot	all					
Plot ID numbers	Histograms	Box Plots	✓ Merge	Binary Channels		
CM Mask (Ma)	Retrievals overlapped	d 🔽 Tissue Mask	V Plot Individual CMs			
Parameters for EVALUATION						
Minimum Intersection value	50					
Intersection mode (may/ref)	ref					
intersection mode (may rely	i ci					
******* Parameters for Manual Mask Generation **********						
Number of vertices of polygon	8					
X splits	3					
Y splits	2					
			Generate Automatic mask	Generate Manual mask	Exit	
		-				

A pop-up window will appear, in which mouse **double-clicking** allows setting the vertices of the polygon (which are numbered to help following the line connections). When one CM delineation is finished, the user can move to the next CM by pressing ESC.



At the end of the manual delineation, the image and the generated mask are presented:



If the user selects *Input Mask*, the software will go on to parse the generated image "e_mM.tif" within the directory where the executable is located (not within any subfolder). If "*Input Mask*" is deselected and the *Evaluate* option is selected, the software will evaluate the correspondence between the automatic mask and the manual mask when the "*Generate Automatic Mask*" button is pressed. These results will appear in the newly generated subfolder.

 Automatic 	O Supervised	
Add	C Independent	
🔲 Input Mask	🔽 Equalize	🔽 Evaluate

In addition, the user can configure associated parameters like the minimum percentage of match required between the two masks and the evaluation method (i.e. intersection area

between the two masks divided by the reference area (*ref*) or by the maximum area between reference (*manual*) and test (*automatic*), which is called "max" method. If a label different from *max* or *ref* is specified, then *ref* method will be used.

******	Parameters for EVALUATION **********	
	Minimum Intersection value	50
	Intersection mode (max/ref)	ref

Once the execution has finished, press the *Exit* button to exit the program and view the written files:

File	Description			
e_X_autocoinc_data.txt	Individual CM info for CMs of the automatic mask presenting high			
	intersection with manually detected CMs			
e_X_evaluation_output.txt	Evaluation summary			
e_X_manucoinc_data.txt	Individual CM info for CMs of the manual mask presenting high			
	intersection with automatically detected CMs			
e_X_MaxAnd.tif CMs with high coincidence between manual and automatic masks				
e_X_Mm_Ma_cont.tif	Overlap between manual and automatic masks			



AUTOMATIC ANALYSIS OF THREE-CHANNEL IMAGE (a)

To perform the same analysis with an image with three separated channels, those should be named under the same identifier, for example "a", which should be entered in the graphical interface in the field "*File label pattern*". In addition, specify that there are 3 images in Number *of images* (1 or 3). In addition, the values of the parameters to process that image,

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such as the binarization threshold and parameters related to noise reduction and dilation, should be adjusted. In the following example, the image is not equalized and the parameter values are set out as in Table 1 of the main manuscript. If there is no equalization, the parameters regulating binarization are those marked in red in the following image:

	Automatic	C Supervised					
	Add	C Independent					
Fi	Input Mask	Equalize	Evaluate				
	Number of images (1 or 3)	3					
	File label pattern (no ext)	a	Input extension	.tif	Output extension	.tif	
	scaling (units/pixel)	0.21					
	Equalized binary threshold	70	Binary threshold for c4	254			
	Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	3	Dilation matrix rank in c1 (CM	3	Dilation iterations in c1 (CM) 3
	Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	3	Dilation matrix rank in c2 (CX)	3	Dilation iterations in c2 (CX) 5
	Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	3	Dilation matrix rank in c3 (INT	3	Dilation iterations in c3 (INT) 3
	irst Filter minimum area (um**2)	100	Padding scale factor	2			
Fir	st Filter minimum perimeter (um)	40					
	Second Filter L min (um)	20	Second Filter L max (um)	200			
	Second Filter W min (um)	5	Second Filter W max (um)	50			

The values of the parameters related to erosion and dilation for noise removal are set in the fields on the right part of the screen. In the bottom part of the screen, values for the parameters related to area, perimeter, length and width filters are set.

With the following parameter values, the software can be run by pressing the *"Generate Automatic Mask"* button:

 Automatic 	C Supervised					
Add	C Independent					
Input Mask	Equalize	Evaluate				
Number of images (1 or 3)	3					
File label pattern (no ext)	a	Input extension	.tif	Output extension .tif		
scaling (units/pixel)	0.21					
Equalized binary threshold	70	Binary threshold for c4	254			
Binary threshold for c1(CM)	8	Noise removal matrix rank in c1 (CM)	3	Dilation matrix rank in c1 (CM) 3	Dilation iterations in c1 (CM) 3	
Binary threshold for c2(CX)	15	Noise removal matrix rank in c2 (CX)	3	Dilation matrix rank in c2 (CX) 3	Dilation iterations in c2 (CX) 5	
Binary threshold for c3(INT)	2	Noise removal matrix rank in c3 (INT)	3	Dilation matrix rank in c3 (INT) 3	Dilation iterations in c3 (INT) 3	
First Filter minimum area (um**2)	100	Padding scale factor	2			
First Filter minimum perimeter (um)	40					
Second Filter L min (um)	20	Second Filter L max (um)	200			
Second Filter W min (um)	5	Second Filter W max (um)	50			
Second Filter R min	1					
Gamma correction	0.5					
Big scale bar lenght (um)	100	Small scale bar lenght (um)	20			
Small window size (um)	150					
Select CM ID plot	all					
Plot ID numbers	Histograms	Box Plots	Merge	Binary Channels		
CM Mask (Ma)	Retrievals overlapped	Tissue Mask	Plot Individual CMs			
Parameters for EVALUATION						
Minimum Intersection value	50					
Intersection mode (max/ref)	ref					
(
Parameters for Manual Mask Generation						
Number of vertices of polygon	8					
X splits	1					
Y splits	1					
			Generate Automatic mask	Generate Manual mask Exit		

The software will then generate an "*out_quantifout_quantif_X*" folder with the processing results. To access this material in video form, the user is referred to the <u>online tutorial</u>.