DMM_Analisis and Analisis_Drosophila User Manuals

DMM Analisis

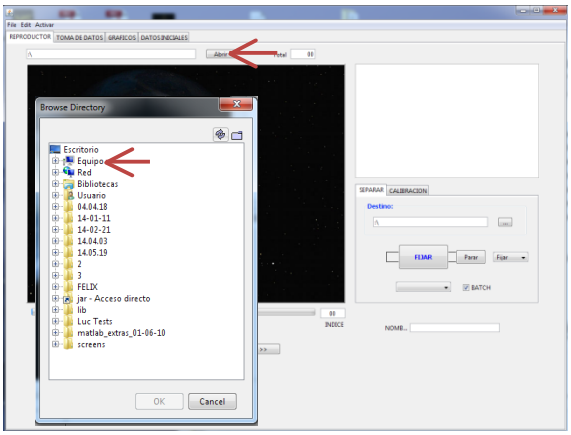
Modules

I. Reproductor

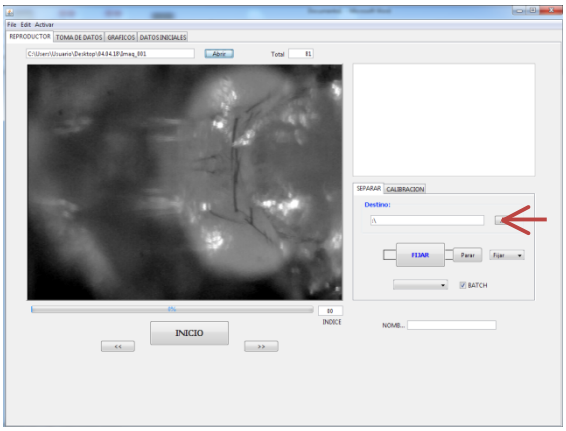
a. This section is primarily used for the separation of raw data from a filming experiment into individual movies. The raw data from a filming experiment is one file containing an image sequence of every animal on the disc. This section of the software is used to create image sequences of every animal. In order to do this, you select the first image of all images individually, and the software will compile the image sequence based on the first image. The filming experiment uses a disc that completes a rotation every 12 minutes. The software compiles images by selecting a new image every 12 minutes based on the time stamp of the first image.

b. Separation Process

i. Begin by loading the file containing all of the raw data (typically a hard drive directory). For PC users, the hard drive directories are accessed in **Equipo.**



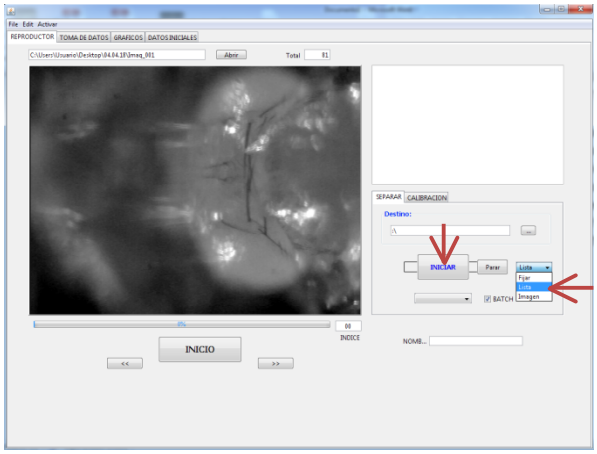
ii. Next, specify the folder for the separated files using the **…** button



iii. In order to specify the first picture for each animal, use the **FIJAR** button. To move to the next picture the **>>** button will move one image at a time. The **<<** button will move in reverse.

NOTE: It is important that you do not use the first image that appears as the first animal, as it is likely not the first animal in the experiment. Move forward through the movie until you find the first separator to be sure you have the first animal.

iv. The program is designed so that pressing **FIJAR** twice accidentally will not register twice on the same image, but it CAN register twice for the same animal. Be careful not to do this as you will have to start over again. Once all of the animals have been specified, use the drop down menu to select **Lista**. Then click **INCIAR** to begin separation. This will likely take a LONG time. Upon completion it will ask if you want to delete the list of names. Click **Si**.

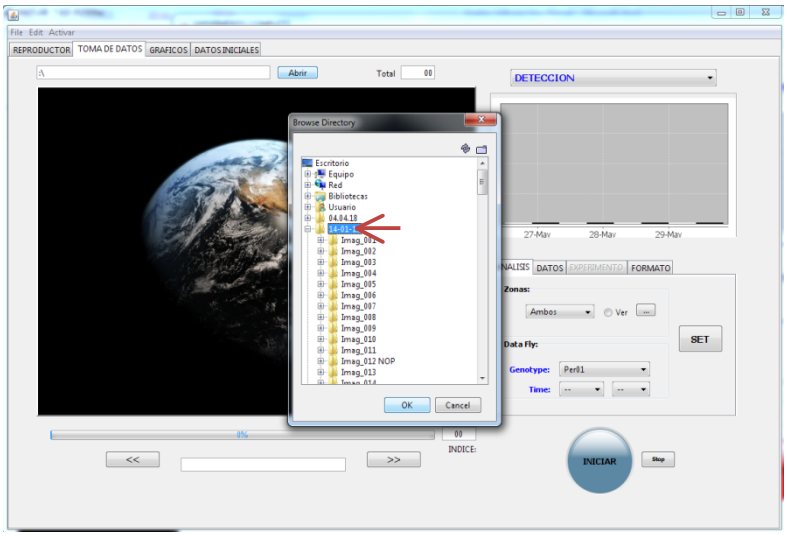


II. Toma De Datos

a. This module is designed for analysis of the separated files. After the **Reproductor** section separates the raw data into time lapse image sequences, the next step is to run the analysis algorithms. In order to do this, you need to specify the area that will be analyzed. Generally, the head area provides the most useful data output, and the algorithms were designed to analyze this area.

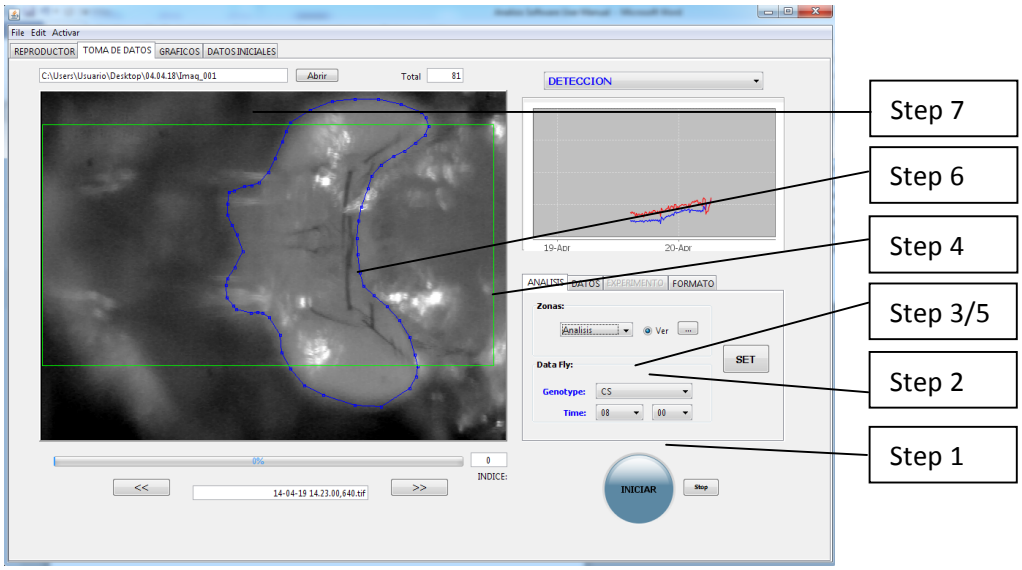
NOTE: Before using this section, you need to manually go into each separated file and remove the photos from after the emergence. Save the first photo of an empty pupal case, but delete the rest. This will allow the program to better determine the time of emergence.

i. Begin by loading the output file from the **Reproductor** section. Do not click on an individual **Imag** file, only the parent file and click **OK**.



ii. Next, you need to select the both a broad region of interest and a specific one. The broad region is a crop of the movie that will localize all measurements to this area. The specific region of interest is an outline of the head region that gives the analysis algorithm a place to start. All necessary buttons are located under the analisis tab for this part. First, specify the **gentotype**

under **Data Fly** and the collection time (step 1). Next, click the **Ver** box under **Zonas** (step 2). This should cause a red box to appear. Under the dropdown menu under **Zonas**, select **Busqueda** (step 3). This will allow you to resize the red box and outline the whole fly (step 4). After that, select **Analisis** under the same dropdown menu (step 5). The box should turn green. Now you can outline the head region of the fly by clicking a border (step 6). Every time you click it will make a blue dot connected to the previous blue dot by a line. Double clicking will connect that dot to the first dot to close the circle. When this is done, you can move to the next fly. Click the directory box at the top and press down on the keyboard to bring up the list of animals in the directory. Select the next animal and press enter(step 7)



iii. One all of the animals have been outlined, go to the drop down menu that says **DETECCION** and select **Experimento Completo**. This will cause the **Experimento** tab to become accessible. Navigate to this tab, and make sure all the animals you wish to analyze are selected in the range. Then click the large **INCIAR** button to begin the analysis. This will take several hours, and the results will be usable in the **Graphicos** tab and the **ANALISIS_DROSOPHILA** program.

III. Graficos

a. This section is used for curve visualization and analysis. The data files created from the **Toma De Datos** section are viewable here. There are several useful analysis tools that can be used to calculate times, slopes, and other data about the curves as well as a high pass filter useful for looking at general trends.