How to use the Excel table and the macros for fire salamanders identification (salamander.xlsm)

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Introduction:

The main purpose of this table isn't to be competitive with IA image recognition software, but to propose an easy method for every person which want to carry out a Catch-Mark-Recatch (CMR) survey without any animal manipulation and with minimal image standardization.

The table can be use alone or with another Excel table containing complementary information on the individuals to be identified (date, location, transect number, observation number (ex: 4th salamander observed on the transect number 1).

All the tables, instructions and codes lines are available in open access on Github (LINK). You are free to modify the code lines the way you want and keep us in touch if you have improved the code or add some functions.

Cells to fill:

Figure 1: General view of the table

The table contains 2 types of cells to fill: the mandatory ones (necessary to run the algorithms), and the optional ones (but advised for a more efficient use of the table).

Mandatory cells:

Spot number: spot numbers located on the back of the salamanders (see spot number part)

M3 /L4 / N4: spot and links between spots located on the nose (see head part)

L9 / M9 / N9: spots located on the neck (see neck part)

ID: to fill only if the individual is already known (see procedure part)

New_ID: automatically filled.

Optional cells :

Date: JJ/MM/AAAA format

Sex: male / female

Age: fill the way you want

Num_add: automatically filled

Num_transect: transect number (1,2,3,4,5,6)

Num_obs: observation number (1, 2, 3…)

X et Y: GPS coordinates, useful to sort individuals by observation distance

AO column: cells coordinate to help the algorithm to look for additional information

Head:

A nose spot is considered from the moment some yellow can be seen on the nose. A link is considered is a **continuous** spot links the eye to the nose (Fig. 2). **Warning, some individuals have spots on both eye and nose, but they aren't connected.** If there is no spot on the nose, you don't have to fill the 2 other cells (Fig. 2).
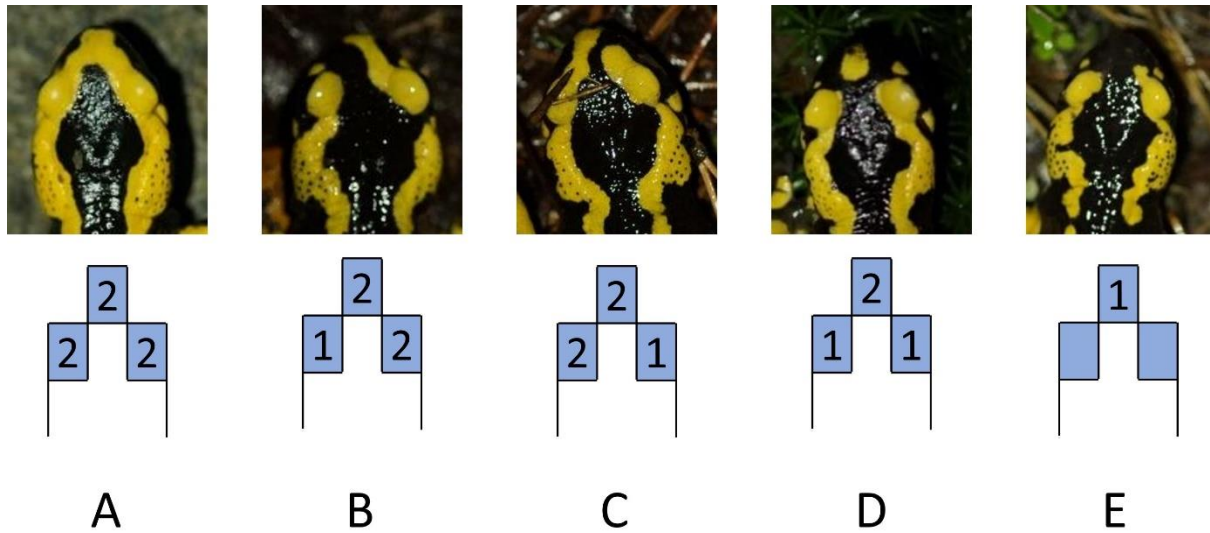

Figure 2: Different nose patterns and their equivalent for the table
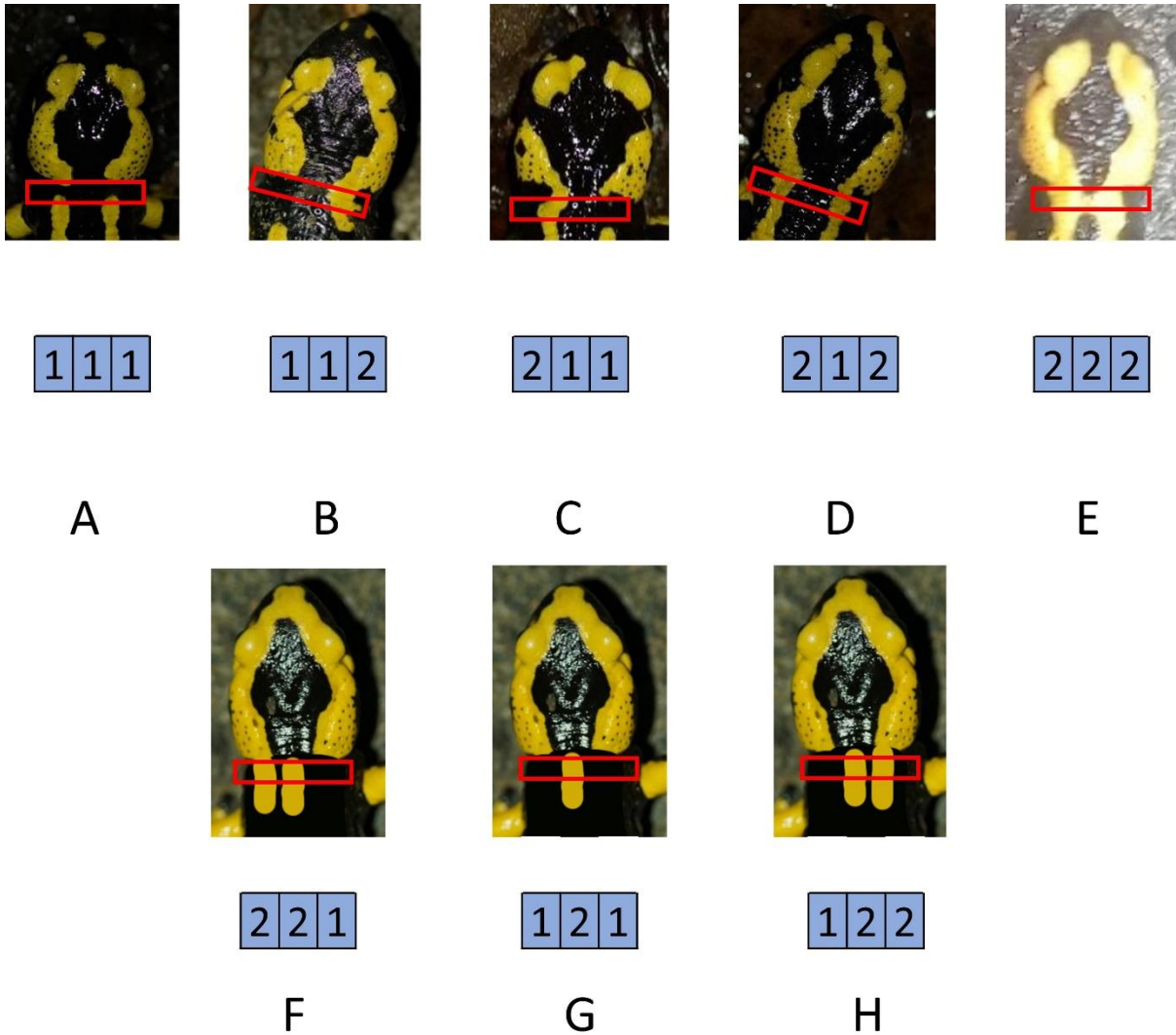
Neck:

Figure 3: Different neck patterns and their table equivalent

The neck is the area located behind the parotoid glands (Fig. 3). **Warning, some individuals show some parotoid glands that are not completely yellow.** It can lead to input errors and to identifications issues.

Spot numbers:

Area: between the back of the front limbs and the back of the rear limbs, only the spots located on the parallel lines. Do not hesitate to draw a line between legs or to place a ruler to determine if a spot belongs to the selection or not.

3 spots

6 spots

5 spots

3 spots

4 spots

7 spots

Procedure:

The procedures without and with another table will be detailed. If you want to use another table, you can go directly to the second part.

One table:

Step 1:

Press the **« Update database »** button to update the data used for individual identification. It's not strictly necessary to press this button. However, it's recommended to do it at the begining and/or at the end of the identification of the full transect.

Step 2:

Fill the cells of the nose, neck, and spot number. You also could fill the date cell to have a history of the catch dates. Then press the **« Match »** button.

Step 3:

If the individual is known, add its ID number below the **ID** cell, then press **Update**.

If the individual is unknown, press the **«New individual»** button.

Step 4:

Once the individual was identified, you can press the **"Clean"** button and go to the next individual.

Salamander plus a second table :

Step 1:

Open both table in parallel (Salamander and your table). Press the **« Update database »** button to update the data used for individual identification. It's not strictly necessary to press this button. However, it's recommended to do it at the beginning and/or at the end of the identification of the full transect.

Step 2:

In the AO column (Fig. 1); add all the information to help the algorithm gather the right information at the right places in your table. Don't forget to add the extension of your file after its name (ex; data_base.xlsx).

Step 3:

Add the date, transect number and observation number of the individual. Check that the observations numbers are continuous. The observation number will automatically take the value n+1 after every identification.

Step 4:

Press the **"Location »** button to add the individual's coordinates.

Step 5:

Fill the cells of the nose, neck, and spot number. You also could fill the date cell to have a history of the catch dates. Then press the **« Match »** button.

Step 6:

If the individual is known, add its ID number below the **ID** cell, then press **Update**.

If the individual is unknown, press the **«New individual»** button.

Step 7:

Once the individual has been identified, you can press the **"Add to table"** button to add the salamander's ID to your table.

Step 8:

Once the individual was identified, you can press the **"Clean"** button and go to the next individual.

Bugs and potential problems:

If during the creation of a new Excel sheet for an individual an error message appears (Fig. 4), check that the number in the cell below **New ID** fits with the last sheet +1.

If you realize that an individual is a duplicate (ex: n°7 and n°45 are identical), copy the information of n°45 in the n°7 sheet (date, sex, locations) then erase all the n°45 criteria (nose, neck , spot number). **Do not delete the sheet.** If you do, the continuity in the sheet's numbers will be broken and the algorithm won't be able to work correctly anymore.

Microsoft Visual Basic

Erreur d'exécution '9':

L'indice n'appartient pas à la sélection.

| Continuer | Fin | Débogage | Aide |

Figure 4: error message