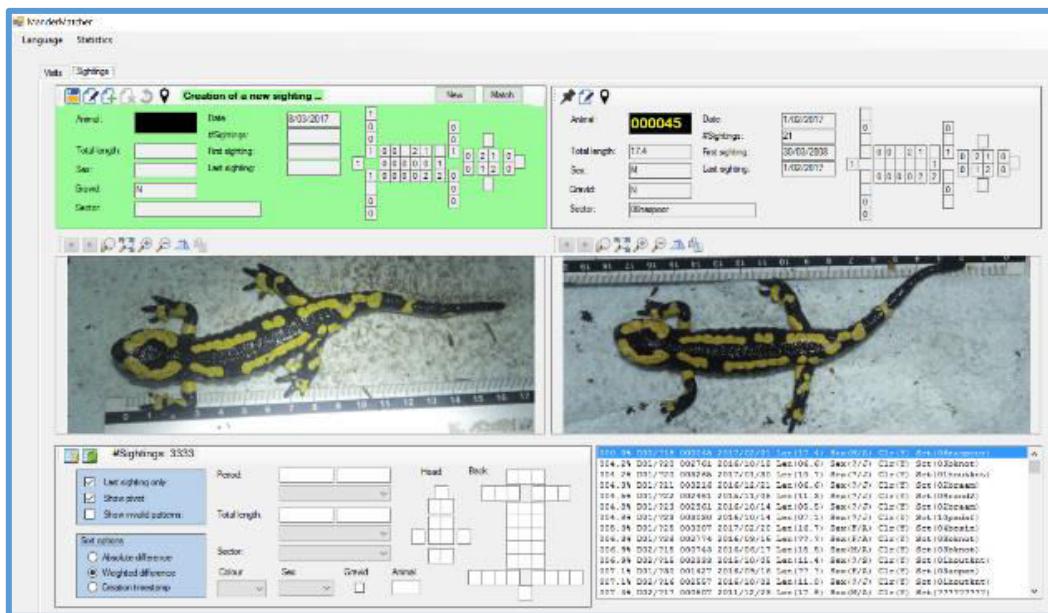


# ManderMatcher

an integrated software tool for population studies of  
the fire salamander *Salamandra salamandra*  
and its spotted relatives



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For support, updates, how to get started and tools for data analysis, we strongly advise you to get in touch with us through the above e-mail address.

**manual version 2 for program version 02.02**

**09/03/2017**

# ManderMatcher?

**ManderMatcher** is mainly a tool for recognition of individual fire salamanders *Salamandra salamandra* based on their unique spot pattern, and it is partially inspired (with regard to how to or how not to match animals) by available literature (Klewen, 1985; Kopp-Hamberger, 1998; Carafa & Biondi, 2004; Šukalo et al., 2013). Yet, the program can do much more than that. It is a complete platform for storing a myriad of relevant data on fire salamander specimens observed in the wild. Mainly data collected by a standardised count methodology are targeted. Besides data on the individual animal records (pattern (for recognition), sex, size, concise ecological features, site details, ...), weather-related and other environmental data can be stored. Future releases intend to expand towards tools for exploratory data analyses, graphs, mapping, ....

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# 1. Preparation

## 1.1 Installation

Download the zip file at [www.hylawerkgroep.be/jeroen](http://www.hylawerkgroep.be/jeroen), open it and copy its content to a folder of your choice.

The zip file contains:

- *ManderMatcher Vii.jj.exe*: the actual program
- *ManderMatcher.mdb*: the MS Access database in which all data is saved and which is freely accessible to the user (e.g. for data analysis)
- *ManderMatcherSetup.mdb*: a MS Access database with fixed components for the program to use – not intended for user access
- *Interop.ADODB.dll*: essential technical file, which requires no further explanation here
- Three folders:
  - *Images*: this is where all photographs are stored once they and the associated data are properly entered
  - *ImagesIn*: the most important folder, especially for first use; here, the user has to place photographs associated with new observational data.  
*!!! Attention: these photographs will be renamed and moved to the Images folder. You may want to make a copy of the original files in a different folder.*
  - *ImagesOut*: in this folder, photograph files are saved with meaningful names, being copies of the (fairly anonymous) files in *Images* which are then labelled by the program with the relevant information (o.a. identification number of the sighting and of the individual, and the date of observation) – see chapter 6.

### Important

- Each version of the program (and everything tied to it) can only be used for a single site.
- For ease of use, uncheck the boxes of the warnings that pop up with first use of the .exe and .mdb files.

## 1.2 Setup

A few items in the *ManderMatcher.mdb* database need to be set manually before use.

### 1.2.1 Sectors

For future analysis, distinguishing a number of parts within the counted transect (or zone) is recommended. These sectors can be e.g. areas with homogeneous habitat characteristics. Later, this allows to investigate relations between these characteristics and the observed animal data. The sectors are to be defined in the table *TabFsmSct*. Below is listed what each field in this table should contain.

Field	Description
SctCde (Sector Code)	<b>Sector code</b> Alfanumerical, free to choose code (9 characters)
SctNme (Sector Name)	<b>Sector name</b> Free text (30 characters)
SctDsc	<b>Sector description</b>

(Sector Description)	Free text (unlimited length)
----------------------	------------------------------

The last field is not mandatory, but it can be used to document the delimitating features of each sectors (verbally, coordinates, ...).

The sector name shows up in a drop-down list during data entry.

## 1.2.2 Transects

You may define multiple transects (or zones, if preferable). A transect is, however, always defined as the sum of a number of sectors. To obtain standardised data and to allow optimal analysis, repeating a fixed transect is advisable. The transects are defined in *TabFsmTrjSct*.

Field	Description
<i>TrjCde</i> <a href="#">(Trajectory Code)</a>	<b>Transect code</b> Alfanumerical, free to choose (9 characters)
<i>SctCde</i> <a href="#">(Sector Code)</a>	<b>Sector code</b> A sector code of those listed in table <i>TabFsmSct</i>

In the first field, the chosen transect code is repeated as many times as there are sectors in the transect. The second column contains the code names of those sectors, matching those of the field *SctCde* in *TabFsmSct*.

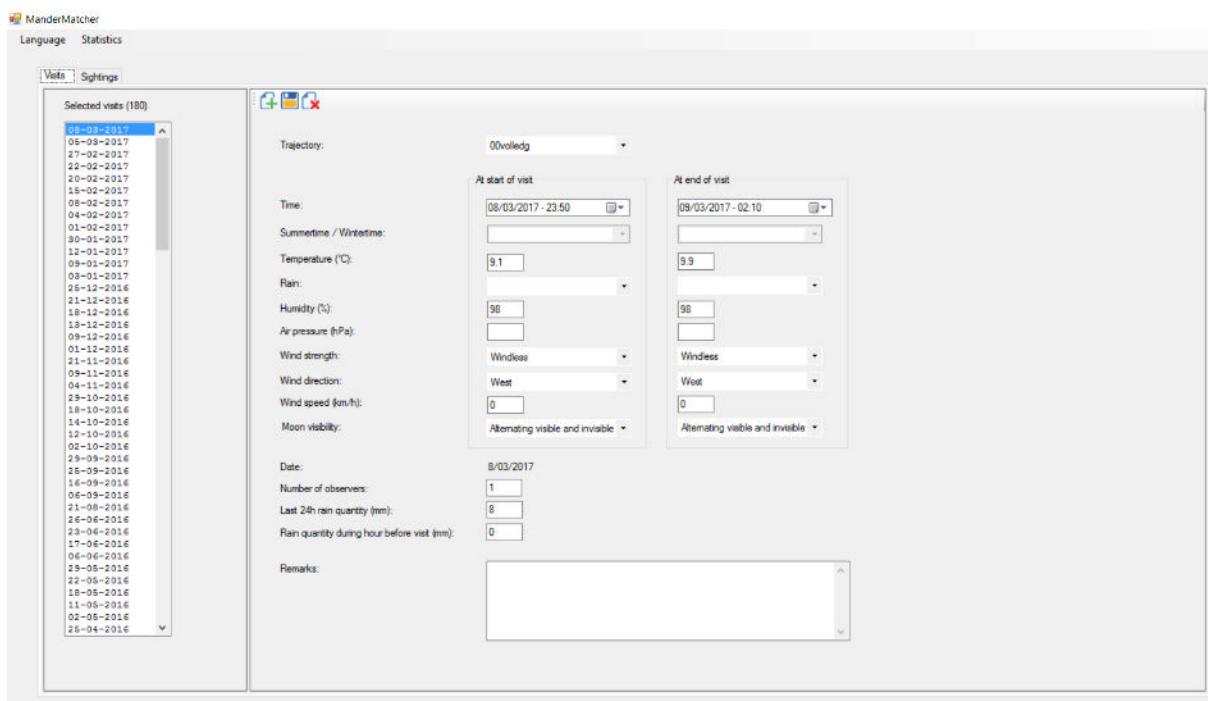
## 2. Outline – the essentials

We briefly discuss the different steps. Subsequent chapters elaborate on most aspects.

The program consists of **three windows**, two of which are readily available as tabs after launch of the program: **Visits** and **Sightings**. From the Sightings tab, the third window can be accessed via the New sighting button. This opens a new window, the **Individual Sighting**.

### 2.1 Creating a visit

Prior to entering data of individual records, we need to create a visit to which these data can be attributed. This visit is a moment in time when salamanders were counted and to which a series of environmental variables, including weather data, can be linked. After launching the program, the tab Visits appears automatically.



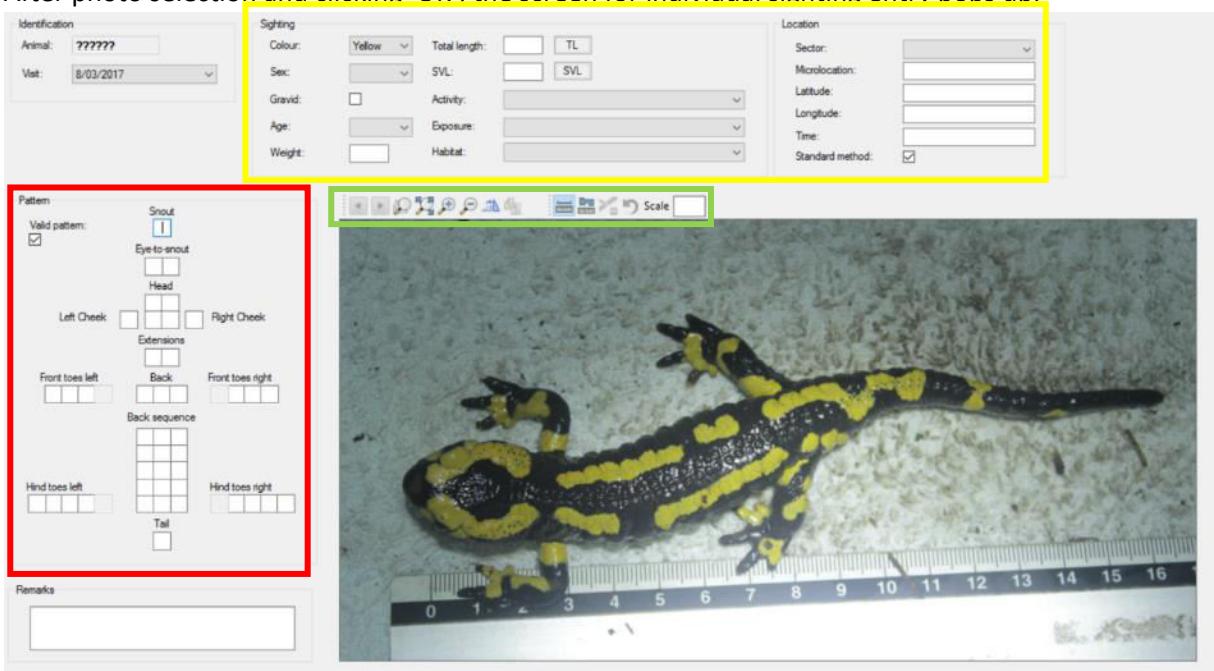
At the left, a box contains the saved visits, ordered chronologically reversed. At the right, details of the highlighted visit are displayed.

- 1) Click to create a new visit.
- 2) Fill out the only mandatory fields: Time at start of visit and time at end of visit (as dd/mm/yyyy hh:mm). These are used to automatically deduce the nearest sunset, regardless of whether the visit started before or after midnight. It is this date that serves as unique identifier of the visit. You can add additional data now or later – see Appendix B for explanation on the various variables.
- 3) Save (.

Note that the highlighted date in the list at the left is the one to which observation records will be added in the next step (data entry). Make sure to select the proper visit before moving on.

## 2.2 Entering sightings

- 1) Go to the tab Sightings. Among other things, this screen is used to find recaptures.
- 2) Assuming that the database was empty at the moment of first use, we skip this window for now and click , leading to the window for entry of individual sighting records.
- 3) First, you are asked to select photos from the *ImagesIn* folder, to which you already copied new photographs. You are about to enter data for each sighting of each individual animal, so select all photographs related to a single animal within a single visit.
- 4) After photo selection and clicking 'OK'. the screen for individual sighting entry pops up.



- 5) All data related to this sighting will be entered through this window.

**Red rectangle:** pattern characteristics. Here, we code the spot pattern for individual recognition of animals – see [chapter 3](#). If more than one photo has been selected, the photos can be browsed by clicking the small arrows above the photo box to the left (upper left in green rectangle).

**Yellow rectangle:** data on the animal and where it was found – see [chapter 4](#).

**Green rectangle:** handling of photographs and making measurements. To measure, the animal needs to be properly photographed – see [chapter 4](#).

## 2.3 Detecting recaptures

- 1) After data entry on the individual sighting and clicking 'OK', you are redirected to the Sightings tab again.

The screenshot shows the software interface for 'Creation of a new sighting'. On the left, there is a photograph of a yellow-spotted salamander (fire salamander) next to a ruler. On the right, a list of previous sightings is displayed, ordered by decreasing similarity to the new sighting. The list includes columns for ID, Date, #Sightings, First sighting, Last sighting, Total length, Sex, Gravid, and Sector. Some entries in the list are highlighted in yellow, indicating they are similar to the new sighting.

ID	Date	#Sightings	First sighting	Last sighting	Total length	Sex	Gravid	Sector
000045	1/02/2017	21	30/03/2008	1/02/2017	17.4	M	N	Osnaspoor
000422	9/12/2016	14	1/12/2011	9/12/2016	16.4	M	N	01houtknt
006.1%	2017/02/21	1	2017/02/22		13.2			
026.1%	2017/02/21	1	2017/02/22		16.8			
026.3%	2009/04/08	1	2016/10/18		13.9			
026.3%	2016/10/18	1	2016/10/18		13.9			
026.3%	2016/10/14	1	2017/02/22		14.9			
026.3%	2017/02/22	1	2017/02/22		10.4			
026.7%	2014/12/21	1	2014/12/21		18.2			
026.7%	2013/04/09	1	2017/01/12		17.0			

The new sighting is shown at the left. If the database contains some records already, at the right at the bottom a list of already available records is shown, ordered by decreasing similarity to the newly entered sighting at the left. Browsing through this list allows to detect a previous sighting of the same individual. To facilitate comparison, differences are highlighted in yellow (see below).

This screenshot shows the 'Creation of a new sighting' screen with a different set of data. The photograph of the salamander is identical to the one above. Below it, a filter panel is open, allowing the user to refine the list of previous sightings. The filter panel includes checkboxes for 'Last sighting only', 'Show pivot', and 'Show invalid patterns', and dropdown menus for 'Period', 'Total length', 'Head', 'Back', and 'Sector'. The list of previous sightings on the right side of the screen also includes highlighted differences in yellow.

ID	Date	#Sightings	First sighting	Last sighting	Total length	Sex	Gravid	Sector
000422	9/12/2016	14	1/12/2011	9/12/2016	16.4	M	N	01houtknt
026.1%	2017/02/21	1	2017/02/22		13.2			
026.1%	2017/02/21	1	2017/02/22		16.8			
026.3%	2009/04/08	1	2016/10/18		13.9			
026.3%	2016/10/18	1	2016/10/18		13.9			
026.3%	2017/02/22	1	2017/02/22		14.9			
026.3%	2017/02/22	1	2017/02/22		10.4			
026.7%	2014/12/21	1	2014/12/21		18.2			
026.7%	2013/04/09	1	2017/01/12		17.0			

The box at the lower left offers options for how to compare and for reducing the list with filter criteria – see [chapter 5](#).

- 2) Once established whether the new sighting concerns a new individual or a recaptured one, a final decision is saved to the database by clicking the “New” (sighting is not a recapture) or “Match” (sighting is a recapture of the animal selected at the right). The program automatically then attributes the unique identification number of the animal concerned to the new sighting and asks if you would like to save it. As we assume visits to aim at observing each animal just once, each individual animal can be entered only once per visit. Entry of accidental within-visit recaptures will lead to joining all photos with a single observation record.

## 3. Coding the pattern

### 3.1 Introduction

You now roughly know which steps to take. In this chapter, we will now focus on the various definitions of the variables/characteristics that are used to build up each animal's code for recognition. It is quite a read, which may be overwhelming at first. Yet, after some time of practical use, a manual quickly becomes unnecessary and pattern entry goes swiftly.

The spot pattern is coded by means of 44 characteristics.

Coding the entire pattern requires clear and detailed photographs of the upper surface and sides of the animal. To limit fieldwork in case of large numbers and/or high abundance, it is however possible to limit this to one or a few clear pictures of the upper surface of the animal. Fields of characteristics that are not apparent from the available photos are left blank (see below) and are not used by the matching algorithm. This somewhat enhances the possibility of obtaining identical patterns, albeit intensive use of the program has shown that even then, animals can still be matched with sufficient ease.

When in doubt, it is best to leave the characteristic blank. This leads to a less powerful use of the algorithm, yet it is preferred over potentially creating 'false' differences. However, it is possible to complete characteristics with their values during previous sightings of the same animal, provided that enough certainty is available to assume that those values did not alter in the meantime.

Patterns may change over time. In adults, these changes are fairly limited and infrequent. In younger individuals, however, they may be sizeable, up to altering the global outlook of the animal. Once you acquire experience with the program, you will be able to anticipate certain changes in young animals. It is, however, advised to strictly code what you see, not what you imagine that might come. If not, you are 'distorting the truth' and making it impossible to trace pattern changes. Given some experience, you can also consider to enhance the chance of recognition of an animal at a future sighting by leaving certain characteristics blank.

### 3.2 Definitions

The spot pattern is part of the sighting data and is, as such, entered in the window 'Individual Sighting' (saved in the sightings table *TabFsmSgh* in *ManderMatcher.mdb*). Next, we discuss the spot pattern in detail, going through it in the from-top-to-bottom order by which you will enter the values automatically or by using the tab key. Each section starts with an illustration showing where the discussed characteristics are located in the entry window. Other sighting data (location, activity, habitat, etc. ...) are discussed in chapter 4.

We start off by defining some scientific terms to indicate specific parts of the salamander body.

**Cloaca:** the combined opening of the digestive, reproductive and urinary tracts, externally visible as a slit on the lower base of the tail

**Dorsal:** related to the back

**Dorsolateral:** related to where back and flanks meet

**Lateral:** related to the flanks or sidewise view of the animal

### 3.2.1 Head

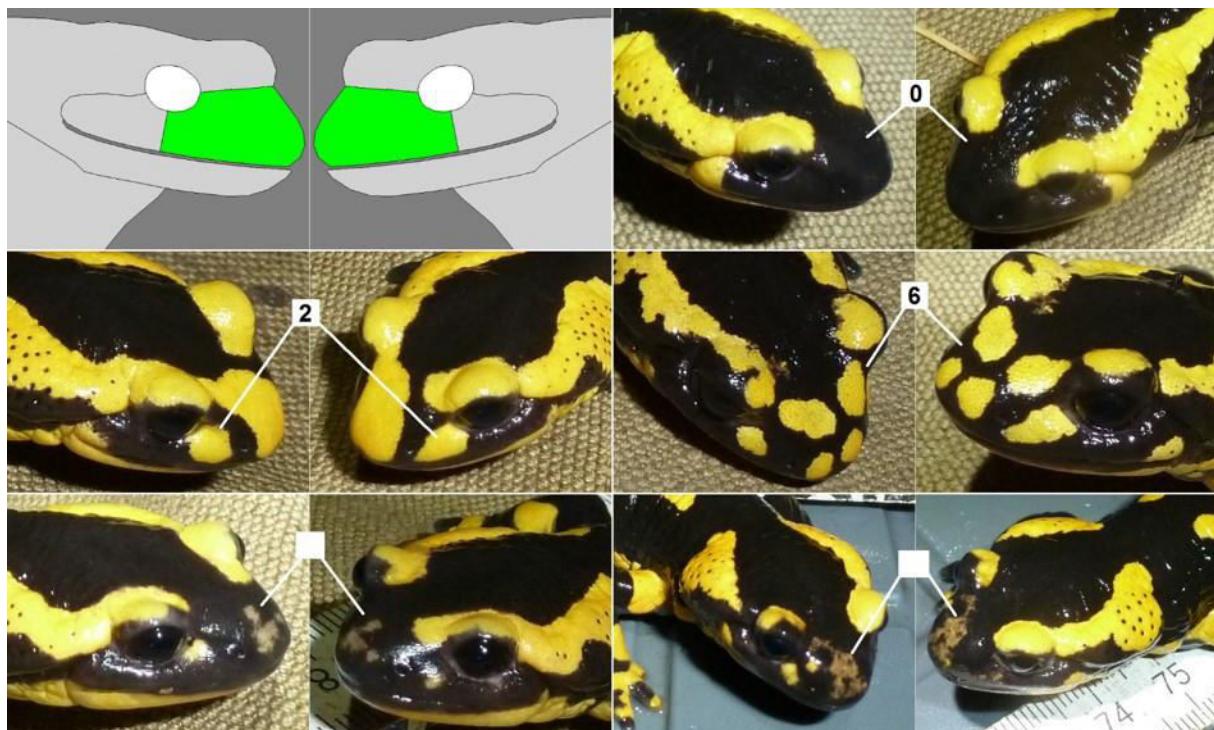
#### 3.2.1.1 Snout

<b>Identification</b> Animal: ?????? Vet: 8/03/2017	<b>Sighting</b> Colour: Yellow Total length: <input type="text"/> TL Sex: <input type="text"/> SVL: <input type="text"/> SVL Gravid: <input type="checkbox"/> Activity: <input type="text"/> Age: <input type="text"/> Exposure: <input type="text"/> Weight: <input type="text"/> Habitat: <input type="text"/>	<b>Location</b> Sector: <input type="text"/> Microlocation: <input type="text"/> Latitude: <input type="text"/> Longitude: <input type="text"/> Time: <input type="text"/> Standard method: <input checked="" type="checkbox"/>
<b>Pattern</b> Valid pattern: <input checked="" type="checkbox"/>  Eye-to-snout  Head  Left Cheek: <input type="checkbox"/>  Right Cheek  Extensions  Front toes left: <input type="checkbox"/>  Back: <input type="checkbox"/>  Front toes right  Back sequence  Hind toes left: <input type="checkbox"/>  Tail: <input type="checkbox"/>  <b>Remarks</b> <input type="text"/>		



#### Entry option 1 – Lateral coding

Requires photographs portraying the entire snout, on top and on the sides, requiring more time effort in the field (and at the desk) than the dorsal coding (see below). To be entered: the **number of obvious, isolated and clearly delimited spots on the ‘snout’**. By ‘snout’, we mean the area shown in green in the below illustration, bordered towards the tail by a vertical line running through the centre of the eye, and on top by a line connected the anterior corners of the eyes. Eye spots which run down until way across the snout (as shown in the first picture on the second row of the illustration below) are ignored. Occasionally, spots are present but as vague as a cloud of milk in a cup of coffee (see both example in the third row). In such cases, the field is left blank.

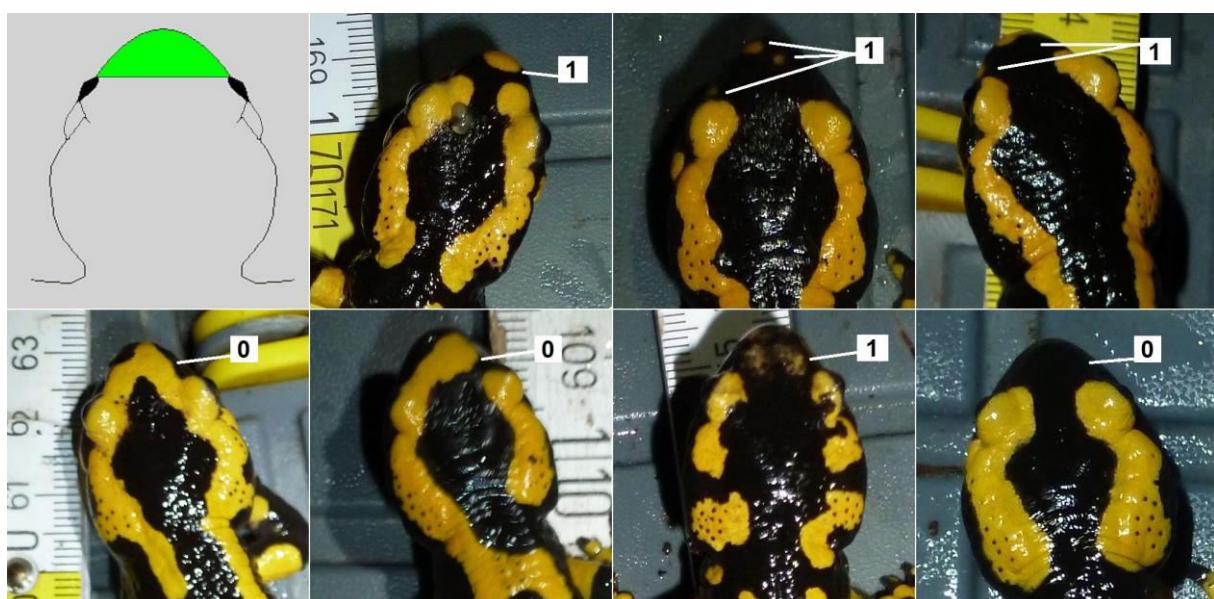


From experience, it is apparent that snout spots tend to grow and/or become more numerous with age/size.

#### [Entry option 2 - Dorsal coding](#)

Less powerful, but does not require lateral pictures, so less laborious in the field. Here, 'snout' is defined as the green area on the upper cheek, as indicated in the grey picture below. To the rear, it is bordered by a line connecting the anterior corners of the eyes. A dorsal view complicates the counting of the exact number of spots, so only presence or absence of spots is coded. Allowed values:

- 0: no snout spots
- 1: one or multiple snout spots



### 3.2.1.2 Cheeks

Identification		Sighting		Location	
Animal:	??????	Colour:	Yellow	Total length:	TL
Mat:	8/03/2017	Sex:		SVL:	SVL
		Gravid:	<input type="checkbox"/>	Activity:	
		Age:		Exposure:	
		Weight:		Habitat:	
Pattern		Scale [ ]			
Valid pattern: <input checked="" type="checkbox"/>					
Snout  Eye-to-snout  Head  Left Cheek  Right Cheek  Extensions  Back  Front toes left  Back sequence  Hind toes left  Tail 					
Remarks					

As these characteristics are best coded from lateral view pictures, these are the fields which are left most commonly blank by observers using dorsal photographs only. Dorsal coding might be possible with decent photographs, but may be unreliable with varying angles of photography. We leave such use up to user discretion. Coding the cheeks requires full view of the upper cheeks, so lateral pictures are in fact indispensable. These two characteristics indicate presence of yellow pigmentation on the left and right 'cheek', as well as the level in which this pigmentation is connected to the yellow spot(s) on the eyes and the parotoid glands (see below). By 'cheek', we mean the area coloured green in the grey picture below, bordered by a vertical line running through the centre of the eye at the front and bordered by a clear ridge at the top and at the rear. Alllowed values:

- 0: no yellow pigmentation
- 1: yellow present, unconnected to eye or parotoid spot
- 2: yellow present, connected to eye or parotoid spot (possibly excluding a narrow hue of black in the skin fold between parotoid gland and cheek ridge, as shown in the 4th example below)



From experience, the cheek spots appear to be part of the most stable side of the head. They are shaped already in very young individuals and will only rarely alter afterwards.

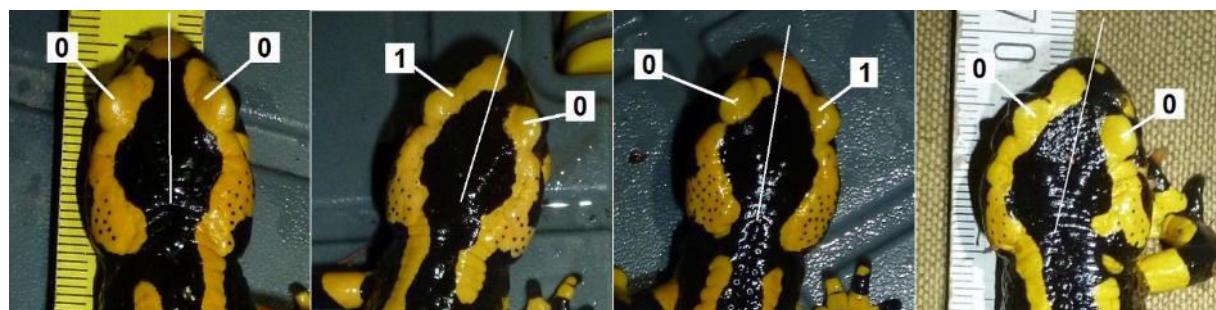
### 3.2.1.3 Dorsal

#### Eye-to-snout

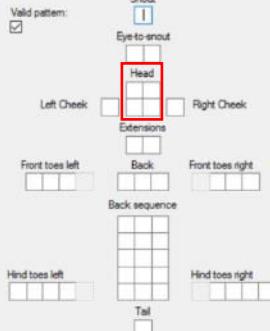
Two characteristics indicating how far the left (A) and right (B) eye spots (see below) continue across the centre of the snout. We note their combination in what follows as 'AB'. Allowed values:

- 0: does not cross
- 1: crosses

If both snout spots run across the snout, merging at the snout tip, both characteristics receive a '1' value. Asymmetrically positioned eye spots might lead to interpretation errors. Yet, always apply the rule of crossing the centre of the snout strictly, coding incomplete snoutwards extensions as '00' or leaving the characteristic blank in case of doubt (see 4<sup>th</sup> photo below).



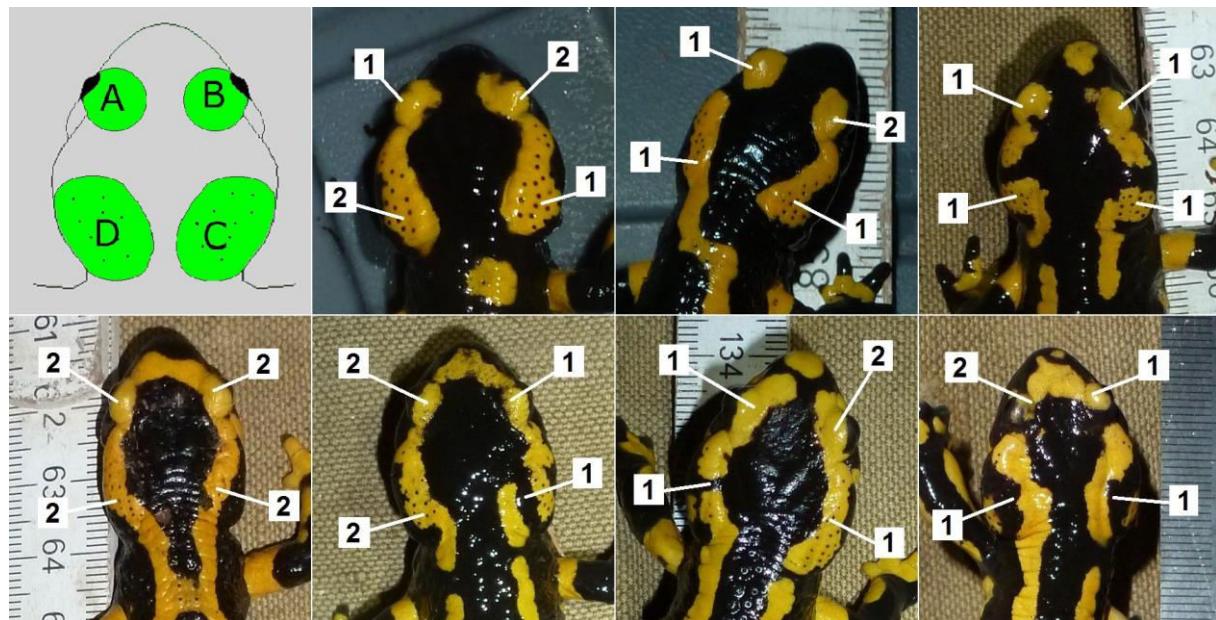
## Central

Identification		Sighting	Location
Animal: ??????	Valid pattern: <input checked="" type="checkbox"/>	Colour: Yellow	Total length: <input type="text"/> TL
Mat: 8/03/2017		Sex: <input type="text"/>	SVL: <input type="text"/> SVL
		Gravid: <input type="checkbox"/>	Activity: <input type="text"/>
		Age: <input type="text"/>	Exposure: <input type="text"/>
		Weight: <input type="text"/>	Habitat: <input type="text"/>
Pattern		Scale: <input type="text"/>	
Valid pattern: <input checked="" type="checkbox"/>  Snout <input type="checkbox"/> Eye-to-snout <input type="checkbox"/> <b>Head</b> <input checked="" type="checkbox"/> Left Cheek <input type="checkbox"/> Right Cheek <input type="checkbox"/> Extensions <input type="checkbox"/> Front toes left <input type="checkbox"/> Back <input type="checkbox"/> Front toes right <input type="checkbox"/> Back sequence <input type="checkbox"/> Hind toes left <input type="checkbox"/> Hind toes right <input type="checkbox"/> Tail <input type="checkbox"/>			
Remarks: <input type="text"/>			

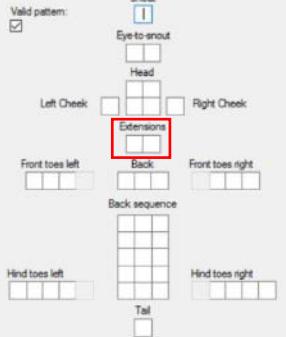
Four characteristics, related to four positions on the head: both eyes and both parotoid glands (= elongated glands behind the eyes). They are coded in a clockwise order as follows: left eye (A), right eye (B), right parotoid (C) and left parotoid (D). Their combination is given here as 'ABCD'. Each indicates (i) presence of yellow pigmentation on the related position (1 out of 4) and (ii) whether this pigmentation is connected to pigmentation on the next position (in the described ABCD clockwise sequence) and as such appears as a single continuous spot. Allowed values:

- 0: no pigmentation (all-black)
- 1: pigmentation present, not connected to next position
- 2: pigmentation present, connected to next position

Pattern 1212, visible as a 'crescent moon' and a 'waning moon', is by far the most common combination. Examples are provided below.



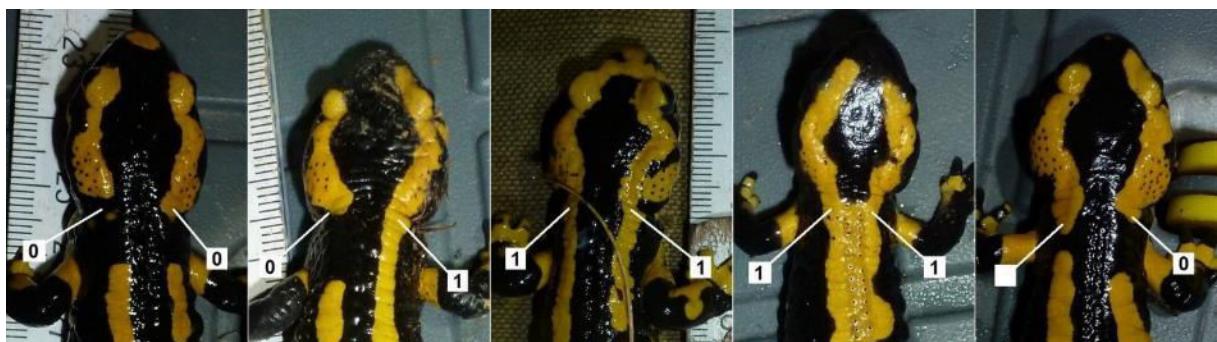
## Parotoid extensions

Identification		Sighting		Location	
Animal:	???????	Colour:	Yellow	Total length:	TL
Mat:	8/03/2017	Sex:		SVL:	SVL
Gravid:	<input type="checkbox"/>	Gravid:		Activity:	
Age:		Age:		Exposure:	
Weight:		Weight:		Habitat:	
Pattern		<input checked="" type="checkbox"/> Valid pattern: 			
		<input type="checkbox"/> Snout <input type="checkbox"/> Eye-to-snout <input type="checkbox"/> Head <input type="checkbox"/> Left Cheek <input type="checkbox"/> Extensions (highlighted) <input type="checkbox"/> Right Cheek <input type="checkbox"/> Front toes left <input type="checkbox"/> Back <input type="checkbox"/> Front toes right <input type="checkbox"/> Back sequence <input type="checkbox"/> Hind toes left <input type="checkbox"/> Hind toes right <input type="checkbox"/> Tail			
Remarks					

Two characteristics, indicating whether the parotoid spots continue towards the rear onto the back of the animal. Allowed values:

- 0: absent or does not reach anterior edge of front leg insertion
- 1: present and passes anterior edge of front leg insertion

Intermediate or doubtful cases are best left blank.



**!!! Attention:** while these spots run onto the back, they are not coded as part of the back and tail spots (see below). In the latter section, only spots which are not connected to head spots are coded.

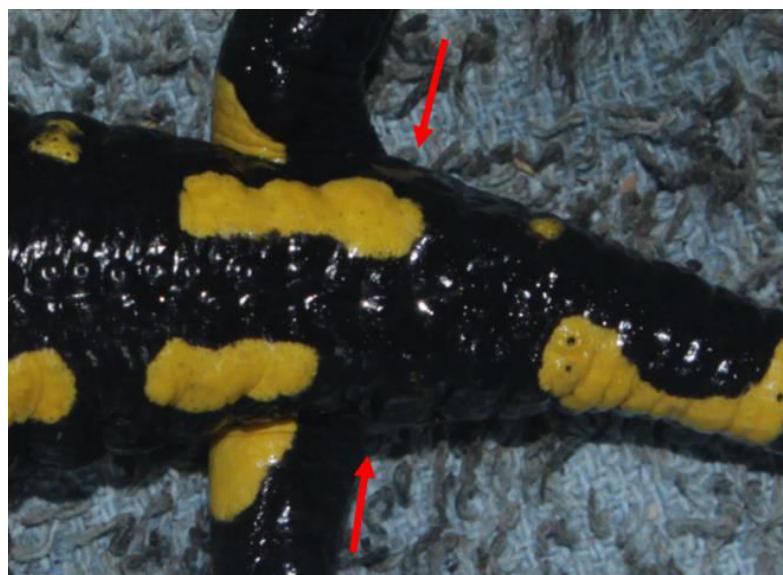
### 3.2.2 Back and tail

<b>Identification</b>	<b>Sighting</b>	<b>Location</b>																								
Animal: ??????	Colour: Yellow Total length: <input type="text"/> TL Sex: <input type="text"/> SVL: <input type="text"/> SVL Gravid: <input type="checkbox"/> Age: <input type="text"/> Activity: <input type="text"/> Weight: <input type="text"/> Exposure: <input type="text"/> Habitat: <input type="text"/>	Sector: <input type="text"/> Microlocation: <input type="text"/> Latitude: <input type="text"/> Longitude: <input type="text"/> Time: <input type="text"/> Standard method: <input checked="" type="checkbox"/>																								
<b>Pattern</b>																										
Valid pattern: <input checked="" type="checkbox"/> <table border="1"> <tr><td>Snout</td><td><input type="text"/></td></tr> <tr><td>Eye-to-snout</td><td><input type="text"/></td></tr> <tr><td>Head</td><td><input type="text"/></td></tr> <tr><td>Left Cheek</td><td><input type="text"/></td></tr> <tr><td>Right Cheek</td><td><input type="text"/></td></tr> <tr><td>Extensions</td><td><input type="text"/></td></tr> <tr><td>Front toes left</td><td><input type="text"/></td></tr> <tr><td>Back</td><td><input type="text"/></td></tr> <tr><td>Back sequence</td><td><input type="text"/></td></tr> <tr><td>Hind toes left</td><td><input type="text"/></td></tr> <tr><td>Hind toes right</td><td><input type="text"/></td></tr> <tr><td>Tail</td><td><input type="text"/></td></tr> </table>	Snout	<input type="text"/>	Eye-to-snout	<input type="text"/>	Head	<input type="text"/>	Left Cheek	<input type="text"/>	Right Cheek	<input type="text"/>	Extensions	<input type="text"/>	Front toes left	<input type="text"/>	Back	<input type="text"/>	Back sequence	<input type="text"/>	Hind toes left	<input type="text"/>	Hind toes right	<input type="text"/>	Tail	<input type="text"/>	<input type="button"/> Scale <input type="text"/>	
Snout	<input type="text"/>																									
Eye-to-snout	<input type="text"/>																									
Head	<input type="text"/>																									
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Back	<input type="text"/>																									
Back sequence	<input type="text"/>																									
Hind toes left	<input type="text"/>																									
Hind toes right	<input type="text"/>																									
Tail	<input type="text"/>																									
Remarks:	<input type="text"/>																									

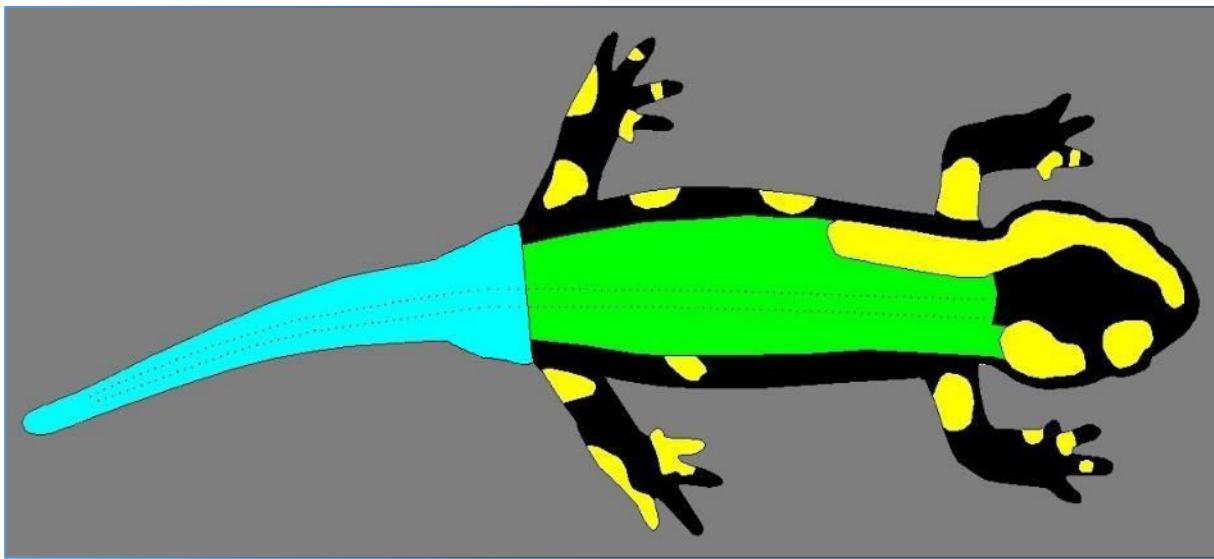
The ‘back section’ is delimited ...

- 1) to the front: by the posterior ridge of the parotoid glands,
  - 2) to the rear: by the first cross-ridge of the transversal tail rings (see first illustration below)  
and
  - 3) to the sides: by either
    - (a) the outer edge of the dorsolateral spot rows that are typical for most individuals of the subspecies *S. s. terrestris* and *S. s. fastuosa*,
- or
- (b) the dorsolateral wart rows present on both sides of the body for all taxa without spots typically arranged in two rows on both sides of the back.

The ‘tail section’ starts where the back section ends (blue in second illustration below).



\* Most populations of *S. s. terrestris* and *S. s. fastuosa*

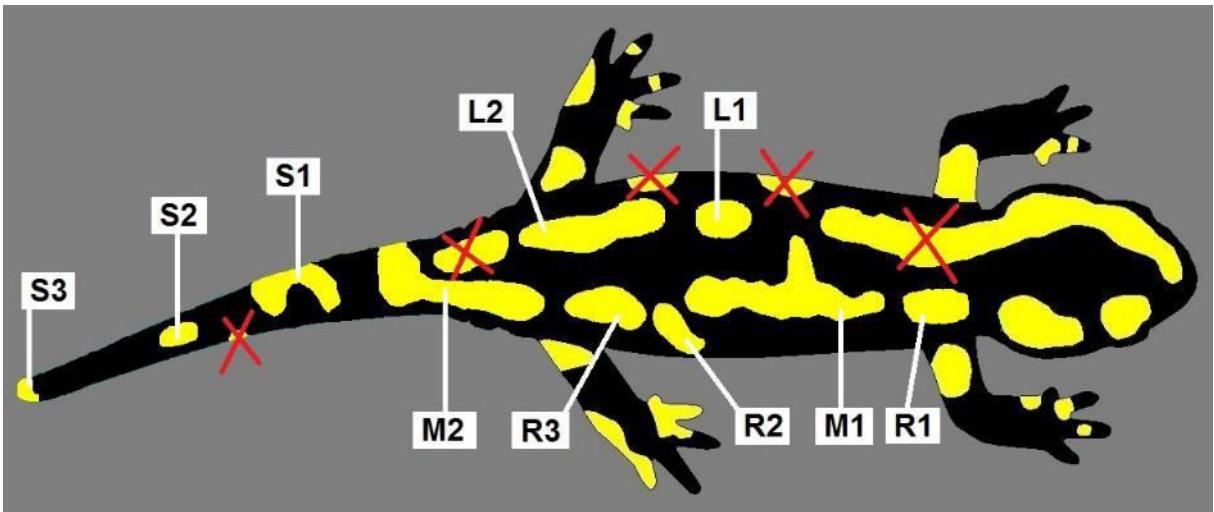


Spots are considered 'back spots' when at least partially located in the back section, even if most of them are located outside the section (see below - M2, R2), yet (as discussed) excluding spots connected to those on the head.

Left (L) and right (R) back spots are defined as spots which do not cross the double row of gland pores that runs along the centre of the back (see above).

Back spots crossing both pore rows are counted as 'middle spots' (M), even if most of them is located to the left or the right of the back (M1) or on the tail (M2 – note that the crossing of the gland pores even only takes place on the tail!).

Tail spots (S) are strictly restricted to the tail section and cross the double gland pore row at least once.



Applying the above definitions, these are the **four main characteristics**:

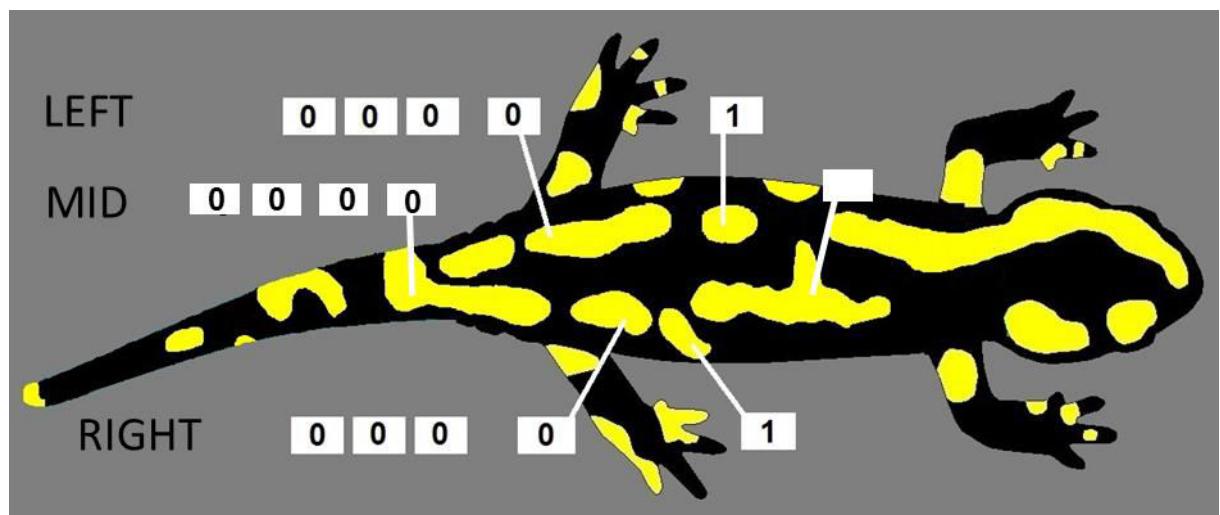
- number of left back spots,
- number of middle back spots,
- number of right back spots and
- number of tail spots.

Additionally, we define a number of **indicators of relative length**. These indicate how a left, middle or right back spot's length relates to that of the spot following it (towards the rear). Allowed values:

- 0: no subsequent left or right back spot present after the considered spot
- 1: the spot is shorter than the subsequent spot
- 2: the spot is longer than the subsequent spot

Three times five indicators are provided for the left, middle and right spots, allowing to code length differences of up to six spots in each of the three spot groups. If less than six spots are present, the series of indicators is completed with zeroes. If no spots or only a single spot are present, all indicator have '0' value. In case of doubt, indicators should be left blank.

Below is an example of the encoding of the left and right spot indicators of relative length. There are only two middle spots, resulting in a blank first indicator (as both spots are of fairly comparable length) followed by four zeroes.



Below an example of the entire back-and-tail encoding is provided. In this case, there are no middle back spots, resulting in five zeroes for the middle back spot indicators of relative length.



#### \* Other taxa

In other taxa where spots are less clearly arranged into the three areas (left, right and middle) of the back, attributing spots to either (or none) of these areas requires somewhat more careful use of the relevant definitions. We will mainly limit ourselves to highlight those definitions which differ from the definitions provided for the subspecies *fastuosa* and *terrestris*.

Let's begin with defining what a back spot is and what not. The borders of the back (and how to deal with them) towards the front and the rear of the animal are identical to those described for the subspecies *fastuosa* and *terrestris* (see above). The lateral borders, however, are different. With dorsolateral spot rows missing, we define them by considering the position of the dorsolateral wart rows. Any spot crossing the two imaginary lines connecting the centre of these warts on each side of the body and any spot which is fully located between both lines, is treated as a back spot. Spots located further towards the flanks are considered flank spots and are not considered any further.

The below illustration shows the position of the right side border of the back as a red line running through the dorsolateral warts. The same applies for the left side border. The elongated spot crossing the line is treated as a back spot, whereas the round spot lower on the right flank is not.

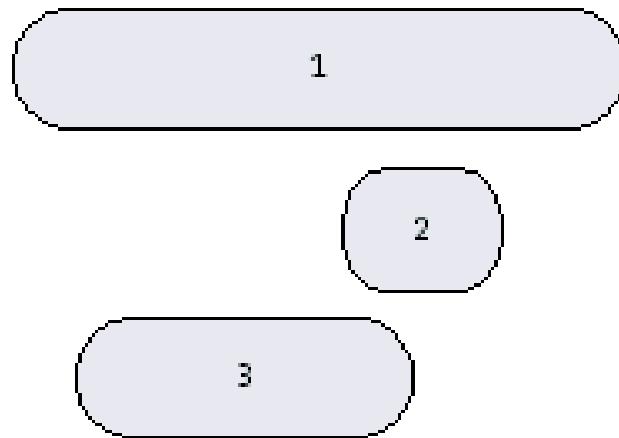


As the wart rows may be less obvious depending on lighting in the photographs, it is recommended to take multiple photographs of each animal.

Now that we sorted that out, the **four main characteristics** are the same as with the striped subspecies/populations: number of left back spots, number of middle back spots, number of right back spots and number of tail spots.

A final hurdle comes with the **indicators of relative length**. Their allowed values are the same as discussed above for the striped subspecies. The order of spots (in the three back areas: left, middle, right) by which the indicators will be derived, however, are not as clear-cut. Indeed, these spots may be arranged in more chaotic fashion than in the tidy rows or lines we find in most *terrestris* and *fastuosa*. However, given the right definition, the same indicators can be derived.

Considering the below figure with the right side facing towards the head and the left side towards the tail, the order of spot within each of the three areas is determined by the front edge of each spot, i.e. the edge closest to the head, regardless of any other feature of the spot, including rear edge or spot width. Thus, the numbers given to the below spots allow for indicators of relative length to be given, even while these spots may overlap along the head-tail axis and are not arranged along a straight line into a clear series. As with the striped subspecies, only the length of the spot in the head-tail direction is taken into account.



With these definitions, the pattern of animals from the major part of the distribution of the *Salamandra* genus is easily coded.



© Bobby Bok



© Laura Bok





*Salamandra corsica*



# Left = 2  
# Mid = 1  
# Right = blank  
# Tail = 3

L rel length indicators: blank-0-0-0-0  
M rel length indicators: 0-0-0-0-0  
R rel length indicators: blank-blank-0-0-0

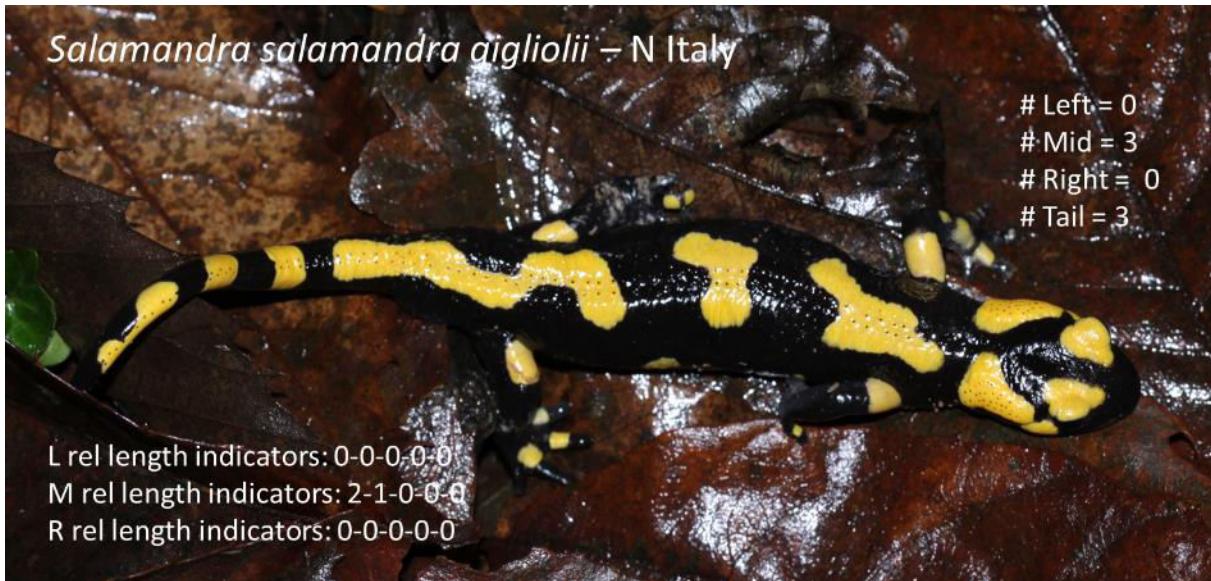
© Wouter Beukema

*Salamandra salamandra longirostris*



# Left = 4  
# Mid = 0  
# Right = 4  
# Tail = 4

L rel length indicators: blank-blank-2-0-0  
M rel length indicators: 0-0-0-0-0  
R rel length indicators: 1-2-1-0-0



Potential limitation for use in certain taxa with either very few (e.g. southern *S. s. gigliolii*) or very numerous spots and specks (some of the Iberian subspecies, as well as e.g. *S. infraimmaculata semenovi*) is noted. The former case may lead to a high portion of identical codes, yet coding does not present any difficulty. In the latter case, coding is possible, but requires even more strenuous application of the definitions. It may be advisable to consider using other methods.

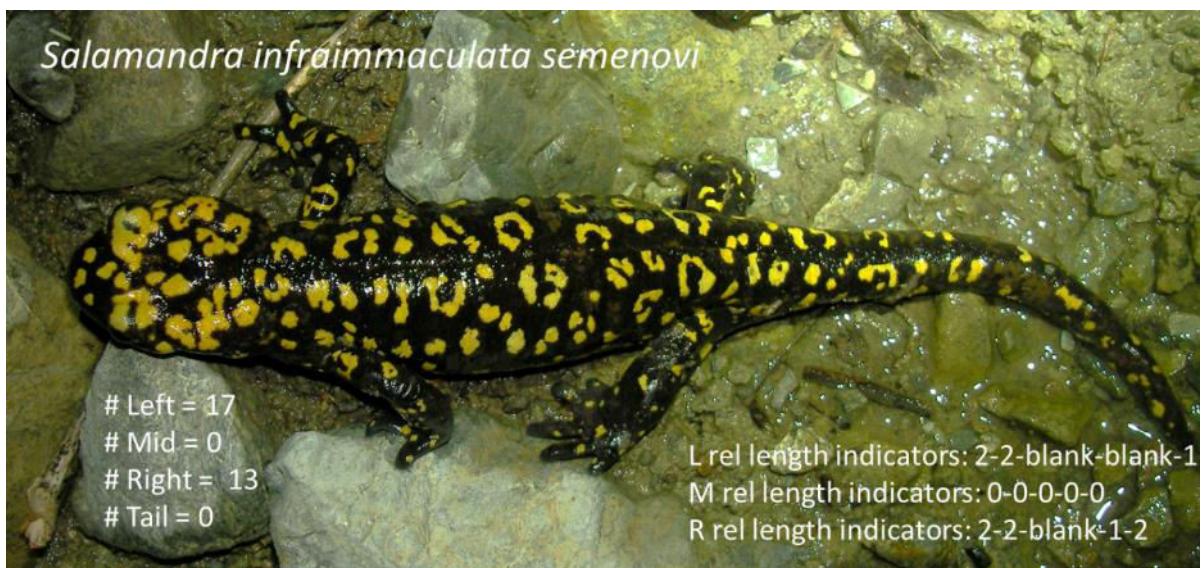


*Salamandra salamandra crespoi*



© Bobby Bok

*Salamandra infraimmaculata semenovi*



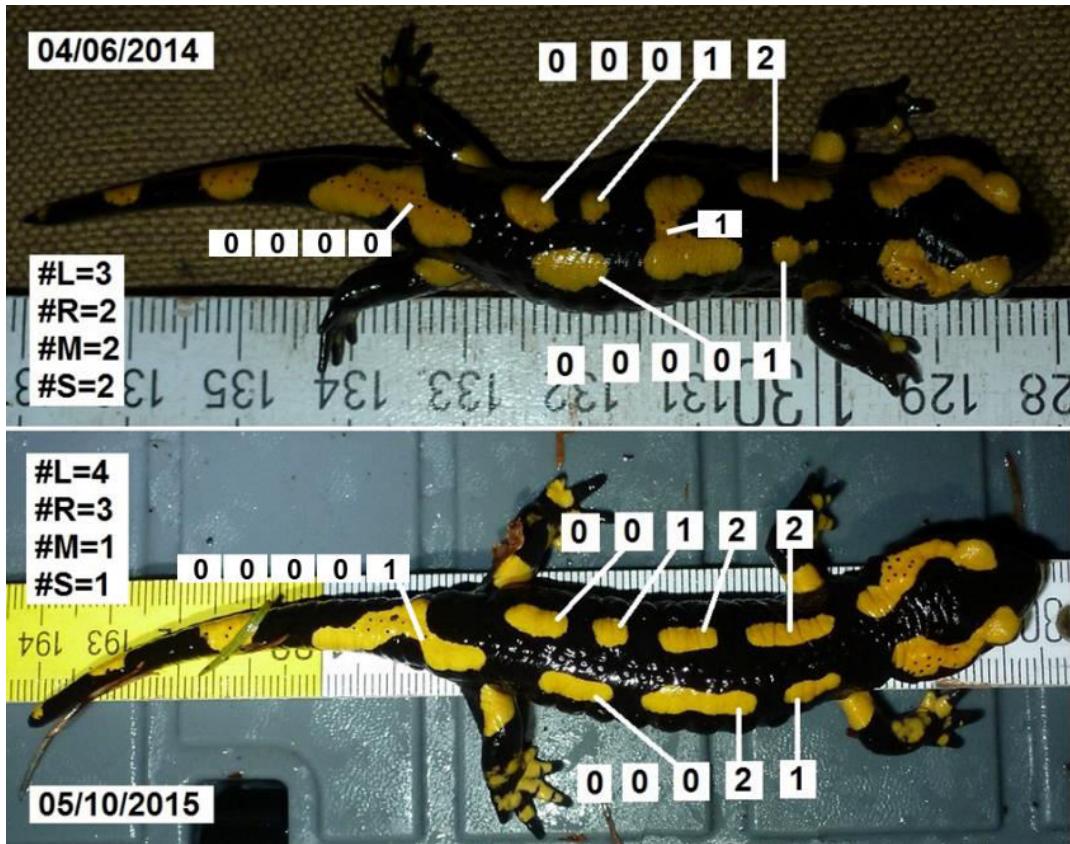
© Bobby Bok

If spot delimitation is unclear, characteristics are best left blank. Note that most taxa show (as in most animals/subspecies) a mixture of black and yellow toes; apart from the back section of the code, toe pattern combination offers high discerning power. As such, the code contains enough characteristics to allow for the algorithm to remain functional with blanks.

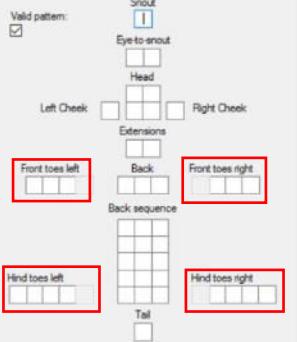
The back section appears to be the most unstable part of the pattern. While largely stable in adult animals, severe changes in the first years after metamorphosis are highly likely. Juveniles often display wide spots with irregular edges, which usually break up into the more typical pattern with two dorsolateral rows of spots at a more advanced age.

Below is an example of two sightings of the same animal. From the first until the second sighting, total length increased by 5.3 cm (from 9 to 14.3 cm). The middle spot on the centre of the back fell apart, while the second tail spot retreated to the side of the tail, resulting in a fairly different pattern.

In case of doubt, zooming in onto the unique constellation of gland pores on the parotoid glands may help, although these pores may move from inside a spot to outside of it due to shrinking of that spot.



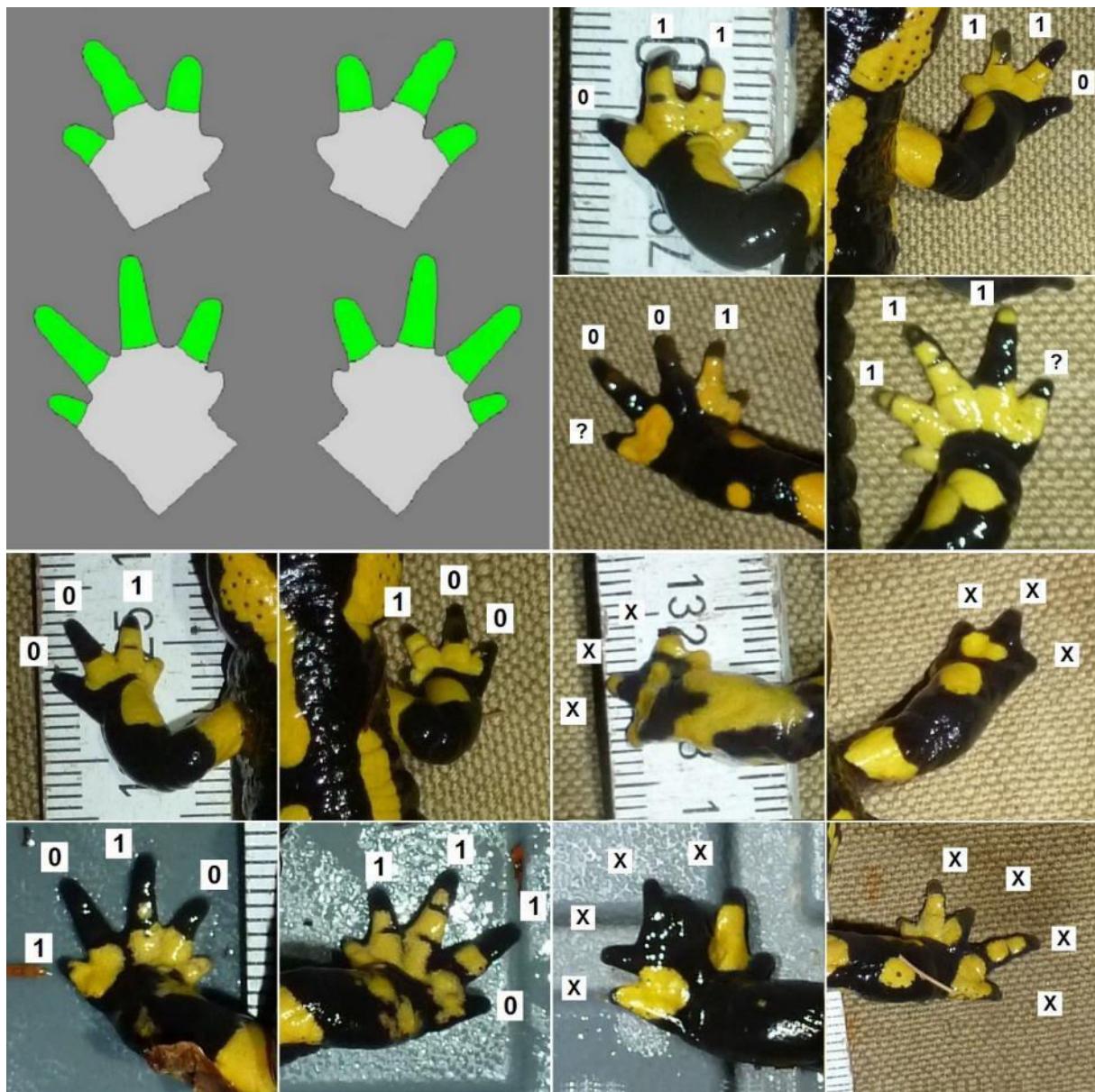
### 3.2.3 Toes

<b>Identification</b> Animal: ?????? Visit: 8/03/2017	<b>Sighting</b> Colour: Yellow Sex: <input type="checkbox"/> Gravid: <input type="checkbox"/> Age: <input type="checkbox"/> Weight: <input type="checkbox"/> Total length: <input type="text"/> TL SVL: <input type="text"/> SVL Activity: <input type="text"/> Exposure: <input type="text"/> Habitat: <input type="text"/>	<b>Location</b> Sector: <input type="text"/> Microlocation: <input type="text"/> Latitude: <input type="text"/> Longitude: <input type="text"/> Time: <input type="text"/> Standard method: <input checked="" type="checkbox"/>
<b>Pattern</b> Valid pattern: <input checked="" type="checkbox"/>  <b>Remarks</b> <input type="text"/>		
		

The green parts of the figure below indicate which parts of the toes are considered for coding the toe pigmentation. At the side of insertion of the toes onto the foot, the toes are delimited by the base of the first phalanx, which is often visible as a narrow black fold (which may or may not be situated within a yellow background). The toe characteristics indicate presence of pigmentation for (1) the three outer toes of each front foot and (2) the four outer toes of each hind foot. The inner toes of the feet are not considered, as these are often inconspicuous and/or not visible in dorsal photographs.

Allowed values:

- 0: no pigmentation present
  - 1: pigmentation present
- X: clear signs of malformation, albeit by birth or due to predation or (larval or postlarval) cannibalism, including higher than normal numbers of toes (4 front, 5 hind) lead to assigning 'X' to all toe characteristics of that foot.



### 3.2.4 Valid pattern indicator

The screenshot shows a software interface for recording herpetological sightings. At the top, there are three main sections: Identification, Sighting, and Location.

- Identification:** Fields for Animal ID (??????), Visit date (8/03/2017), and other metadata.
- Sighting:** Fields for Colour (Yellow), Total length (TL), Sex, SVL, Gravid status, Activity, Age, Exposure, Weight, and Habitat.
- Location:** Fields for Sector, Microlocation, Latitude, Longitude, Time, and Standard method (checked).

**Pattern:** This section contains a grid for entering pattern codes. A red box highlights the "Valid pattern" checkbox, which is checked. The grid includes fields for Snout, Eye-to-snout, Head, Left Cheek, Right Cheek, Extensions, Front toes left, Back, Front toes right, Back sequence, Hind toes left, Hind toes right, and Tail.

**Remarks:** A text input field for additional notes.

**Image:** A photograph of a fire salamander (Salamandra salamandra) with distinct yellow dorsal stripes on a black background. It is placed next to a metric ruler for scale.

This indicator is a checkbox, located at the upper left of the pattern code entry fields. Its default setting is 'on'. You can turn it off for sightings which allow too few characteristics to be entered to allow proper matching. Invalid patterns can be omitted from the selected list in the Sightings tab/window (see chapter 5).

## 4. Entering other individual sighting data

The screenshot shows the 'Individual Sighting' data entry interface. It includes sections for Identification (Animal: ??????, Date: 8/03/2017), Sighting (Colour: Yellow, Sex: Male, Gravid: No, Age: Adult, Weight: 10g, Total length: TL, SVL: SVL, Activity: Day, Exposure: Sun, Habitat: Forest), Location (Sector: 1, Microlocation: 1, Latitude: 52.3, Longitude: 4.9, Time: 10:00, Standard method: checked), Pattern analysis (Snout: 1, Eye-to-snout: 1, Head: 1, Left Cheek: 1, Right Cheek: 1, Extensions: 1, Front toes left: 1, Back: 1, Front toes right: 1, Back sequence: 1, Hind toes left: 1, Hind toes right: 1, Tail: 1), a photo of a yellow and black fire salamander next to a ruler, and a Remarks field.

In chapter 4, we explain which individual record data can be entered and stored. After entry of all required/available data, the Individual Sighting can be closed by clicking 'OK'. Subsequently, the sighting can be matched with the available previously saved sightings in the database, as briefly explained in chapter 2 and elaborated further in chapter 5.

The above illustration indicates the content of this chapter. The yellow rectangle contains a number of individual-specific variables. We will cover these more or less from left to right and from top to bottom.

The green rectangle contains photo manipulation features, as well as length measurement tools.

Conclusively, we discuss a number of rather self-explanatory fields in the 'Individual Sighting' data entry screen.

### 4.1 Colour

Some populations contain a small portion (ca. 1%) of striking, orange-coloured specimens. Allowed values (fixed list):

- Yellow
- Orange

## 4.2 Sex

Allowed values (fixed list):

- Female
- Male

This field is to be left blank in case of unclear sex.

## 4.3 Gravid

A checkbox for females only.

## 4.4 Age

Allowed values (fixed list):

- Adult
- Juvenile
- Subadult

Seifert (1991) set the limit between juvenile and subadult at 12 cm and the one between subadult and adult at 16 cm (although he adds further distinction for males and females). Obviously, these are generalisations, as individual animals may very well become fertile at 15.5 or 16.5 cm.

From the above, we can deduce that Age (in the absence of a better alternative) is actually readily available by deduction from our own length measurements (see below). Yet, we maintain Age as a separate variable, e.g. because of animals with an incomplete tail.

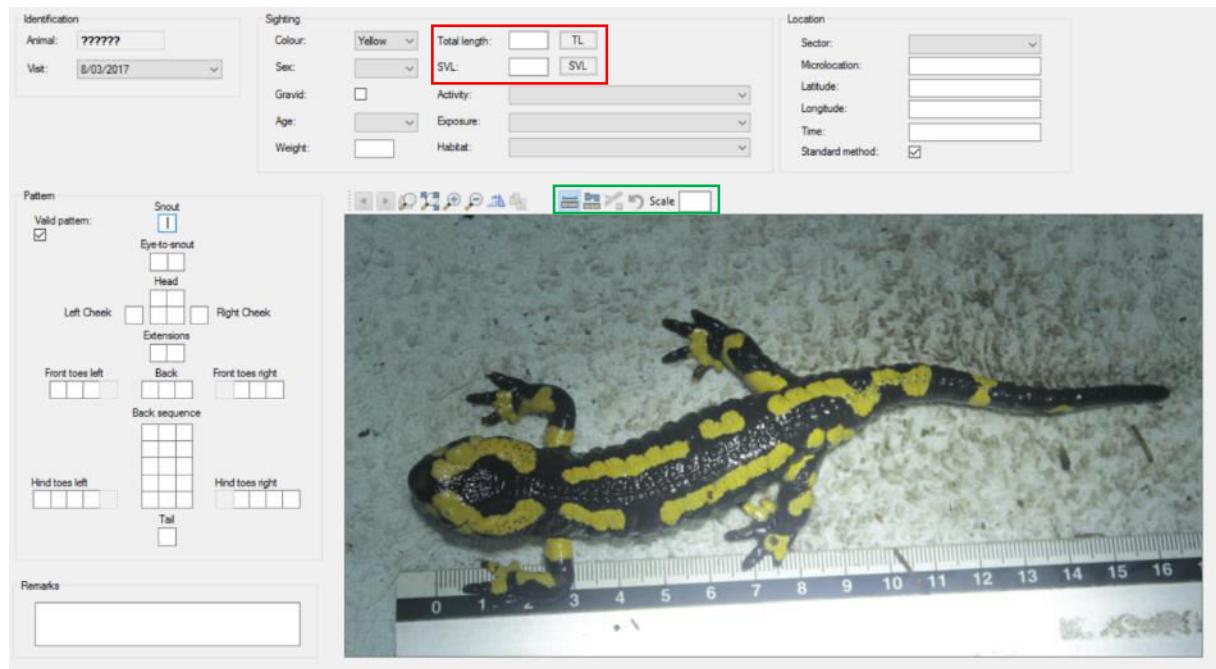
Using a different value to distinguish between subadult and adult animals may be worth considering. From experience, we know that proper recognition of recaptures depends on pattern stability. This stability seems already fairly in place at 14 cm, allowing for definition of the subadult-adult distinction rather based on pattern stability than on Seifert's fertility assessment.

## 4.5 Weight

A numeric value in grams.

## 4.6 Length measurements

The fields Total length and SVL allow to save two length measurements. Below, we explain the measuring process.



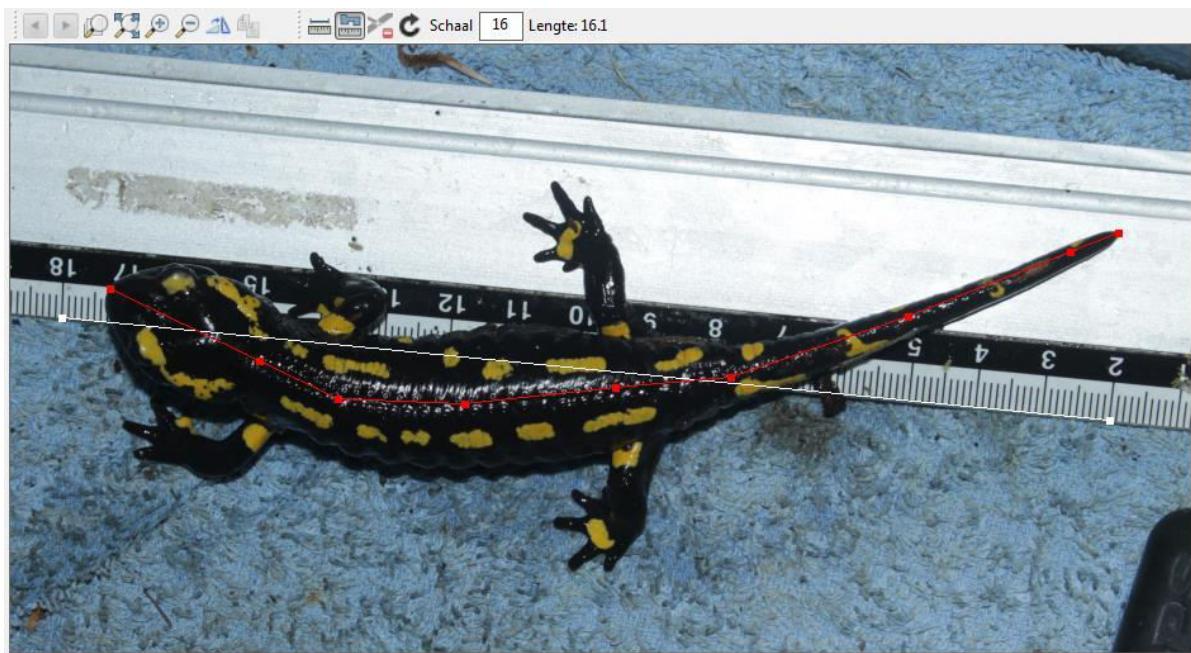
In the above illustration, the green rectangle indicates the buttons for measuring the animal, while the red rectangle indicates the fields to which, by pushing the buttons, the measurements are saved in the database. We perform two measurements: total length (TL) and snout-vent length (SVL, which basically is TL with the tail – see below).

- 1) At the start, the Scale measurement button is switched on by default. Use the right mouse button to cover a meaningful distance along an object of known length (e.g. a ruler), by clicking twice (start and end point). The calibration line appears in white.
- 2) Enter the actual calibration line length in the 'Scale' box.
- 3) To perform the actual measurement, first click the 'Object measurement' button . Starting at the snout tip, now measure the animal with the right mouse button by drawing multiple straight segments along the body axis of the animal.
- 4) Pause for a first time at the third cross-ridge on the base of the tail. This ridge matches the end of the cloacal opening and is traditionally considered as the end of the body (without tail).
- 5) Hit the 'SVL' button higher up, in order to save the measurement to the SVL field.
- 6) Now continue measuring until the tip of the tail.
- 7) Hit the 'TL' button to copy the total length to the Total length field.

Useful:

- Standardise your measuring by allowing following the centre of the back, namely in between the two rows of gland pores.
- Delete the last measurement point with the button.
- Double click with the right mouse button to erase the white calibration line or the red measurement line. To erase both at once, use the button.

- While performing measurement, you can zoom with the mouse wheel. Navigating the picture is also possible with the provided zoom buttons and the hand icon which appears when clicking on the picture with the left mouse button.
- Lens effects, angle of photographing, etc. can cause measuring errors. Therefore, try to position the animal as stretched out as possible next to the ruler and observe a 90° angle with the surface on which animal and ruler are located when photographing. Position the salamander close enough to the ruler. Using a background with subdivisions of fixed length (e.g. graph paper) offers the most accurate results.



## 4.7 Activity

Together with the two variables discussed in the next two sections, Activity allows to document how the animal was found by choosing from a list of (fixed) options.

Activity may demonstrate the yearly activity cycle of the population, with certain activities being tied to seasonal patterns. The impact of observer disturbance needs to be minimised, affecting as such the search method. Use your torch light so the beam only hits newly discovered animals when they are within viewing distance. More simply put, shine your light close to where you are and not too far ahead.

Allowed values (fixed list):

- Moving: only if you may assume the movement was not caused by the observer
- Immobile, without further detail: the most frequently observed state
- Immobile, with stretched front legs: as if ‘standing guard’, as also seen in male common toads during spring migration
- Ascending the trunk of a tree or similar: a special type of ‘standing guard’
- (possibly) Depositing larvae: for females positioned in water. While hard to distinguish, animals in water with the sole purpose of moisture absorption are entered as ‘Immobile, without further detail’.
- Body to body interaction between males: may relate to combat as well as futile mating attempts. Both categories are hard to tell apart.
- Mating, in amplexus: male and female in mating hold.

- Eating
- Dead

## 4.8 Exposure

The degree to which an animal is exposed to air and sight potentially reflects its yearly activity cycle and/or its response to environmental conditions. Partially hidden animals are frequently observed when humidity is sufficient but wind speed is high.

Allowed values (fixed list):

- Fully exposed: dier is volledig zichtbaar of heeft duidelijk geen intentie zich te verbergen
- Partially hidden: schuilplaats verlatend of inkruipend
- Entirely hidden, observed by flipping objects: only for animals found when turning over stones, logs, etc. To be avoided, as it is (1) unsuitable as standardised count method and (2) it causes disturbance of moisture maintenance and shelter availability.

## 4.9 Habitat

An indication for the ecological meaning of where the animal was found.

- Open area, bare ground (paths, trails, ...): compare with the next option, but on naked soil. Open spots have been cited as being used for finding a mate.
- Open area, forest floor (dead leaves, ...): likely indicates a not ‘consciously’ chosen location, albeit usually away from shelter (and as such, clearly related to an ‘Activity’). For animals found on the forest floor (dead leaves, detritus, ...), without being explicitly associated with a structural element.
- Associated with (living) tree: Obviously, the woods are full of trees. What is meant, however, are animals located on or along the edges of tree roots. This may be related to hydration by catching water running down along the tree trunk, to use of trees as landmarks, to territorial behaviour, ...
- Associated with dead wood: for animals found on or in the immediate vicinity of stumps, fallen trunks, piles of wood, .... Dead wood may provide shelter as well as being used as a vantage point.
- Associated with vegetation: (possibly hiding) in (dense) vegetation.
- Associated with stagnant water (ponds, ...): mainly females to deposit larvae.
- Associated with running water - streams etc.: mainly females to deposit larvae.
- Paved road: on paved road.
- Associated with other notable structure.

While the offered values are certainly debatable, applying your own personal and clear definitions of each of them may allow to document habitat use through space and time.

## 4.10 Sector

Sectors are a practical tool for rough localisation of observations. The sector of a given sighting is chosen from a fixed, user-specified list (see chapter 1).

## 4.11 Microlocation

A free to use field for additional details on the site of observations, e.g. a code for a certain terrain feature, left or right side of the transect, .... Best filled out with values of a self-defined fixed set, but not enforced by the program.

## 4.12 Latitude & longitude

The most commonly used set of geographical coordinates, map date WGS84. These are the coordinates used by most GPS devices, as well as Google Maps, Google Earth, ....

## 4.13 Time

Time of observation of the animal, to be entered as dd/mm/yyyy hh:mm:ss.

## 4.14 Standard method

Use this to specify if a sighting was made following a (your!) standard protocol. This may mean that a fixed transect has been surveyed, during which the observer counted salamanders the same way each time, preferably using the same torch, the same number of observers, the same search effort, the same route, ... Standardisation is critical for analysis of repeated visits. The default value is 'on'.

## 5. Matching and filtering

Now that you have properly entered all individual sighting details, you may finally hit the 'OK' button and start searching for past sightings of the same animal. This matching process is executed on the 'Sightings' tab. Note, however, that a lot of what is written below can also be used for data exploration, without having entered a new sighting first.

In chapter 1, we already briefly explained how to find matches (previous captures). At the left, the newly entered sighting is shown, at the right the already available sightings are sorted by decreasing similarity with that newly sighted animal.

At the top, you may also find buttons to edit the selected sightings (left and right). Hovering over the buttons reveals explanatory popups, allowing us to limit the below explanation to the less than obvious aspects.

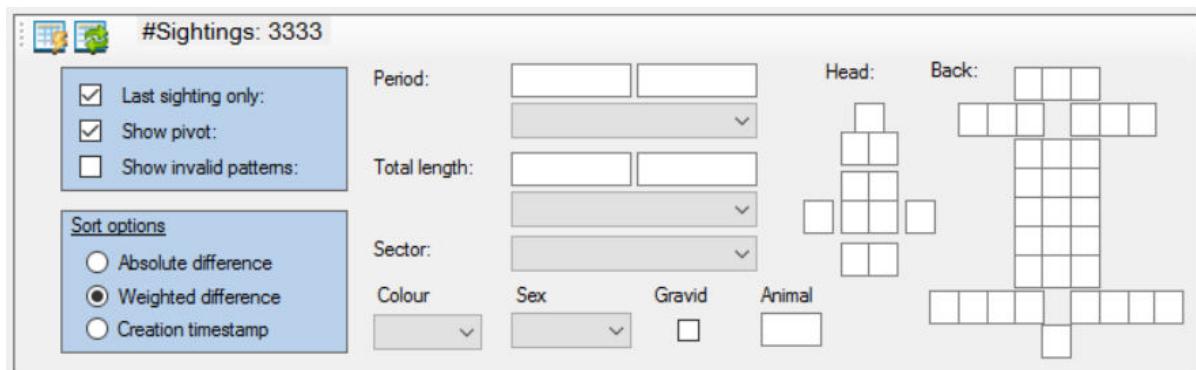
: At the end of the matching process, this button saves the new sighting, be it as the first sighting of a new individual, or an additional sighting of a known specimen. As long as the new sighting has not been saved, its entire heading is displayed against a green background.

: This (re)opens the 'Individual Sighting' data entry screen, allowing editing. Changes are saved automatically when closing the 'Individual Sighting' data entry screen, i.e. without having to hit the save button.

: We used this button before; starts the entry of a new sighting.

: This button is not relevant during the matching process of a new sighting, but can be used to compare a saved sighting with the rest of the database. By clicking it, the sighting selected at the right is moved to the left, after which the matching algorithm is automatically executed.

Conclusively, we can reduce the list of sightings at the right by using the selection or filter criteria at the lower left.



Many of the fields shown in the above illustration are readily recognisable, as they are also part of the 'Individual Sighting' data entry screen. Below we run through the options.

*Last sighting only*: In contrast to common exploration, it is desirable to only use the most recent sighting of each animal for matching new sightings.

*Show pivot*: If saved already in the database, you can decide whether the animal shown at the left has to be in the list at the right or not.

*Show invalid patterns*: to filter out invalid pattern sightings or not (see chapter 3).

*Sort options:*

- *Absolute difference*

The 44 pattern characteristics of the animal at the left are compared to those of the animal selected at the right. The number of characteristics of different value is counted. A characteristic which was left blank is not taken into account. The sightings in the list at the right are sorted by decreasing similarity. Only useful if a sighting is fixed to the left part of the screen. If not, sightings are sorted automatically by '*Creation timestamp*' (see below).

- *Weighted difference*

Sorting by '*Absolute difference*' may allow sightings with a lot of blank characteristics to rank high (as they do not contribute to the matching process), while differences may still be considerable. Sorting by '*Weighted difference*' accounts for this. The number of differences is divided by the number of non-blank characteristics of both animals (left and right), expressed as a percentage. This percentage determines the sorting order.

- *Creation timestamp:*

Sorts the list at the right in reversed chronology of data entry, with the latest entry at the top of the list. Useful to retrace your steps when entering multiple sightings.

*Period:* The first box defines the lower date limit of the (to be) selected sightings (formaat dd/mm/yyyy). Only sightings on or after that date are selected. The second box, at the right of the first one, does the opposite, setting an upper date limit. A simple dropdown menu allows filtering based on the sighting in the left half of the screen.

*Totale lengte:* As with *Period*, limits may be set to the total length of the animal of each sighting. Again, a dropdown menu allows filtering based on the sighting in the left half of the screen. To account for possible measuring errors, however, a margin of error is applied. To alter the value of this margin, see Appendix A.

*Animal:* to filter sightings of a single animal only by its identification number.

The remaining fields are, as mentioned, fairly obvious, as they were already discussed when describing the sighting entry process (chapters 3 and 4).

Changing the value of any of the checkboxes or dropdown menus automatically causes an update of the list at the right. To apply entered values in the remainder of the fields, click the 'Apply criteria' button . A 'Clear criteria' button  is also available.

## 6. Creating named copies of photographs

From the rather anonymous content of the *Images* folder, a copy of the photos of each sighting can be made, showing the sighting details in the file name.

- Identification number of animal => FsmXXXXXX (where X = digit)
- Date of sighting => yyyy-mm-dd
- Identification number of sighting => SghXXXXXX (where X = digit)
- Identification number of photograph => ImgXXXXXXXX (where X = digit)

These copies are created by hitting the  button, located above each photo frame.

## 7. Analysis

Those familiar with MS Access may easily export data for analysis. We intend to provide a myriad of graphs and analysis tools in the future.

To be continued...

## 8. Appendices

### 8.1 Appendix A - Preferences

For optimal use, a number of features can be set inside the database to fit your personal preference.

#### 8.1.1 Language

*ManderMatcher.mdb => TabFsmPrf => LggCde*

Allowed values:

- 'NDL': Dutch
- 'ENG': English

In the menu at the upper left of the screen, the language can be set to your preference. This is, however, reset when you close the program. To fix the language default to your liking, adjust the above field in the database.

#### 8.1.2 Sort preference

*ManderMatcher.mdb => TabFsmPrf => SrtCde*

Allowed values:

- 'ABS': absolute difference
- 'LOG': weighted difference
- 'CRT': creation timestamp

See chapter 5. The default setting can be altered in the database.

#### 8.1.3 Margin of error for length filter

*ManderMatcher.mdb => TabFsmPrf => MsrMgnLen*

Allowed values: error margin, in cm.

See chapter 5. Specifies the margin of error that is taken into account due to potential measuring error. The initial value is set to 1 cm.

#### 8.1.4 Zoom step size

*ManderMatcher.mdb => TabFsmPrf => ZomStpFct*

Allowed values: decimal number between 0 and 1

You can zoom with the zoom buttons or the mouse wheel. The size of each step is initially set to 0.01. It is advisable to adjust this value in relation to the resolution of your photographs.

### 8.1.5 Last sighting only

*ManderMatcher.mdb => TabFsmPrf => ShwLstSghOlyFlg*

Allowed values: on/off

Sets the default value for 'Last sighting only' (see chapter 5).

### 8.1.6 Show pivot

*ManderMatcher.mdb => TabFsmPrf => ShwPvtSghFlg*

Allowed values: on/off

Sets the default value for 'Show pivot' (see chapter 5).

### 8.1.7 Show invalid patterns

*ManderMatcher.mdb => TabFsmPrf => ShwlvlPatFlg*

Allowed values: on/off

Sets the default value for 'Show invalid patterns' (see chapter 5).

## 8.2 Appendix B – visit-associated variables

For entry of visited-related data, see chapter 2. A full list of the variables which may be entered is given in Appendix C. Here, we only offer further explanation for the less obvious ones.

The only mandatory variables are time at start of visit and time at end of visit. Among other things, this allows calculation of visit duration, % of time with moonlight during the visit, ... This type of derived variables are useful for further data analysis. In fact, the same goes for all other variables. The more you enter, the more you can do with your data.

Temperature, humidity, air pressure, wind speed, rainfall and visibility of the moon are often mentioned as factors affecting the activity level of fire salamanders. To allow analysis of changes in these variables, the program allows saving both a start and end value for these variables.

The visit-related data are entered via the 'Visits' tab/screen and are saved in the database in the visits table (*TabFsmVst*).

### 8.2.1 Trajectory

Select the chosen transect – see chapter 1. Use this for standardised counts. If not, it is impossible to tell afterwards whether a sector/area has been counted yielding 0 sightings, or whether it was omitted.

### 8.2.2 Date

Date of nearest sunset. Automatically deduced, with the eve of the night of visiting as determining. This is the main variable of the visit, or its 'name'.

### 8.2.3 Temperature, rain quantity, humidity, wind speed, air pressure, ...

You can collect these yourself or obtain them from a nearby weather station.

The program allows to enter cumulative rain quantity (in mm) of the previous 24 hours and of the last hour before the start of the visit. Given the localised nature of rain fall, local data are essential. The same applies for humidity.

#### 8.2.4 Rain

This variable allows to save your own, subjective assessment of rain fall intensity during the visit.

Allowed values (fixed list):

- No precipitation
- Mist falling / Drizzle
- Showers / Periods with rain
- Continuously raining

#### 8.2.5 Wind strength

As local wind force may be influenced by local topography (e.g. hilltop vs. sheltered valley), you can note your own, subjective assessment of the force of the wind.

Allowed values (fixed list):

- Windless
- Light breeze / Moderate wind
- Stiff breeze / Strong wind
- Stormy
- 

#### 8.2.6 Moon

Contradictory findings have been published on the influence of moonlight. Certain authors deem it beneficial for orientation, while others state it would limit activity. At the moment, the program only allows to note whether the moon was visible during the visit or not. A future version will offer automatic deduction of moon-related variables (luminosity, duration of moonshine during visit, ...).

##### 7.2.6.1 *Moon visibility*

This variable allows to note whether the moon is visible during the visit and, if invisible, what causes it to be invisible.

Allowed values (fixed list):

- Absent (not yet risen)
- Visible
- Invisible (due to clouds)
- Alternating visible and invisible

#### 8.2.7 Remarks

Free text field for additional information.

## 8.3 Appendix C – Tables in the ManderMatcher.mdb database

### 8.3.1 Visits – TabFsmVst

Field	Description
Vstldf (Visit Identification)	<b>Unique identification code</b> Alphanumeric, 6-character code, automatically generated
Dte (Date)	<b>Visit date</b> Date, in DD/MM/YYYY.
TrjCde (Trajectory Code)	<b>Trajectory</b> A transect code, as defined in table TabFsmTrjSct
ObsNbr (Observer Number)	<b>Number of observers</b> Integer
StgTme (Starting Time)	<b>Time at start of visit</b> Date-time, as DD/MM/YYYY HH:MM
StgDayTmeSav (Starting Daytime Savings)	<b>Time at start of visit – daylight saving time indicator</b> Allowed values (fixed values): <ul style="list-style-type: none"> <li>• S – <a href="#">Summer time</a></li> <li>• W – <a href="#">Winter time</a></li> </ul> Only relevant during the last Sunday of October between 2:00AM and 3:00AM.
EndTme (Ending Time)	<b>Time at end of visit</b> Date-time, as DD/MM/YYYY HH:MM
EndDayTmeSav (Ending Daytime Savings)	<b>Time at end of visit – daylight saving time indicator</b> Allowed values (fixed values): <ul style="list-style-type: none"> <li>• S – <a href="#">Summer time</a></li> <li>• W – <a href="#">Winter time</a></li> </ul> Only relevant during the last Sunday of October between 2:00AM and 3:00AM.
StgTmp (Starting Temperature) EndTmp (Ending Temperature)	<b>Temperature at start/end of visit</b> Number (°C) with 1 decimal digit
RaiStgCde (Rain Starting Code) RaiEndCde (Rain Ending Code)	<b>Rain at start/end of visit</b> Allowed values (fixed values): <ul style="list-style-type: none"> <li>• NONE – No precipitation</li> <li>• MIST – Mist falling / Drizzle</li> <li>• SHOW – Showers / Periods with rain</li> <li>• RAIN – Continuously raining</li> </ul>
HumStgPct (Humidity Starting Percentage) HumEndPct (Humidity Ending Percentage)	<b>Humidity at start/end of visit</b> Percentage, als een gehele waarde tussen 1 en 100
AirPsrsTgVal (Air Pressure Starting Value) AirPsrsEndVal (Air Pressure Ending Value)	<b>Air pressure at start/end of visit</b> Integer (hPa)
WndStgSpd (Wind Starting Speed) WndEndSpd (Wind Ending Speed)	<b>Wind speed at start/end of visit</b> Number (km/h) with 1 decimal digit
WndSpdStgCde (Wind Speed Starting Code) WndSpdEndCde (Wind Speed Ending Code)	<b>Wind force at start/end of visit</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• NONE – Windless</li> <li>• LGHT – Light breeze / Moderate wind</li> </ul>

	<ul style="list-style-type: none"> <li>STRG – Stiff breeze / Strong wind</li> <li>STRM – Stormy</li> </ul>
WndDirStgCde <a href="#">(Wind Direction Starting Code)</a> WndDirEndCde <a href="#">(Wind Direction Ending Code)</a>	<b>Wind direction at start/end of visit</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>NN – North</li> <li>NW – Northwest</li> <li>WW – West</li> <li>ZW – Southwest</li> <li>ZZ – South</li> <li>ZO – Southeast</li> <li>OO – East</li> <li>NO – Northeast</li> </ul>
MonVisStgCde <a href="#">(Moon Visibility Starting Code)</a> MonVisEndCde <a href="#">(Moon Visibility Ending Code)</a>	<b>Moon visibility at start/end of visit</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>ABST – Absent (not yet risen)</li> <li>VISI – Visible</li> <li>INVI – Invisible (due to clouds)</li> <li>ALTN – Alternating visible and invisible</li> </ul>
Lst24hRaiQty <a href="#">(Last 24 Hours Rain Quantity)</a>	<b>Rain quantity of last 24h</b> Number (mm) with 1 decimal digit
Lst1hRaiQty <a href="#">(Last 1 Hour Rain Quantity)</a>	<b>Raining quantity of last 1h</b> Number (mm) with 1 decimal digit
RemTxt <a href="#">(Remark Text)</a>	<b>Remarks</b> Free text

### 8.3.2 Sectors – TabFsmSct

Field	Description
SctCde <a href="#">(Sector Code)</a>	<b>Sector code</b> Alphanumeric, 9-character code, user-defined
Veldnaam: SctNme <a href="#">(Sector Name)</a>	<b>Sector name</b> Free text (30 characters)
Veldnaam: SctDsc <a href="#">(Sector Description)</a>	<b>Sector description</b> Free text (unlimited character size)

### 8.3.3 Trajectories – TabFsmTrjSct

Field	Description
TrjCde <a href="#">(Trajectory Code)</a>	<b>Trajectory code</b> Alphanumeric, 9-character code, user-defined
SctCde <a href="#">(Sector Code)</a>	<b>Sector code</b> A sector code, as defined in TabFsmSct

### 8.3.4 Preferences – TabFsmPrf

Field	Description
LggCde <a href="#">(Language Code)</a>	<b>Language preference</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>NDL – Dutch</li> <li>ENG – English</li> </ul>
SrtCde <a href="#">(Sort Code)</a>	<b>Sort option preference</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>ABS – decreasing absolute difference</li> </ul>

	<ul style="list-style-type: none"> <li>LOG – decreasing weighted difference</li> <li>CRT – decreasing creation timestamp</li> </ul>
MsrMgnLen <i>(Measure Margin Length)</i>	<b>Margin of error for length filter</b> Number (mm) with 2 decimal digits
ZomStpFct <i>(Zoom Step Factor)</i>	<b>Zoom step size</b> Percentage, decimal number from 0.00 to 1.00
ShwLstSghOlyFlg <i>(Show Last Sighting Only Flag)</i>	<b>Last sighting only</b> Yes/no
ShwPvtSghFlg <i>(Show Pivot Sighting Flag)</i>	<b>Show pivot</b> Yes/no
ShwlvlPatFlg <i>(Show Invalid Pattern Flag)</i>	<b>Show invalid patterns</b> Yes/no
LonDeg <i>(Longitude Degree)</i>	<b>Longitude (*)</b> Number (degrees) with 5 decimal digits From -180.00000 to 180.00000
LatDeg <i>(Latitude Degree)</i>	<b>Latitude (*)</b> Number (degrees) with 5 decimal digits From 0.00000 to 90.00000
TmeZon <i>(Timezone)</i>	<b>Time zone (*)</b> Negative or positive integer
SubSpc <i>(Subspecies)</i>	<b>Subspecies</b> Text; for potential use in future versions

(\*) Longitude, latitude and time zone are needed to deduce location-related statistics (sunset, moonrise, etc.) and to map sightings. These features will become available in future version of the program.

### 8.3.5 Sightings – TabFsmSgh

Field	Description
SghIdf <i>(Sighting Identification)</i>	Unique sighting number Alphanumeric, 6-character code, automatically generated
FsmIdf <i>(Firesalamander Identification)</i>	Link with individual animal number Alphanumeric, 8-character code, determined bij selection of either the 'Match' or the 'New' button.
VstIdf <i>(Visit Identification)</i>	Link with visit – visit number Unique number, as defined in visits table (TabFsmVst)
EyeLftCde <i>(Eye Left Code)</i> EyeRgtCde <i>(Eye Right Code)</i> PtdLftCde <i>(Parotoid Left Code)</i> PtdRgtCde <i>(Parotoid Right Code)</i>	<b>Left/Right Eye/Parotoid</b> Allowed values: <ul style="list-style-type: none"> <li>0: no pigmentation (all-black)</li> <li>1: pigmentation present, not connected to next position</li> <li>2: pigmentation present, connected to next position</li> </ul>
PtdExtLftCde <i>(Parotoid Extension Left Code)</i> PtdExtRgtCde <i>(Parotoid Extension Right Code)</i>	<b>Parotoid extensions</b> Allowed values: <ul style="list-style-type: none"> <li>0: absent or does not reach anterior edge of front leg insertion</li> <li>1: present and passes anterior edge of front leg insertion</li> </ul>
ChkLftCde <i>(Cheek Left Code)</i> ChkRgtCde <i>(Cheek Right Code)</i>	<b>Cheeks</b> Allowed values: <ul style="list-style-type: none"> <li>0: no yellow pigmentation</li> <li>1: yellow present, unconnected to eye or parotoid spot</li> <li>2: yellow present, connected to eye or parotoid spot</li> </ul>
SntSptNbr <i>(Snout spot number)</i>	<b>Number of snout spots</b> Integer
EyeLftExtCde <i>(Eye Left Extension Code)</i> EyeRgtExtCde	<b>Eye-to-snout extensions</b> Allowed values: <ul style="list-style-type: none"> <li>0: does not cross centre of snout</li> </ul>

(Eye Right Extension Code)	<ul style="list-style-type: none"> <li>• 1: crosses centre of snout</li> </ul>
BckLftSptNbr (Back Left Spot Number) BckRgtSptNbr (Back Right Spot Number) BckMidSptNbr (Back Mid Spot Number)	<b>Number of left/right/middle back spots</b> Integer
TaiSptNbr (Tail Spot Number)	<b>Number of tail spots</b> Integer
BckLftLenCde1/2/3/4/5, (Back Left Length Code) BckMidLenCde1/2/3/4/5, (Back Mid Length Code) BckRgtLenCde1/2/3/4/5 (Back Right Length Code)	<b>Relative spot length indicators</b> Allowed values: <ul style="list-style-type: none"> <li>• 0: no subsequent left, mid or right back spot present after the considered spot</li> <li>• 1: the spot is shorter than the subsequent spot</li> <li>• 2: the spot is longer than the subsequent spot</li> </ul>
ToeFrnLftCde1/2/3 (Toe Front Left Code) ToeFrnRgtCde1/2/3 (Toe Front Right Code)	<b>Front toes left/right</b> Allowed values: <ul style="list-style-type: none"> <li>• 0: no pigmentation present</li> <li>• 1: pigmentation present</li> <li>• X: clear signs of malformation, albeit by birth or due to predation or (larval or postlarval) cannibalism, including higher than normal numbers of toes (4 front, 5 hind) lead to assigning 'X' to all toe characteristics of that foot.</li> </ul>
ToeHndLftCde1/2/3/4 (Toe Hind Left Code) ToeHndRgtCde1/2/3/4 (Toe Hind Right Code)	<b>Hind toes left/right</b> Allowed values: <ul style="list-style-type: none"> <li>• 0: no pigmentation present</li> <li>• 1: pigmentation present</li> <li>• X: clear signs of malformation, albeit by birth or due to predation or (larval or postlarval) cannibalism, including higher than normal numbers of toes (4 front, 5 hind) lead to assigning 'X' to all toe characteristics of that foot.</li> </ul>
SexCde (Sex Code)	<b>Sex</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• F – Female</li> <li>• M – Male</li> </ul>
AgeCde (Age Code)	<b>Age class</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• A – Adult</li> <li>• J – Juvenile</li> <li>• S – Subadult</li> </ul>
GvdFemCde (Gravid Female Code)	<b>Gravid female</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• Y – clearly gravid</li> <li>• N – not or not obviously gravid</li> </ul>
ClrCde (Color Code)	<b>Colour</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• Y – Yellow</li> <li>• O – Orange</li> </ul>
BdyLen (Body Length)	<b>Total length</b> Decimal number (cm) Format nn,n

SvtLen (Snout-Vent Length)	<b>Snout-vent length</b> Decimal number (cm) Format nn,n
Wgh (Weight)	<b>Weight</b> Decimal number (cm) Format nn,n
SctCde (Sector Code)	<b>Sector</b> A sector code, as defined in table TabFsmSct
MicLocCde (Micro Location Code)	<b>Microlocatie</b> Alfanumerical, 9-character code, free entry
CrdLatDeg (Coordinate Latitude Degree)	<b>Latitude</b> Decimal number (degrees) Format nn,nnnnn - from 0.00000 to 90.00000
CrdLonDeg (Coordinate Longitude Degree)	<b>Longitude</b> Decimal number (degrees) Format nn,nnnnn - from -180.00000 to 180.00000
ActCde (Activity Code)	<b>Activity</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• MOVE - Moving</li> <li>• IMMO - Immobile, without further detail</li> <li>• PUSH - Immobile, with stretched front legs</li> <li>• CLIM - Ascending the trunk of a tree or similar</li> <li>• BIRT - (possibly) Depositing larvae</li> <li>• MM&amp;&amp; - Body to body interaction between males</li> <li>• AMPL - Mating, in amplexus</li> <li>• EATT - Eating</li> <li>• DEAD - Dead</li> </ul>
HabCde (Habitat Code)	<b>Habitat</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• PATH - Open area, bare ground (paths, trails, ...)</li> <li>• LEAF - Open area, forest floor (dead leaves, ...)</li> <li>• TREE - Associated with (living) tree</li> <li>• WOOD - Associated with dead wood</li> <li>• VEGE - Associated with vegetation</li> <li>• POOL - Associated with stagnant water (ponds, ...)</li> <li>• STRM - Associated with running water - streams etc.</li> <li>• ROAD - Paved road</li> <li>• OTHR - Associated with other notable structure</li> </ul>
ExpCde (Exposure Code)	<b>Exposure</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• FULL - Fully exposed</li> <li>• PART - Partially hidden</li> <li>• NULL - Entirely hidden, observed by flipping objects</li> </ul>
SghTme (Sighting Time)	<b>Time of observation</b> Date-time, as DD/MM/YYYY HH:MM:SS
StaMthFlg (Standard Method Flag)	<b>Standard method indicator</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• Y – Standard</li> <li>• N – Not standard</li> </ul>
VldPatFlg (Valid Pattern Flag)	<b>Valid pattern indicator</b> Allowed values (fixed list): <ul style="list-style-type: none"> <li>• Y – Valid</li> <li>• N – Invalid</li> </ul>

CrtTms <a href="#">(Creation Timestamp)</a>	<b>Time of creation of record</b> Date-time, as DD/MM/YYYY HH:MM:SS
LupTms <a href="#">(Last Update Timestamp)</a>	<b>Time of last edit of record</b> Date-time, as DD/MM/YYYY HH:MM:SS

### 8.3.6 Sightings - Photographs – TabFsmSghImg

This table links the photographs to the sightings (automatically generated numbers).

Field	Description
Sghldf <a href="#">(Sighting Identification)</a>	<b>Sighting number</b> as defined in the sightings table (TabFsmSgh)
Imgldf <a href="#">(Image Identification)</a>	<b>Unique photograph identification number</b> Alphanumeric, unique, 8-character code, generated by the program.
RegTms <a href="#">(Registration Timestamp)</a>	<b>Time of photography</b> Date-time, as DD/MM/YYYY HH:MM:SS Not yet operational.

### 8.3.7 Sightings - Remarks – TabFsmSghRmk

This table contains the free remarks of each sighting.

Field	Description
Sghldf <a href="#">(Sighting Identification)</a>	<b>Sighting number</b> as defined in the sightings table (TabFsmSgh)
RmkTxt <a href="#">(Remark Text)</a>	<b>Remarks</b> Free text

## 8.4 References

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