APHIS User Manual

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Automatic Photo Identification Suite

Version 1.0.0

Fundació Balear d'Innovacio i Tecnologia (Govern de les Illes Balears)
Population Ecology Group - Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

Disclaimer

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The software was developed with greatest care and tested extensively on different computer systems. We found no errors in the released product versions. Nevertheless, there is no guarantee, that the software will run error-free on each system. We will not take any liability for incompatibilities with hardware-components and other software products and their components.

The software is provided "as is", without any guarantee on the suitability for a certain case of application.

No liability whatsoever will be accepted in case of data loss caused by using the software. Using the software is at the sole risk of the user. Fundació BIT and IMEDEA will take no liability for damages resulting from the direct or indirect use of the software.

Project partners and acknowledgements

APHIS development has been funded by the Population Ecology Group of IMEDEA (Instituto Mediterraneo de Estudios Avanzados), being the members of this research group involved in software requirements and functionality definition as well as in testing phases. Dr. Giacomo Tavecchia conceptualized and impulsed the idea, he has participated in every decision taken since the beginning to the end of the project. Dr. Tavecchia and José Manuel Igual Gómez conducted a sequence of sampling campaigns of *Podarcis lilfordi* specifically designed to test APHIS, sharing for the benefit of the project their experience in capture-recapture procedures. Andreu Rotger Vallespir has become the most active user and reviewer of the APHIS 1.0 functional beta version.

On the other hand, Fundación BIT (formerly Fundación iBit) has been in charge of software programming. Dr. Óscar Moya supervised the tasks of the developers team, ensuring that APHIS functionality fulfilled the requirements defined by the Population Ecology Group. Pep Lluis Mansilla and Sergio Madrazo worked hard transforming ideas to the working piece of code we denominate APHIS and that you can download from .http://imedea.uib-csic.es/bc/ecopob/

We specially appreciate the support of the authors of I3S, Jurgen den Hartog and Renate Reijns, which kindly and rapidly respond to all our questions when we were putting efforts on understanding the I3S code and method.

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1. Introduction

This manual guides you through the use of APHIS v.1.0. This software suite includes two photo-identification procedures:

1) a pixel-based comparison of a given region or ROI (Image template matching, ITM)
2) a comparison of user-defined spots pattern (Spots Pattern Matching, SPM).

The first procedure has been originally created for APHIS, whereas the second procedure is an extension of the already existing procedure implemented in software I3S (see chapter 4).

The second procedure also implements a database filtering system that uses qualitative parameters to avoid unnecessary comparisons. Both procedures share a common user interface, the characteristic of which are described in the following sections.

The photo-identification consists in the comparison of a **sample**, i.e. a picture of an individual of unknown identity, against a set of **candidates,** i.e. pictures of individuals of known identity present in the database. The **database**, in this case is a simple file structure that uses folders to store any images of each individual. In APHIS the database will be a folder with as many sub-folders as individuals identified.

The software assists photo-identification by applying algorithms to calculate similarities among the sample images and the candidates, returning a **score** value per comparison that will be used to order candidates for a posterior **visual inspection**. During the final inspection the user decides whether the sample is a **match** with a candidate or not. If the sample is a match, the image will be stored under the existing folder of the candidate picture. Alternatively, it will be stored as a **new individual,** creating a new folder in the database. Note that APHIS prompts the folder name using successive numbers, but users can write a different one**.**

The photo-matching is done in three steps.

1) Pre-processing. Before comparisons, users are asked to prepare samples by selecting reference points on each picture. This phase is different in SPM and ITM (see below).
2) Matching. During matching, the software compares the sample pre-processed images with those already presented in the database and delivers a series of potential matches (maximum an hundred potential matches), from the more to the less plausible.
3) Visual inspection. In this last phase, users inspect the potential matches and decided whether a match has been found or not.

In SPM we implemented a database **filtering system** which allows the user to define a filter, e.g. male of female, to reduce the set of valid candidates, avoiding unnecessary comparisons against the whole database. Filters have been thought to describe qualitative characters or **features** that distinguish unequivocally one individual from another, such as the gender or the location. User can define as many filters as necessary that will be combined to preselect the candidates that have to be compared to the sample. We have called this functionality **multichar filtering.** The use of such filters is not necessary, but in large database can reduce considerably computing efforts and waiting times during the analysis.

APHIS stores the results in text files. These files are formatted as comma-separated *CSV* to allow its

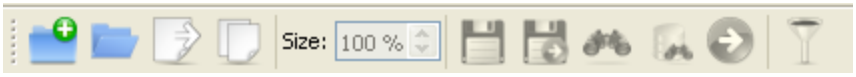
inspection on a spread-sheet. *CSV* files can be opened by commonly used programs as Microsoft Office or Open Office [1] among others.

The APHIS software also includes the particular concept of **project** which is used to define a study of a single species or population in determined conditions (i.e. from the same geographical location if migration is implausible, or studied during a segment of time) or analysed with a particular algorithm (ITM or SPM). Finally, the program offers two batch processes. The first one can be activated to open a set of samples for pattern edition (**Open Batch**) and the second one to compare among each of the previously edited samples and the candidates already in the database (**Search Batch**).

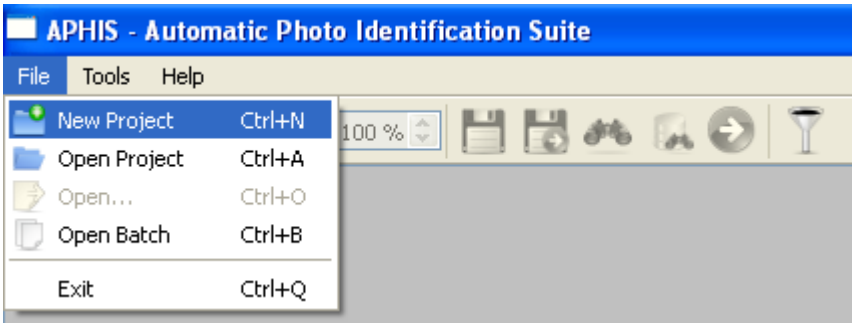
2. How to begin

When APHIS is launched a main window appears. The main Menu is divided in three categories (File, Tools and Help) and gives access to APHIS controls. The submenus also display key shortcuts to most operations.

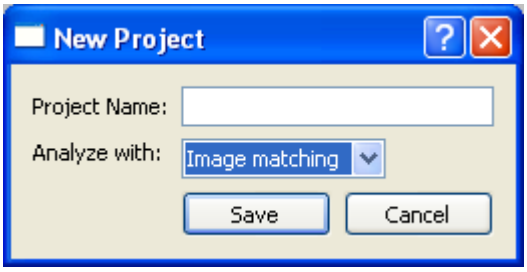
A set of short-cuts to the most common operations. Only lightened buttons are active in a given moment.



On the File option, users can chose between opening an existing project or create a new one.



When a new project is created, the user is asked to specify the name of the project and the procedure that will be used in photo matching (ITM or SPM).



1 It can be downloaded for free at http://www.openoffice.org/

Differences between these procedures are outlined in chapters 3 and 4. The ITM procedure is faster but is more affected by image characteristics. It should be preferred when images are homogeneous in terms of light and resolution and when individuals present highly defined spots or contrasted colors. The SPM procedure is well adapted when photos are heterogeneous or when animal characteristics are not well distinguishable, however the pre-processing phase is usually longer than the one in the ITM procedure. Once the matching procedure has been defined, a project sub-folder is created and stored in the directory "ProyectosFOTOID" or "ProyectosI3S", under ITM and SPM procedures, respectively. APHIS will create a project file with *.pis* extension, a database sub-folder where the candidates will be stored, a sub-folder where edited samples will be placed since processed and a last sub-folder that will contain the reports and logs generated during the analysis. Project name and characteristics will appear in the information displayed on the right part of the window.

A new project is a *tabula rasa* where no information has been provided to the software to perform any analysis. As photo-identification is based on the use of a minimum repository of images to compare your sampled individuals with, it is mandatory to create a database to proceed to the next steps. When only one image has been taken, it is possible to create a database using the *Open* function (from the *File Menu*, *Toolbar* or simply by pressing *Ctrl+O*). However users commonly begin with a set of images of individuals. In this case one should use the *Open Batch* function (from the *File Menu*, *Toolbar* or simply by pressing *Ctrl+B)*. In each case, APHIS will ask to select the folder that contains the image/s. Note that each processed image will be separated in a sub-folder representing a single individual.

Once the first image is displayed user can control its zoom level and position either with the mouse wheel or with the size selector of the toolbar and the scroll bars that surround the image. After these preliminary steps, it is time to define the references for each image. Here the procedures differ and the steps to follow will be outlined in the next chapters.

3. Image Template Matching (ITM)

Introduction

The ITM procedure implements the *matchTemplate* function of the Open Computer Vision libraries[2]. The *matchTemplate* is a preprogrammed function of OpenCV that slides a template image patch over an input image looking for matches. This method provides three different algorithms and their normalized versions in order to calculate a matrix of likelihoods of match per comparison. APHIS implements the normalized version of the correlation coefficient algorithm, which is the most accurate of the three. Normalization is used to minimize the effect of lightning differences among template while calculating matching scores.

During the ITM pre-processing step the user selects two reference points for each picture. They should be easily recognizable parts of the animal, e.g. shoulders or eyes, or species-characteristic.

2 http://opencv.org/

For the lizard in Photo 1, the two references were the two upper corners of the larger scales on the first four-scale horizontal pectoral line (Photo 1.1). Depicting a reference system is necessary to ensure accurate two dimensional comparisons of sample and candidate. The reliability of matching scores will depend on the reproducibility of this selection across pictures.

References will be used in ITM to align the individual with the horizontal axis (Photo 1.2), crop a region of interest which proportions will be dependent of the pixel distance among references (Photo 1.3), resize the image to a fixed resolution being the resulting image named as **pattern** (Photo 1.4) and, finally to divide the pattern in six non-overlapping contiguous **templates** extracted automatically from the lower half of the pattern (Photo 1.5). Steps (2) to (5) are automatically performed by the software and do not need supervision. The only supervised task is marking the two reference points.

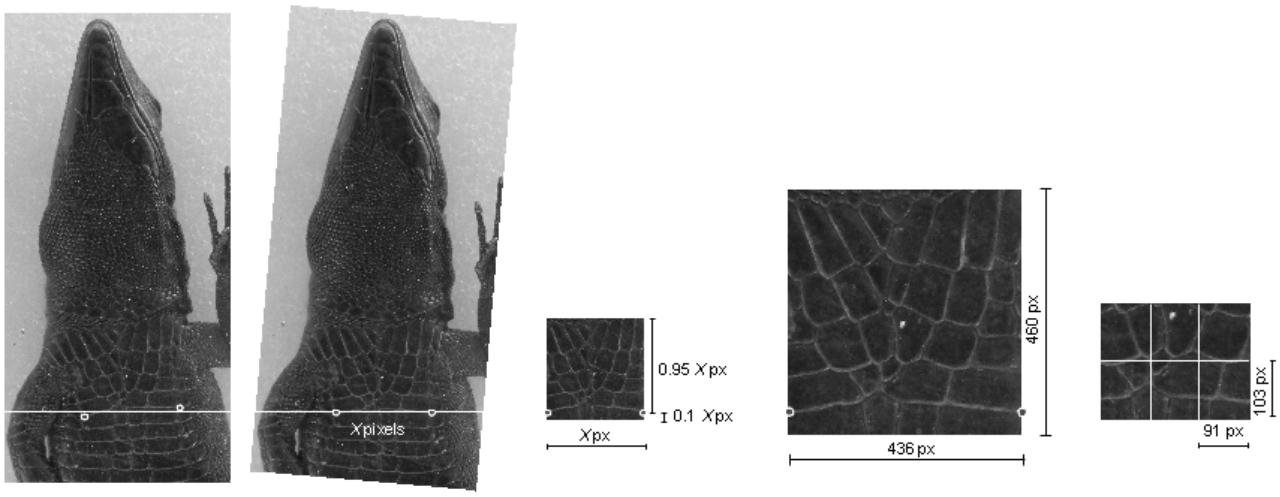


Photo 1.

The six resulting templates extracted from a single sample are individually compared with the candidate pattern and the scores resulting from the six comparisons are added up to produce the final sample-candidate matching score. APHIS delivers an ITM score list per comparison where candidates are ordered, from highest to lowest, by their matching likelihood (the final score). Individual template scores range from -1 to 1, this being the score obtained when the template is a portion of the own input image. Therefore a value of 6 would be a perfect sample-candidate match.

Using non-overlapping templates the effect of local image defects has less impact on the final score, enabling real matches to be well positioned in the score list ahead of random ones.

Creating a new or opening an existing ITM project

A new project can be created from the menu bar, toolbar or with the *Ctrl + N* key short-cut. A window will open asking you to give a name to the project and to chose the analytical procedure to

apply. In this case the *Image Matching* option should be selected. The ITM new project sub-folder is placed under *ProyectosFOTOID*. There you will find a file with the *.pis* extension, a database sub-folder where the candidates will be stored, a sub-folder where edited samples will be placed since processed and a last sub-folder that will contain the reports and logs generated during the analysis.

Once familiar with the analytical procedure it can be helpful to browse this folder/sub-folder structure using the File Explorer from Windows. That can give you a better understanding on how APHIS manages the files used in the project, thus enhancing your user experience and helping you to use the software more efficiently.

An existing project can be opened from the menu bar, tool bar or with the *Ctrl + A* key short-cut. ITM projects are stored with the *.pis* extension and found under the *.../APHIS/ProyectosFOTOID* folder.

Once the project is opened a lateral panel is displayed in the interface. At this time, only the project name and the procedure used for the analysis are indicated, but more valuable information and functionality will be incorporated to this area as you progress in the analysis.

***Warning**: APHIS was programmed and tested in Windows XP systems. Windows 7, 8 and 10 changed the accessibility to files under the Program Files Folder (*C:\Program Files (x86)*) . The consequence is that Project Folders are not visible when you browse with the Windows Explorer to the APHIS folder. Follow the instructions in Annex 1 to find that folders.*

Create the project database

When creating a new project, as photo-identification is based on the use of a minimum repository of images to compare your sampled individuals with, it is mandatory to create a database to proceed to the next steps (see end of Chapter 2 for how to begin database).

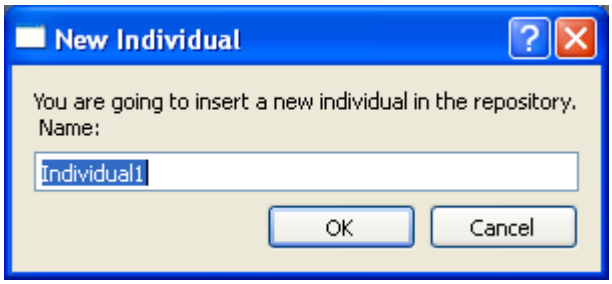
Once an image is displayed as a single image or as the first one of a batch, it appears on the main window. User can control its zoom level and position either with the mouse wheel or with the size selector of the toolbar and the scroll bars that surround the image.

The next two left click of the mouse will position the references (Photo 1.1). The first reference to set must be the left one, the second the right one. The sequence is not trivial as APHIS needs to know which one is on the left side of the animal and which is on the right. A reference can be deleted right clicking on it.

After setting the references, user can switch to the handy buttons from the toolbar.

At this stage, with a new project where no repository or candidate images are present, images should be simply saved in the database. Press the *Save* button (with the disk image) to open one

image or the *Save & Next* button (the disk image with a green arrow) if you are in a batch process. Both store the pattern and templates in the database. You can also discard an image if it does not achieve the necessary quality to be taken into consideration for the analysis. Keep doing that with all the images you opened. APHIS will give automatically a name to the individual you save, however it is possible to edit this name before passing to the next image. Note that APHIS will treat all these unmatched images as belonging to different individuals. Users should make sure that each image saved as candidate belongs to a different individual.



***Warning**: while creating the database using* Open Batch *it is required that each image belongs to a different individual. Two photographs from the same individual would be treated as belonging to different animals because matching algorithms have still not been applied to detect such circumstance.*

Analyse of image/s

Once at least one sample is in the database it is possible to proceed to search for matching images. There are three steps for the analysis of sample image/s: the **pre-processing**, the **matching** and the phase of **post-processing** (or visual inspection).

PRE-PROCESSING: First open the sample with the *Open* button or a set of samples with the *Open Batch* button. Each image should be pre-processed by marking the references as when creating the database. Two references are positioned by the first two left click of the mouse. Users should take in mind that these references should be the same on every picture. The pre-processing phase can be stopped at any time. Edited samples will be temporally stored in the project's *Captures* folder for the matching processed. After the matching process these temporary files will be moved to individual sub-folders of the database or discarded. The *General Info* tab has a section that lists the samples contained temporarily in the *Captures* folder and a button to delete them if this is user's decision. It also contains an *Image Information* section that displays the name of the image file and the date and time of capture and a *Finger Print Information* section informing of the number of references already marked on the active sample (Photo 2).

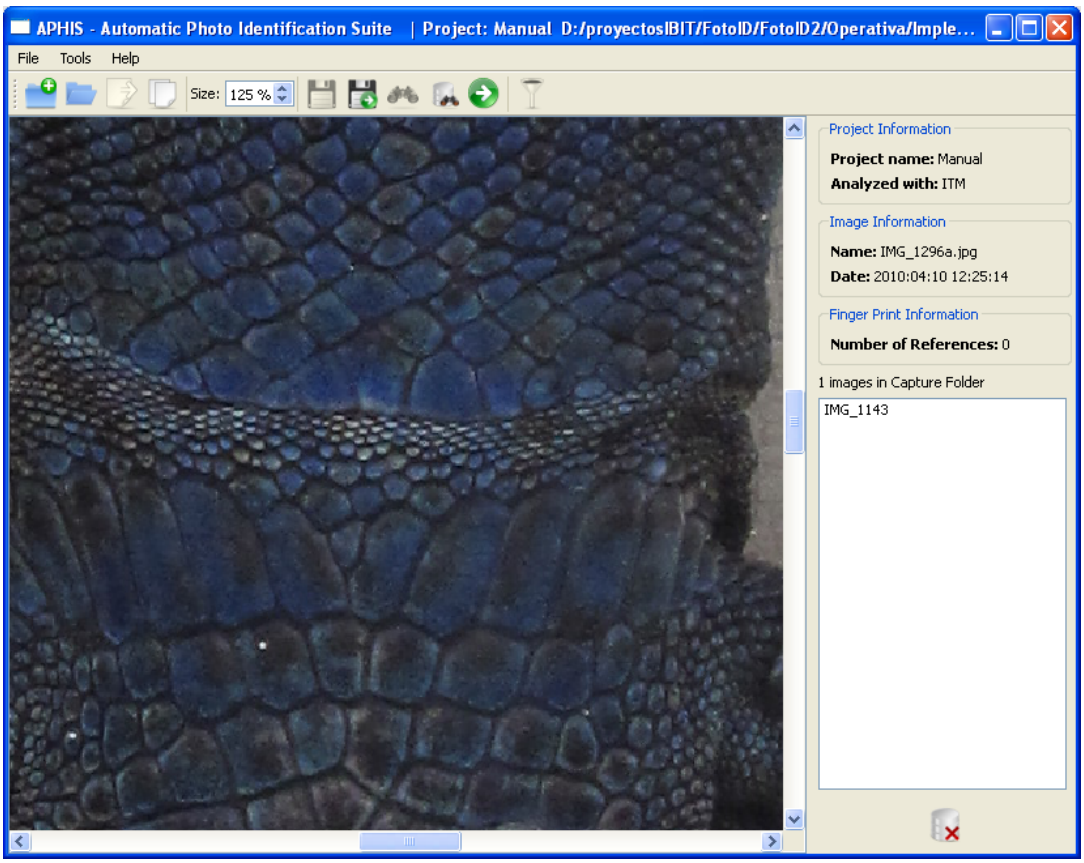


Photo 2

MATCHING: When pre-processing is finished, the matching phase begins by pressing the *Search* or *Search Batch* button (depending whether a single image or multiple images have been pre-processed). The software will calculate similarity indexes for each sample-candidate pair. If images are processed by batch, results will be presented only when all samples have been analysed. The matching phase is automatic and does not need supervision. This is true for single as well as multiple images. APHIS will display the results for each image sequentially.

VISUAL INSPECTION: For each image, APHIS displays in the lateral panel the first fifty options considering their likelihood values. Users can browse them from highest to lowest scores to visually compare the sample and candidate. After the inspecting phase the image can be registered using the *Match* button, if a match has been accepted, or as a new individual with the *New* button, if a match has not been found. User can also discard the image using the *Discard Sample* button (Photo 3). A match occurs when the sample and the selected candidate images are from the same individual. The sample image will be stored in the subfolder of the matching candidate in the database or on a new subfolder if it belongs to a new individual. In APHIS each subfolder represents one individual. The visual matching task will be then repeated for each sample image.

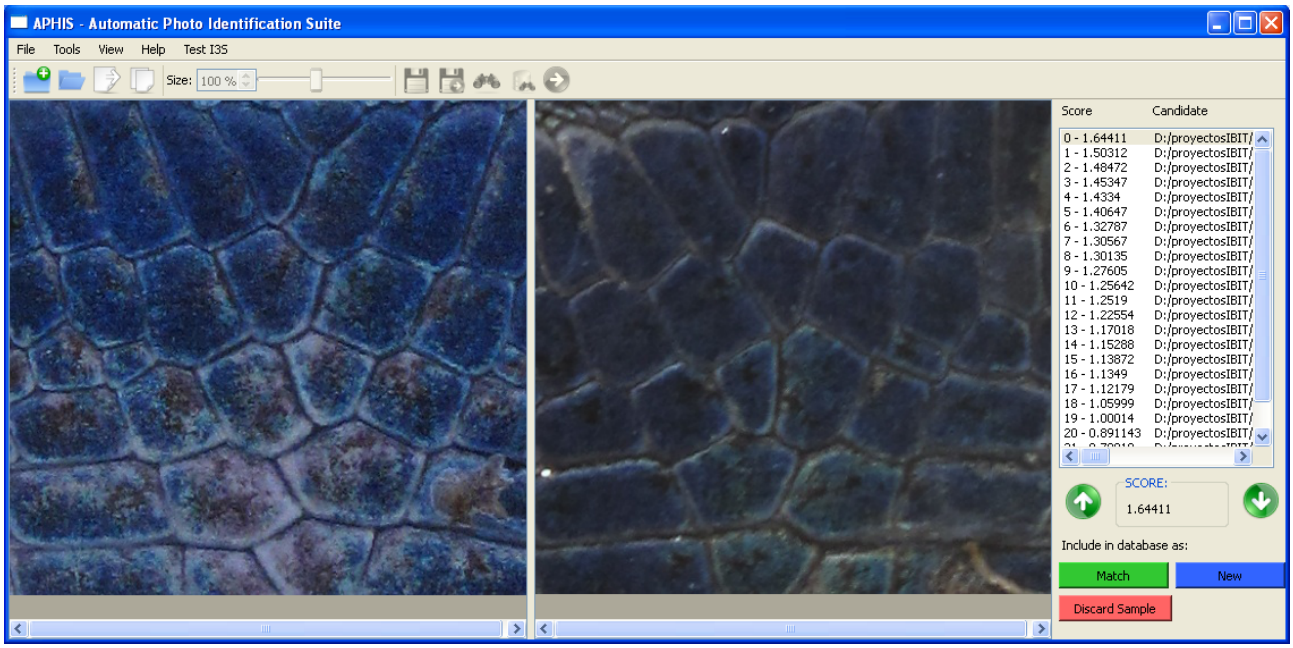


Photo 3

4. Spots Pattern Matching (SPM)

Introduction

SPM is based on the algorithm implemented in the freely available[3] software I^{3}S. In this case, during the preprocessing of a sample picture the user delimits the region of interest with three references and marks the set of spots within that will be compared during matching the defined area. The coordinates of each spot in the space delimited by the references form a fingerprint-like statistic.

During the analysis, the spatially-corrected cloud of spots from the sample is compared with the fingerprints stored in a repository. This correction is the result of an affine transformation of the sample pattern mapped onto that of the candidate one. Matching scores are calculated as the sum of metric distances between spots from every pair created in a sample-candidate comparison divided by the square of the total number of spot pairs. Lowest scores point to likely matches, being the number of spot pairs used during calculation relevant to the resulting score value although it is not yet clear to what extent. Numbers in the range of 20 to 40 spots would in general ensure enough pairs for the matching, however we recommend you to do some preliminary testing with a reduced set of samples to determine the number of spots that will actually require your study.

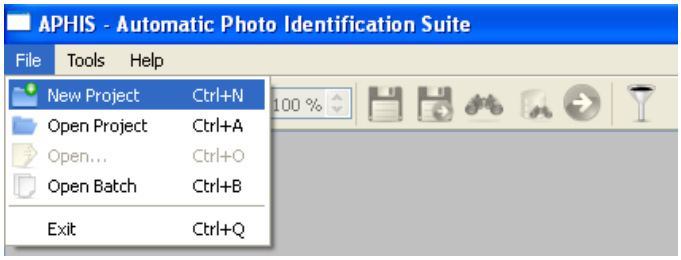
The matching algorithm used by SPM approach in APHIS was directly extracted from the I^{3}S Classic source code respecting its license agreement (GNU Public License v2) and in accordance with its developers. APHIS uses the exhaustive search version of the comparison algorithm

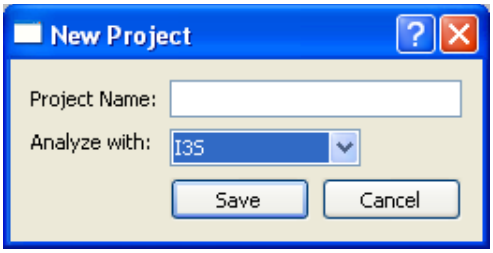
3 http://www.reijns.com/i3s/

described at Van Tienhoven et al. (2007)[4]. The exhaustive search uses every possible three spot pairs as references for different affine transformations, and not only those defined by the user (quick search). Score values are calculated for each transformation and a subsequent comparison with the candidate and the lowest is kept as final result. Exhaustive searches, although computer resources consuming, proved to be far more accurate than simple ('quick') searches. In APHIS, the pre-processing and the matching phases occur separately. This permits to process sequentially a group of samples and then launch the matching calculations for the whole set. Once finished the automated matching, the user is presented with a list of sample-candidate alternatives ordered from lower to higher matching scores. If multiple pictures from the same candidate are available, APHIS only shows this with the lowest score.

Creating or opening a SPM project

Creating and opening project can be done as explained for the previous procedure. A new project can be created from the menu bar, toolbar or with the *Ctrl + N* key short-cut. A window will open asking you to give a name to the project and to choose the analytical procedure to apply. In this case the *I3S* option should be selected.





The APHIS folder containing the new project sub-folder is under the directory *Proyectos I3S*. The file has the *.pis* extension, a database sub-folder where the candidates, spots patterns and, in contrast to the ITM procedure, *multichar filtering* features will be stored, a sub-folder where edited samples will be placed since processed and a last sub-folder that will contain the reports and logs generated during the analysis. As stated before, it is useful to browse this folder/sub-folder structure using the File Explorer from Windows for a better understanding on how APHIS manages the files used in the

4 *Van Tienhoven, A. M., J. E. Den Hartog, R. A. Reijns, and V. M. Peddemors. 2007. A computer-aided program for pattern-matching of natural marks on the spotted raggedtooth shark Carcharias taurus. Journal of Applied Ecology 44:273 - 280.*

project.

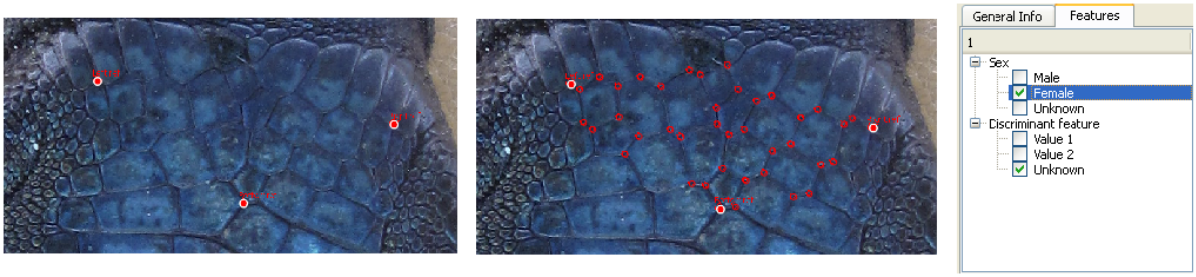
> ***Warning**: APHIS was programmed and tested in Windows XP systems. Windows 7, 8 and 10 changed the accessibility to files under the Program Files Folder (*C:\Program Files (x86)*) . The consequence is that Project Folders are not visible when you browse with the Windows Explorer to the APHIS folder. Follow the instructions in Annex 1 to find that folders.*

An existing project can be opened from the menu bar, tool bar or with the *Ctrl+A* key short-cut. SPM projects are stored with the *.pis* extension and found under the */...APHIS/Proyectos I3S* folder.

Once the project is opened a lateral panel is displayed in the interface. It has two tabs, the *General Info* tab and the *Features* tab. At this time, only the project name and the procedure used for the analysis are indicated in *General Info*, but more valuable information and functionality will be incorporated to this area as you progress in the analysis. The *Features* tab is also empty in a newly created project, but will be used to display and control your choices if you decide to apply *multichar filtering* to the analysis.

Equivalent to the ITM procedure, it is mandatory to create a repository of images to use as set of candidate for photo-matching. Once an image is displayed as a single image or as the first one of a batch, it appears on the main window. User can control its zoom level and position either with the mouse wheel or with the size selector of the toolbar and the scroll bars that surround the image. It is now time to define the references for each image.

In the ITM procedure, the next two left clicks on the image would set the references. In the SPM procedure three references are needed. **The next three left click of the mouse will set the three references sequentially and in a clockwise order (Photo 4.1).** Each reference is labelled to minimize mistakes.



(1) (2) (3)

Photo 4

Note that three references have been chosen to match the requirement of the study, however APHIS can be customized to have more, if necessary.

Once the three references are set, the spots pattern is applied. Here user selects each spot that will be used as a matching feature in the matching phase. In the case of the lizard we marked the intersections between scales so to define a pattern of scales used as a 'fingerprint' (Photo 4.2). A reference or spot can be deleted right clicking on it.

A final option is to define a character for the multichar filtering (Photo 4.3). *Multichar filtering* cannot be fully controlled from the interface. The specific features and their valid values have to be defined in the metadata.xml text file that can be found under the project folder. Users can use any text editor to edit this file. Open metadata.xml and add any feature between the <data> and </data> tags. Each feature name and valid values have to be inserted between a <feature> and a </feature> tags. There must always be an opening and a closing tag per data block. The same applies for the feature name and values. For a better a understanding follow the next example:

```
<?xml version='1.0' encoding='utf-8'?>
<data>
        <feature>
                <name>Sex</name>
                <value>Male</value>
                <value>Female</value>
                <value>Unknown</value>
        </feature>
</data>
```

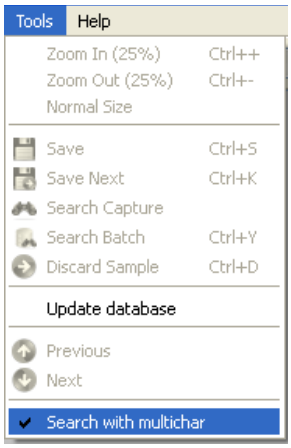
The previous text shows the basic contents of a typical *metadata.xml* file. By default, each project has a predefined *Sex* feature with *male*, *female* and *unknown* as valid values. It is mandatory to include the *unknown* value because phenotypic characters are not always black and white. If you want, for example, to introduce a new feature as skin pigmentation with values *bluish* and *greenish* edit the file in the following manner:

```
<?xml version='1.0' encoding='utf-8'?>
<data>
        <feature>
                <name>Sex</name>
                <value>Male</value>
                <value>Female</value>
                <value>Unknown</value>
        </feature>
        <feature>
                <name>Skin_pigmentation</name>
                <value>Bluish</value>
```

```
            <value>Greenish</value>
            <value>Unknown</value>
        </feature>
    </data>
```

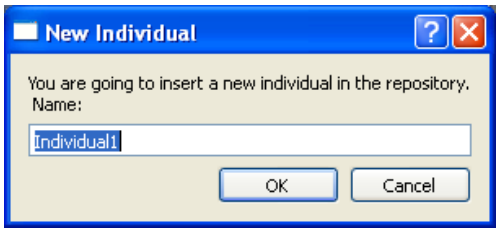
> ***Warning***: *Do not use Special symbols or spaces on name or value denominations. If you want to separate words in those names use an underscore. Neither delete the <?xml version='1.0' encoding='utf-8'?> header. Not following this instructions can lead to unexpected behaviours of the multichar filtering.*

Once edited this file reopen APHIS and you will see the features and values in the corresponding tab of the lateral panel. During edition simply check or uncheck feature values for each individual.



After setting the references, user can switch to the handy buttons from the toolbar.

At this stage, with a new project where no repository or candidate images are present, user should press the *Save* button or the *Save & Next* button when in a batch process. Both store the pattern and templates in the database. Users can also discard an image if it does not achieve the necessary quality to be taken in consideration for the analysis. Keep doing that with all the images you opened. APHIS will give automatically a name to the individual you save this way, however it is possible to edit this name before proceeding to the next image or finishing the process.



***Warning**: while creating the database using* Open Batch *it is required that each image belongs to a different individual. Two photographs from the same individual would be treated as belonging to different animals because matching algorithms have still not been applied to detect such circumstance.*

Analyse of image/s

Once a project with at least one sample in the database is open it is possible to proceed to the matching analysis. The three phases of pre-processing, matching and visual inspection (post-processing) are similar to the ones described for ITM. However, the supervised tasks are different.

PRE-PROCESSING: Users should first open a sample with the *Open* button or set of samples with the *Open Batch* button (Photo 5).

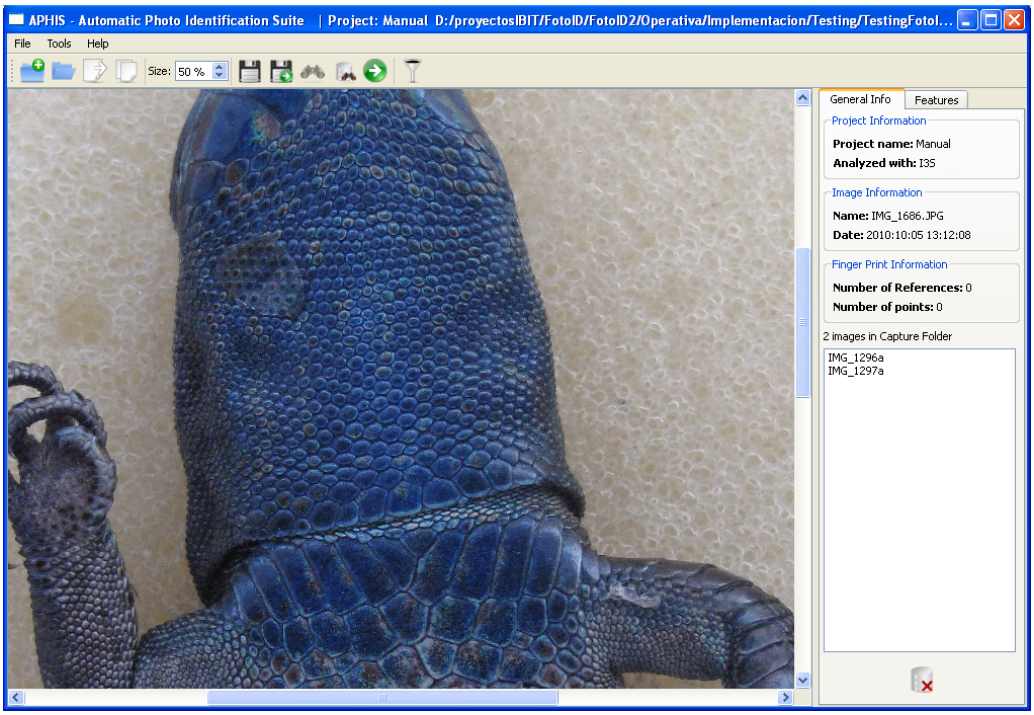


Photo 5.

Three references should be marked on each image. These are positioned clockwise by the first three left click of mouse. Each reference is labelled to help in this process. Subsequently user should mark with the left click of the mouse spots, scars or other characteristics that are used for individual recognition. Images are then automatically taken as repository.

The pre-processing phase can be stopped at any time. Edited samples will be temporally stored in the project's *Captures* folder ready to be analysed. The *General Info* tab has a section that lists the samples contained by the *Captures* folder and a button to delete them if this is your decision. It also contains an *Image Information* section that displays the name of the image file and the date and time of capture and a *Finger Print Information* section informing of the number of references and spots already marked on the active sample.

The pre-processing phase in SPM procedure is longer than the one in the ITM, depending on how many spots, scars or other characteristics have to be marked.

MATCHING: When finished with the preprocessing of the samples, users can press the *Search* or *Search Batch* button (the right option depends of the *Open* option you used one step before). The software will calculate similarity indexes for each sample-candidate pair and display in the lateral panel the first fifty options considering this likelihood values.

VISUAL INSPECTION: after the matching phase, APHIS delivers the results from from highest to lowest scores. Here users can visually compare the sample and candidate pair (Photo 6). Once taken a decision it can be registered using the *Match*, *New* or *Discard Sample* buttons. *Match* means that that both, the sample and the selected candidate are the same individual. It will store the sample in the subfolder of the matching candidate in the database. Therefore, each subfolder represents one individual. Pressing *New* you indicate that no candidate matches with the sample and that it should be stored as new individual. Finally, one can discard a comparison if you don't want to include the sample in the database. This supervised task is equivalent to the one in the ITM procedure and it bound to last the same time.

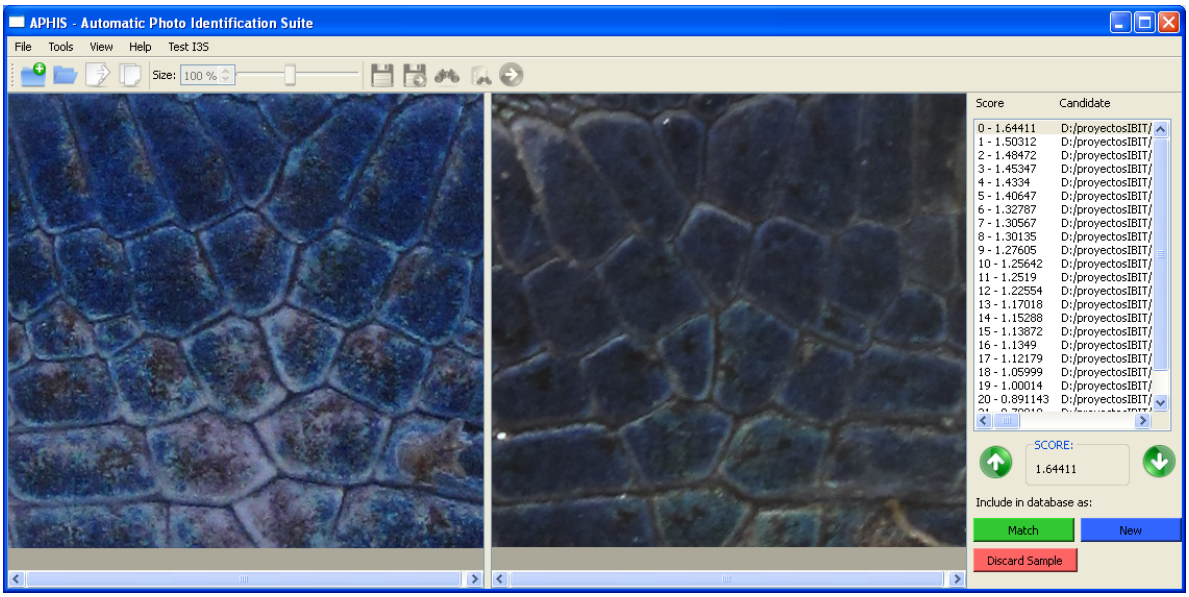


Photo 6

5. Tracking the results

APHIS stores the results in text files. These files are formatted as comma-separated *CSV* to allow its inspection on a spread-sheet. *CSV* files can be opened by commonly used programs as Microsoft Office or Open Office [5] among others.

In some cases, the program will open a menu asking you to rename a file. Note that repeated file or individual names are not allowed in APHIS to avoid confusion during results inspection.

5 It can be downloaded for free at http://www.openoffice.org/

Under the Project Folder you will find a *results/logs subfolder* containing four files, namely *Chains.csv*, *Dates.csv*, *DatesAndChains.csv* and *Rename.csv*. *Chains.csv* contains a row per individual with its name in the first column and sample names that belong to it in adjacent columns. *ChainsAndDates.csv* includes also sampling dates of each sample. *Dates.csv* only the dates. And *Rename.csv* a history of renamed samples to let you track denomination changes in filenames. Under the *results subfolder* is also created a registry for each analysis run, they provide a detail of scores obtained per sample-candidate pair displayed in the results lists.

ChainsAndDates.csv includes also sampling dates of each sample. *Dates.csv* only the dates. And *Rename.csv* a history of renamed samples to let you track denomination changes in filenames.

***Warning**: APHIS was programmed and tested in Windows XP systems. Windows 7, 8 and 10 changed the accessibility to files under the Program Files Folder (*C:\Program Files (x86)*) . The consequence is that Project Folders are not visible when you browse with the Windows Explorer to the APHIS folder. Follow the instructions in Annex 1 to find that folders.*

6. Update the database (for advanced and ventured users)

Frequent users of APHIS might be tempted to "manage" the repository and capture folder contents. This can be dangerous because deleting some files can corrupt the whole project.

A first **GOLD RULE** is to make a full copy of your Project Folder before doing any change to its contents. Keep this copy in a safe place and if something goes wrong, simply substitute the corrupted folder by this backup.

***Warning**: APHIS was programmed and tested in Windows XP systems. Windows 7, 8 and 10 changed the accessibility to files under the Program Files Folder (*C:\Program Files (x86)*) . The consequence is that Project Folders are not visible when you browse with the Windows Explorer to the APHIS folder. Follow the instructions in Annex 1 to find that folders.*

Files can be moved across subfolders if, for example, a sample was incorrectly matched with an existing individual or one can delete a sample that is producing mess in your analysis, etc.

However, if these actions are made while APHIS is open, during pre-processing or visual inspection, the software will not be aware of the changes and can react unexpectedly. To avoid this one should use the *Update database* function in the *Tools* menu. Once updated, the program will know about the changes and behave correctly.

You can also edit the metadata file contents, but we do not recommend to do that as far as it is easy to edit them reopening the sample inside APHIS and using the interface selectors to check or uncheck a value.

7. Final remarks

APHIS is a new freely-available software for individual recognition by photo-identification. The main aspect that distinguish it from other routines is that it reduces supervised tasks to the minimum. This makes APHIS especially suitable for the analyses of a large number of photos. Also, it includes two different routines, the ITM and the SMP, to better meet users' needs and a multi-character filtering for a more efficient search in large database. In the ITM routine (Chapter 3) pre-processing phase is reduced to the setting of two references. For expert as well as new users, this per-processing task would take 2-3 seconds per image. However the routine has some pitfalls. Deciding two reference points that can be easily recognized in any picture is not an easy task. It is helpful to have a little knowledge of the anatomy of the species under study and find out a reference system unequivocally and easily recognisable in all samples. A second problem is that ITM performance is highly affected by image quality and diligent usage. Heterogeneous sampling conditions in luminosity, focus or other distortions as dirt over the animal, can affect the analysis. An inconsistent setting of references has also dramatic impact on the result. Therefore ITM has to be taken as a "rigid" procedure and cannot be considered as a definitive solution for all ecological studies. Despite these drawbacks, when image characteristics are homogeneous across the samples and two body references are easily recognised, ITM is a very fast an efficient method for photo matching. The second procedure, SPM, uses the existing I3S algorithm, which is based on pair-wise comparison of the distance between points defined by the user an three references points. The pre-processing phase is about ten times longer than in the ITM and depends on user 's experience and on the minimum number of points that need to be compared. On the other hand it does not rely on photo quality or characteristics as the ITM procedure. As a rule of thumb we advice to work with ITM only when luminosity, definition and image quality can be standardized.

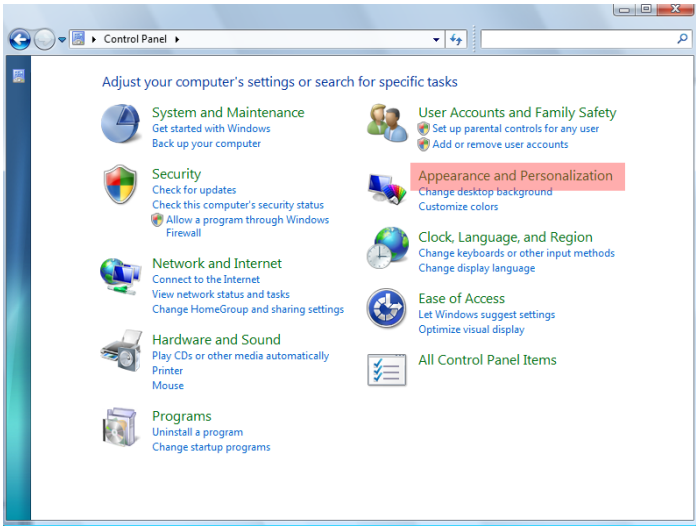
Annex 1. Finding the Project Folders in Windows 7,8 and 10.

Accessing Project Folders under Windows 7

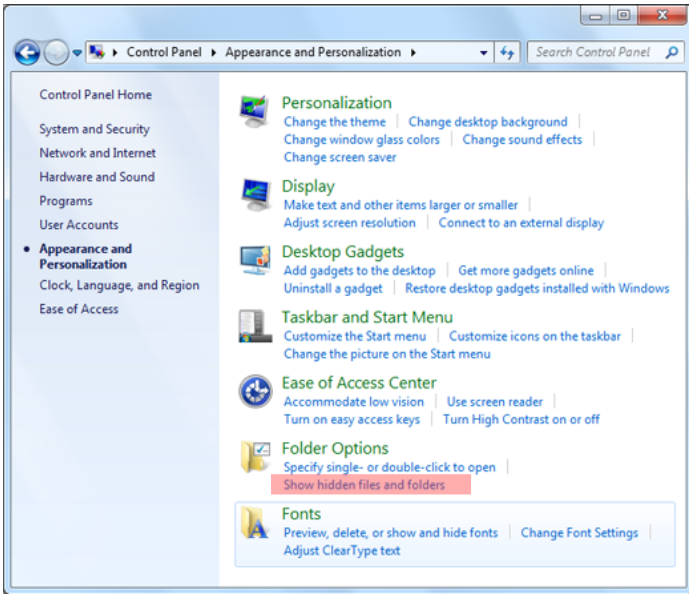
1- Click on the *Start button* in the lower left corner of your screen (Windows flag).

2- Click on the Control Panel menu option. It will open a new Window.

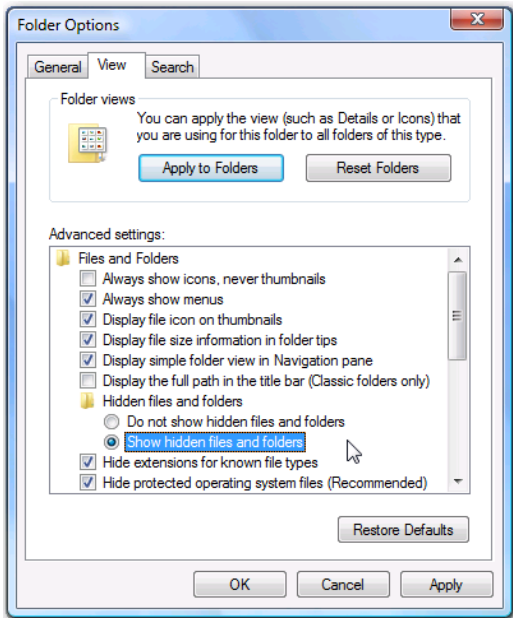
3- Click on *Appearance and Personalization* .



4- Click on the *Show hidden files and folders* option



5- Select the radio button *Show hidden files and folders*.



6- Press the *Apply* button and then the *OK* button.

7- Now you can use the Windows Explorer window to browse to the APHIS Project Folders which will be under the path:

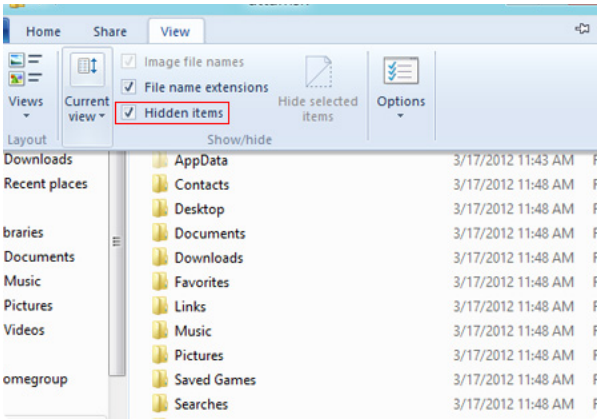
C:\Users[your_user_folder]*\AppData\Local\VirtualStore\Program Files (x86)\APHIS*

You have to substitute [your_user_folder] by your Windows user name.

Accessing Project Folders under Windows 8

1- Use a Windows Explorer window to browse to your user folder (*C:\Users*[your_user_folder]) where [your_user_folder] is your Windows user name

2 - Unhide the *AppData* folder, clicking on *View* on the menu bar and checking *Hidden items*.



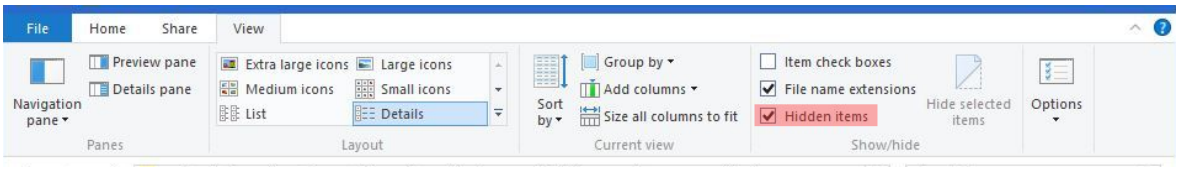
3- Now you can browse to the APHIS Project Folders which will be under the path:

C:\Users[your_user_folder]*\AppData\Local\VirtualStore\Program Files (x86)\APHIS*

Accessing Project Folders under Windows 10

1- Use a Windows Explorer window to browse to your user folder (*C:\Users*[your_user_folder]) where [your_user_folder] is your Windows user name

2 - Unhide the *AppData* folder, clicking on *View* on the menu bar and checking *Hidden items*.



3- Now you can browse to the APHIS Project Folders which will be under the path:

C:\Users\[your_user_folder]\AppData\Local\VirtualStore\Program Files (x86)\APHIS