SonoChiro® 4.0

User guide

Florian Cantori, Alexandre Haquart

Florian Cantori, Alexandre Haquart - December 2017

Chapter 1. Introduction

Foreword for SonoChiro® regulars: At first glance the difference between SonoChiro® V3 and V4 will seem minor to the user. Required settings are almost identical. The great novelty of version 4 lies in the data validation mode through SonoView, a new software developed for the validation of SonoChiro®'s results. This tutorial follows the usual process of sound identification developed with the first SonoChiro® versions (preparation of audio files ⇒ prediction ⇒ validation).

> For a quick update of your user experience, boxes such as this one underline the novelties and the important steps of the process.

Chapter 2. Software installation and launching

2.1. Installation

- Run *SonoChiro_Setup.exe*
- Follow setup instructions
- Launch SonoChiro® from your desktop or your *Start* menu.

2.2. Launching platform

Through the program menu: Start menu ⇒ programs ⇒ SonoChiro-4.0
Or through the icon on your desktop:

A launching platform for different tools will open. It grants access to 4 softwares:

Version: 4.0.4
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Contact : Technical assistance
Website : Le Club Biotope
Société Biotope - BP58 - 34140 Mèze - France

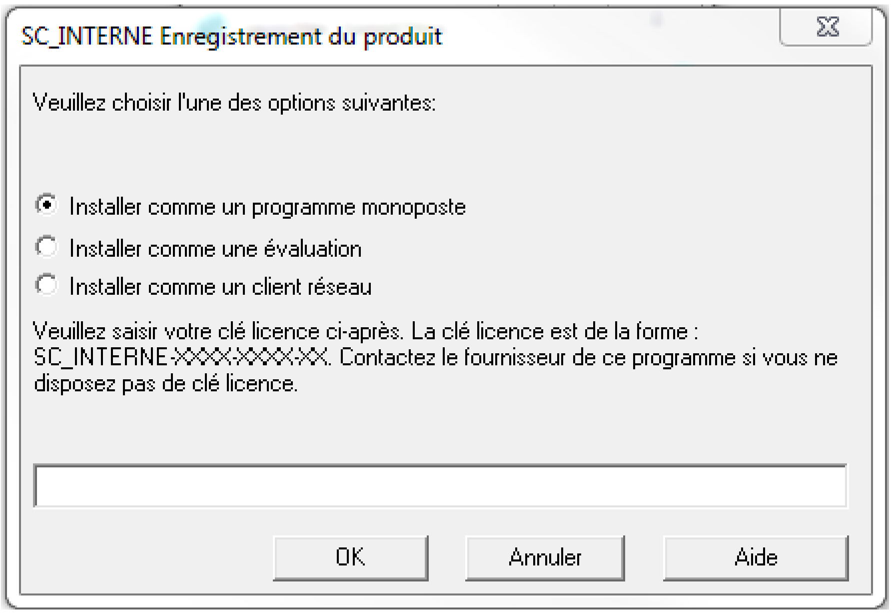
1. **SonoChiro**®: the new SonoChiro® software.
2. **SonoView**: validation tool for SonoChiro®'s results.
3. **SonoSearch** : audio file sorting tool.
4. **SonoDemux** : audio file splitting tool.

2.3. Product registration

Software protection only applies to SonoChiro®. To activate the registration process you have to execute the program.

An internet connexion is required for this step !

- Among the available options, choose *Install as a single-user program*
- Enter the license key in your possession (you received it per e-mail) and validate
- Enter your contact details in the new window and validate
- Protection will be verified shortly and SonoChiro® will launch

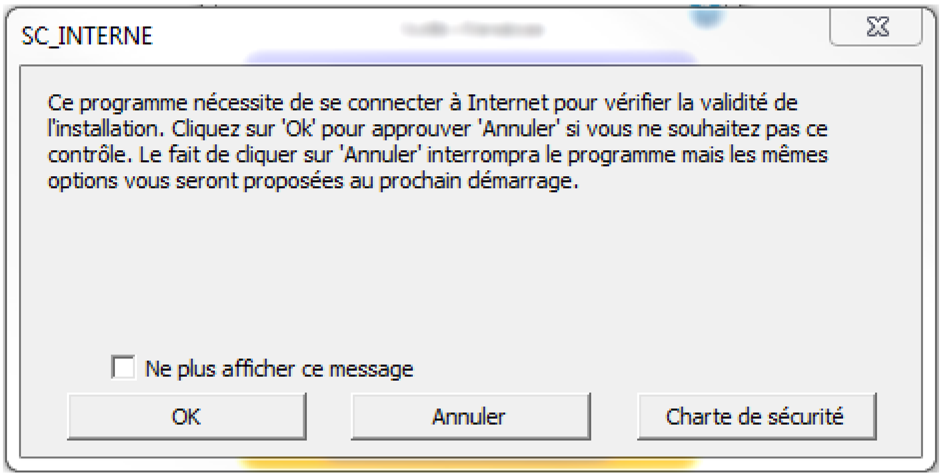


SC_INTERNE Enregistrement du produit

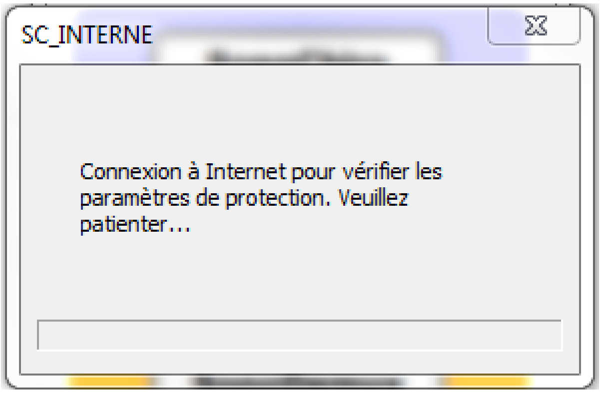
Veuillez choisir l'une des options suivantes:

● Installer comme un programme monoposte
○ Installer comme une évaluation
○ Installer comme un client réseau

Veuillez saisir votre clé licence ci-après. La clé licence est de la forme : SC_INTERNE-XXXX-XXXX-XX. Contactez le fournisseur de ce programme si vous ne disposez pas de clé licence.



Ce programme nécessite de se connecter à Internet pour vérifier la validité de l'installation. Cliquez sur 'Ok' pour approuver 'Annuler' si vous ne souhaitez pas ce contrôle. Le fait de cliquer sur 'Annuler' interrompra le programme mais les mêmes options vous seront proposées au prochain démarrage.



Connexion à Internet pour vérifier les paramètres de protection. Veuillez patienter...

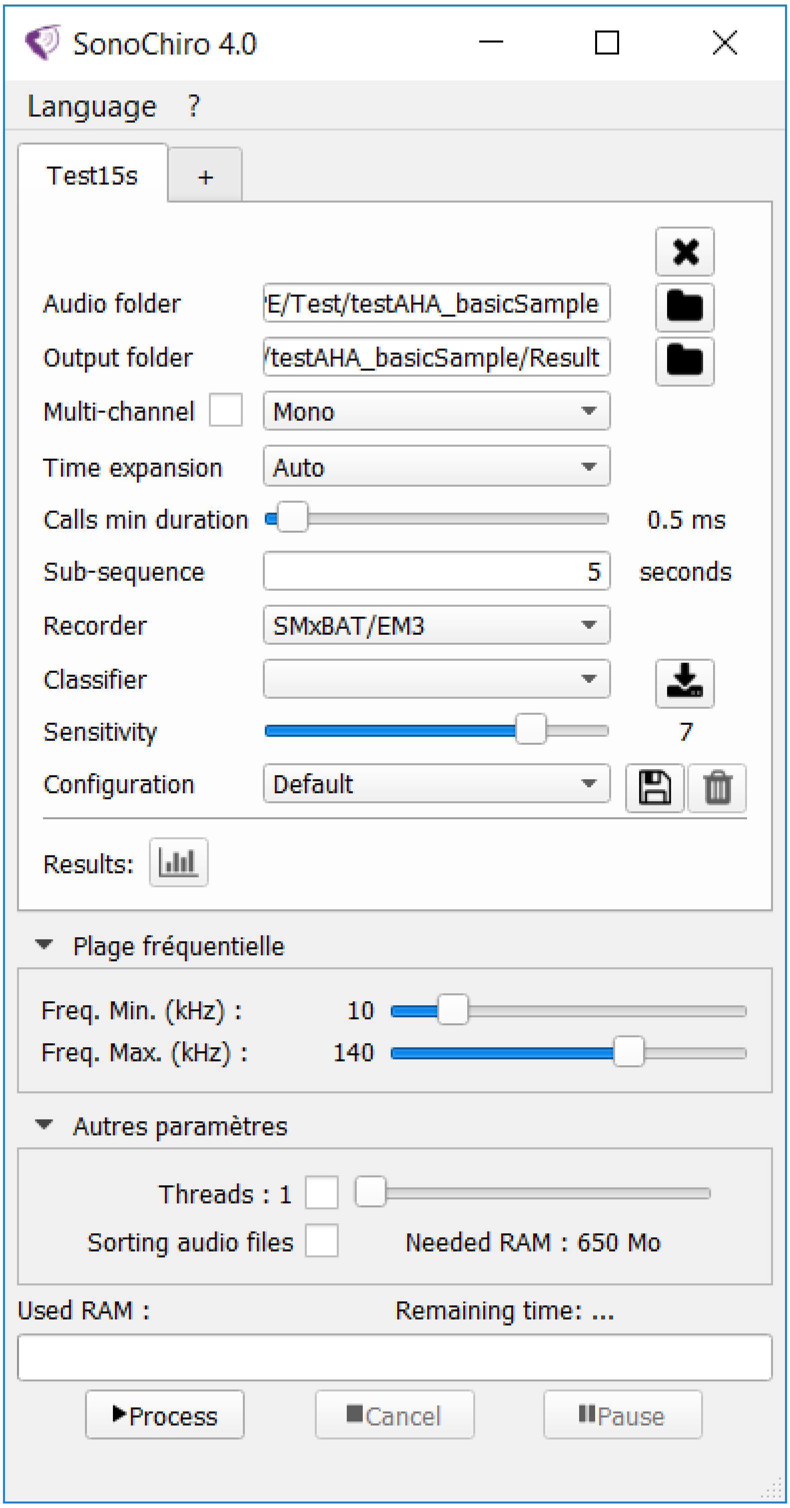
Chapter 3. Quick start

For users in a hurry passing from version 3 to version 4, we will here try to summarise the main novelties offered by the software and give some keys to facilitate the transition between both versions. You now have access to a software suite, accessible through the launching platform. Through this interface you can access both SonoChiro® V4 and SonoView, the software for result validation, but also to other small softwares, SonoDemux for sound splitting and to SonoSearch for audio files sorting.

3.1. SonoChiro®

SonoChiro® version 4 presents a very similar interface to version 3. However additional options are available:

- Queue manager
- Mono or Stereo analysis option
- Automated checking of time expansion format
- Automated splitting of long files (*Analysis bit*)
- Calculation speed optimisation
- Bandwidth analysis



Audio folder 'E/Test/testAHA_basicSample

Output folder /testAHA_basicSample/Result

Multi-channel ☐ Mono

Time expansion Auto

Calls min duration 0.5 ms

Sub-sequence 5 seconds

Recorder SMxBAT/EM3

Classifier

Sensitivity 7

Configuration Default

Freq. Min. (kHz) : 10

Freq. Max. (kHz) : 140

Threads : 1 ☐

Sorting audio files ☐

Needed RAM : 650 Mo

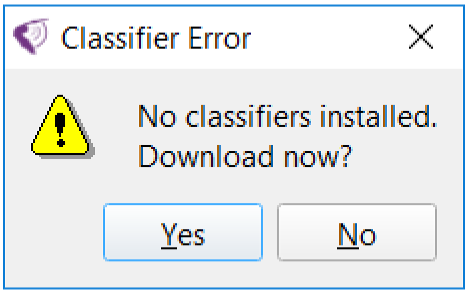
Used RAM :

Remaining time: ...

SonoChiro® V4 analysis results come out as:

- a `.sqlite3` project, readable with SonoView.
- a CSV file, readable with a spreadsheet (the format is quite the same as in V3)

Example 1. SonoChiro® - First utilisation of SonoChiro®

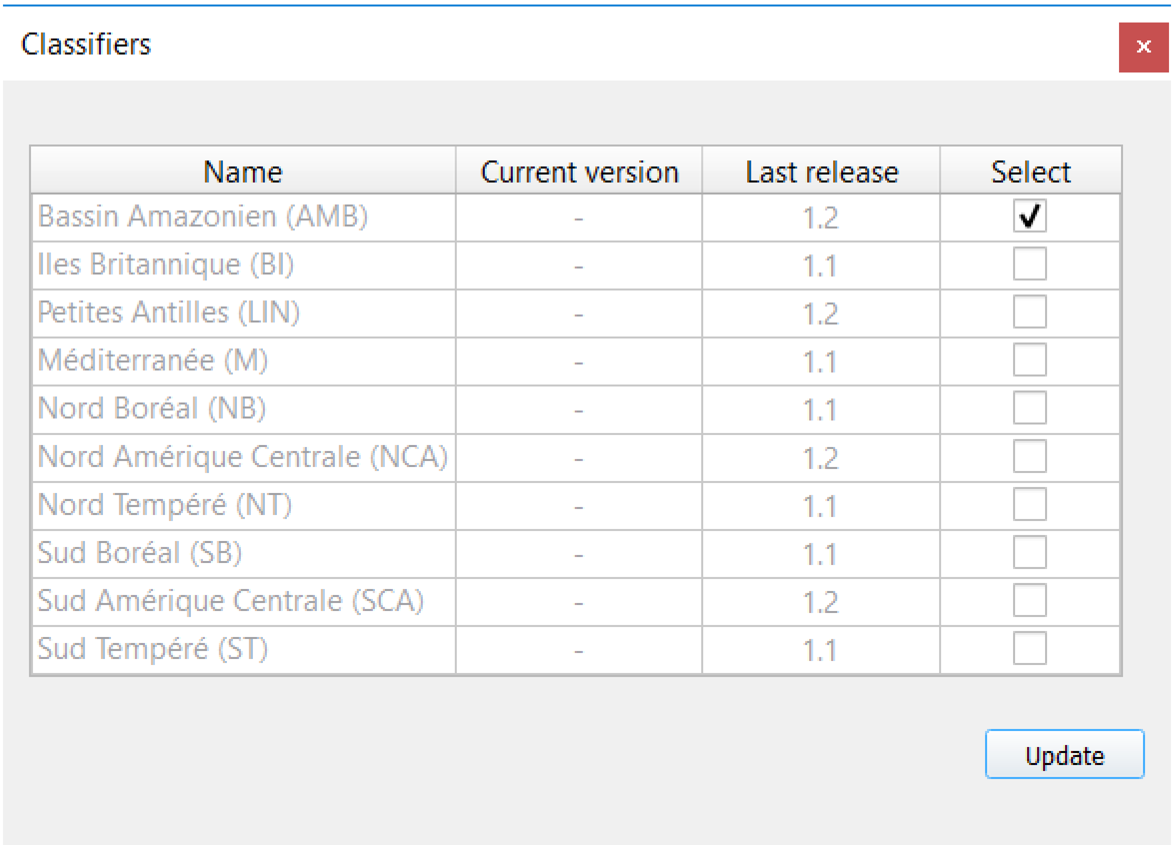


Classifier Error

No classifiers installed. Download now?

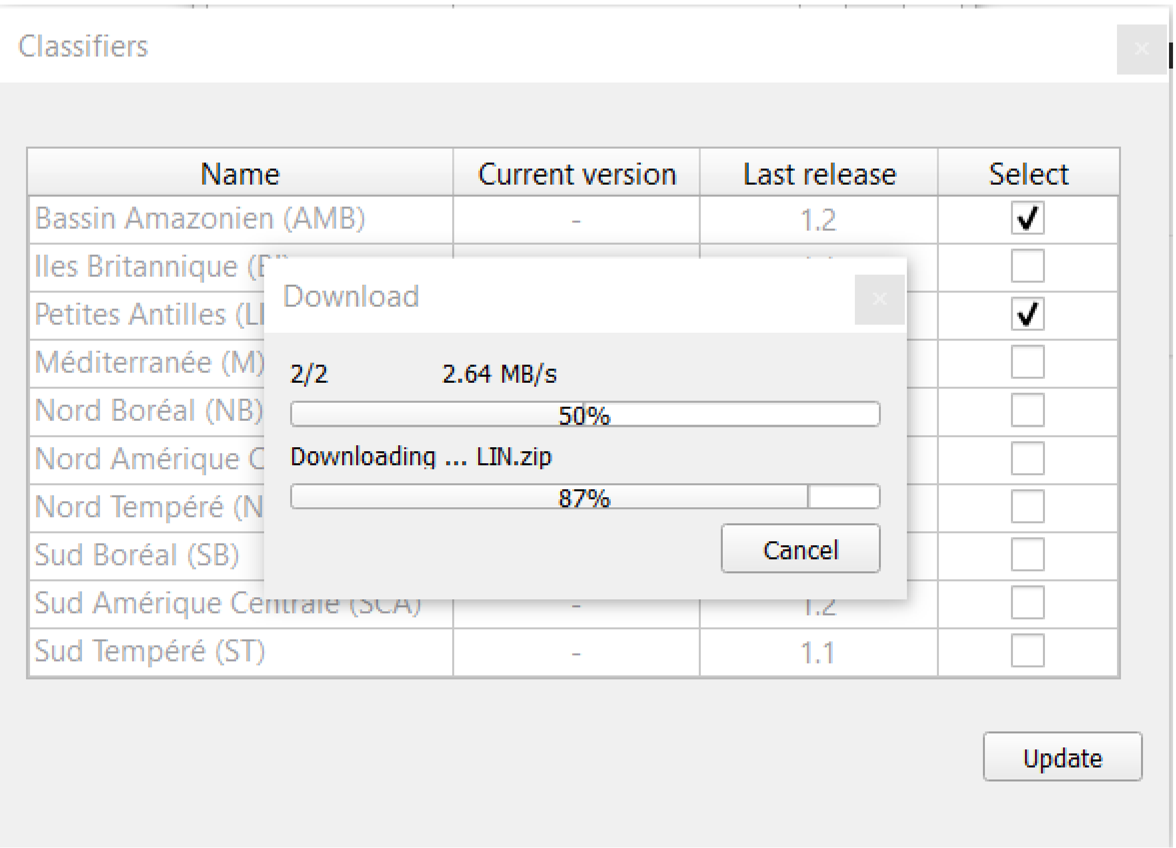
During the first launch, the software detects the absence of classifiers and offers to download them. After validation:

- Select the desired classifier(s) and download them
- At the end of the downloading process, check for classifiers in the selection option.



Classifiers

Name	Current version	Last release	Select
Bassin Amazonien (AMB)	-	1.2	☑
Iles Britannique (BI)	-	1.1	☐
Petites Antilles (LIN)	-	1.2	☐
Méditerranée (M)	-	1.1	☐
Nord Boréal (NB)	-	1.1	☐
Nord Amérique Centrale (NCA)	-	1.2	☐
Nord Tempéré (NT)	-	1.1	☐
Sud Boréal (SB)	-	1.1	☐
Sud Amérique Centrale (SCA)	-	1.2	☐
Sud Tempéré (ST)	-	1.1	☐



Name	Current version	Last release	Select
Bassin Amazonien (AMB)	-	1.2	☑
Iles Britannique (			☐
Petites Antilles (L			☑
Méditerranée (M)			☐
Nord Boréal (NB)			☐
Nord Amérique C			☐
Nord Tempéré (N			☐
Sud Boréal (SB)			☐
Sud Amérique Centrale (SCA)	-	1.2	☐
Sud Tempéré (ST)	-	1.1	☐

Download

2/2 2.64 MB/s

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Downloading ... LIN.zip

87%

To uninstall a classifier, go back to the selection interface and right click on a classifier to delete one.

If the list of classifiers appears empty, check the status of your internet connection.

3.2. SonoView

SonoView gathers most of the tools you usually use to validate sounds, with some extra user-friendly items:

- Table with sorting tools
- Sonograms of measured sounds
- Direct links between window display and audio files
- Data sorting, deletion and export options.

		File	Check	ID	Contact	Group	IGp	Species	ISp	Calls	Fdom	Fmin	IntMed	IQual
			filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre
1	🔍	Test15s_par...		Myospp	Principale	Vessp	10	Myospp	10	13	0	0	0	7
2		Test15s_par...		parasi	Secondaire	parasi	2	parasi	2	3	0	0	0	6
3	🔍	Test15s_par...		parasi	Principale	parasi	10	parasi	10	0	0	0	0	0
4	🔍	Test15s_par...		Myospp	Principale	Vessp	10	Myospp	10	9	51	50	79	8

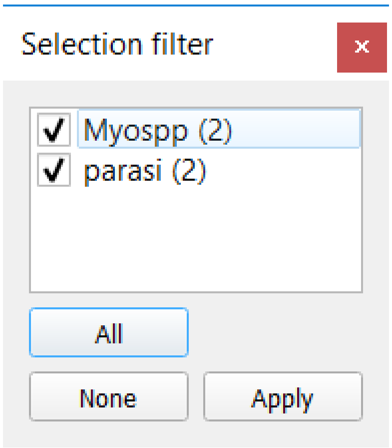
Sequence (0/3) - Micro 0

Example 2. SonoView - quick start

- In Sonoview, File ⇒ open a project ⇒ `project.sqlite3` (analysis result of SonoChiro® V4)
- 🔍 To view a sequence
- Use the mouse wheel to scroll sonograms from left to right
- 👁 To read the audio file in an external software
- filtre For data filtering
- Use <, >, = for numeric data filters

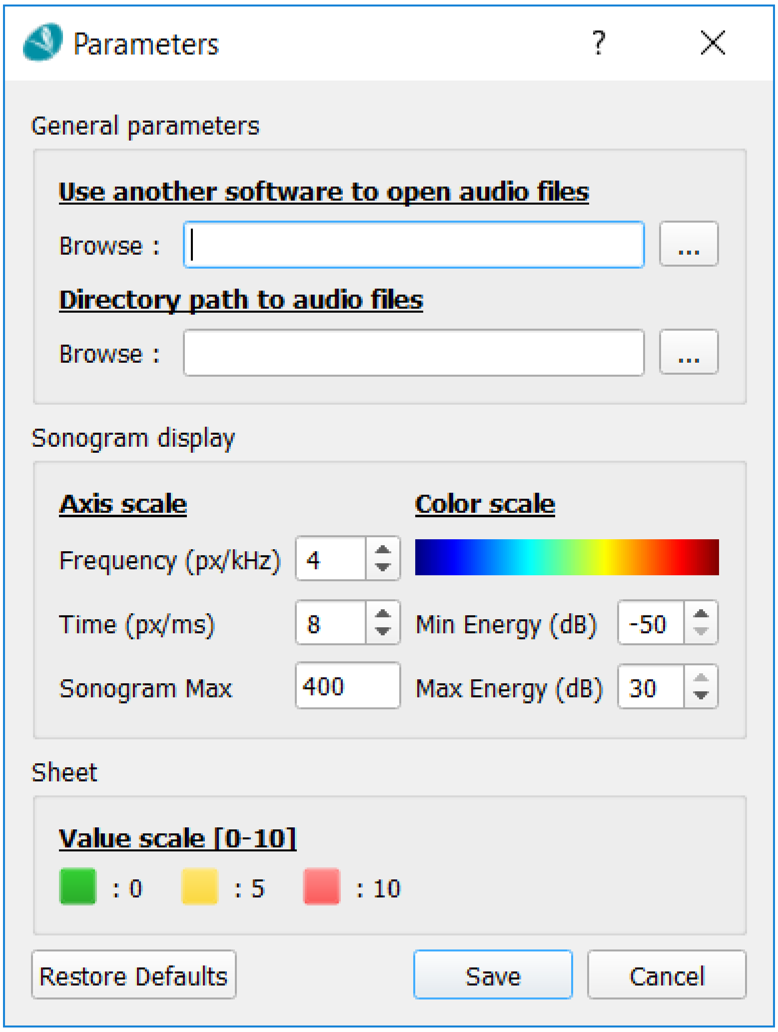
Example 3. SonoView - Opening a project and basic actions

- Open a new project in SonoView (menu 'File' => 'Open a project') by selecting the sqlite3 file created during a previous analysis of SonoChiro®
- Use sorting and filtering options to organise your work (use the relevant columns among 'Date', 'Hour', 'Calls', 'Species', 'Fdom' …).
    - For the validation column: '=0' not validated, '=1' validated and '=2' pertinent



    - For text columns, select the items to display (see figure)
    - For numeric columns, use '>', '<' and/or '='
- Take a look at the sonogram of a sequence you want to verify
- Edit the 'ID' field if necessary
- Mark sequences as 'pertinent' with right click => 'Mark as pertinent' and check for the appearance of a yellow star on the validation button.

Example 4. SonoView - Preferences manager



Parameters

General parameters

Use another software to open audio files

Browse :

Directory path to audio files

Browse :

Sonogram display

Axis scale

Frequency (px/kHz) 4

Time (px/ms) 8

Sonogram Max 400

Color scale

Min Energy (dB) -50

Max Energy (dB) 30

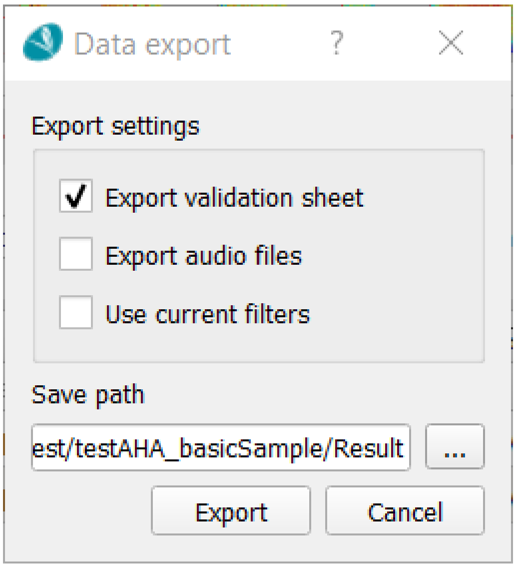
Sheet

Value scale [0-10]

🟩 : 0 🟨 : 5 🟥 : 10

- Open the preferences window (menu 'Settings'=>'Preferences')
- Check the access path to the audio folder
- Select the access path to the external analysis software
- Edit axis and colour scales in the 'Sonogram display' options for an optimal visualisation of sound sequences. Bat calls must clearly stand out from ambient noise for a correct evaluation of sound shapes
- Edit the validation column colours and their value scales in the 'Table' options
- Save and view modifications
- If you want to go back to default, open the preferences window again and restore default values, save and view modifications

Example 5. SonoView - Data export



Export settings

☑ Export validation sheet

☐ Export audio files

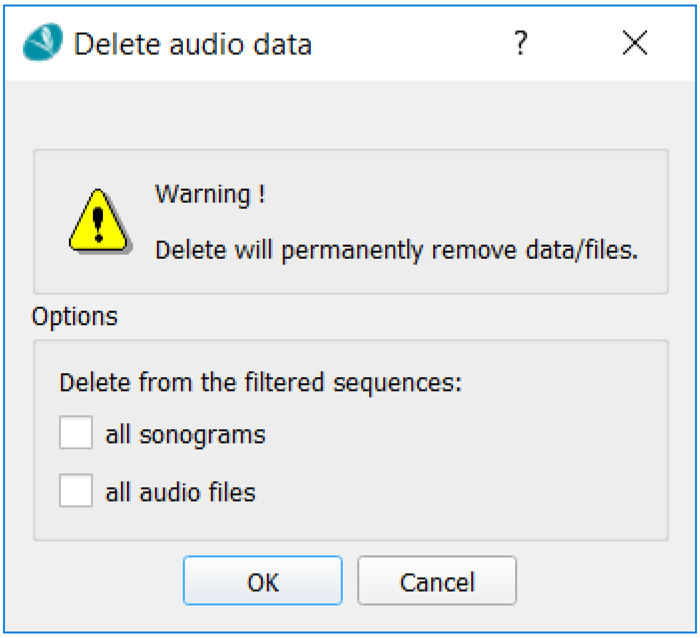
☐ Use current filters

Save path

est/testAHA_basicSample/Result

- Open a project in SonoView and filter the table according to criteria of your choice (Validation, Species, Frequencies…)
- Click on 'File' -> 'Export Data' to open the export window
- Select export options:
  - The validation table will be exported in CSV format
  - Audio file export copies sound files in a new folder
  - 'Use active filters' allows to export only data (validation or audio files) respecting the current filter conditions
- Select the folder for data export
- Export

Example 6. SonoView - Sound files cleaning



Delete audio data

Warning !

Delete will permanently remove data/files.

Options

Delete from the filtered sequences:

☐ all sonograms

☐ all audio files

- Open a project in SonoView and notice its size
- Verify that the button 'File' -> 'Clean sound files' is not clickable
- Filter the table according to criteria of your choice (Validation, Species, Frequencies…)
- Click on 'File' -> 'Sound data cleaning' to open the data deleting window
- Select the export options:
    - Deleting sound images will delete sonograms stored in the sqlite database of the current project
    - Deleting sound files will delete audio files associated to the current project. Because sound files are precious, this options should only be chosen if sound files containing bat sound have been copied in a new folder during the previous step (Data export). If you need to reduce the sound folder size on your disk, you can also use the SonoSearch software to copy in a new folder only sound files that contained a bat sound and then delete the old folder.
- Validate and check that data have been correctly deleted
- Check that your computer disk free space has increased. It may be necessary to empty the recycle bin first.

Chapter 4. Preparing audio files

SonoChiro® only accepts audio files in WAVE format (file name extension .wav)

4.1. Good recording conditions: a time saver !

Microphone environment will change signal transmission, impacting the abilities of SonoChiro® to analyse information. To simplify, SonoChiro®'s worst enemies are (1) Echoes and (2) Parasites. It is in the user's best interest to prevent any of those issues when installing the recording material. Here are some elementary rules to follow in order to optimise recording quality:

1. Keep the microphone away from the ground, at least 1 meter if possible.
2. Use a cable to install your microphone in the best conditions.

3. Bring out your microphone from vegetation. If it is installed on a tree, put it as much as possible at the tip of its branches. Cut leaves around the microphone.
4. Orientate the microphone horizontally or 45° towards the sky, in the direction of an open space, especially if the microphone is directional.
5. More generally, maximise chances that the space between bats and the microphone is not obstructed with any object that may alter sound.

4.2. Audio file name format

The way how your recording files are named is important because SonoChiro® will extract information about location, date and hour. If done properly, this step will help you save a precious time for later analysis. SonoChiro® V4 will extract the timestamp produced by several recorder models:

1. **SM2BAT/SM3BAT/SM4BAT/EM3** : Supports the old SM2 format with milliseconds (ex: `SM2_10_20120726_220303_946.wav`). The format of new recorders is the same (ex: `TF7544_20130516_011832.wav`). For those recorders SonoChiro® considers that file name beginning is a location name (ex : `SmallPond_20130516_011832.wav` → Location: 'SmallPond').
2. **DX500** : The timestamp is found in a « info.txt » file shared with all recorded audio files. Remark: To obtain this text file, you need a firmware version 2.1.1. minimum.
3. **Batlogger** : The timestamp is found in an XML file associated with each audio file. Ex : 15050008.wav ⇒ 15050008.xml

4.3. File duration

In previous versions, files had to be in mono and have a duration inferior to 20 seconds. The V4 handles stereo files and durations of several minutes. To be efficient, automated identification must only apply to short sequences. By convention, 5 seconds is usually used to define a bat pass length. This duration is ideal for SonoChiro®. Above this duration, call diversity may become too important and may not be well handled by the software’s classification process. This duration setting is adjustable in SonoChiro® V4 (see [Analysis bit] section in 'Interfaces'), but if your recording files are really too long (more than 10 minutes) it is recommended to split them with the SonoDemux software (see [launching platform]). This step will avoid potential issues and allow you to clean more easily your folders when deleting empty files.

In SonoDemux, 4 information are required:

- Expected audio file duration
- Time expansion format (x10 or x1)
- Folder containing original recordings
- Folder where split recordings are to be stored

SonoChiro® 4.0

Interfaces

Florian Cantori & Alexandre Haquart

Chapter 1. Introduction

This document presents the different graphical interfaces of SonoChiro®'s new software suite. All graphical elements and their interactions are hereby detailed. If specific interactions are not explicit enough, please do not hesitate to contact Sonochiro support.

Chapter 2. Launcher

The launcher is the first interface to appear when starting the software suite. It is the main menu that will allow you to access the different analysis or data handling tools.

The launcher will also automatically handle software updates (see the Update system section)

2.1. Applications access

Version: 4.0.4
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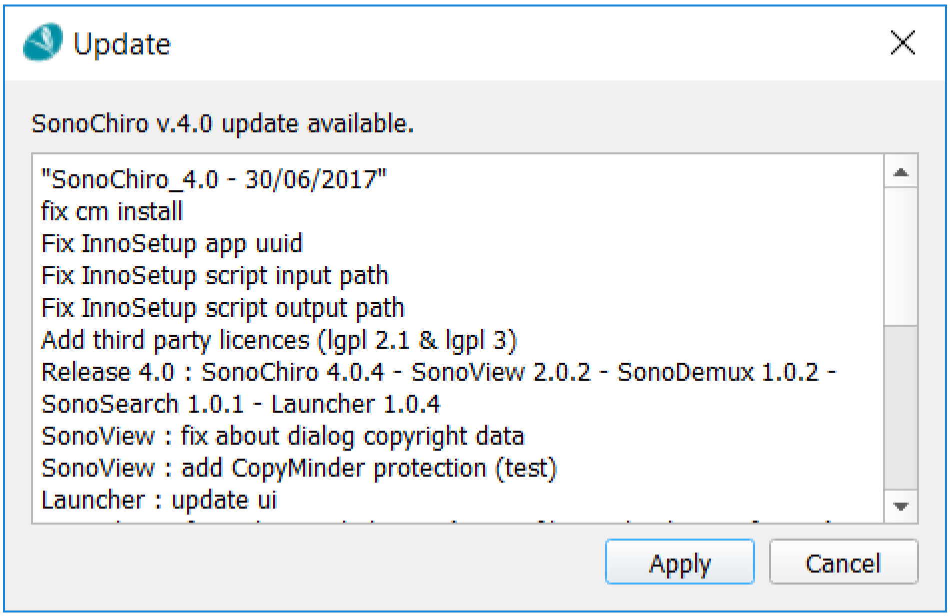
Contact : Technical assistance
Website : Le Club Biotope
Société Biotope - BP58 - 34140 Mèze - France

This interface allows you to access the software suite’s different tools:

1. **SonoChiro®**: automated analysis tool for bat sounds.
2. **SonoView**: visualisation and validation tool for SonoChiro® results.
3. **SonoSearch**: audio file sorting tool.
4. **SonoDemux**: audio file splitting tool.

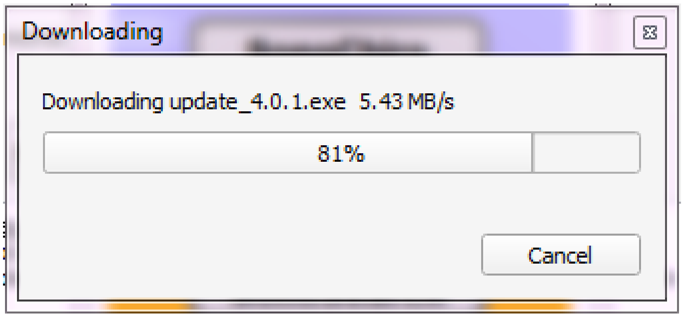
since version 4.0, only one SonoChiro® session can be active on the same computer ! However analyses can be queued (see the 'Processing list' section in Main window).

2.2. Update system



SonoChiro v.4.0 update available.

"SonoChiro_4.0 - 30/06/2017"
fix cm install
Fix InnoSetup app uuid
Fix InnoSetup script input path
Fix InnoSetup script output path
Add third party licences (lgpl 2.1 & lgpl 3)
Release 4.0 : SonoChiro 4.0.4 - SonoView 2.0.2 - SonoDemux 1.0.2 - SonoSearch 1.0.1 - Launcher 1.0.4
SonoView : fix about dialog copyright data
SonoView : add CopyMinder protection (test)
Launcher : update ui

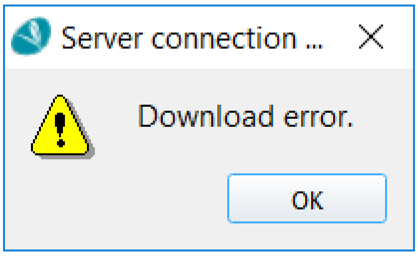


Downloading update_4.0.1.exe 5.43 MB/s

81%

Since its 4.0 version, SonoChiro® possesses an automated update system. Each time a new update is available and ready to be downloaded, the software will systematically inform you and leave you with the choice to apply the update or not.

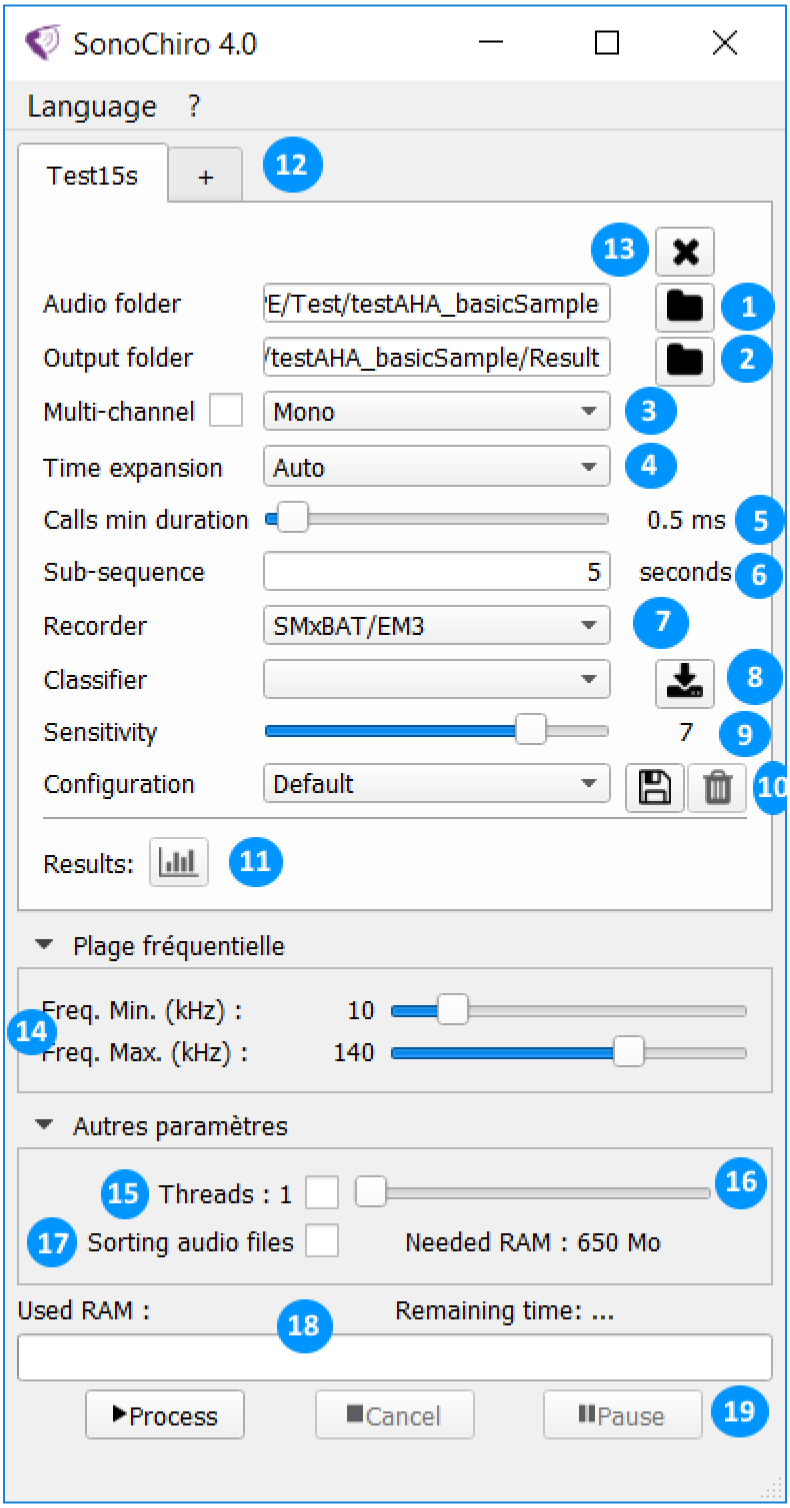
The checking of available updates may fail for different reasons. SonoChiro® will inform you but this will not prevent you from using the current version of the software. If the following error message appears, please check first your internet connection. If the problem remains, please contact the support.



Download error.

Chapter 3. SonoChiro®

3.1. Main window



SonoChiro 4.0

Language ?

Test15s +

Audio folder E/Test/testAHA_basicSample

Output folder /testAHA_basicSample/Result

Multi-channel ☐ Mono

Time expansion Auto

Calls min duration 0.5 ms

Sub-sequence 5 seconds

Recorder SMxBAT/EM3

Classifier

Sensitivity 7

Configuration Default

Results:

Plage fréquentielle

Freq. Min. (kHz) : 10

Freq. Max. (kHz) : 140

Autres paramètres

Threads : 1 ☐

Sorting audio files ☐

Needed RAM : 650 Mo

Used RAM :

Remaining time: ...

1. Selection of the **audio folder**.
2. Selection of the **results folder**. By default SonoChiro® will always store the results folder at the root of the audio folder.
3. **Multi-Channel Option** [Mono, Channel1, Channel2] : SonoChiro® automatically detects whether sounds are in stereo or in mono and ignores this item in the case of a monochannel

audio file.

4. **Time expansion** [x1, x10, Auto]
5. **Minimum call duration**: defines the minimum duration of calls to analyse. This item may be helpful in the presence of parasite sounds.
6. **Analysis bit**: defines the duration of the audio files given to SonoChiro® for analysis. The results will appear as a unique row per bit. If a sound file has a greater duration than this value, several rows will refer to the consecutive bits of same audio file.
7. **Recorder**: selects the recorder used.

> ℹ This selection allows the software to correctly use information contained in the file names (e.g. LocationMic_DateHourMinSec_Ms.wav)

8. **Classifier**: selects the classifier corresponding to the study location. The ⭳ button allows the handling of classifiers (installing, deleting, updating).
   see Classifiers update
9. **Sensitivity**: defines the sensitivity of the prediction. This influences the processing time and the precision of IDs. The standard value is a good compromise.

> ℹ When selecting the audio folder, SonoChiro® will check the format of the first file in the selected folder. It will search for information on date, hour and location name. The expected format is the following: *LOCATIONMIC_DATEHOURMINSEC_MILLISEC* (microphone name is optional).

> ℹ The value `Auto` of the *Time expansion* item lets the software select the correct value. It is chosen by checking the sampling frequency: if F_s<50kHz ⇒ time expansion x10.

10. **Custom settings**: this option allows you to save specific settings and to use them later again with one simple click. You can load existing settings by selecting one from the list. Only the default settings are available when starting for the first time.

Use the 💾 button to save new settings.

Use the 🗑 button to delete the selected settings.

11. **Analysis results** 📊: For each analysis, at the end of the process, a summary can be accessed through this button. Please refer to the Analysis results section for further information.
12. **Processing list**: For performance reasons, it is not possible to open several sessions of SonoChiro® V4 simultaneously in order to analyse several folders. A queue manager has been created to handle the folders to analyse and to define analysis settings for each of them. Analyses may last quite a long time if you need to process nights or weeks of data. This queue manager allows for instance to schedule several analyses in the evening and to find the results on the next day. When a first analysis has been scheduled, you only have to click on the + button at the top of the main window to add a new analysis to the processing list, with its corresponding settings. All you need is to click on the different tabs to go from one analysis to

the other.

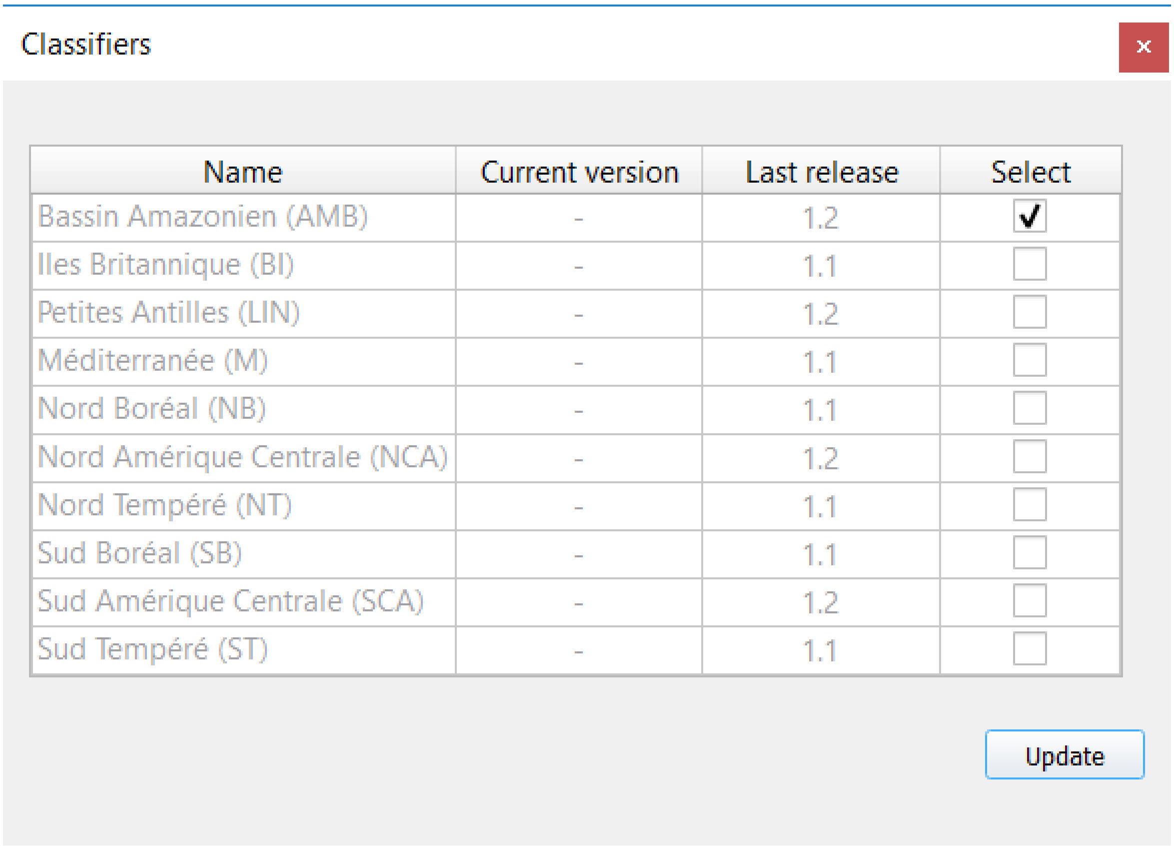
13. ✖ : deleting an analysis from the processing list.
14. **Frequency filter**: SonoChiro® now offers to filter certain frequencies to focus the analysis on a specific bandwidth by entering minimum and maximum frequencies. **$0<f_{min}<70kHz$** and **$10<f_{max}<200kHz$**
15. **Parallel calculation**: SonoChiro® can fully take advantage of the available resources on your computer if you activate this option. With a 4 core processor you may process 4 audio folders simultaneously. Time saved will not exactly be divided by 4 but you will save a significant amount of time.
16. You can **limit** resources used by SonoChiro® to allow the execution of other parallel applications.

> ⚠ It is recommended to limit the number of threads to its maximum -1 to free a minimum of resources for the system environment.

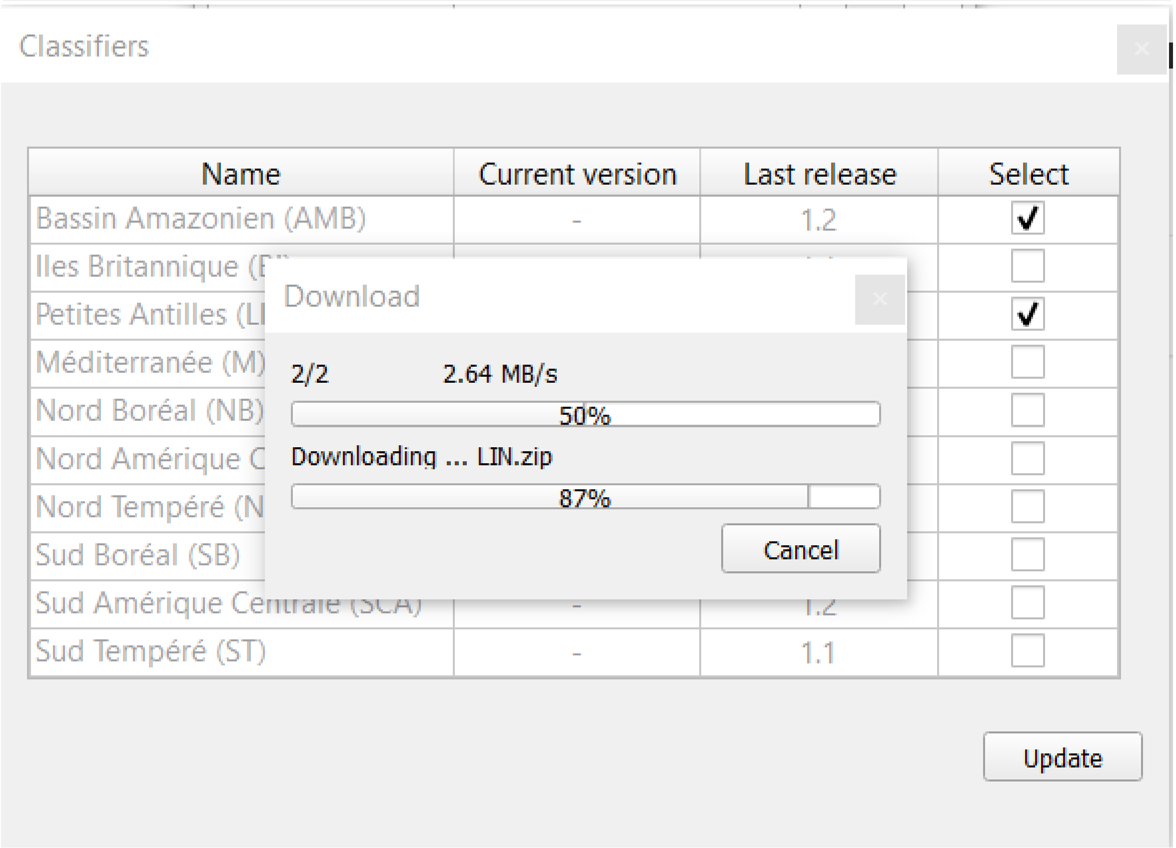
17. **Audio sorting**: During analysis, SonoChiro® will sort out analysed audio files by creating an *Empty* folder for empty files and an *Unknown* folder for files of non supported format.
18. **Progressing bar**: during processing, this is where progression information will be displayed, including:
    - Analysis initialisation
    - Classifier loading (%)
    - File analysis progression (measurements, prediction, total)
    - Time elapsed since start
19. Start and stop analysis.

3.2. Classifiers update

The 📥 button allows to handle classifiers of the study area (setup, deleting and updating).



Name	Current version	Last release	Select
Bassin Amazonien (AMB)	-	1.2	☑
Iles Britannique (BI)	-	1.1	☐
Petites Antilles (LIN)	-	1.2	☐
Méditerranée (M)	-	1.1	☐
Nord Boréal (NB)	-	1.1	☐
Nord Amérique Centrale (NCA)	-	1.2	☐
Nord Tempéré (NT)	-	1.1	☐
Sud Boréal (SB)	-	1.1	☐
Sud Amérique Centrale (SCA)	-	1.2	☐
Sud Tempéré (ST)	-	1.1	☐



Name	Current version	Last release	Select
Bassin Amazonien (AMB)	-	1.2	☑
Iles Britannique (			☐
Petites Antilles (L			☑
Méditerranée (M)			☐
Nord Boréal (NB)			☐
Nord Amérique C			☐
Nord Tempéré (N			☐
Sud Boréal (SB)			☐
Sud Amérique Centrale (SCA)	-	1.2	☐
Sud Tempéré (ST)	-	1.1	☐

2/2 2.64 MB/s

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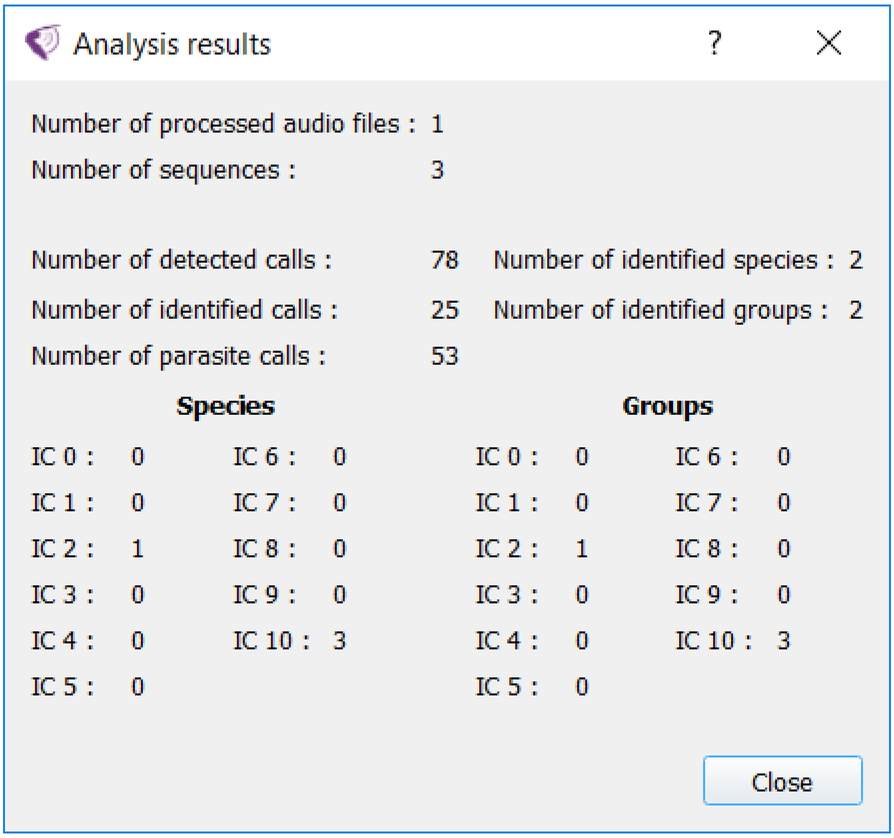
Downloading ... LIN.zip

87%

3.3. Analysis results

For each analysis configured in the interface, at the end of processing, a summary of the ID results is accessible through the 📊 button.



Number of processed audio files : 1
Number of sequences : 3

Number of detected calls : 78
Number of identified calls : 25
Number of parasite calls : 53

Number of identified species : 2
Number of identified groups : 2

Species

IC 0 : 0
IC 1 : 0
IC 2 : 1
IC 3 : 0
IC 4 : 0
IC 5 : 0
IC 6 : 0
IC 7 : 0
IC 8 : 0
IC 9 : 0
IC 10 : 3

Groups

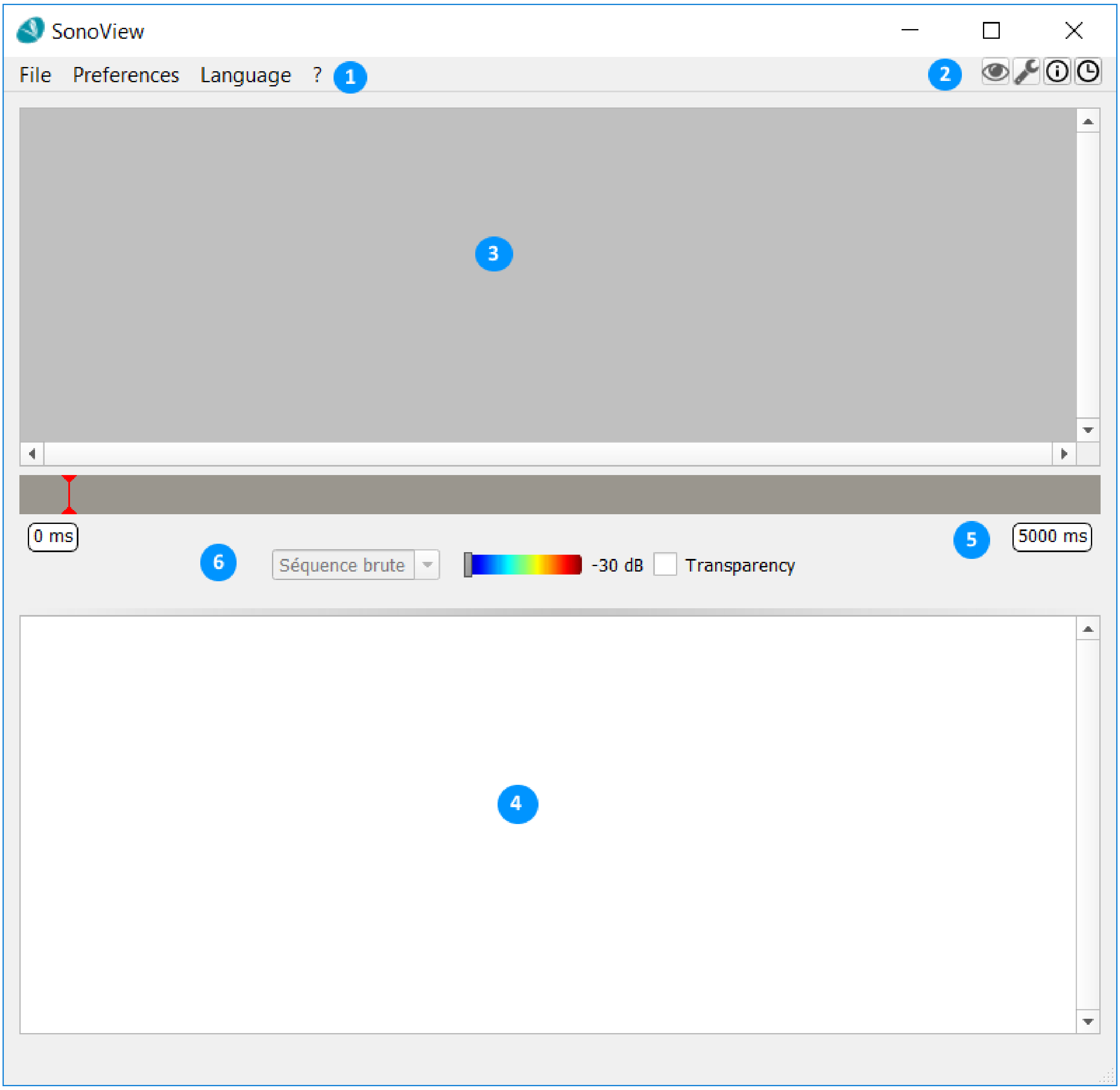
IC 0 : 0
IC 1 : 0
IC 2 : 1
IC 3 : 0
IC 4 : 0
IC 5 : 0
IC 6 : 0
IC 7 : 0
IC 8 : 0
IC 9 : 0
IC 10 : 3

Chapter 4. SonoView

SonoView allows you to open .sqlite projects generated by SonoChiro®.
File → Open a project

Any changes are automatically saved in the .sqlite file. There is no Undo/Redo mechanism available.

4.1. Main items



1. **Menus** : See Preferences and Methodology
2. **Toolbox**: see Toolbox section
3. **Sonogram scene**: see Sonogram scene section

4. **Validation table** : see Validation table
5. **Call position bar in the recording sequence**
6. **Settings** : [visual settings] option.

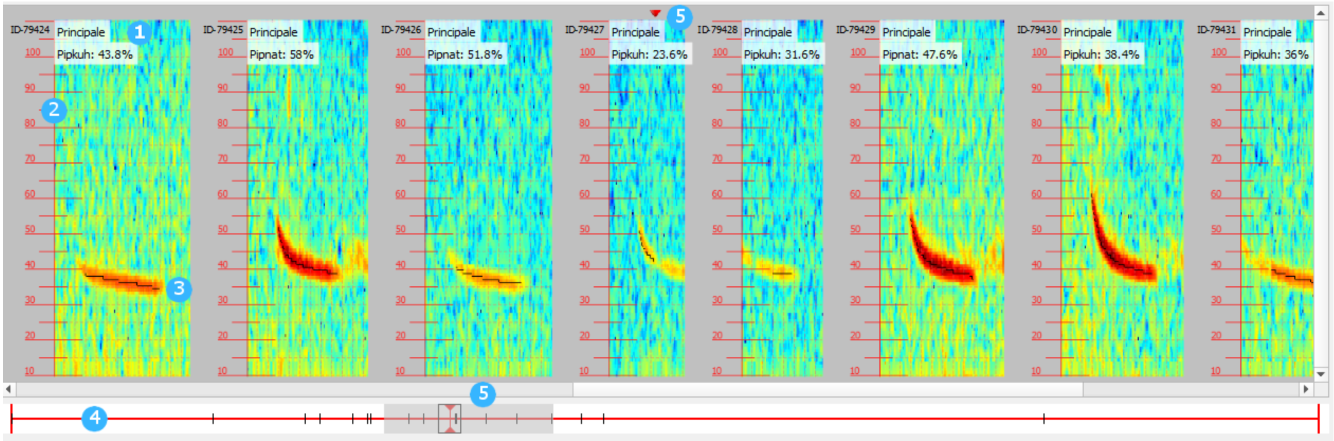
Sonogram scene

'Classic mode'

The classic mode is the default mode when opening SonoView.

If a great amount of calls have been detected in a sequence, all sonograms will not be displayed in the same window. Several actions are possible to move from one sonogram to the other within the same sequence:

- Directly on screen:
    - Mouse wheel: scrolls to the left or to the right on a zoomed out view.
    - Ctrl + wheel : zoom +/-
    - Shift + wheel : scrolls to the left or to the right on a zoomed in view.
    - Right click : « Centre view » allows to centre the call in the middle of the screen and adapts the zoom.
- On the navigation bar:
    - Left click: to go directly to the desired spot in the sequence.
    - Mouse wheel: moves to the left or to the right.



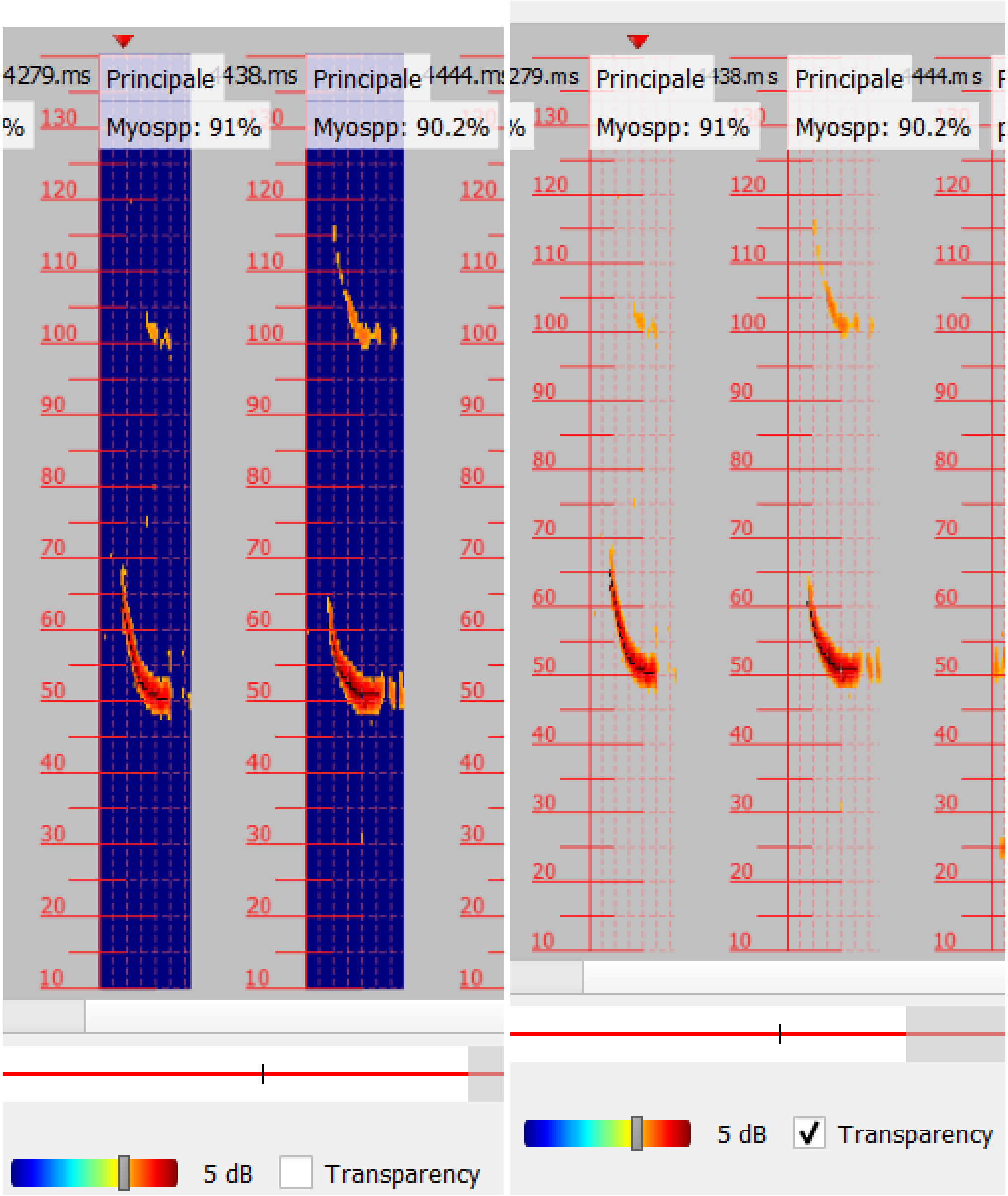
The sonogram scene provides several information:

1. **For each call**, prediction information:
    - The species order of arrival in the sequence (primary, secondary, tertiary)
    - The species name with the highest identification probability and its probability level.
2. **A sonogram image per call** :
    - A fix grid allows to find temporal and frequency marks directly on the sonogram:

    - Every 5 kHz for the frequency axis.
    - Every 1 ms for the time axis.

3. **The signal imprint detected by the software**: all parameters are measured on this imprint by SonoChiro®. It greatly influences the identification results.
4. **Position bar of calls in the sequence**: the ticks indicate the calls position in the sequence. A tooltip gives the exact temporal reference of each call in the sequence.
5. **Position window in the sequence**: The shaded window indicates the sequence segment shown on screen. The red cursor makes the link between the central sonogram and the position bar.

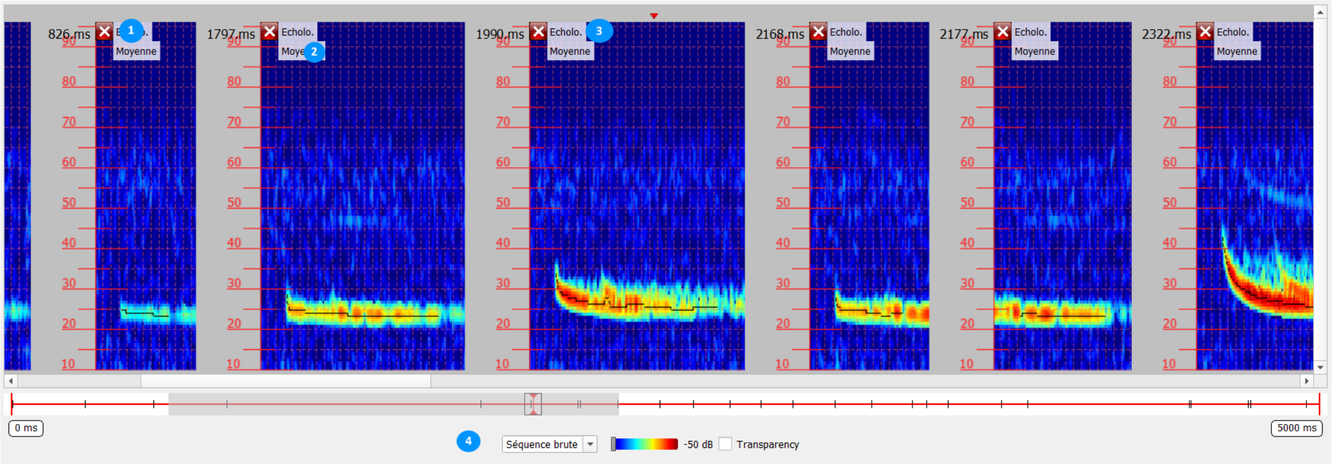
The graphical settings will allow you to bring out calls from the ambient noise by applying a classical high pass filter. You can select its threshold value. A transparency option is also available.



'Edition mode'

Access to this mode is possible through the 🔧 button in the upper right corner of the main window.

This mode is useful if you aim at enhancing classifiers. It allows to clean a sequence from undesirable measures.



1. **Individual call deletion** : ☒
2. **Quality level of measure** (editable)
3. **Call type** (editable)
4. **Type of call filter**

Each modification made in this edition mode is visible in the 'Historic' tool of the Toolbox.

4.2. Validation table

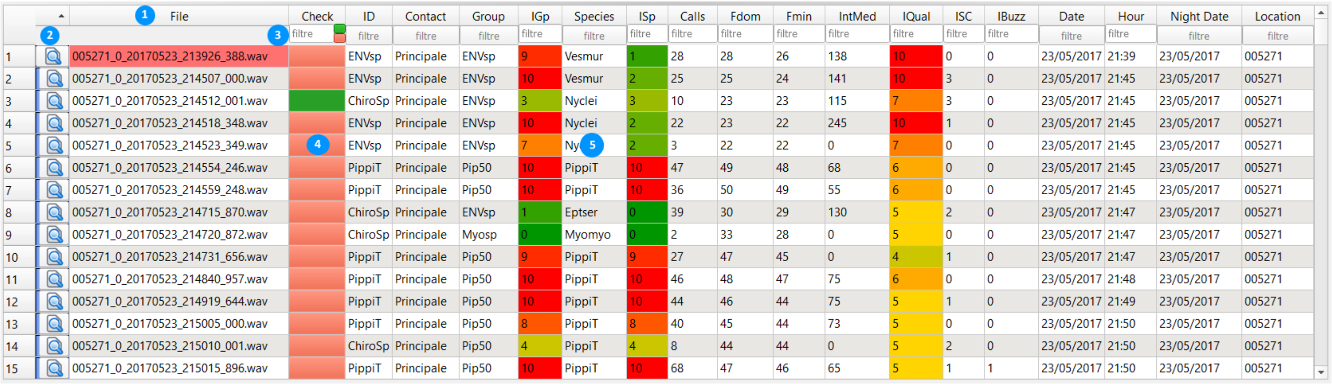
From the left to the right, the table contains the following fields:

Field name	Content	Commentary
Filename	Name of the audio file	An audio file may have several rows depending on the bit duration chosen (see [Analysis bit]) or if several species are present in the sequence.
Check	Validation column	Validated lines are marked in green by the user.
ID	Temporary identification of SonoChiro®.	Depending on the confidence indexes, ID indicates the species (if ISp > 5) else the group (if IGp > 5) else 'ChiroSp'. The user can edit this field to write his final identification after he has checked the audio file, if needed (see VI for more details).
Contact	Contact level of the species in the sequence	Indicates 'Principal' for the most represented species in the sequence, 'Secondary' or 'Tertiary' if it is less represented.

Field name	Content	Commentary
Group	Species group identified by Sonochiro®	(see [Annex Groups/Species])
IGp	Confidence index associated to the species group	Varies from 0 to 10.
Species	Species identified by Sonochiro®	(see [Annex Groups/Species])
ISp	Confidence index associated to the species	Varies from 0 to 10.
Calls	Number of calls on which identification was done	-
Fdom	Median frequency at the maximum energy	-
Fmin	Median minimum call frequency	-
IntMed	Median time interval between calls (proxy for rhythm)	Indicates a null value if the rhythm is regarded as non reliable because several individuals are present or because many echoes are present.
IQual	Quality index of the sequence	Varies from 0 to 10. This value reflects the identification ability of SonoChiro®.
ICS	Confidence index for the presence of social calls	Varies from 0 to 10.
IBuz	Confidence index for the presence of foraging calls (buzz)	Varies from 0 to 10.
Date	Recording date	Format DD/MM/YYYY
Hour	Recording hour	Format HH:MM
Night	Date of the beginning of the night (useful for summary tables).	Format DD/MM/YYYY.
Location	Isolates the beginning of the file name	If the name of the location has been written in the file name, through the recorder settings or with a software (e.g. Lupas Rename, Ant Renamer), the location name will appear.

ℹ in columns "Group" and "Species", the "parasi" value may appear. It indicates that the file probably only contains parasite sounds (i.e. other than bat calls). However, there is a non negligible chance that the file still contains bat calls.

❗ Date, hour and location parameters will be added only if information could be retrieved at the time of the analysis of the audio file (correct file name format or metadata from a recorder).



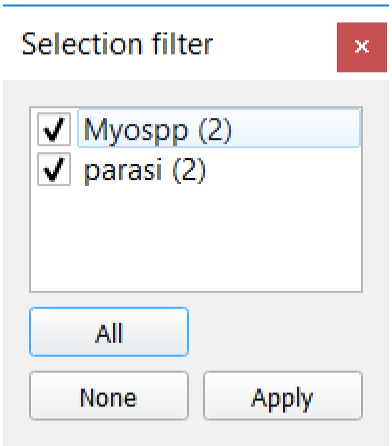
		File	Check	ID	Contact	Group	IGp	Species	ISp	Calls	Fdom	Fmin	IntMed	IQual	ISC	IBuzz	Date	Hour	Night Date	Location
			filtre 🟩🟥	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre	filtre
1	🔍	005271_0_20170523_213926_388.wav	🟥	ENVsp	Principale	ENVsp	9	Vesmur	1	28	28	26	138	10	0	0	23/05/2017	21:39	23/05/2017	005271
2	🔍	005271_0_20170523_214507_000.wav	🟥	ENVsp	Principale	ENVsp	10	Vesmur	2	25	25	24	141	10	3	0	23/05/2017	21:45	23/05/2017	005271
3	🔍	005271_0_20170523_214512_001.wav	🟩	ChiroSp	Principale	ENVsp	3	Nyclei	3	10	23	23	115	7	3	0	23/05/2017	21:45	23/05/2017	005271
4	🔍	005271_0_20170523_214518_348.wav	🟥	ENVsp	Principale	ENVsp	10	Nyclei	2	22	23	22	245	10	1	0	23/05/2017	21:45	23/05/2017	005271
5	🔍	005271_0_20170523_214523_349.wav	🟥	ENVsp	Principale	ENVsp	7	Ny	2	3	22	22	0	7	0	0	23/05/2017	21:45	23/05/2017	005271
6	🔍	005271_0_20170523_214554_246.wav	🟥	PippiT	Principale	Pip50	10	PippiT	10	47	49	48	68	6	0	0	23/05/2017	21:45	23/05/2017	005271
7	🔍	005271_0_20170523_214559_248.wav	🟥	PippiT	Principale	Pip50	10	PippiT	10	36	50	49	55	6	0	0	23/05/2017	21:45	23/05/2017	005271
8	🔍	005271_0_20170523_214715_870.wav	🟥	ChiroSp	Principale	ENVsp	1	Eptser	0	39	30	29	130	5	2	0	23/05/2017	21:47	23/05/2017	005271
9	🔍	005271_0_20170523_214720_872.wav	🟥	ChiroSp	Principale	Myosp	0	Myomyo	0	2	33	28	0	5	0	0	23/05/2017	21:47	23/05/2017	005271
10	🔍	005271_0_20170523_214731_656.wav	🟥	PippiT	Principale	Pip50	9	PippiT	9	27	47	45	0	4	1	0	23/05/2017	21:47	23/05/2017	005271
11	🔍	005271_0_20170523_214840_957.wav	🟥	PippiT	Principale	Pip50	10	PippiT	10	46	48	47	75	6	0	0	23/05/2017	21:48	23/05/2017	005271
12	🔍	005271_0_20170523_214919_644.wav	🟥	PippiT	Principale	Pip50	10	PippiT	10	44	46	44	75	5	1	0	23/05/2017	21:49	23/05/2017	005271
13	🔍	005271_0_20170523_215005_000.wav	🟥	PippiT	Principale	Pip50	8	PippiT	8	40	45	44	73	5	0	0	23/05/2017	21:50	23/05/2017	005271
14	🔍	005271_0_20170523_215010_001.wav	🟥	ChiroSp	Principale	Pip50	4	PippiT	4	8	44	44	0	5	2	0	23/05/2017	21:50	23/05/2017	005271
15	🔍	005271_0_20170523_215015_896.wav	🟥	PippiT	Principale	Pip50	10	PippiT	10	68	47	46	65	5	1	1	23/05/2017	21:50	23/05/2017	005271

The validation table has a **filtering and sorting tool** to ease data validation:

1. **Field names bar**: a simple click on the field name sorts out the column in an ascending order; a second click will sort it out in a descending order.

> Sorting helps organise data display. It can be used with the same aim as filters but is usually less practical. For this reason we generally advise to keep a chronological sorting in order for the consecutive sequences to be grouped together (in the case of a same individual that produced several consecutive recordings for example).

2. **Zoom**: 🔍 a click on the small magnifying glass at the beginning of a line will show the sequences sonograms.
3. **Filter bar**: a click on a cell of this bar will open a filter menu for the text fields or will allow to enter a formula for numeric fields.



Selection filter

☑ Myospp (2)
☑ parasi (2)

For numeric columns, filtering is made through a mathematical criterion:

- « > value »: only displays strictly superior values.
- « < value »: only displays strictly inferior values.
- « = value »: only displays strictly equal values.
- « value1 <> value2 »: only displays values between value1 and value2.

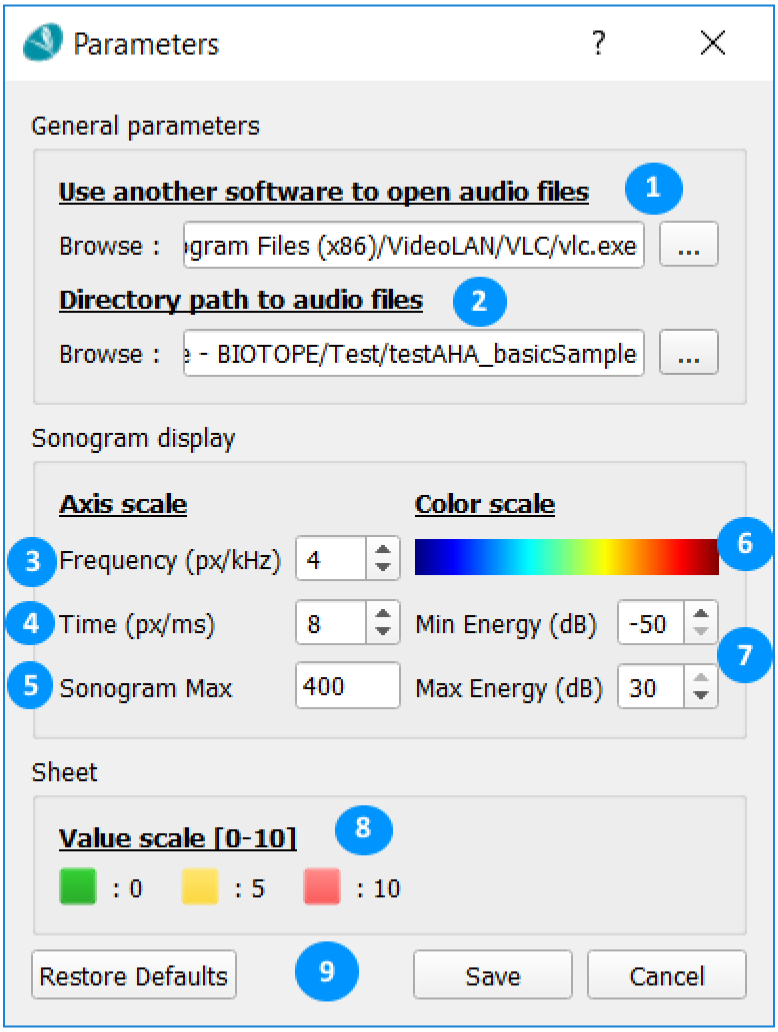
4. **ID validation mark**: marking of the lines validated manually by the user. It is possible to edit this column in two ways:
    - Left click: changing the colour red/green (validated/not validated)

- Right click → Action → "Mark as pertinent": mark with a star for later use.

For the « Val. » column only the mathematical criterion « value » is relevant: « = 0 » returns not validated sequences (in red). « = 1 » returns validated sequences (in green). « = 2 » returns pertinent sequences (with a star).

4.3. Preferences

You can access the window through the Preferences→Parameters menu:


Parameters

General parameters

Use another software to open audio files
Browse : gram Files (x86)/VideoLAN/VLC/vlc.exe

Directory path to audio files
Browse : - BIOTOPE/Test/testAHA_basicSample

Sonogram display

Axis scale
Frequency (px/kHz) 4
Time (px/ms) 8
Sonogram Max 400

Color scale
Min Energy (dB) -50
Max Energy (dB) 30

Sheet

Value scale [0-10]
🟩 : 0
🟨 : 5
🟥 : 10

1. **External analysis software**: access path to an external acoustic analysis software (Batsound.exe, audacity.exe, Syrinx.exe…) to listen to the file and make manual measurements.
2. **Audio folder path**: Path to the location where the current audio files are stored (required for the opening of files in an external software).
3. **Frequency display (px/kHz)**: scale parameters of the frequency axis for sonogram display.
4. **Time display (px/ms)**: scale parameters of the temporal axis for sonogram display.
5. **Max Sonogram**: Maximum number of sound images displayed in the sonogram scene. After several hundreds of calls the software may encounter certain troubles. If the sequence has more calls than the value entered here, images will not be shown.
6. **Colour scale**: several colorimeters are available.

7. **Signal intensity bounds**
8. **Value scale**: conditional confidence index columns formatting and colour choice depending on indexes values.
9. **Settings saving**: it is also possible to put default settings back.

Toolbox

Three buttons give access to different tools: 👁 🔧 🕒

External acoustic analysis software: 👁 Shortcut to open the active sequence in an external acoustic analysis software defined in the 'Preferences' menu. The same action can be done through the table (right click → Other → Open in an external software).

> during the first utilisation you need to indicate the access path to the program to open (the actual location of the program on the computer, not the desktop shortcut). This location is also accessible through the menu Preferences

Adjustable wrench 🔧: This icon gives access to the [Edition Mode]

Historic 🕒: access to the edition historic. This historic lists all operations done in the [Edition Mode] for the current sequence. Each operation can be undone through the table (right click on an item of the list → Undo)

SonoChiro® 4.0

Methodology

Chapter 1. Presentation

1.1. Introduction

SonoChiro® software has been built around the expertise and the know-how of Biotope’s bat experts. The proceedings of this method are hereby reminded to ensure an optimal use of the software.

Biotope is a consulting firm studying numerous territories. For each new study, the following question was at the origin of the motivation to create our tools: « **What are the conservation stakes for bats in this area ?** ». From this question, many other follow:

- « Which species are present ? » (qualitative aspects)
- « What is the state of populations ? » (quantitative aspects)
- « How to count them ? »
- « What are we counting ? », « With what tools ? » (methodological aspects)

The team at the origin of SonoChiro®'s software conception (Jean-Fançois JULIEN from the French National Museum for Natural History, Alexandre HAQUART, Yves BAS, Thierry DISCA) had solid bases in the acoustic identification of bats, notably thanks to the method developed by Michel BARATAUD. **Handling of this methodology is a prerequisite to validate our software’s determinations**. SonoChiro® is indeed only a sorting tool. A very powerful tool but a tool that makes mistakes. The user thus has to **find identification errors**. These errors are scarce or territories with few species, but they can be frequent on territories with a high species diversity or in bad recording conditions.

SonoChiro® is first of all **adapted to automatically handle large acoustic datasets**. Its use allows to very quickly sort out recordings, facilitates the validation of suggested identifications and to « clean » datasets by deleting parasites and unwanted information.

The order of the following chapters will follow the chronological order of a bat expertise, from sound recordings to counting results. This proceeding will allow a better understanding of the different tools and facilitate the use of the software.

1.2. Purpose and framework for the software

SonoChiro® is a software analysing automatically ultrasound recordings of bats, be it in time expansion or in real time. This software provides a valuable help for all users of bat detectors, in particular in case of unattended recorders accumulating large amounts of data. Its diverse functions make it useful in many different contexts of analysis: inventorying species at a site, counting bat passes, quantifying hunting activity (feeding buzzes), highlighting social activity, etc.

SonoChiro® cannot completely substitute for a manual identification since a zero error rate is unattainable in the current state of knowledge and technological advances. However, SonoChiro® has been designed for maximum ease of the treatment of its own mistakes, especially through a set of relevant confidence indices. Thus, the **time saved** through the use of SonoChiro® is considerable. This varies depending on many factors (objectives, recording quality, etc.) but it is **generally greater than 90%**, it even exceeds 99% in many cases.

1.3. Principle of operation

SonoChiro® process recordings in two phases: **detection and classification**.

The **detection** process consists in localizing then characterizing a maximum number of signals potentially emitted by bats. SonoChiro® has indeed been designed to ensure a maximum sensitivity in bat calls detection, in order to detect even the most discrete species, even in case of weak signals and/or poor quality recordings. This approach result in large numbers of parasites being, in this preliminary phase, considered as potential bat calls, but these are easily discarded during the next phase (see Recordings prerequisites).

The **classification** process is backed up by the characterization of previously detected signals. This classification operates on each file on which the software has detected potential bat calls. SonoChiro® determines first if the file contains calls from one or two species of bats. In the first case, the classification operates on all the bat calls detected in the file, considered forming a single “bat pass”. In the second case, the classification operates separately on the two subsets of bat calls, identified as being part of two different “bat passes”.

At the end of this phase, each bat pass benefit from a 5-level identification:

1. An **species identification for each call**: display of the most probable species and its probability level (at the top of sonograms in SonoView)
2. An **identification at species level** ("Species" column), accompanied by a confidence index (ISp) going from 0 to 10.
3. An **identification at a species group level** (Group), thus less accurate but more reliable, also accompanied by a confidence index (IGp) going from 0 to 10.
4. An index of **feeding buzz presence** (Ibuz) highlighting a prey catch, thus a foraging behaviour, also from 0 to 10.
5. An index of **social calls presence** (Ics) highlighting the proximity to a roost for numerous species, also from 0 to 10.

Associating a **confidence index** to each level of identification is an **essential supplement** to the identification itself. SonoChiro® has indeed been designed in such a way that each confidence index closely reflect error risk in the identification. Thus, the user can identify for each analysis, a threshold in the confidence index below which identifications are false or doubtful. He/she can then mass process these “errors” for maximum time saving.

Finally, some complementary quantitative information is added for each bat pass: number of calls, median dominant frequency, median interval and signal quality. (Cf Interface)

1.4. Geographical and taxonomic coverage

SonoChiro® currently covers more than **110 bat species**, 31 of the 39 European species and 80 Neotropical species. Species list can be accessed on the presentation page of classifiers. (Cf

Classifiers)

The learning process of the software has been performed on several millions of calls, recorded all over Europe, from Lithuania to Spain and from Serbia to Ireland, with a minimum of 1,000 calls for each considered species.

Species name codes used by SonoChiro® are formed by 6 letters referring to the first 3 genus letters and the first 3 species letters.

```
ex: Pipistrellus pygmaeus = Pippyg
```

Chapter 2. Recordings prerequisites

SonoChiro® only accepts audio files in WAVE format (file name extension .wav)

2.1. Good recording conditions: a time saver !

Microphone environment will change signal transmission, impacting the abilities of SonoChiro® to analyse information. To simplify, SonoChiro®'s worst enemies are (1) Echoes and (2) Parasites. It is in the user's best interest to prevent any of those issues when installing the recording material. Here are some elementary rules to follow in order to **optimise recording quality**:

1. Keep the microphone away from the ground, at least 1 meter if possible.
2. Use a cable to install your microphone in the best conditions.

3. Bring out your microphone from vegetation. If it is installed on a tree, put it as much as possible at the tip of its branches. Cut leaves around the microphone.
4. Orientate the microphone horizontally or 45° towards the sky, in the direction of an open space, especially if the microphone is directional.
5. More generally, maximise chances that the space between bats and the microphone is not obstructed with any object that may alter sound.

2.2. Audio file name format

The way how your recording files are named is important because SonoChiro® will extract information about location, date and hour. If done properly, this step will help you save a precious time for later analysis. SonoChiro® V4 will extract the timestamp produced by several recorder models:

1. **SM2BAT/SM3BAT/SM4BAT/EM3** : Supports the old SM2 format with milliseconds (ex: `SM2_10_20120726_220303_946.wav`). The format of new recorders is the same (ex: `TF7544_20130516_011832.wav`). For those recorders SonoChiro® considers that file name beginning is a location name (ex : `SmallPond_20130516_011832.wav` → Location: 'SmallPond').
2. **DX500** : The timestamp is found in a « info.txt » file shared with all recorded audio files. Remark: To obtain this text file, you need a firmware version 2.1.1. minimum.
3. **Batlogger** : The timestamp is found in an XML file associated with each audio file. Ex : 15050008.wav ⇒ 15050008.xml

2.3. File duration

In previous versions, files had to be in mono and have a duration inferior to 20 seconds. The V4 handles stereo files and durations of several minutes. To be efficient, automated identification must only apply to short sequences. By convention, 5 seconds is usually used to define a bat pass length. This duration is ideal for SonoChiro®. Above this duration, call diversity may become too important and may not be well handled by the software’s classification process.

> In certain situations (wetlands or tropical regions), when species diversity or individual density is very high, it is even recommended to limit audio sequences duration to 3 seconds.

This duration setting is adjustable in SonoChiro® V4 (see [Analysis bit] section in 'Interfaces'), but if your recording files are really too long (more than 10 minutes) it is recommended to split them with the SonoDemux software (see [launching platform]). This step will avoid potential issues and allow you to clean more easily your folders when deleting empty files.

2.4. Project folder size

Due to performance issue using big SQLite file in SonoView, we recommend to handle small project in SonoChiro®. The maximum recommended size is around 15-20Go. In order to help you to split you big project, we provide an executable, SonoSplitter, in the SonoChiro® program folder (double-click on sonosplitter.exe).

Chapter 3. SonoChiro® settings

Please see interface presentation (Cf Interface)

Chapter 4. Predictions validation

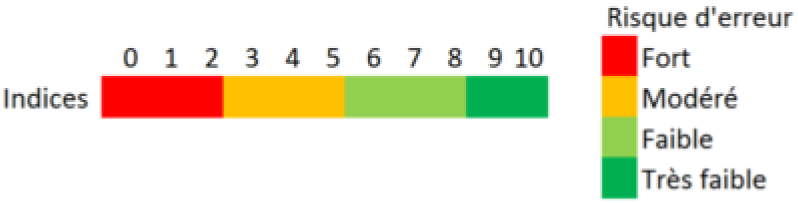
This step requires that a sample of the recordings would be manually checked by “expert judgement”. It therefore requires skills in acoustics.

Validating or correcting can be easily mass processed on your table thanks to **“ID” field**. This column has indeed a vocation to be edited in such as to constitute the final identification at the end of this step.

> The ID column is your "result" column, which you will use for summaries.

4.1. Confidence indexes interpretation

Without going too far into details, here are the explanations concerning the algorithm determining **confidence indexes** attributed to a group (IGp) or a species prediction (ISp). After having targeted calls present in the sequence, SonoChiro® will calculate probabilistic statistics on each of those calls. This index is shown at the top of sonograms in SonoView for each call. This index changes from one call to the other. The software algorithm uses all call indexes to calculate a sequence confidence index.

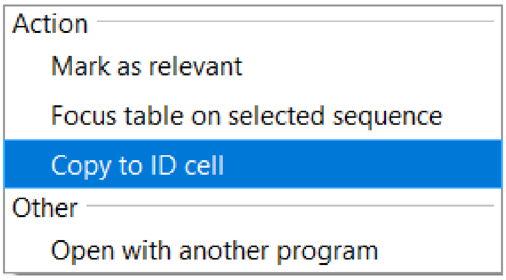


To produce the **final prediction** of the ID column, SonoChiro® uses Species (ISp) and Group (IGp) confidence indexes. ID indicates the species (if ISp > 5) else the group (if IGp > 5) else 'ChiroSp' (Chiroptera sp.). However the **5 value threshold is a careful threshold** and it is often possible to trust inferior indexes values, but the reliability of confidence indexes varies according to different factors:

1. **According to species and species groups**: if many species acoustically close are found in the same geographical area, those species index will systematically be weak. In Europe, it is generally the case for the *Myotis* group for instance.
2. **According to classifiers**, species list varies. The confidence index of a given species will thus depend on the presence or not of another acoustically close species. For instance, *Pipistrellus pygmaeus* index will be more reliable in regions where *Miniopterus schreibersi* is absent (both species) emit modulated frequencies with an end frequency close to 51).
3. **According to recordings quality**: see [Recording prerequisites]
4. **According to reference data**: It happens that a species is not correctly identified. It is often the case when a classifier is being built. This indicates that the present signal is not referenced in our learning database. If you encounter such cases please contact us to help us keep advancing the software. Those cases are rare in European classifiers but they can happen more often in outlying areas because of 'local accents'.

Contrary to other columns, the ID column is editable, this means that you can write any species name. Therefore, be careful to respect species nomenclature if you want to avoid issues with unnecessary synonyms (type parasi and Parasi or Pippg and Ppyg ...)

To avoid typing errors and go faster, rather use cell copy by stretching a cell content to adjacent cells. For this, double click on the small square in the lower right corner of the active cell to copy its content and paste it to all cells underneath. You can also transfer a species name from the Species column to the ID column by right clicking on the Species cell and clicking 'cpy to the ID cell'.



4.2. Different objectives, different approaches

In front of the amount of data produced by Sonochiro®, the user may soon feel overwhelmed. "Where should I start validating this table ?" In other words:

« How to choose the files to be manually checked? »

This choice depends on the user's purpose and his/her requirement in terms of exhaustively and accuracy. Hence, there is no recipe which can fit every situation. We give below two examples of common and contrasting situations for you to get an idea of your possibilities.

4.2.1. Case 1 : You intend to inventory the list of species present on a site

For this purpose, simply check **one single bat pass per species** identified by SonoChiro®: the one which got the highest confidence index and which consequently got the highest probability to belong to the species. Either the identification of **SonoChiro® is right, the species is thus really present, or SonoChiro® is wrong, the species can then be considered as missing.**

For the sake of prudence and completeness, you can check up to three more bat passes among the highest confident ones, but it is useless to go any further because **it is extremely rare that a species is present without its highest confident identifications being right.**

On the event of a tie on the confidence indices, you can add a second criterion by selecting the file with **the highest quality index (IQual) and/or the largest number of calls (NbCalls)**. This can be particularly useful for Myotis species whose confidence indices are generally low and manual identification is difficult.

This method allows checking generally **only 10 to 25 files for 100 to 8000 recorded ones in the case of a whole night** (this ratio would be better or lower according to recording duration). If you do not bother to identify some difficult species groups like Myotis spp., the number of files to be checked is even noticeably lower.

4.2.2. Case n°2 (ambitious): You intend to quantify the activity of each species

If you wish to **quantify the activity of a species**, it becomes necessary to check additional files because the highest confidence index can't be considered representative for the other ones and, if it's valid, giving a guarantee that all files allocated to the species are valid.

But be careful, this doesn't mean to check every single bat passes (generally useless) but to estimate the number of bat passes corresponding to each species. In most cases, a given level of imprecision (±20% for ex.) in this estimate is entirely tolerable since the measured value of activities vary over several orders of magnitude between sites and between species

To simplify analysis it is recommended to first **filter the species group** even if one wishes to identify to the species level, because some errors can be found cross-wide a species group and can be treated more rapidly in this way.

The validation process thus goes group by group, and within those groups, species by species.

The 'aim of this game' consists in **finding the confidence index limit below which automated IDs are not reliable anymore.** This value varies according to species are species groups but also according to recordings quality and classifiers. It is thus difficult to provide here typical values but the user will quickly build an opinion for himself in function of his context.

> Mass validate or correct IDs can be done quickly from your table with the help of the « ID » column. In practice, you will need to use a filter to isolate all rows belonging to such species or such group, according to the desired criteria (Group/Species/Index). You then write the correct species name in the first cell of the « ID » column and double click on the lower right corner of the active cell to copy/paste this content to all lower cells.

For each species or group of species, the process goes as follows:

1. **Identification is right**
    a. A majority of the other bat passes have similar values of confidence index
        i. the species is not rare = **you can validate all the bat passes of the species**
        ii. the species is possibly rare = you check at least 3 more bat passes in order not to overestimate the activity of the species
            A. there is no error = **you can validate all the bat passes of the species**
            B. errors are found = **you check at least a dozen of bat passes to estimate activity accurately**
    b. A majority of the other bat passes of the species have much lower confidence indices than the highest = you check at least two other bat passes among the low confidence indices
        i. there is no error = **you can validate all the bat passes of the species**
        ii. errors are found = you check at least 3 other bat passes to define to which level of

confidence index, errors correspond = **you can validate all the bat passes which are over this confidence level** and pass to B for others

2. **Identification is wrong**: you check at least three other bat passes
    a. The error is systematically the same (a specific species or parasites) = **you correct all the bat passes concerned to the species manually identified**
    b. the bat passes checked did not all correspond to the same species = **you check at least 6 other bat passes in order to estimate the proportion of each species**

> Comment: this protocol intend to be a guide in the initial steps taken by the user. The experience subsequently accumulated will allow the user to progressively deviate from it and/or to ameliorate it, according to analyses purposes. The consideration of additional parameters like the number of calls, the rhythm, the frequencies or the behaviour (feeding buzz / social calls) could in some case improve the management of errors.

4.2.3. You are still overloaded with validation time: some additional solutions

Reducing even further the time of validation is possible at the cost of eliminating the **files from which the error risk is the highest**. SonoChiro® is indeed set by default to be very sensitive and detect as many bat passes as possible, even the weakest and shortest ones (even 1 single call) in poor recording conditions. This setting allows an optimal efficiency in detection, particularly useful for discrete species which benefit from easy manual identification, even in poor conditions (ex: horseshoe bats, Barbastelle…). However, it is reasonable to waive these sensitive settings if you want to gain more time by save yourself a large part of the error management. For this, SonoChiro®'s users have access to five tools:

1. **The Sensitivity setting** chosen before running SonoChiro®. Lowering this setting can drastically reduce the error rate in case of heavily parasitized recordings (ex: bush-crickets). Be careful, dropping sensitivity below 3 can eliminate a large part of the bat passes, particularly when a lot of bats are detected far from the detector (ex: high-flying bats recorded from the ground).
2. **Increasing the minimum duration of calls**. Be careful, this could rapidly eliminate species which make very short calls when they are hunting, Plecotus and Myotis particularly. This setting is thus not advised if these species are sought after.
3. **Increase the minimum detection frequency** to 12kH for instance. Careful, this setting must not be used in *Tadarida teniotis* distribution area (emits as low as 9-10 kHz). This setting can avoid the recording of numerous parasite sounds, notably Orthoptera.
4. Filtering a posteriori bat passes contain only a few calls (**NbcCalls** > **2**), hence, making their identification much less reliable. Be careful, filtering bat passes over 2 calls would sometimes eliminate species calling with very slow rhythm (ex: Greater Noctule or Free-tailed Bat).
5. Filtering a posteriori bat passes of bad quality recording (**Iqual** > **2**). Be careful, filtering on this criterion could eliminate a large part of bat passes if the environment of the microphone is much cluttered (forest understorey, tunnel, etc.).

Chapter 5. Data export and file cleaning

5.1. Export

After having analysed your SQLite project, you will probably need to export results to a table for quantitative analysis (.csv file).

```
File -> Export data
```

This menu will allow you to export your data as a whole or partially of you check the "Active filters" box.

You can also extract audio files of interest in this way.

5.2. Cleaning

Automated ultrasound recorders produce a non negligible amount of data. A part of these recordings may be of no interest because they are empty or because they do not contain any bat sound. It is possible to delete those files with SonoChiro®.

```
File -> Sound files cleaning
```

This menu will allow you to **delete audio files** displayed on your table (active filter). You can also **delete images** of the current project. Deleting images for the most common species for instance will save a non negligible space on your disk. Those deletions will not prevent the current project from functioning correctly, but data will be missing.

SonoChiro® 4.0

The classifiers

Chapter 1. Europe

1.1. Geographical and taxonomic coverage

SonoChiro® currently covers 31 of the 39 European species (see list below). Training has been done on several millions of calls recorded throughout Europe, from Lithuania to Spain, and from Serbia to Ireland with a minimum of 1,000 calls for each species.

Table 1. List of European bat species treated by SonoChiro®

Code	Scientific name	English name
Barbar	*Barbastella barbastellus*	Western Barbastelle Bat
Eptnil	*Eptesicus nilssonii*	Northern Bat
Eptser	*Eptesicus serotinus*	Serotine Bat
Hypsav	*Hypsugo savii*	Savi’s Pipistrelle Bat
Minsch	*Miniopterus schreibersii*	Schreibers' Bent-winged Bat
Myoalc	*Myotis alcathoe*	Alcathoe Whiskered Bat
Myobec	*Myotis bechsteinii*	Bechstein’s Bat
Myobly	*Myotis blythii*	Lesser Mouse-eared Bat
Myobra	*Myotis brandtii*	Brandt’s Bat
Myocap	*Myotis capaccinii*	Long-fingered Bat
Myodas	*Myotis dasycneme*	Pond Bat
Myodau	*Myotis daubentonii*	Daubenton’s Bat
Myoema	*Myotis emarginatus*	Geoffroy’s Bat
Myomyo	*Myotis myotis*	Greater Mouse-eared Bat
Myomys	*Myotis mystacinus*	Whiskered Bat
Myonat	*Myotis nattereri*	sensu stricto "northern Natterer’s Bat"
MyospA	*Myotis* cf. *nattereri sp. A*	southern type Natterer’s Bat
Nyclas	*Nyctalus lasiopterus*	Greater Noctule Bat
Nyclei	*Nyctalus leisleri*	Leisler’s Bat
Nycnoc	*Nyctalus noctula*	Noctule
Pipkuh	*Pipistrellus kuhlii*	Kuhl’s pipistrelle bat
Pipnat	*Pipistrellus nathusii*	Nathusius' Pipistrelle Bat
PippiM	*Pipistrellus pipistrellus*	Common Pipistrelle Bat type “Mediterranean”
PippiT	*Pipistrellus pipistrellus*	Common Pipistrelle Bat type “Temperate”
Pippyg	*Pipistrellus pygmaeus*	Soprano Pipistrelle
Pleaur	*Plecotus auritus*	Brown Big-eared Bat
Pleaus	*Plecotus austriacus*	Grey Long-eared Bat

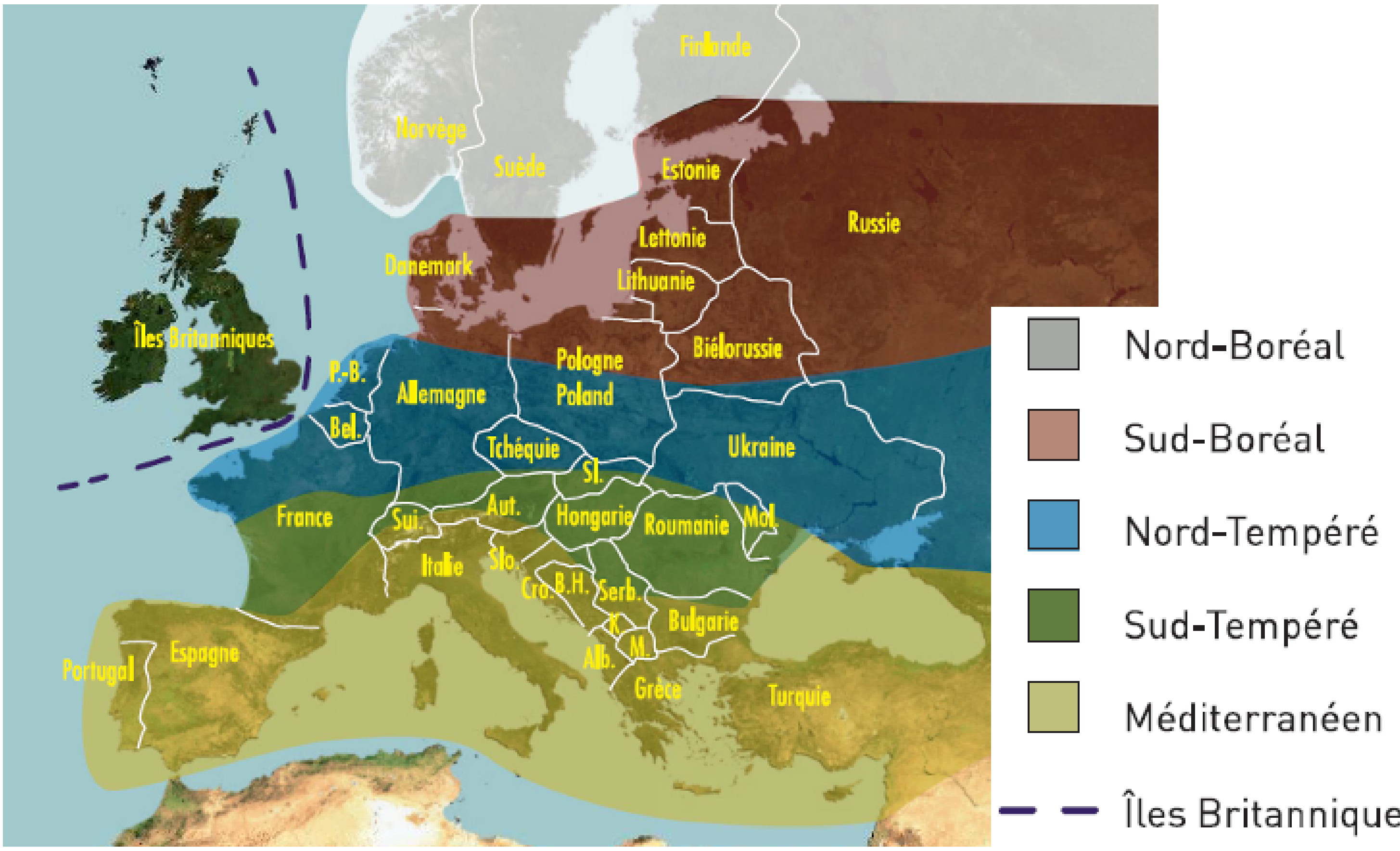
Plemac	*Plecotus macrobullaris*	Alpine Long-eared Bat
Rhieur	*Rhinolophus euryale*	Mediterranean Horseshoe Bat
Rhifer	*Rhinolophus ferrumequinum*	Greater Horseshoe Bat
Rhihip	*Rhinolophus hipposideros*	Lesser Horseshoe Bat
Tadten	*Tadarida teniotis*	European Free-tailed Bat
Vesmur	*Vespertilio murinus*	Particoloured Bat

You’ll notice that the list contain 33 entities for 31 species. Two taxa, each usually considered as a single species, has indeed been split in two entities, on the basis of recent publications for Natterer’s Bat (Puechmaille *et al.* 2011 ; Salcini *et al.* 2011) and on the basis of noticeable differences in calls for the Common Pipistrelle, between individuals from the Mediterranean Basin and those from temperate regions.

In addition, the temporary absence of eight of the European species will cause little harm to SonoChiro® users, wherever recordings originate from. For seven of these eight species, no reliable criteria regarding their calls has indeed been described because they emit almost identical calls from commoner species which are covered by SonoChiro®. Hence, if these species are recorded by a user, they will be assigned to their commoner “acoustic counterpart”. There remains Blasius’ Horseshoe Bat (Rhinolophus blasii) whose range is restricted to southern Balkans. In the current state of SonoChiro®, this species will be most often assigned to its closest species: the Mediterranean Horseshoe Bat.

The difficulties of identification of some species (ex: Plecotus spp., Myotis spp., etc) led us to define species groups in order to offer a second level of identification, less accurate but more reliable. These groups are detailed in the table below.

A workbook entitled « SpList_Geo.ods » gives the connections between species and groups which slightly vary between geographical regions. This workbook can be downloaded here: http://www.leclub-biotope.com/en/index.php?controller=attachment&id_attachment=20



⬜ Nord-Boréal

🟫 Sud-Boréal

🟦 Nord-Tempéré

🟩 Sud-Tempéré

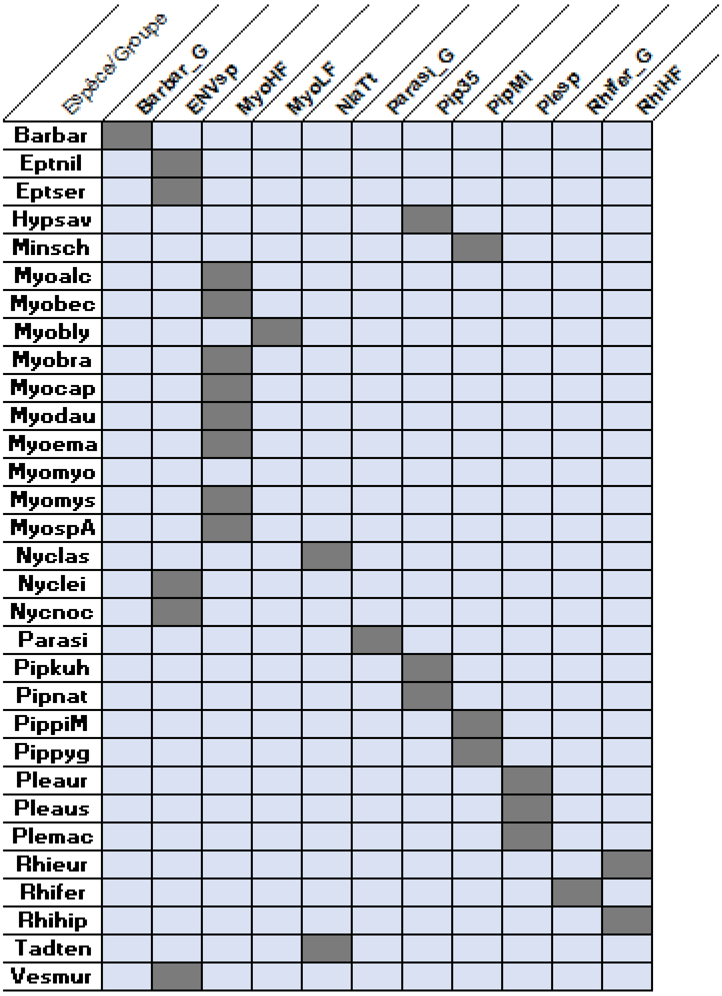
🟨 Méditerranéen

– – Îles Britanniques

1.2. European Bat classifiers

1.2.1. M - Mediterranean

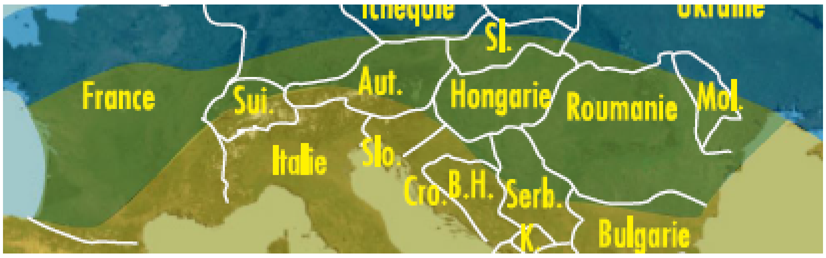
30 species, 11 groups

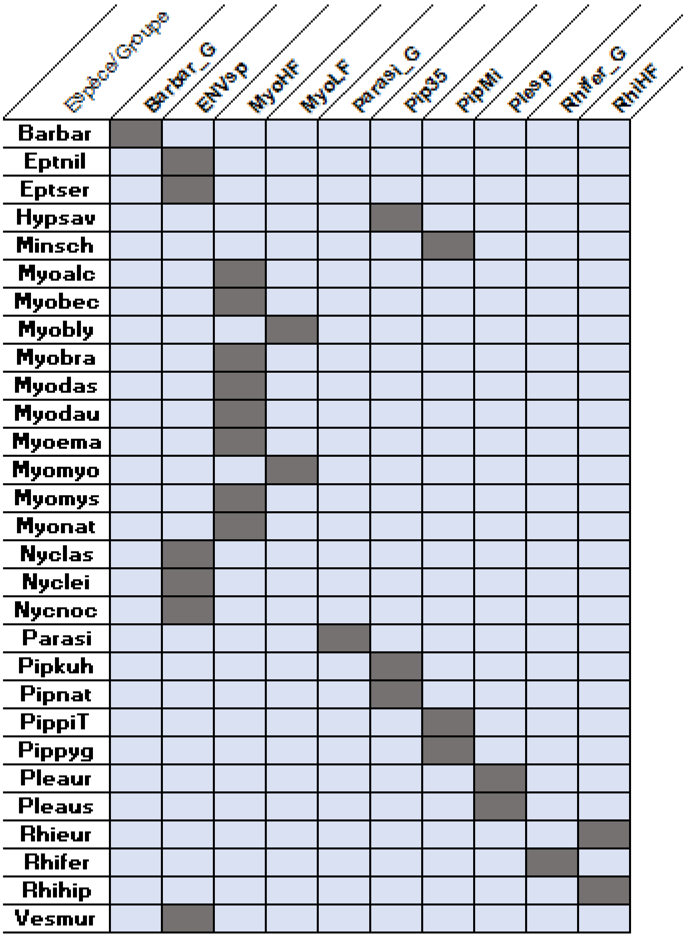


Espèce/Groupe	Barbar_G	ENVsp	MyoHF	MyoLF	NlaTt	Parasi_G	Pip35	PipMi	Plesp	Rhfer_G	RhiHF
Barbar	■										
Eptnil		■									
Eptser		■									
Hypsav							■				
Minsch								■			
Myoalc			■								
Myobec			■								
Myobly				■							
Myobra			■								
Myocap			■								
Myodau			■								
Myoema			■								
Myomyo											
Myomys			■								
MyospA			■								
Nyclas					■						
Nyclei		■									
Nycnoc		■									
Parasi						■					
Pipkuh							■				
Pipnat							■				
PippiM								■			
Pippyg								■			
Pleaur									■		
Pleaus									■		
Plemac									■		
Rhieur											■
Rhifer										■	
Rhihip											■
Tadten					■						
Vesmur		■									

1.2.2. ST - South temperate

28 species, 10 groups

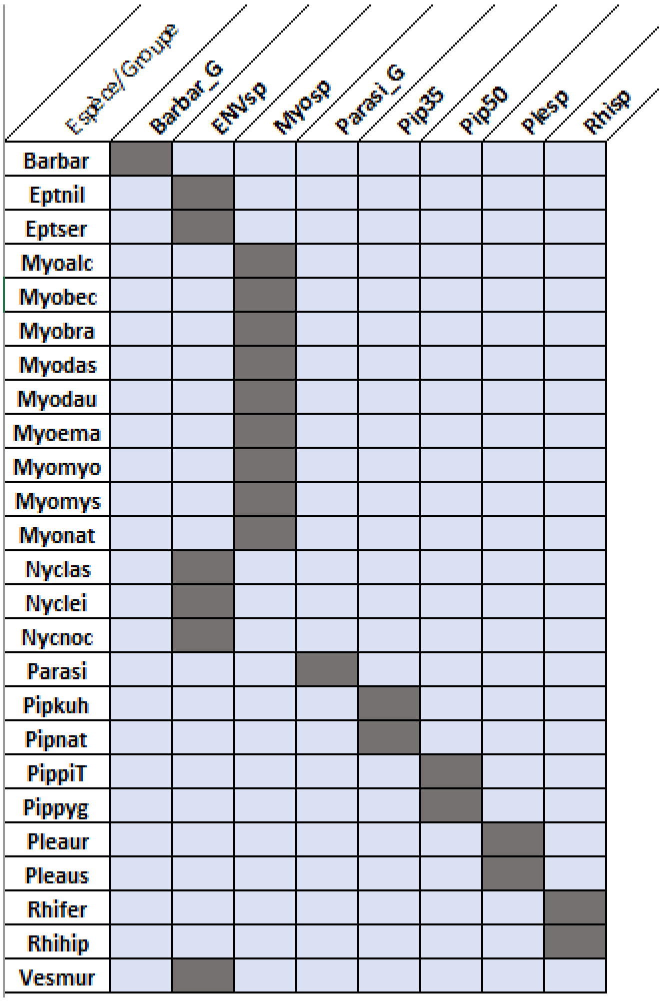




Espèce/Groupe	Barbar_G	ENVsp	MyoHF	MyoLF	Parasi_G	Pip35	PipMi	Plesp	Rhifer_G	RhiHF
Barbar	■									
Eptnil		■								
Eptser		■								
Hypsav						■				
Minsch							■			
Myoalc			■							
Myobec			■							
Myobly				■						
Myobra			■							
Myodas			■							
Myodau			■							
Myoema			■							
Myomyo				■						
Myomys			■							
Myonat			■							
Nyclas		■								
Nyclei		■								
Nycnoc		■								
Parasi					■					
Pipkuh						■				
Pipnat						■				
PippiT							■			
Pippyg							■			
Pleaur								■		
Pleaus								■		
Rhieur										■
Rhifer									■	
Rhihip										■
Vesmur		■								

1.2.3. NT - North temperate

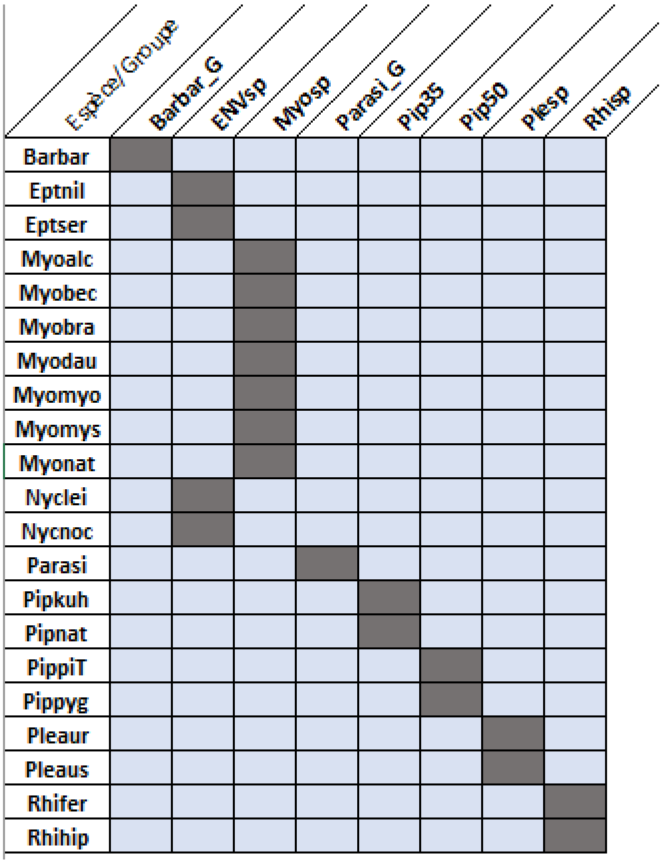
24 species, 8 groups



Espèce/Groupe	Barbar_G	ENVsp	Myosp	Parasi_G	Pip35	Pip50	Plesp	Rhisp
Barbar	■							
Eptnil		■						
Eptser		■						
Myoalc			■					
Myobec			■					
Myobra			■					
Myodas			■					
Myodau			■					
Myoema			■					
Myomyo			■					
Myomys			■					
Myonat			■					
Nyclas		■						
Nyclei		■						
Nycnoc		■						
Parasi				■				
Pipkuh					■			
Pipnat					■			
PippiT						■		
Pippyg						■		
Pleaur							■	
Pleaus							■	
Rhifer								■
Rhihip								■
Vesmur		■						

1.2.4. BI - British Isles

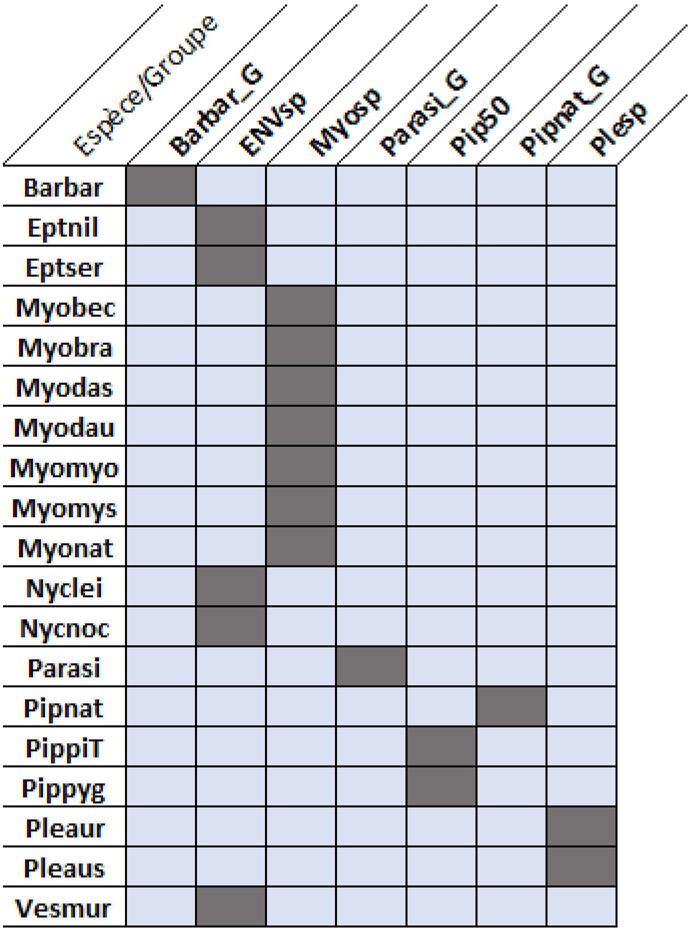
20 species, 8 groups



Espèce/Groupe	Barbar_G	ENVsp	Myosp	Parasi_G	Pip35	Pip50	Plesp	Rhisp
Barbar	■							
Eptnil		■						
Eptser		■						
Myoalc			■					
Myobec			■					
Myobra			■					
Myodau			■					
Myomyo			■					
Myomys			■					
Myonat			■					
Nyclei		■						
Nycnoc		■						
Parasi				■				
Pipkuh					■			
Pipnat					■			
PippiT						■		
Pippyg						■		
Pleaur							■	
Pleaus							■	
Rhifer								■
Rhihip								■

1.2.5. SB - South Boréal

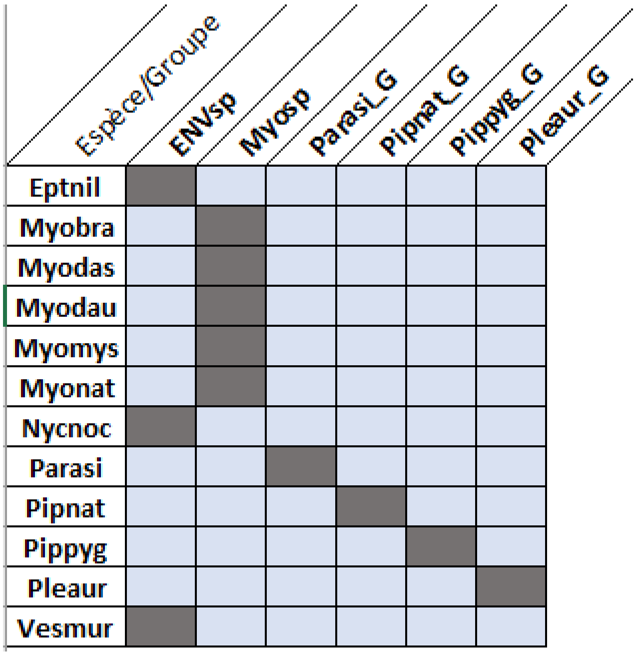
18 species, 7 groups



Espèce/Groupe	Barbar_G	ENVsp	Myosp	Parasi_G	Pip50	Pipnat_G	Plesp
Barbar	■						
Eptnil		■					
Eptser		■					
Myobec			■				
Myobra			■				
Myodas			■				
Myodau			■				
Myomyo			■				
Myomys			■				
Myonat			■				
Nyclei		■					
Nycnoc		■					
Parasi				■			
Pipnat						■	
PippiT					■		
Pippyg					■		
Pleaur							■
Pleaus							■
Vesmur		■					

1.2.6. NB - North Boréal

11 species, 6 groups



Espèce/Groupe	ENVsp	Myosp	Parasi_G	Pipnat_G	Pippyg_G	Pleaur_G
Eptnil	■					
Myobra		■				
Myodas		■				
Myodau		■				
Myomys		■				
Myonat		■				
Nycnoc	■					
Parasi			■			
Pipnat				■		
Pippyg					■	
Pleaur						■
Vesmur	■					

Chapter 2. Neotropics

2.1. Geographical and taxonomic coverage

SonoChiro® currently covers **82 species** in Neotropical areas (see list below).

Training has been done on several millions of calls recorded in French Guyana, Mexico and Venezuela, with a minimum of 1,000 calls per each species.

```
AMB : Amazonian Basin
LIN : Lesser Indies
SCA : Southern Central America
NCA : Northern Central America
```

2.1.1. A

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Ardnic	*Ardops nichollsi*	Phyllostomidae		X		
Artjam	*Artibeus jamaicensis*	Phyllostomidae		X		
Artlit	*Artibeus lituratus*	Phyllostomidae		X		

2.1.2. B

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Balio.	*Balantiopteryx io*	Emballonuridae			X	
Bracav	*Brachyphylla cavernarum*	Phyllostomidae		X		

2.1.3. C

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Carper	*Carollia perspicillata*	Phyllostomidae		X		
Cencen	*Centronycteris centralis*	Emballonuridae	X		X	
Cenmax	*Centronycteris maximiliani*	Emballonuridae	X			
Censen	*Centurio senex*	Phyllostomidae	X		X	X
Chiimp	*Chiroderma improvisum*	Phyllostomidae		X		
Corbre	*Cormura brevirostris*	Emballonuridae	X			X
Cynabr	*Cynomops abrasus*	Molossidae	X			
Cynpar	*Cynomops paranus*	Molossidae	X			
Cynpla	*Cynomops planirostris*	Molossidae	X			X
Cynspp	*Cynomops spp*	Molossidae			X	X

2.1.4. D

Code	BINOMIAL	Family	[AMB]	[LIN]	[NCA]	[SCA]
Dicalb	*Diclidurus albus*	Emballonuridae	X		X	X
Dicing	*Diclidurus ingens*	Emballonuridae	X			
Dicscu	*Diclidurus scutatus*	Emballonuridae	X			

2.1.5. E

Code	BINOMIAL	Family	[AMB]	[LIN]	[NCA]	[SCA]
Eptchi	*Eptesicus chiriquinus*	Vespertilionidae	X			X
Eptfur	*Eptesicus furinalis*	Vespertilionidae	X		X	X
Eptfus	*Eptesicus fuscus*	Vespertilionidae	X		X	X
Eptgua	*Eptesicus guadeloupensis*	Vespertilionidae		X		
Eptspp	*Eptesicus fuscus/guadeloupensis*	Vespertilionidae		X		
Eumaur	*Eumops auripendulus*	Molossidae	X		X	X
Eumgla	*Eumops glaucinus*	Molossidae	X		X	X
Eumhan	*Eumops hansae*	Molossidae	X		X	X
Eumund	*Eumops underwoodi*	Molossidae			X	X

2.1.6. F

Code	BINOMIAL	Family	[AMB]	[LIN]	[NCA]	[SCA]
Furhor	*Furipterus horrens*	Furipteridae	X			X

2.1.7. G

Code	BINOMIAL	Family	[AMB]	[LIN]	[NCA]	[SCA]

Glospp	*Glossophaginae spp*	Phyllostomidae	X	X	X	X

2.1.8. L

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Lasblo	*Lasiurus blossevillii*	Vespertilionidae	X		X	X
Lascin	*Lasiurus cinereus*	Vespertilionidae	X		X	X
Lasega	*Lasiurus ega*	Vespertilionidae	X		X	X
Lasegr	*Lasiurus egregius*	Vespertilionidae	X			X
Lasint	*Lasiurus intermedius*	Vespertilionidae			X	X
Lonaur	*Lonchorhina aurita*	Phyllostomidae	X		X	X
Loninu	*Lonchorhina inusitata*	Phyllostomidae	X			

2.1.9. M

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Macmac	*Macrophyllum macrophyllum*	Phyllostomidae	X		X	X
Molbar	*Molossus barnesi*	Molossidae	X			
Molmol	*Molossus molossus*	Molossidae	X	X	X	X
Molruf	*Molossus rufus*	Molossidae	X		X	X
Molsin	*Molossus sinaloae*	Molossidae	X		X	X
Monple	*Monophyllus plethodon*	Phyllostomidae		X		
Mormeg	*Mormoops megalophylla*	Mormoopidae	X		X	X
Myoalb	*Myotis albescens*	Vespertilionidae	X		X	X
Myoele	*Myotis elegans*	Vespertilionidae	X		X	X
Myokea	*Myotis keaysi*	Vespertilionidae	X		X	X

Myomar	*Myotis martiniquensis*	Vespertilionidae		X		
Myonig	*Myotis nigricans*	Vespertilionidae	X		X	X
Myorip	*Myotis riparius*	Vespertilionidae	X			X
Myosim	*Myotis simus*	Vespertilionidae	X			
Myospp	*Myotis dominicensis/martiniquensis/nigricans*	Vespertilionidae		X		
Myovel	*Myotis velifer*	Vespertilionidae			X	

2.1.10. N

Code	*BINOMIAL*	Family	[AMB]	[LIN]	[NCA]	[SCA]
Natmex	*Natalus mexicanus*	Natalidae			X	X
Natspp	*Natalus spp*	Natalidae	X			
Natstr	*Natalus stramineus*	Natalidae		X		
Nocalb	*Noctilio albiventris*	Noctilionidae	X		X	X
Noclep	*Noctilio leporinus*	Noctilionidae	X	X	X	X
Nyclat	*Nyctinomops laticaudatus*	Molossidae	X		X	X

2.1.11. P

Perkap	*Peropteryx kappleri*	Emballonuridae	X		X	X
Permac	*Peropteryx macrotis*	Emballonuridae	X		X	X
Pertri	*Peropteryx trinitatis*	Emballonuridae	X	X		
Phydsp	*Phyllostomidae spp*	Phyllostomidae	X		X	
Phylsp	*Phyllostomus spp*	Phyllostomidae	X		X	X

Procen	*Promops centralis*	Molossidae	X		X	X
Ptedav	*Pteronotus davyi*	Mormoopidae	X	X	X	X
Ptegym	*Pteronotus gymnonotus*	Mormoopidae	X		X	X
Ptep70	*Pteronotus personatus 70*	Mormoopidae	X			
Ptep80	*Pteronotus personatus 80*	Mormoopidae	X		X	X
Ptepar	*Pteronotus parnellii*	Mormoopidae		X	X	X
Ptepер	*Pteronotus personatus*	Mormoopidae	X			
Pter53	*Pteronotus rubigionosa*	Mormoopidae	X	X		
Pter59	*Pteronotus rubigionosa*	Mormoopidae	X	X		

2.1.12. R

Rhospp	*Rhogeessa spp*	Vespertilionidae	X		X	X
Rhynas	*Rhynchonycteris naso*	Emballonuridae	X		X	X

2.1.13. S

Sacbil	*Saccopteryx bilineata*	Emballonuridae	X		X	X
Saccan	*Saccopteryx canescens*	Emballonuridae	X			
Sacgym	*Saccopteryx gymnura*	Emballonuridae	X			
Saclep	*Saccopteryx leptura*	Emballonuridae	X		X	X
Stulil	*Sturnira lilium*	Phyllostomidae		X		
Stutho	*Sturnira thomasi*	Phyllostomidae		X		

2.1.14. T

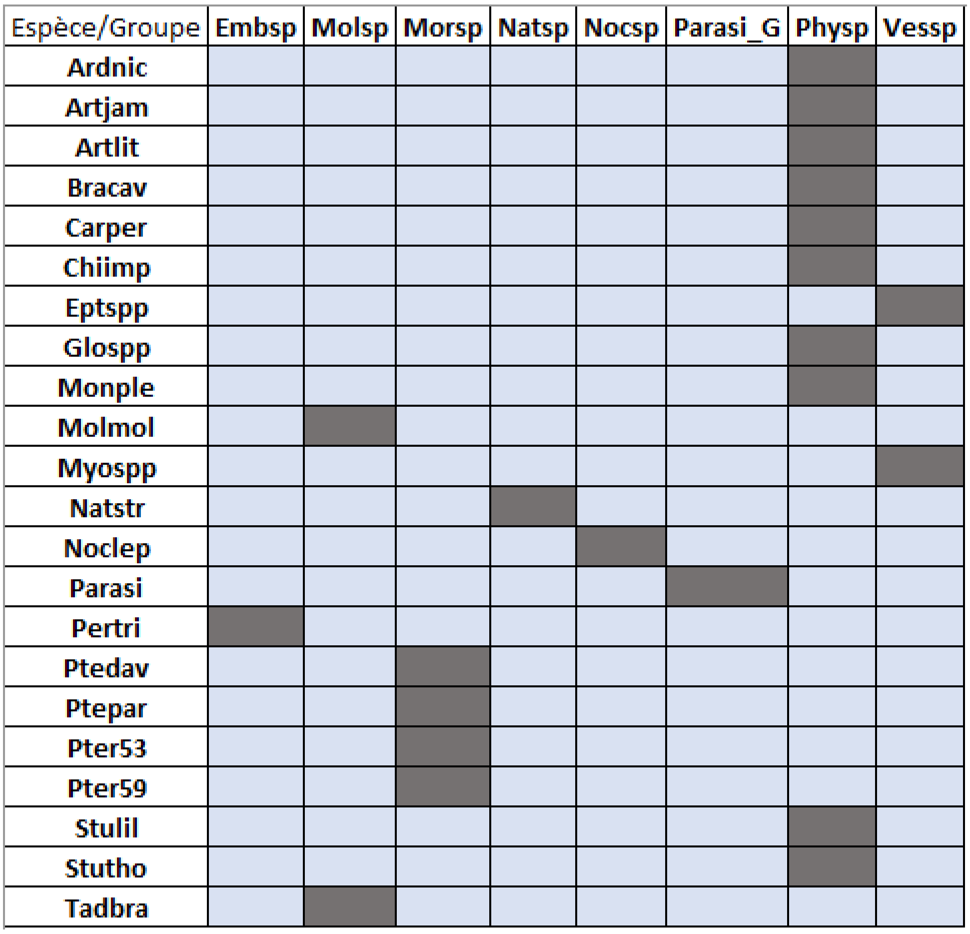
Tadbra	*Tadarida brasiliensis*	Molossidae	X	X	X	X
Thyspp	*Thyroptera spp*	Thyropteridae	X		X	X

2.2. Neotropical bat classifiers

2.2.1. RE, REtest2 - Reunion Island

In progress, no commercialisation planned.

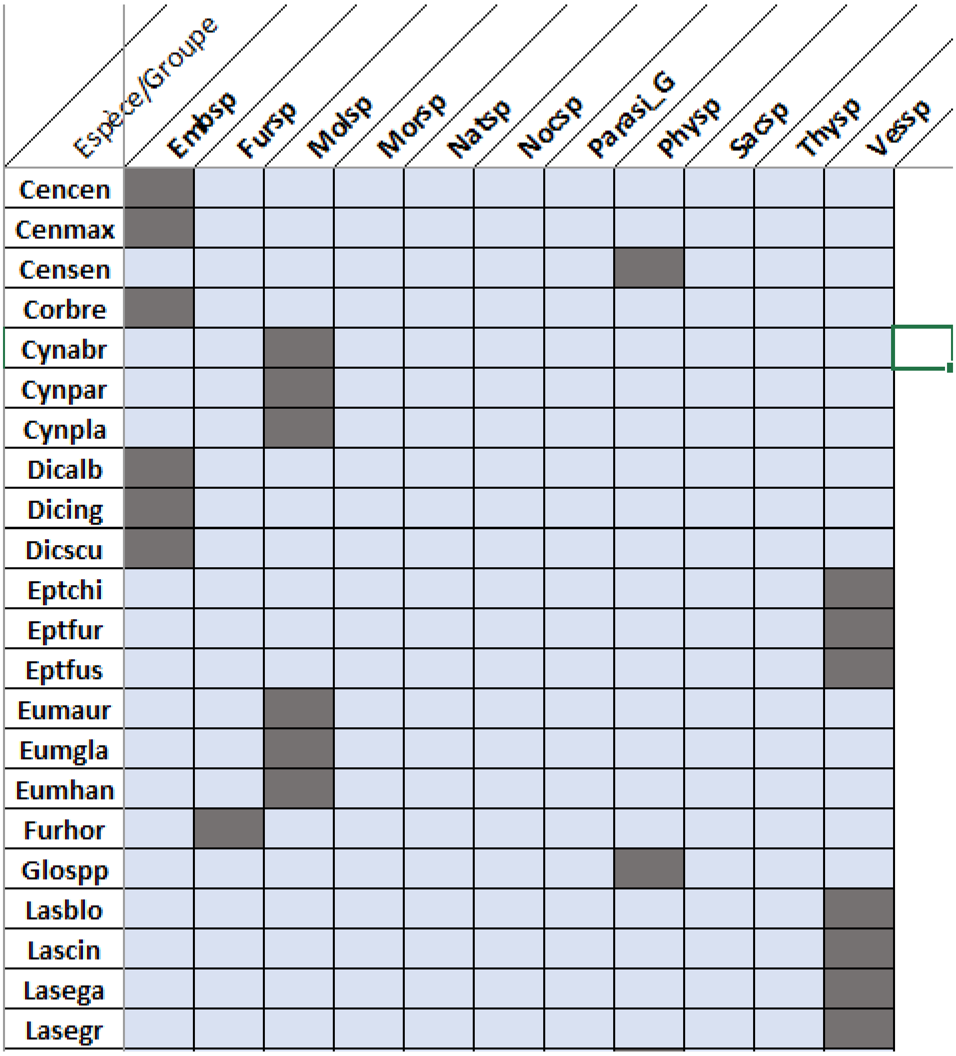
LIN - Lesser Indies



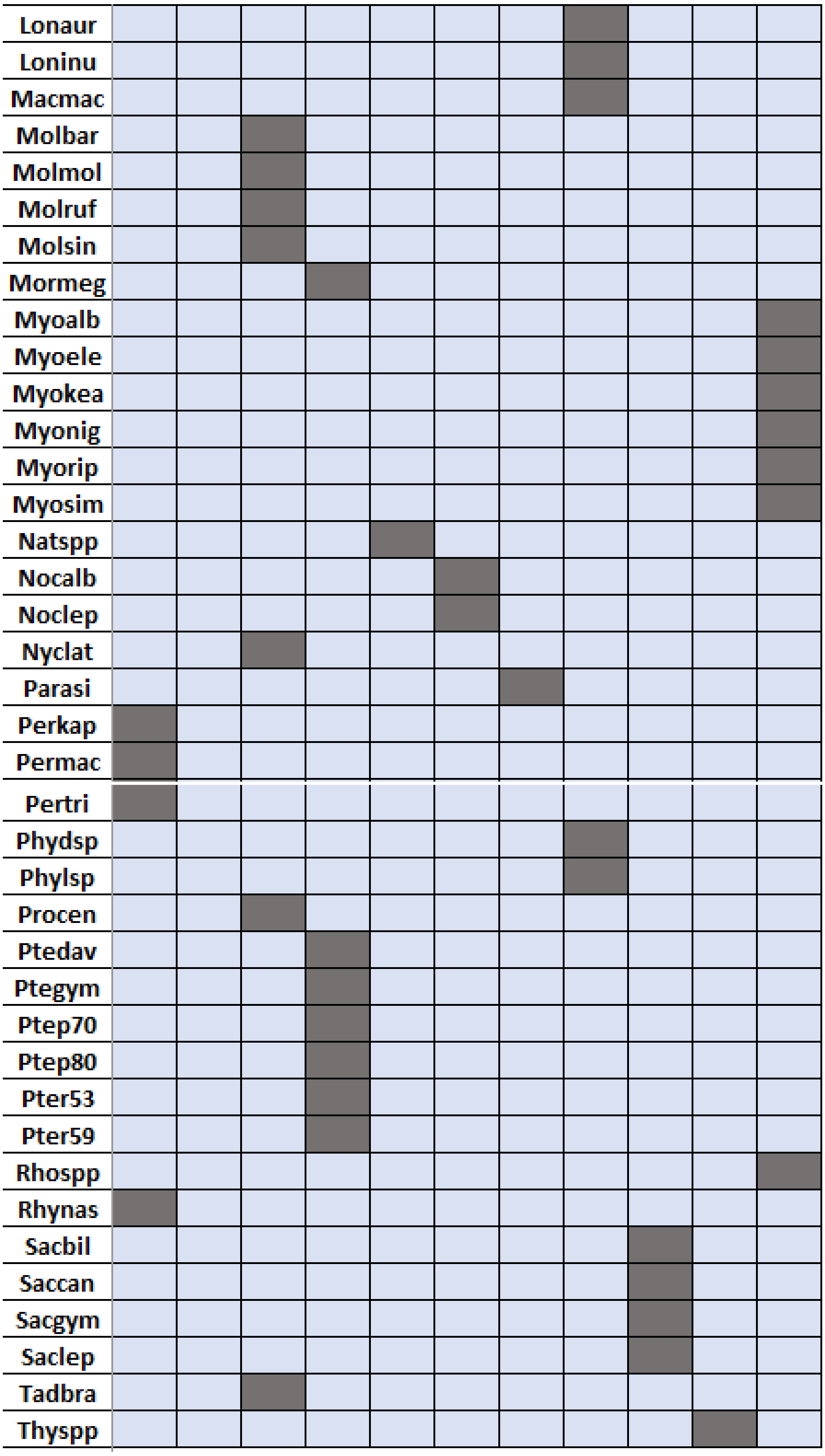
Espèce/Groupe	Embsp	Molsp	Morsp	Natsp	Nocsp	Parasi_G	Physp	Vessp
Ardnic							■	
Artjam							■	
Artlit							■	
Bracav							■	
Carper							■	
Chiimp							■	
Eptspp								■
Glospp							■	
Monple							■	
Molmol		■						
Myospp								■
Natstr				■				
Noclep					■			
Parasi						■		
Pertri	■							
Ptedav			■					
Ptepar			■					
Pter53			■					
Pter59			■					
Stulil							■	
Stutho							■	
Tadbra		■						

Species / Acoustic group connection

AMB - Amazonian Basin



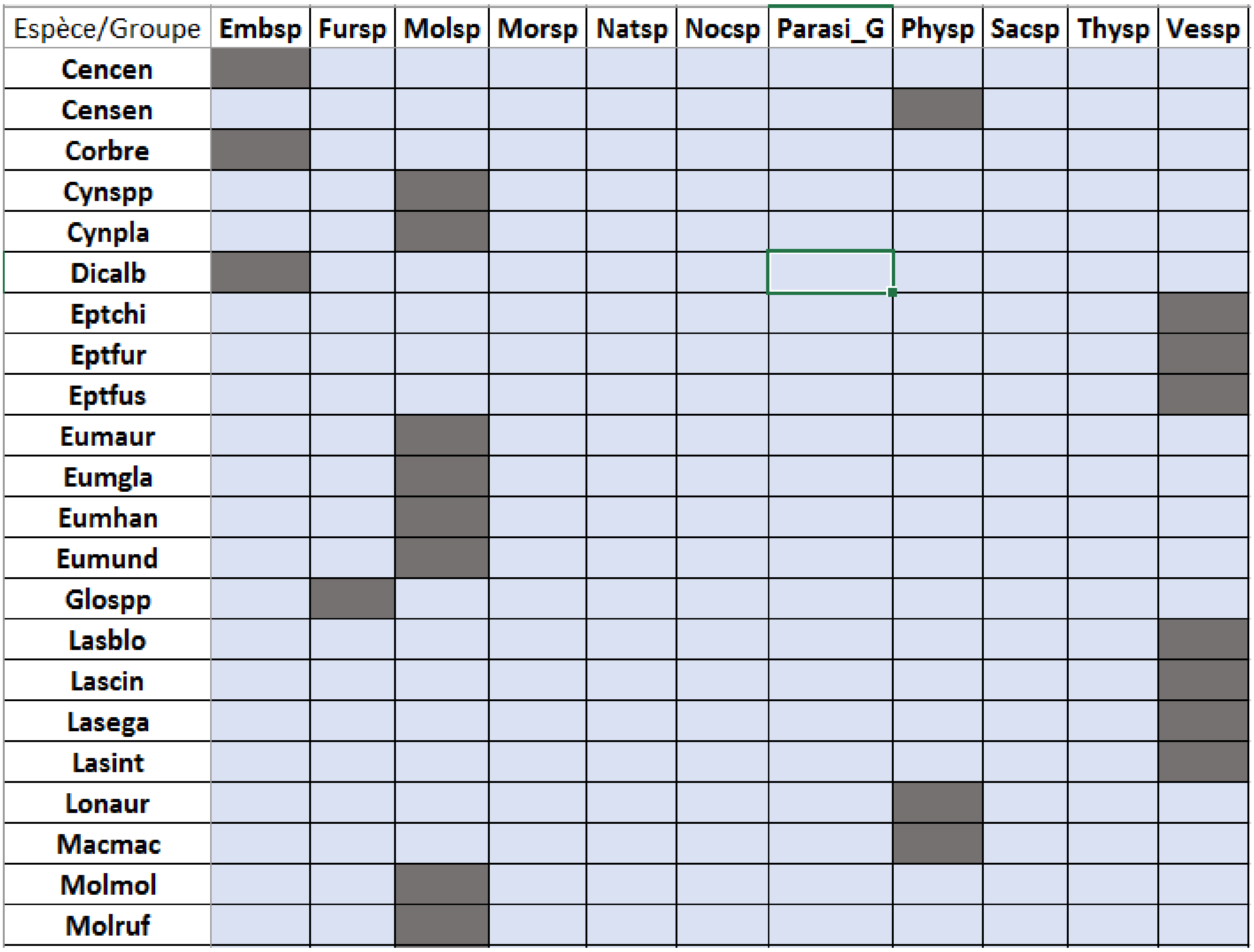
Espèce/Groupe	Embsp	Fursp	Molsp	Morsp	Natsp	Nocsp	Parasi_G	Physp	Sacsp	Thysp	Vessp
Cencen	■										
Cenmax	■										
Censen								■			
Corbre	■										
Cynabr			■								
Cynpar			■								
Cynpla			■								
Dicalb	■										
Dicing	■										
Dicscu	■										
Eptchi											■
Eptfur											■
Eptfus											■
Eumaur			■								
Eumgla			■								
Eumhan			■								
Furhor		■									
Glospp								■			
Lasblo											■
Lascin											■
Lasega											■
Lasegr											■



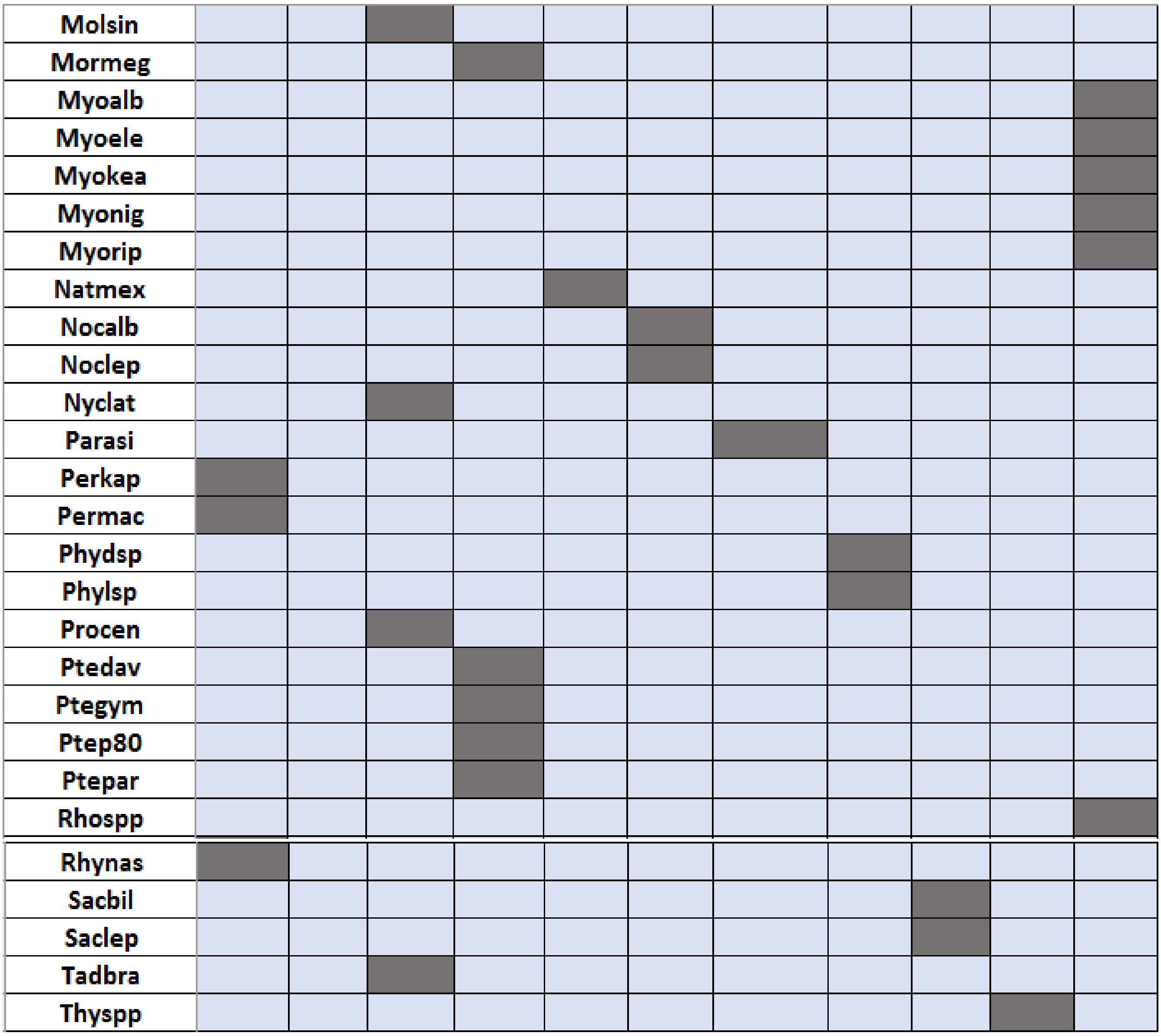
Lonaur								■			
Loninu								■			
Macmac								■			
Molbar			■								
Molmol			■								
Molruf			■								
Molsin			■								
Mormeg				■							
Myoalb											■
Myoele											■
Myokea											■
Myonig											■
Myorip											■
Myosim											■
Natspp					■						
Nocalb						■					
Noclep						■					
Nyclat			■								
Parasi							■				
Perkap	■										
Permac	■										
Pertri	■										
Phydsp								■			
Phylsp								■			
Procen			■								
Ptedav				■							
Ptegym				■							
Ptep70				■							
Ptep80				■							
Pter53				■							
Pter59				■							
Rhospp											■
Rhynas	■										
Sacbil									■		
Saccan									■		
Sacgym									■		
Saclep									■		
Tadbra			■								
Thyspp										■	

Species / Acoustic group connection

SCA - Southern Central America



Espèce/Groupe	Embsp	Fursp	Molsp	Morsp	Natsp	Nocsp	Parasi_G	Physp	Sacsp	Thysp	Vessp
Cencen	■										
Censen								■			
Corbre	■										
Cynspp			■								
Cynpla			■								
Dicalb	■										
Eptchi											■
Eptfur											■
Eptfus											■
Eumaur			■								
Eumgla			■								
Eumhan			■								
Eumund			■								
Glospp		■									
Lasblo											■
Lascin											■
Lasega											■
Lasint											■
Lonaur								■			
Macmac								■			
Molmol			■								
Molruf			■								



Molsin			■								
Mormeg				■							
Myoalb											■
Myoele											■
Myokea											■
Myonig											■
Myorip											■
Natmex					■						
Nocalb						■					
Noclep						■					
Nyclat			■								
Parasi							■				
Perkap	■										
Permac	■										
Phydsp								■			
Phylsp								■			
Procen			■								
Ptedav				■							
Ptegym				■							
Ptep80				■							
Ptepar				■							
Rhospp											■
Rhynas	■										
Sacbil									■		
Saclep									■		
Tadbra			■								
Thyspp										■	

Species / Acoustic group connection

2.2.2. NCA - Northern Central America

Espèce/Groupe	Embsp	Molsp	Morsp	Natsp	Nocsp	Parasi_G	Physp	Sacsp	Thysp	Vessp
Balio_	■									
Cencen	■									
Censen							■			
Cynspp		■								
Dicalb	■									
Eptfur										■
Eptfus										■
Eumaur		■								
Eumgla		■								
Eumhan		■								
Eumund		■								
Glospp							■			
Lasblo										■
Lascin										■
Lasega										■
Lasint										■
Lonaur							■			
Macmac							■			
Molmol		■								
Molruf		■								
Molsin		■								
Mormeg			■							
Myoalb										■
Myoele										■
Myokea										■
Myonig										■
Myovel										■
Natmex				■						
Nocalb					■					
Noclep					■					
Nyclat		■								
Parasi						■				
Perkap	■									
Permac	■									
Phydsp							■			
Phylsp							■			
Procen		■								
Ptedav			■							
Ptegym			■							
Ptep80			■							
Ptepar			■							
Rhospp										■
Rhynas	■									
Sacbil								■		
Saclep								■		
Tadbra		■								
Thyspp									■	

Species / Acoustic group connection