

*TETTRIs*

*Transforming European Taxonomy through Training, Research, and Innovations*

## **Deliverable 6.2**

# **Free, user-friendly web-platform for integrative species delimitation analyses, inc. video tutorials**

WP 6/MNHN

**Document:** Deliverable  
**Version:** v.03  
**Date:** 24/05/2024

Date: 24/05/2024 1 / 12 Doc version: v03

## TETTRIs related product

| Identification              | Value  |
|-----------------------------|--|
| Title                       | D6.2 - Free, user-friendly web-platform for integrative species delimitation analyses, inc. video tutorials            |
| Author(s)                   | Teddy Bruy, Aurélien Miralles, Tony Robillard Magalie Castelin, Nicolas Puillandre, Julie Bouché, Benoit Fauvet-Messat |
| Affiliation                 | MNHN   |
| Contributors (Affiliation)  |  |
| Publisher                   | CETAF  |
| Identifier of the publisher |  |
| Doc. Version                | v01  |
| Resource                    | Report   |
| Publication year            | 2024   |
| Sensitivity                 | Low – Public document  |
| Date                        | 02/05/2024   |
| Citation                    |  |

### Abstract:

This document introduces the Spart explorer web platform developed under Task 6.3. This tool enables integrative species delimitation analyses through a free, user-friendly web platform. Species hypothesis can be inferred from a DNA alignment in FASTA format using ASAP or ABGD methods. Limes then compares the different partitions qualitatively and associates them with a score independently of the method used. Last but not least, Spart explorer lets you graphically visualise results, whether generated or imported from pre-existing data. In this document, we present several screenshots showing the graphical user interface and the various options available, as well as a link to a video which has the same purpose. We conclude by mentioning the limitations and prospects for improvement of this web platform.

### Keywords:

Species delimitation, species delimitation workflow, integrative species delimitation, integrative taxonomy, use-friendly web-platform, Spart explorer, ABGD, ASAP, Limes, Spartviewer, species hypothesis, partition.

| Settings                 | Value  |
|--------------------------|--|
| <b>DELIVERABLE</b>       |  |
| Deliverable title:       | Free, user-friendly web-platform for integrative species delimitation analyses, inc. video tutorials |
| Deliverable n°:          | D6.2   |
| <b>WORK PACKAGE</b>      |  |
| Work Package             | 6  |
| Work Package Leader      | MeiseBG  |
| Task                     | T6.3   |
| Task Leader              | MNHN   |
| Type:                    | Document   |
| Lead beneficiary:        | MNHN   |
| Citation:                | ORCID:   |
| Due date of deliverable: | 31/05/2024   |
| Actual submission date:  | 31/05/2024   |
| Deliverable status:      | Submitted  |

### Document Control Information

| Settings                 | Value  |
|--------------------------|--|
| Document Title:          | 6.2 Free, user-friendly web-platform for integrative species delimitation analyses, inc. video tutorials                     |
| Project Title (Acronym): | TETTRIs  |
| Document Owners:         | Teddy Bruy, Aurélien Miralles, Tony Robillard<br>Magalie Castelin, Nicolas Puillandre, Julie Bouché,<br>Benoit Fauvet-Messat |
| Project Coordinator      | Technical Coordinator, CETAF<br>Financial Frederik Hendrickx , RBINS   |
| Doc. Version:            | v03  |
| Sensitivity:             | Public   |
| Date:                    |  |

### Document Approver(s) and Reviewer(s):

NOTE: All Approvers are required. Records of each approver must be maintained. All Reviewers in the list are considered required unless explicitly listed as Optional.

| Name           | Role     | Institution | Action   | Date       |
|----------------|----------|-------------|----------|------------|
| Peter Warth    | Reviewer | SMNS        | Review   | 14/05/2024 |
| Carl Vangestel | Reviewer | RBINS       | Review   | 14/05/2024 |
| Teddy Bruy     | Author   | MNHN        | Review   | 24/05/2024 |
| Ana Casino     | Approver | CETAF       | Approved | 31/05/2024 |

### Document history:

The Document Author is authorised to make the following types of changes to the document without requiring that the document be re-approved:

- Editorial, formatting, and spelling
- Clarification

To request a change to this document, contact the Document Author or Owner. Changes to this document are summarised in the following table in reverse chronological order (latest version first).

Date: 24/05/2024 3 / 12 Doc version: v03

| Revision | Date       | Created by                   | Short Description of Changes |
|----------|------------|------------------------------|------------------------------|
| v01      | 02.05.2024 | Teddy Bruy                   | Final Draft                  |
| v02      | 14.05.2024 | Peter Warth & Carl Vangestel | Comments                     |
| v03      | 24.05.2024 | Teddy Bruy                   | Adoption of Comments         |
|          | 31.05.2024 | Ana Casino                   | Approved                     |

**Configuration Management: Document Location**

The latest version of this controlled document is stored in [location](#)

## Table of contents

|  |           |
|--|-----------|
| <b>Table of contents</b>               | <b>5</b>  |
| 1. Introduction                        | 6         |
| 2. Tools                               | 6         |
| 2.1 ABGD                               | 6         |
| 2.2 ASAP                               | 7         |
| 2.3 LIMES                              | 7         |
| 2.4 Visualisation (with Spartviewer)   | 7         |
| 2.5 Data file formats                  | 7         |
| 3. Screenshots                         | 7         |
| 4. Perspective and future developments | 12        |
| <b>APPENDIX 1</b>                      | <b>12</b> |
| <b>REFERENCES:</b>                     | <b>12</b> |

## 1. Introduction

Over the past few years, the supply of bioinformatics tools for alpha-taxonomic research has exploded, demonstrating that the discipline is now well on the way to its digital transition. However, much remains to be done to facilitate dialogue between the multiple species delimitation approaches available and the heterogeneous types of data they mobilise. As a first step in this direction, we developed Spart explorer, a user-friendly web platform dedicated to integrative species delimitation.

Spart explorer is a user-friendly tool which infers species hypotheses based on DNA sequences, using two popular species delimitation tools, ABGD and ASAP. The platform also implements LIMES, which can compare different partitions. Species partitions obtained on the platform or uploaded from local files can then be compared in a dynamic and intuitive graphic representation (Spartviewer), associated to a phylogenetic tree, to facilitate result interpretation and comparison in an integrative taxonomy framework.

The flexibility of Spart explorer allows it to perform different workflows, independently from each other or combined. The most basic workflows enable for instance exploratory species delimitation from mitochondrial sequence alignment (with ABGD and/or ASAP), and the visualisation of the results obtained ; the visualisation and statistical comparisons of partitions inferred from other delimitation tools (multilocus molecular delimitation, morphological delimitation, or partitions illustrating, for example, the species classification currently accepted by the community); or the online conversion between Spart and SpartXML species partition format. Finally, all these functionalities can be combined along a same integrated operational workflow.

The platform will be open to the public very shortly. The link is as follows: <https://spartexplorer.mnhn.fr/>

## 2. Tools

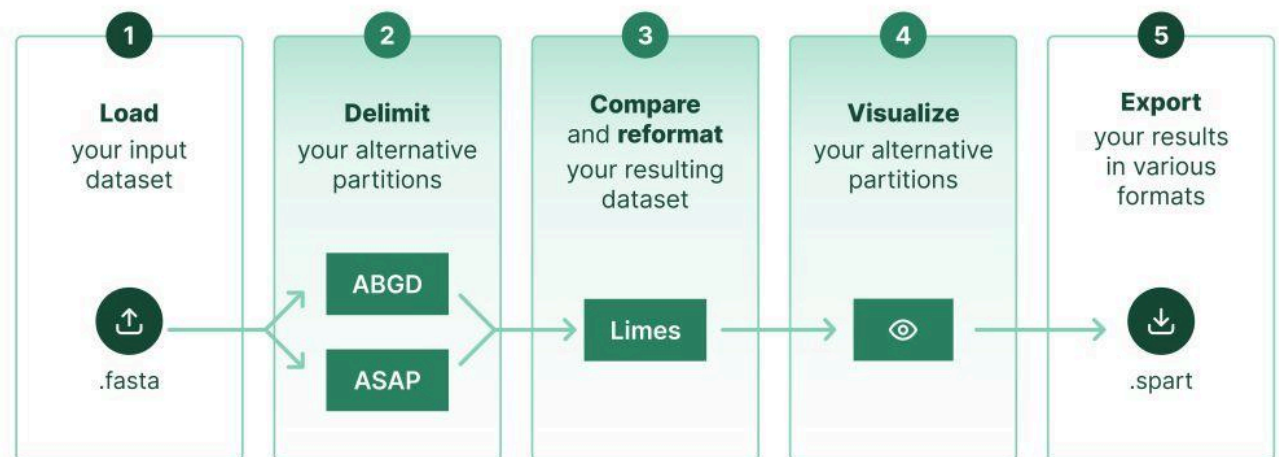


Figure 1: overview of the Spart explorer processing chain

### 2.1 ABGD

ABGD (Automatic Barcode Gap Discovery, Puillandre et al. 2012) is a fast, simple method to split a sequence alignment data set into species hypotheses. The method uses a distance threshold estimated from the distribution of genetic distances between specimens from the same species (intraspecific diversity) and from different species (interspecific diversity).

Date: 24/05/2024 6 / 12 Doc version: v03

## 2.2 ASAP

ASAP (Assemble Species by Automatic Partitioning, Puillandre et al. 2020) implements a hierarchical clustering algorithm that only uses pairwise genetic distances, thus avoiding the computational burden of phylogenetic reconstruction, to propose species hypotheses. ASAP proposes species partitions ranked by a scoring system that uses no biological prior insight of intraspecific diversity.

## 2.3 LIMES

LIMES (Ducasse et al. 2019) is an automatic calculation tool which qualitatively compares species partitions obtained by distinct SD approaches, regardless of their respective theoretical backgrounds, and even in absence of reference topology. LIMES can also merge, extract and export SPART files.

## 2.4 Visualisation (with Spartviewer)

Spartviewer is the very first tool for automatic visualisation of species partitions, developed as part of the present project. Several alternative species partitions can be simultaneously visualised through a segmented bar chart produced by SpartViewer. In these representations, now commonly used in the literature, each segmented and multicoloured vertical bar represents a possible partition of the whole dataset of individuals staked as a column, of which each segment represents a distinct subset, i.e. a primary species hypothesis. SpartViewer has been designed to enable "at-a-glance" the comparison of alternative partitions which are aligned side by side. The algorithm will always assign the same colour to subsets inferred identically in two or more partitions (i.e. those subsets that show the same exact content in individuals), although a same subset colour in two or more alternative partitions does not necessarily mean that these subsets are identical, even if they present similarities (for instance, if one is including the other).

## 2.5 Data file formats

Spart explorer manages .fasta input files (sequence alignment) and produces standard species partition files (.spart, .spartXML) as output (Miralles et al. 2022).

# 3. Screenshots

Several logos were developed and presented at the TETTRIs All Hands Meeting in January 2024. The one selected (Figure 2) features a magnifying glass, in reference to research. The roundness of the typography symbolizes the living world. We also decided to use the color palette used for TETTRIs (#216114A, #7AC1DC, #FF8E3E).



Figure 2: Spart explorer logo


On the Spart explorer homepage (Figure 3), two options are displayed. On the one hand, "Delimitation" to import DNA alignments in a fasta file for species delimitation analyses purposes. On the other hand "Visualisation and comparison" with the possibility to import partitions from previous analyses, including the possibility to use a dataset from multiple DNA markers data, morphological data, geographical data, etc.

## Spart explorer

### A taxonomic web platform to infer, compare and visualise species partitions

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Integer ultricies justo nec sagittis venenatis. Sed sit amet tincidunt sapien. Vivamus interdum auctor ex nec pulvinar. Ut placerat id turpis a dignissim. Morbi sed iaculis augue, et faucibus quam. Nulla dignissim massa et velit volutpat orci.


#### Delimitation



Delimit aligned DNA sequences into candidate species

[Let's go →](#)

#### Visualisation and comparison



Visualise, merge and compare various species partition file

[Let's go →](#)

#### Tools used in Spart Explorer

##### ABGD

ABGD (Automatic Barcode Gap Discovery) is a fast, simple method to split a sequence alignment data set into candidate species that should be complemented with other evidence in an integrative taxonomic approach.

##### ASAP

ASAP (Assemble Species by Automatic Partitioning) is a method to build species partitions from single locus sequence alignments. ASAP is the implementation of a hierarchical clustering algorithm that only uses pairwise genetic distances, avoiding the computational burden of phylogenetic reconstruction. Importantly, ASAP proposes species partitions ranked by a new scoring system that uses no biological prior insight of intraspecific diversity.

##### Limes

LIMES is an automatic calculation tool which qualitatively compares species partitions obtained by distinct SD approaches, regardless of their respective theoretical backgrounds, and even in absence of reference topology. The program implements four different previously published indexes, and allows their automated calculation.

[Contact us](#)
[Terms of Use](#)
[Privacy policy](#)
[Legal notice](#)








Figure 3: Spart explorer homepage

Once the delimitation option has been selected, you can import a fasta file containing aligned sequences. It will then be possible to choose the tool used (ASAP or ABGD) and an advanced choice of parameters (Figure 3). The option of being notified by email has been added in the event of analyses of large datasets that may take a long time to complete. However, our experience shows that even for thousands of sequences, results are quite rapid.



## Délimitation

### Choose a file

Drag a file here to upload or

sequence.fast

This is a MEGA CSV distance file

### Choose a tool

ABGD  ASAP

Advanced options

Select the substitution model to compute the distances:

Jukes-Cantor(JC69)
  Kimura (K80)
  Simple Distance (p-distances)

**ABGD Options**

X

Relative gap width

Minimal a priori value - Pmin

Maximal a priori value - Pmax

Number of steps in [Pmin,Pmax]

Number of bins

for distance distribution

**ASAP Options**

Split groups below this probability

Number of best scores

Fixed seed value

If you don't want to use a fixed seed value, leave -1

### Restitution

If you load a large amount of data, your results may take time to display.

Notify me by email when my results are ready

\*Mandatory fields

→

Figure 3: Userflow delimitation input

Graphical representations of the analysis results can then be used to highlight the most coherent partition (figure 4). In addition, tables display the ten best partitions generated for each method. These include the number of subsets per partition and offer the option of downloading details in Spart format.

Please quote the Spart Explorer platform and the ABGD tool in your publications. [Learn more](#)

## Delimitation results

[← Visualize and compare →](#)


Figure 4: Userflow delimitation output

Finally, SpartViewer allows users to visualize and compare the different partitions (Figure 5) either from the scores generated on the platform, or by importing them. Several manipulations are available making the platform user-friendly, such as:

- Filter by source (ABGD, ASAP...)
- Sort by number of subsets or by score value
- Reset to the standard settings

Date: 24/05/2024 10 / 12 Doc version: v03

- Add or delete partition
- move a partition (column) using mouse
- Download the visualisation



Figure 5: SpartViewer userflow delimitation output

At the top of the page, we've added a tab with a general presentation of the tool, as well as a link to a FAQ giving users the possibility of an independent usage of Spart explorer. At the bottom of the page, links to contact information and RGPD information have been included.

A video has been recorded (available [here](#)) showing the operability of the platform through:

1. the homepage, including the introduction of the tool and the general process
2. the settings of the delimitation tools
3. the execution of the tools and delimitation results (including the associated credits and the download option of the generated files)
4. the editorial and FAQ pages

Date: 24/05/2024 11 / 12 Doc version: v03

## 4. Perspective and future developments

Spart explorer provides an entirely operable tool that serves the needs of the community and fully encompasses the promises made in the grant agreement. Although providing fully operational workflows, it represents a proof-of-concept offering only a very small glimpse of the potential offered by online species delimitation workflows. Implementation of other molecular species delimitation methods would be the most obvious improvements, but many other functionalities are also conceivable at every stage of the pipeline. In a second step, upstream applications might for instance be developed to allow interoperability with pre-existing databases (ex. to search and import sequences from existing repositories) or to prepare data (ex. alignment tools). More interestingly are downstream applications facilitating interpretations of the results under various contexts. This may for instance consist in tools allowing comparisons of alternative partition hypotheses by plotting them on other datasets, such as geographic distribution maps, phased haplotype networks or morphological datasets. Others applications might even intervene later, at the very end of the process, to facilitate the work of formal species description, either in extracting diagnostic molecular or morphological traits (by combining species partition and "specimen/character" morphological matrix), or in providing intra- and interspecific p-distances statistics for each delimited subsets. Examples of extension are in fact so numerous and variable according to the approach used or taxa studied that it is virtually impossible to anticipate them all.

## APPENDIX 1

| ID | Reference or Related Document      | Source or Link/Location |
|----|------------------------------------|-------------------------|
| 1  | SpartExplorer Video                | <a href="#">LINK</a>    |
| 2  | ASAP video tutorial                | <a href="#">LINK</a>    |
| 3  | ABGD video tutorial                | <a href="#">LINK</a>    |
| 4  | LIMES video tutorial               | <a href="#">LINK</a>    |
| 5  | SpartExplorer website              | <a href="#">LINK</a>    |
| 6  | Puillandre <i>et al.</i> 2024 book | <a href="#">LINK</a>    |

## REFERENCES:

Ducasse, J., Ung, V., Lecointre, G., Miralles, A. (2020). LIMES: a tool for comparing species partition. *Bioinformatics*, 36, 2282–2283.

Puillandre, N., Brouillet, S., & Achaz, G. (2021). ASAP: assemble species by automatic partitioning. *Molecular Ecology Resources*, 21(2), 609-620.

Puillandre, N., Lambert, A., Brouillet, S. & Achaz, G. (2012) ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology*, 21, 1864–1877.

Puillandre, N., Miralles, A., Brouillet, S., Fedosov, A., Fischell, F., Patmanidis, S. & Vences, M. (2024) Species delimitation and exploration of species partitions with ASAP and Limes. In *DNA Barcoding: Methods and Protocols* (pp. 313-334). New York, NY: Springer US.

Miralles, A., Ducasse, J., Brouillet, S., Flouri, T., Fujisawa, T., Kapli, P., Knowles, L. L., Kumari, S., Stamatakis, A., Sukumaran, J., Lutteropp, S., Vences, M., & Puillandre, N. (2022). SPART: A versatile and standardized data exchange format for species partition information. *Molecular Ecology Resources*, 22, 430–438.

Date: 24/05/2024 12 / 12 Doc version: v03