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SPARTEXPLORER

EXPLORE SPECIES PARTITIONING ON A SINGLE-LOCUS DATASET IN JUST A FEW CLICKS

TETTRIs

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Target group

The user spectrum includes integrative taxonomists, phylogenetists and molecular ecologists.

Goal

To develop a user-friendly web platform that facilitates integrative **species delimitation** by enabling researchers to efficiently explore, compare, and interpret multiple lines of evidence within a **unified interface**.

Summary/Description

SPART EXPLORER is a user-friendly web platform intended to enable quick and easy online exploration of the **various possible competing species partitions hypotheses**. This first version implements two popular delimitation tools for single locus dataset (ABGD and ASAP), and provides an innovative graphic interface allowing visual and statistical comparisons of alternative species partitions.

SOILMATS course | Photo by Iasmi Stathi

You Will Need

- A **single-locus DNA** alignment in fasta to be analysed by ASAP and/or ABGD
- Optionally, the **visualisation interface** also allows users to complement the set of ABGD and/or ASAP species partitions by uploading additional spart files (for instance obtained from other delimitation tools exporting results in spart files, or created by hand). To be compatible, these complementary spart files must present the same characteristics as those previously inferred (i.e. same number of individuals with identical identifiers).

A web platform: SPART EXPLORER is accessible at https://spartexplorer.mnhn.fr/. All its functionalities are free of charge and do not require the creation of a login account. All analyses launched have a unique url, valid for one month by default, but automatically renewed after each new access, therefore enabling users to return to the latest analysis status, whatever its state of progress. Users can also be notified by email in the event of analyses of large datasets that may take a long time to complete.

Steps to implement the Course

1 Open your browser and go to https://spartexplorer.mnhn.fr/.

2 Click on the button « let’s go » (Delimitation).

3 Upload your aligned fasta. file.

4 Choose a delimitation tool (ASAP and/or ABGD), with parameters by default or advanced options.

5 Click on « confirm » to launch the analysis.

6 Visualize your results, compare the alternative partitions inferred with the indexes calculated by LIMES and through an interactive graphical interface.

7 Export your results through various formats (species partitions in .spart, graphics in .svg and .png, and other kinds of results in .txt).

8 Optionally, you can load complementary .spart partitions at this stage to compare them with the newly inferred ones.

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Timeframe

The whole process usually takes **1 – 3 minutes**, depending on how heavy your dataset is.

Estimated Budget (Indicative)

The service is free of charge.

What went well / Even better if

If you notice any bugs or if you have any suggestion to improve the platform, please report them.

- via e-mail to amiral@mnhn.fr puillandre@mnhn.fr

Outputs and Indicators

You now possess one or several preliminary species partitions that provide support for evaluating your species hypotheses using an integrative approach.

Photo by Iasmi Stathi

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