## Instructions for abstract submission on ARPHA Conference Abstracts (ACA) platform

1. Prepare your abstracts in any text editor you like but follow these guidelines:
   - The abstract should be in English.
   - The abstract should be up to a maximum of **250 words** (without title and authors);
   - The abstract is concise and may contain the following information:
     o the reason(s) for the research;
     o the research method;
     o main results;
     o the significance of the results in relation to the reason(s) for the research;
     o possible applications of the results or advice for follow-up research.
   - The ACA platform offers many fields to fill in besides the abstract itself. We ask you to fill in at least the following fields:
     o Title (add if it is a 'Poster' or 'Oral' presentation)
     o Author(s)
     o Keywords
     o Presenting author
     o Presented at
     o Affiliation(s) (to be filled in on your ARPHA-profile page; see point 3)
   - The abstract should not contain references, figures or tables, neither should you upload supplementary files;
   - A maximum of 5 keywords is allowed.
   - In the field 'Presented at', you fill in: "11th International Dormouse Conference (May 9-13, 2022)"

   See the appendix for an example of an abstract published on ACA.

2. To submit the abstract, go to the Dormouse Conference Collection on the ACA website: https://aca.pensoft.net/collection/212/

3. Register or log in on the website. If you don't have an account for ACA yet, you find instructions for registration here:
   https://arphahub.com/manual#CreatenewARPHAaccount

4. Click the **Start new Abstract** button in the top right corner of the page.

5. You will be redirected to your manuscript, where you can add co-authors, text, keywords, references or any other necessary element from the options in the left-hand menu. Start writing.
   Note: Use the Tips and Tricks concise guide, if needed, or contact the ACA editorial office via the Helpdesk button.

6. Select a relevant conference collection from the **Collections** button located in the top menu.
   *Note: Please select "**The 11th International Dormice Conference**" from the dropdown list.*

Collections button
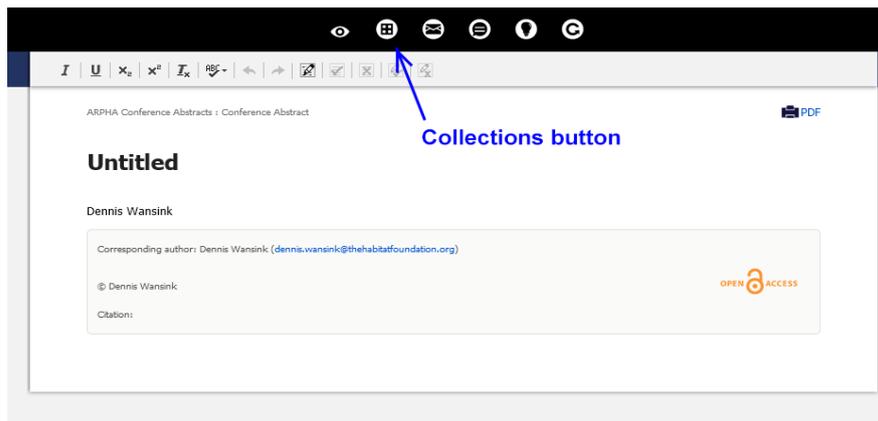
7. When ready, click the **Validate** button at the bottom of your screen.
   Note: At this step, an automated technical check will run through your submission and alert you if there are any mandatory elements missing.
   Note: If the system finds some technical problems in your manuscript, a pop-up window will show you each issue encountered. Please click on the links for each error and the system will guide you to the relevant place, where the issue should be addressed.

8. Once you have resolved all issues (if any) and the technical validation is successfully completed, click the **Submit for technical review** button, which will have appeared at the bottom of your screen.
   Note: At this step, your manuscript will be sent to the conference organisers or the respective session convener for approval.

9. An email will notify you about the reviewer's decision. If the manuscript is **returned for correction**, you will have to address the issues and re-submit for technical review.
   Note: The manuscript can go through a few technical review rounds before it is approved for submission.

10. When your manuscript is **approved** for submission by the reviewers, click the **Submit to** the journal button, which will have appeared at the bottom of your screen.
    Note: Please carefully go through the submission screens, providing the requested information to finalise your submission.
    Note: When asked about the article processing charges, you have to select the following option: "I have a special agreement via direct contact with the journal prior to submission to receive a full or partial fee waiver for this submission" and indicate in the free text field the name of the collection: 'The 11th International Dormice Conference'. You will find details on the process [here](#).

11. Click Finish on the last submission screen.

Congratulations, your abstract is now successfully submitted to ACA!

IMPORTANT: To revisit your unfinished submission(s), please log in through the ARPHA Writing Tool (https://arpha.pensoft.net/) and click the **See more** button. You will be redirected to a dashboard where you can see all your recent manuscripts and their current status.

Appendix Example of an abstract on ACA

Title: Establishment of a national monitoring program based on environmental DNA for amphibians and the chytrid fungus *Batrachochytrium dendrobatidis* (Poster)

Authors: Omneya Ahmed Osman, Johan Andersson, Tomas Larsson, Mats Töpel, Alexander Eiler

Abstract

National monitoring programs provide the basis for evaluating the integrity of ecosystems, their responses to disturbances, and the success of actions taken to conserve or recover biodiversity. In this study, we successfully established a national program for the invasive chytrid fungus *Batrachochytrium dendrobatidis* (Bd) based on dual TaqMan assays. Amphibian diversity based on metabarcoding of the mitochondrial 12S rRNA gene was also performed. Assays were optimized for sensitive detection of target species from a wide range of amphibian ponds with variable potential of inhibitions for eDNA based detection. An amphibian mock community of 5 species was used to validate the metabarcoding approach while internal standards were used in the case of the dual TaqMan assays. First sampling of over 170 ponds in Norway resulted in Bd detection in 12 environmental samples and one swab sample taken over multiple years indicating the establishment of Bd in Norway. Five amphibian species *Bufo bufo, Lissotriton vulgaris, Triturus cristatus, Rana arvalis* and *Rana temporaria* as predicted from data in long-term citizen science reporting systems were widely detected in the collected eDNA samples. Our large scale-monitoring program indicates a low risk of a Bd outbreak and amphibian decline caused by chytridiomycosis but continued monitoring is recommended in the future. These findings indicate that eDNA is an effective method to detect invasive species, and to monitor endangered amphibian species. Still, several shortcomings (such as PCR inhibitors and sample volume) were identified that need to be addressed to improve eDNA-based monitoring at the national level.

Keywords

chytridiomycosis, TaqMan assay, metabarcoding

Presenting author

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