



Conference Abstract

Challenges in data analyses and data storage for metabarcoding

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Received: 02 Mar 2021 | Published: 04 Mar 2021

Citation: Fontaneto D, Franc A (2021) Challenges in data analyses and data storage for metabarcoding. ARPHA Conference Abstracts 4: e65361. <https://doi.org/10.3897/aca.4.e65361>

Abstract

The working group of the DNAquanet COST Action dealing with data analyses and data storage for the use of metabarcoding approaches in biodiversity assessment, namely Working Group 4, had two main goals. On the one hand the comparison of the available analytical pipelines, while keeping track of new advances in bioinformatics, and on the other hand to deal with potential issues in data storage and sharing in the era of big data. Such activities were carried out through discussions at meetings of the COST Action, organisations of workshops, online surveys, and meta-analyses. The main achievements of the first line of activity, comparing pipelines, will be summarised in the first of the talks of the session, dealing with differences in clustering algorithms to obtain clusters of sequences that are then used for subsequent analyses and inference. The other talks in the session will introduce different pipelines and approaches that are currently developed to improve the way biological monitoring can be performed. The main achievement of the second line of activity, on data storage and sharing, will be summarised in the first flash talk of the session, dealing with the current scenario and potential pitfalls related to sharing the raw data from massive sequencing. The other flash talks in the session will provide examples on the applications of different approaches to analyse biodiversity using DNA sequence data. We are confident that the pluralism in approaches and applications that will be presented in the session will provide supporting discussions and interactions for a convergence towards the optimisation of the pipelines and the best use of data from metabarcoding.

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Presented at

1st DNAQUA International Conference (March 9-11, 2021)