

'ABACUS' – a cloud-based tool for standardising marine biological data recording



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Introduction

Many thousands of marine biological samples are collected and analysed on an annual basis to satisfy statutory monitoring commitments (e.g. Water Framework Directive (WFD), Habitats Directive) and conditions of licences granted for marine activities. These include seabed samples that undergo macrobenthic, particle size distribution and chemical analysis, water samples analysed to monitor planktonic communities and scientific trawl samples to assess fish and other mobile species. Despite the requirement for these analytical processes to be conducted by laboratories participating in recognised quality control schemes (e.g. the NE Atlantic Marine Biological Quality Control (NMBAQC) scheme) and in line with best practice guidance (Worsfold et al. 2010, Mason 2016, Turner et al. 2016), there remain fundamental issues surrounding the recording of non-standardised marine biological data. These issues stem from inter-analyst and inter-laboratory variability in sample analysis methodologies, recording practices, species naming, the use of taxonomic qualifiers and so on. This is thought to be the root cause for widespread mis-interpretation of trends in marine biological communities which, in some cases, can have serious consequences for both Statutory Nature Conservation Bodies (SNCBs) and private sector organisations legally obligated to conduct robust marine ecological monitoring.

This is aptly demonstrated by the contrasting results presented in Figure 1. Drawing conclusions based on the non-standardised data would lead one to believe that there were clear and statistically significant differences between the species composition between years (demonstrated by the lack of overlap of points for each year).

However, when considering the correctly standardised dataset it is clear there was little difference between years (demonstrated by the overlap of points for each year). This type of oversight could potentially have severe consequences for private sector organisations planning marine developments / activities and for regulatory bodies with legal duties to detect and report impacts on protected features.

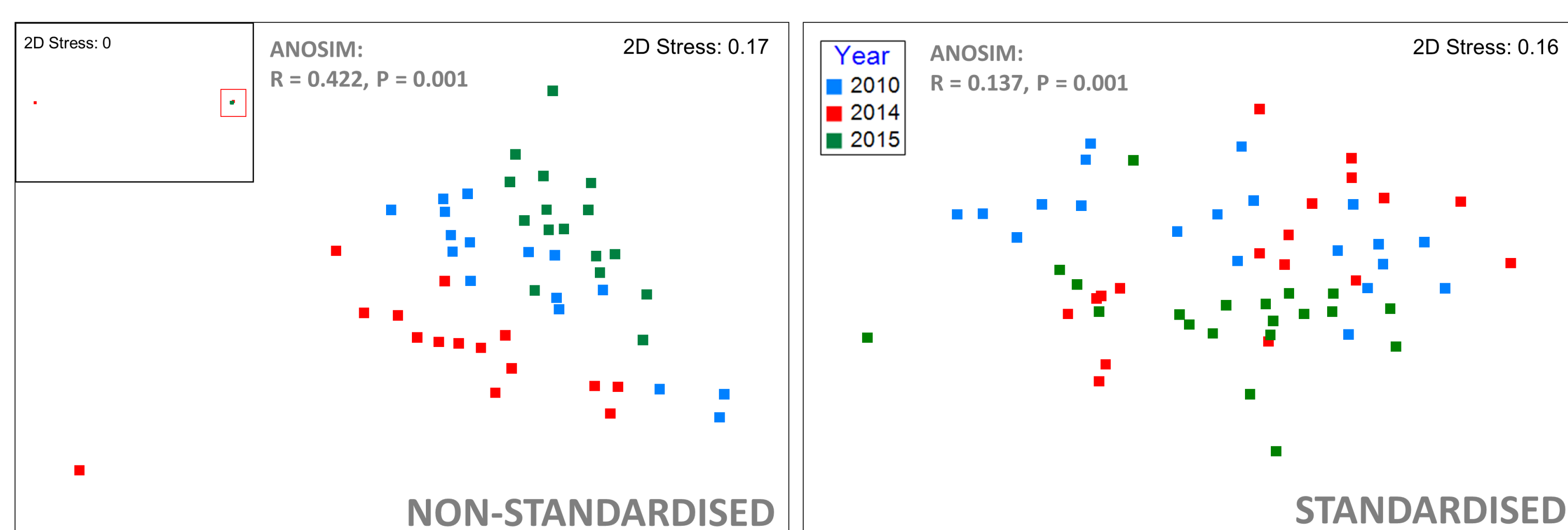


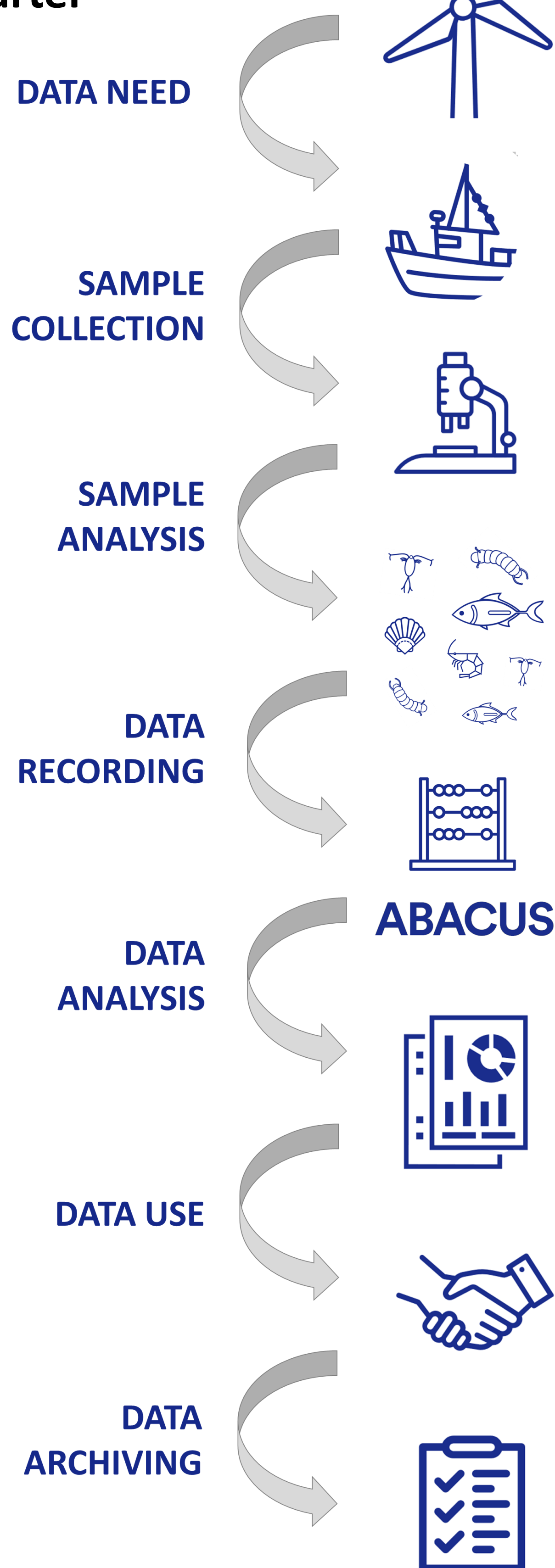
Figure 1. Non-metric MDS ordination plots of square-root transformed Bray-Curtis similarity epibenthic abundance data from single beam trawl samples taken during the pre- and post-construction surveys at a UK offshore windfarm. Left: inconsistent nomenclature over time. Right: standardised nomenclature over time. *note that the non-standardised plot is presented as a subset of points (shown with red box) from the main MDS displayed in the top left.

To address this ever-apparent issue, this poster presents the web-based data management application 'ABACUS' (v1.0) that has been developed to act as a platform for marine scientists to record, quality assure, store and export standardised marine biological data in line with internationally recognised data standards (e.g. MEDIN, GEMINI, ISO).

Acknowledgements

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Methods



Development Process - ABACUS has been developed using the latest Microsoft technologies (ASP.NET CORE, MVC, C#, Microsoft SSOL Server Database) and is encrypted using industry standard SSL and HTTPS. As part of the development of v1.0, a number of demonstration versions were tested by a team of taxonomists during analysis of hundreds of macrobenthic samples at Ocean Ecology Limited's (OEL) laboratory. Further testing and developments are underway with the aim of making v2.0 available to other organisations in 2019.

Species Recording - Samples can be tracked through key analysis stages including log in, elutriation, extraction, identification, biometric measurements and biomass. Quality Control stages are available for extraction and identification to improve quality or for the supervision and training of less experienced analysts. During the identification analysis stage, a web service provides a direct link to the World Register of Marine Species (WoRMS) database. Typing a few characters of any scientific name will automatically return a list of matching taxa. Selecting one of the taxa will retrieve a collection of data from the WoRMS database including taxonomic classification data, authority, AphiaIDs and other attribute data (e.g. AMBI groups) as well as other species information including Species Directory Codes (SDCs).

Data Exports - Marine Environmental Data and Information Network (MEDIN) compliant data export functionality is provided as standard, which has been funded by MEDIN and validated by The Archive for Marine Species and Habitats Data (DASSH). Fully MEDIN compliant exports can be created and downloaded with just a few clicks, skipping error-prone and slow manual processes. Users are also able to customise data exports based on data type (e.g. count or biomass data) and subsets of samples and/or sampling events.

Users - Being cloud based, analysts can sign into ABACUS via a web browser from any device with an internet connection. Through an admin dashboard selected users can manage access permissions of others as well as creating user profiles for external partners. When signed in, user activity can be recorded providing a full audit trail of data recording, quality control actions (e.g. amending a species name) and data exports.

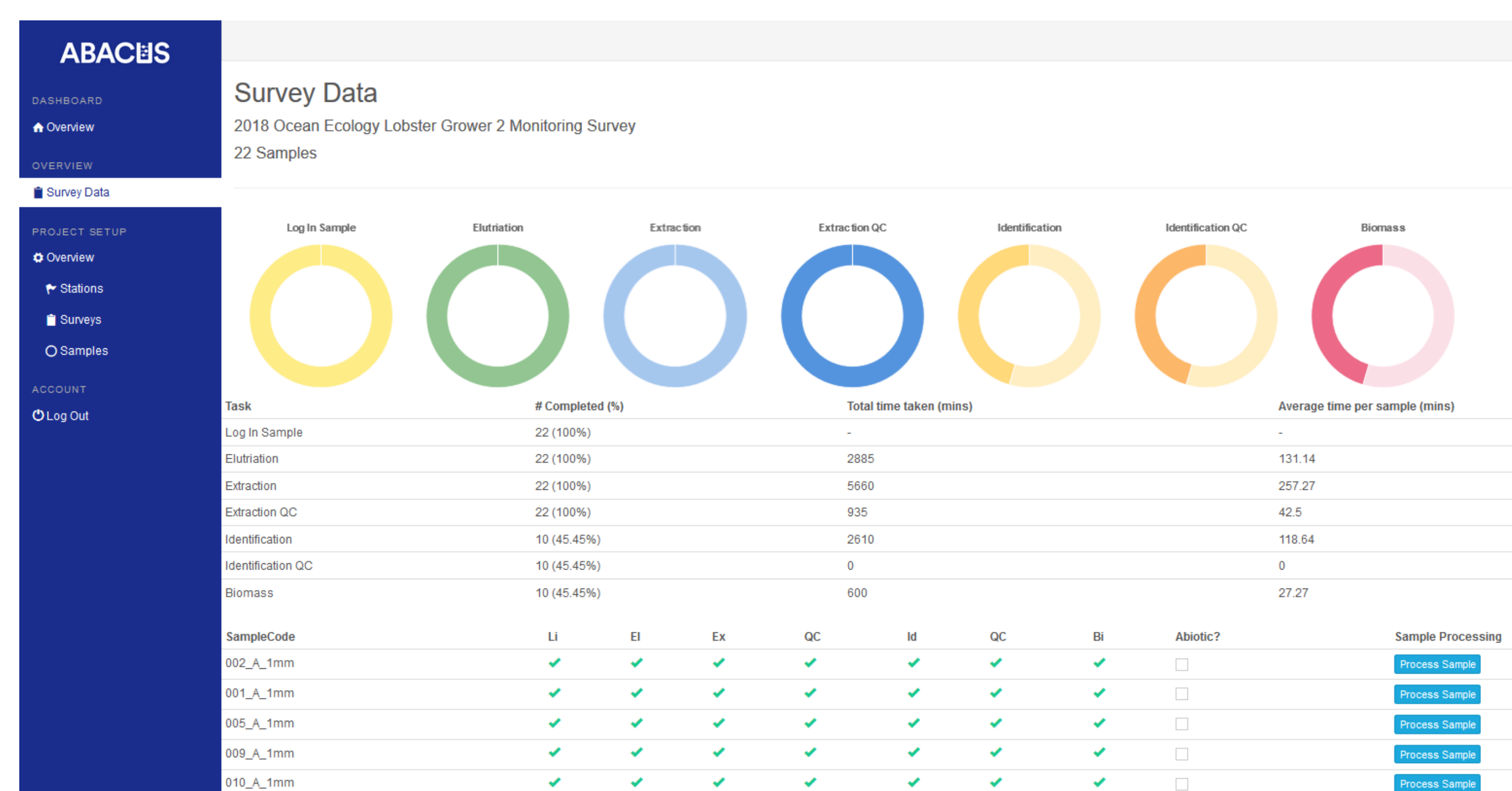


Figure 2. Example web-browser screen shots taken within ABACUS.

Discussion

With the rapid global growth predicted for a number of marine sectors (e.g. offshore windfarms and deep-sea mining), the adoption of ABACUS by laboratories working on behalf of developers and regulatory bodies may well help to minimise consenting bottlenecks and conversation oversights as well as significantly increase archiving of data with Data Archiving Centres (DACs). As such there is significant scope for ABACUS to act as an invaluable tool for scientists working in many marine sectors and publically funded organisations as well as for academics conducting marine biological research.

References

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- Worsfold AT, Hall D, Reilly MO (2010) Guidelines for processing marine macrobenthic invertebrate samples: a Processing Requirements Protocol.