

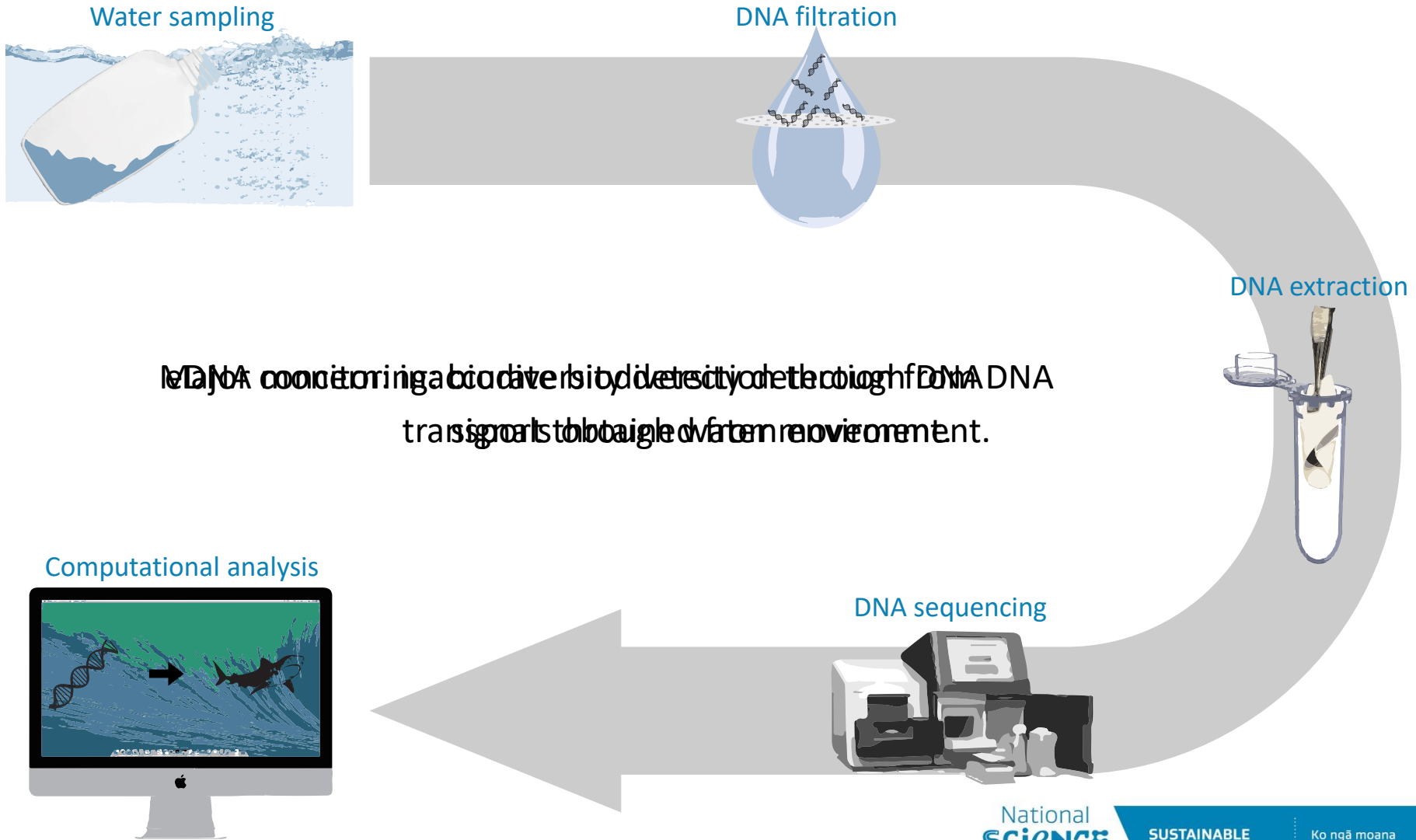
Quantifying marine biodiversity using environmental DNA (eDNA)

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eDNA monitoring: methodology

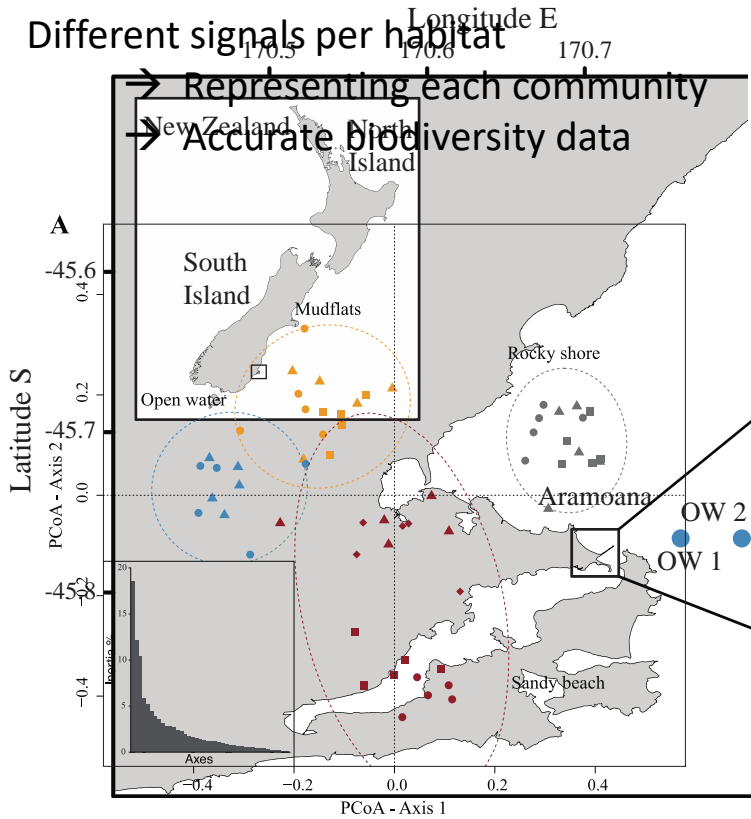


eDNA monitoring can detect the presence of DNA signals through water movement. This allows for the detection of biodiversity through DNA signals through water movement.

Accuracy of the eDNA monitoring method

Different signals per habitat

Small overlap in species detection shows limitations in both survey methods.



Traditional survey

- Chordata:**
 - Forsterygion malcomi*
 - Cnemidocarpa bicornuta*
 - Didemnum candidum*
 - Didemnum densum*
 - ⊕ *Notoclinops segmentatus*
 - ⊕ *Obliquichthys maryannae*
- Arthropoda:**
 - Chamaesipho columna***
- Bryozoa:**
 - Cribricellina cribraria*
- Chlorophyta:**
 - ⊕ *Canterpa brownii*
 - ⊕ *Cladophora crinalis*
 - ⊕ *Cladophora verticillata*
 - ⊕ *Codium fragile*
 - ⊕ *Codium gracile*
 - ⊕ *Enteromorpha intestinalis*
 - ⊕ *Ulva lactuca*
 - ⊕ *Wittrockiella lyalli*
- Echinodermata:**
 - ⊕ *Ophiosamnis maculata*
 - ⊕ *Pentagonaster pulchellus*
 - Pseudochinus huttoni*
- Mollusca:**
 - Cellana ornata*
 - Cominella nassoides*
 - ⊕ *Cryptaconchus porosus*
 - ⊕ *Maoricolpus roseus*
 - Mytilus edulis*
 - ⊕ *Sypharochiton pelviserpentis*
- Rhodophyta:**
 - Champia novae-zelandiae*
 - Gelidium pusillum*
 - Gigartina clavifera*
 - Gigartina decipiens*
 - Pachymenia lusoria*

eDNA survey

- Arthropoda:**
 - Acartia jiletti*
 - Bosmina meridionalis*
 - Calanus australis*
 - Calocalanus tenuis*
 - Clausocalanus ingens*
 - Clausocalanus pargens*
 - Ctenocalanus citer*
 - Daphnia pulex*
 - Euphausia lucens*
 - Evadne nordmanni*
 - Hemigrapsus crenulatus*
 - Jasus edwardsii*
 - Macrophthalmus hirtipes*
 - Nyctiphanes australis*
 - Oithona similis*
 - Oncaea waldemari*
- Chordata:**
 - Austrominius modestus*
 - Forsterygion flavonigrum*
 - Caesioperca lepidoptera*
 - Helicolenus dactylopterus*
- Echinodermata:**
 - Australostichopus mollis*
 - Coccinasterias muricata*
 - Evechinus chloroticus*
 - Patriella regularis*
- Bryozoa:**
 - Chaperiopsis cervicornis*
 - Hippomenella vellicata*
 - Membranipora membranacea*
- Chlorophyta:**
 - Lobosphaera incisa*
- Rhodophyta:**
 - Audouinella hermannii*
 - Sirodotia suecica*
 - Gracilaria truncata*

- Chordata:**
 - Aplodactylus arcidens*
 - Ascidia ahodori*
 - Galaxias brevipinnis*
 - Galaxias maculatus*
 - Gobiomorphus cotidiamus*
 - Latridopsis forsteri*
 - Maurolucis australis*
 - Maurolucis muelleri*
 - Nemadactylus macropterus*
 - Notolabrus fucicola*
 - Retropinna retropinna*
 - Sprattus antipodum*
 - Trachurus japonicus*
 - Trachurus symmetricus*
- Echinodermata:**
 - Ophiactis resiliens*
 - Ophiomeris fasciata*
 - Ophiopteris antipodum*
 - Patriella mortenseni*
- Mollusca:**
 - Aulacomya atra*
 - Potamopygus estuarinus*
 - Tavera spissa*

Open water

Sandy beach

Rocky shore

Mudflats



Conclusions

eDNA can become a powerful tool to aid conservation management strategies.

➔ Used by ecologists in conjunction with established methods

1. Easy-to-follow guidelines for field and lab work.
2. Semi-automated computational pipeline for data-analysis.

Minimal training is needed: providing the necessary information

Workshops

eBook

Collaboration

Sampling procedures

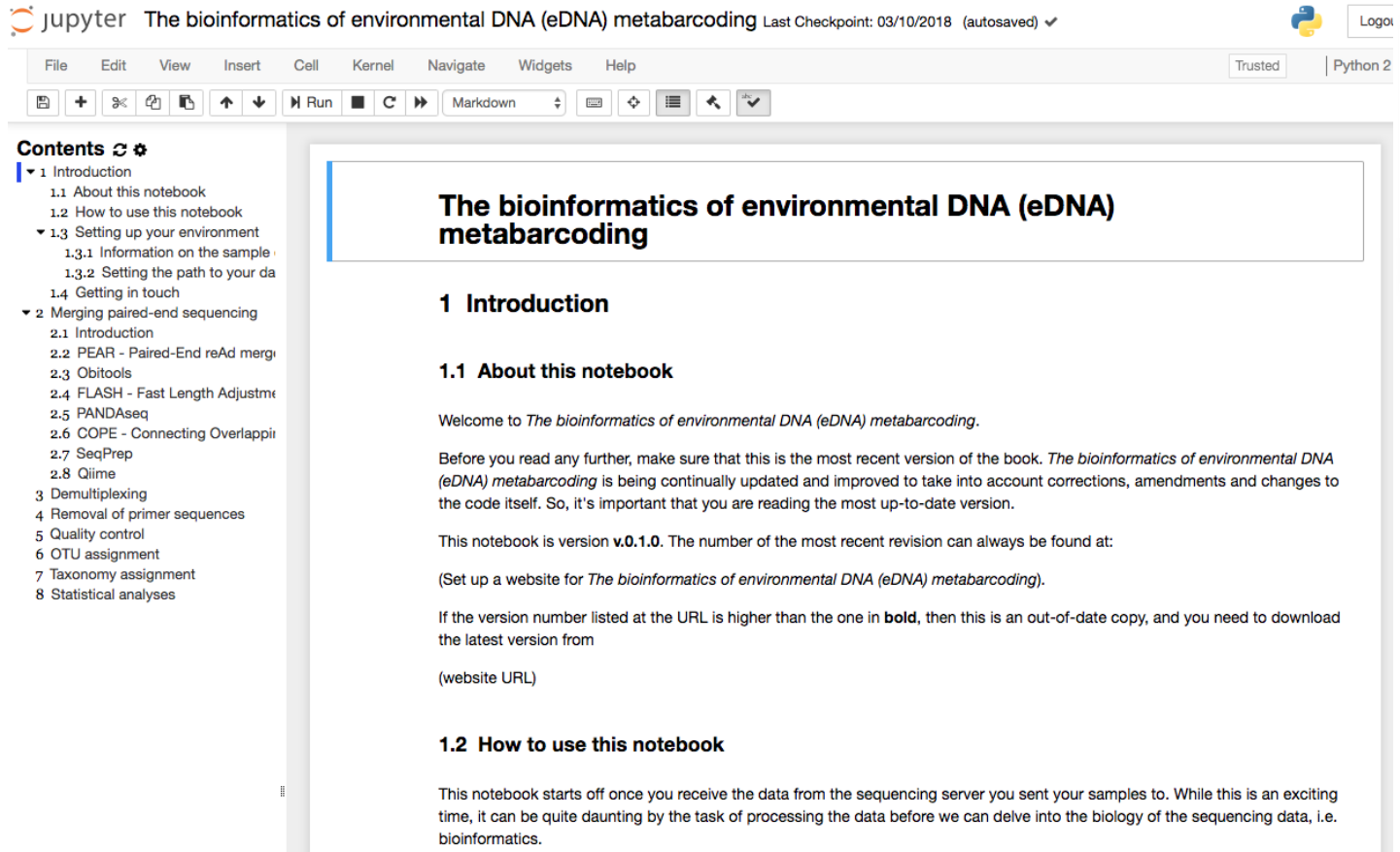


Laboratory procedures



Computational analysis





The screenshot shows a Jupyter Notebook interface. At the top, the title is "The bioinformatics of environmental DNA (eDNA) metabarcoding" with a last checkpoint of "03/10/2018 (autosaved)". The interface includes a menu bar (File, Edit, View, Insert, Cell, Kernel, Navigate, Widgets, Help) and a toolbar with icons for file operations, running, and editing. On the left, a "Contents" sidebar lists the notebook's structure, with "1 Introduction" selected. The main content area displays the title and the beginning of the "1 Introduction" section, including a sub-section "1.1 About this notebook".

The bioinformatics of environmental DNA (eDNA) metabarcoding

1 Introduction

1.1 About this notebook

Welcome to *The bioinformatics of environmental DNA (eDNA) metabarcoding*.

Before you read any further, make sure that this is the most recent version of the book. *The bioinformatics of environmental DNA (eDNA) metabarcoding* is being continually updated and improved to take into account corrections, amendments and changes to the code itself. So, it's important that you are reading the most up-to-date version.

This notebook is version **v0.1.0**. The number of the most recent revision can always be found at:

(Set up a website for *The bioinformatics of environmental DNA (eDNA) metabarcoding*).

If the version number listed at the URL is higher than the one in **bold**, then this is an out-of-date copy, and you need to download the latest version from

(website URL)

1.2 How to use this notebook

This notebook starts off once you receive the data from the sequencing server you sent your samples to. While this is an exciting time, it can be quite daunting by the task of processing the data before we can delve into the biology of the sequencing data, i.e. bioinformatics.



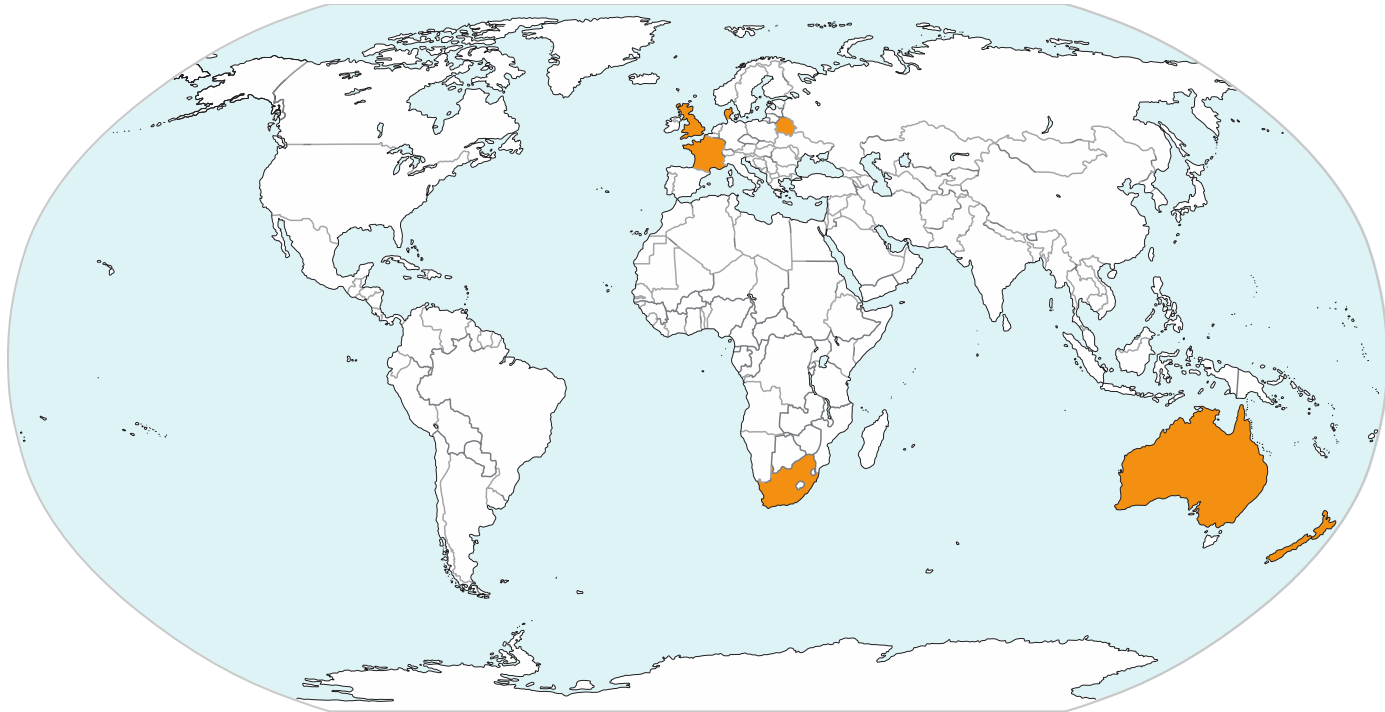
Oscar Ortega

Workshops

eBook

Collaboration

Collaborative projects: setting up, advancing, or promoting eDNA research



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