

# **Passive eDNA collection enhances aquatic biodiversity analysis**

Jeanne Harabedian

# Motivation

## Environmental DNA (eDNA) Metabarcoding

- Novel method for assessing biodiversity wherein **samples are taken from the environment** via water, sediment or air from which **DNA is extracted**, and then **amplified using general or universal primers** in polymerase chain reaction and **sequenced** using next-generation sequencing to generate thousands to millions of reads.
- Metabarcoding removes the need for multiple taxonomic experts by **automatically matching the DNA samples** to a taxonomic identity from an existing database
- Because the identity matching is automated, the limitations come purely from how many samples can be metabarcoding

# Motivation

## Room for Improvement?

- Main objective → **more samples**
- Increase the amount of samples that one can collect by **switching from active filtering to passive filtering**

## Active Filtering

- Collect water samples (1 L - 20 L, depends on the environment) and actively pump the water through membranes to collect eDNA samples
- Extremely time and energy intensive, requiring specialized equipment

# Design and Implementation

## Their Approach

- They present the alternative of switching from the active pump system to a passive membrane collection system
- Using two membranes:
  - **positively charged nylon** to catch eDNA particles by charge attraction
  - **non-charged cellulose ester** to catch eDNA particles by entrapment
- They attached these membranes to an oyster aquaculture frame with mesh pockets and submerged underwater



# Evaluation

## Varying Climate

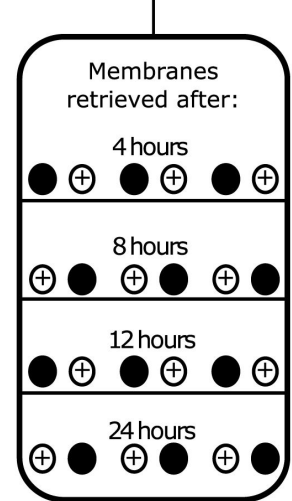
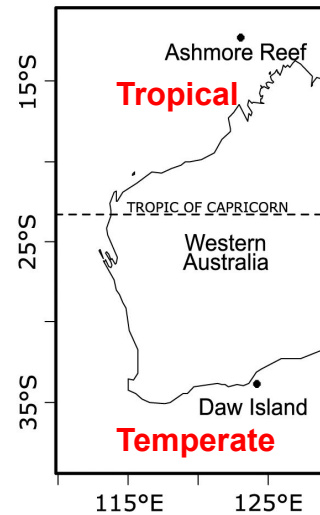
- They tested their system in two different climates
  - **Tropical Waters** in the Ashmore Reef
  - **Temperate Waters** around Daw Island

## Varying Collection Time

- They tested how varying the particle collection time affected the overall taxa identification

## Compared Against Active Filtering in all Cases

- In all tests at both locations they compared against active filtering (using 9 L of water) as their ground truth



# Sample Post Processing

## Standard Methods Used for all eDNA Sequencing

- One-step quantitative polymerase chain reaction (qPCR) were performed with each sample and a universal primer
  - Primer is picked based on the fact that they're **targeting fish taxa**
- PCR outputs also include controls
  - **Positive Control:** DNA sample of a fish that should not be in the environment that they collected, but should be identified with 100% accuracy
    - All identified the known fish with 100% accuracy
    - Minimum reads in the positive control was 36, therefore a conservative cutoff for their application was 40 reads
  - **Negative Control:** use deionized water instead of DNA sample
    - No sample produced more than 5 reads for any species
- They compare these outputs against a database of known fish (different for each region)
  - < 80% match: sample discarded
  - 80 % < match < 90 % : family
  - 90 % < match < 97 % : genus
  - > 97 % : species



# Supplementary Data and Results - Daw

**Table 2 Taxa detected at Daw Island.**

Family name	Taxon name	Passive filtration										Active filtration	
		Charged					Non-charged						
		4 h	8 h	12 h	24 h	34 h	4 h	8 h	12 h	24 h	34 h		
Aplodactylidae	<i>Aplodactylus</i> sp.			B	B	B	B	B	B	B	B	B	B
Arripidae	<i>Arripis georgianus</i>	B	B	B	B	B	B	B	B	B	B	B	B
	<i>Arripis</i> sp.	B	B	B			B	B	B	B			B
Aulopidae	<i>Latropiscis purpurissatus</i>		B				B						B
	<i>Centroberyx</i> sp.	P											
Berycidae	<i>Lophonectes</i> sp.												
Callionymidae	<i>Repomucenus calcaratus</i>	P					P		P				
	<i>Pseudocaranx sp.</i>	B	B	B	B		B	B	B	B			B
Carangidae	<i>Pseudocaranx wrighti</i>		B										B
	<i>Seriola lalandi</i>		B	B			B						B
	<i>Trachurus</i> sp.				B								B
Cheilodactylidae	<i>Cheilodactylus</i> sp.						P						
	<i>Cheilodactylidae</i> —unknown 1	P	P				P		P				
	<i>Nemadactylus valenciennesi</i>									P			
Chironemidae	<i>Chironemus georgianus</i>	P		P			P		P				
	<i>Chironemus maculosus</i>		B	B	B			B	B				B
Clinidae	<i>Heteroclinus adelaidae</i>	B			B								B
	<i>Heteroclinus eckloniae</i>						B						B
Clupeidae	<i>Clupeidae</i> —unknown 1	B	B				B						B
	<i>Sardinops sagax</i>	B	B	B	B	B	B	B	B	B			B
Congridae	<i>Gnathophis longicauda</i>												
	<i>Bathyrahis brevicaudata</i>			B	B								
Dinolestidae	<i>Dinolestes lewini</i>												
Dussumieridae	<i>Etrumeus jacksoniensis</i>	B		B	B		B	B	B				B
	<i>Engraulis australis</i>	B			B		B	B	B	B			B
Enoplosidae	<i>Enoplosus armatus</i>		B	B					B	B			B
	<i>Paragaula melbournensis</i>						B	B	B	B			B
Hemiramphidae	<i>Hyporhamphus melanachir</i>	B		B			B	B	B	B			B
	<i>Iso rhotophilus</i>												A

**Table 2 (continued)**

Family name	Taxon name	Passive filtration										Active filtration	
		Charged					Non-charged						
		4 h	8 h	12 h	24 h	34 h	4 h	8 h	12 h	24 h	34 h		
Kypnosidae	<i>Girella</i> sp.		B	B	B	B	B	B	B	B	B	B	B
	<i>Kypnosus gladius/sydneyanus</i>	B	B	B	B	B	B	B	B	B	B	B	B
Labridae	<i>Scorpius</i> sp.				B		B	B	B	B	B	B	B
	<i>Achoerodus</i> sp.	B	B	B	B		B	B	B	B	B	B	B
Labridae	<i>Australabrus maculatus</i>	B	B				B	B	B	B	B	B	B
	<i>Bodianus</i> sp.									P		P	
Labridae	<i>Eupetrichthys angustipes</i>	B	B	B	B		B	B	B	B	B	B	B
	<i>Halichoeres brownfieldi</i>	B	B				B	B	B	B	B	B	B
Labridae	<i>Labridae</i> —unknown 1												B
	<i>Notolabrus fucicola</i>									B			B
Labridae	<i>Notolabrus parilus</i>									B	B	B	B
	<i>Ophthalmolepis lineolata</i>									B	B	B	B
Labridae	<i>Pictilabrus laticlavus</i>	B	B	B	B		B	B	B	B	B	B	B
	<i>Carcharodon carcharias</i>												
Monacanthidae	<i>Acanthaluteres</i> sp.	B	B								B	B	B
	<i>Monacanthidae</i> —unknown 1										B	B	B
Moridae	<i>Nelussetta ayraulti</i>	P									P		
	<i>Scobinichthys granulatus</i>											B	B
Moridae	<i>Lotella rhacina</i>	B											B
	<i>Pseudophycis barbata</i>												A
Mullidae	<i>Upeneichthys</i> sp.	B								B		B	B
	<i>Upeneichthys stotti</i>	B	B	B	B		B	B	B	B	B	B	B
Myliobatidae	<i>Myliobatis australis</i>									B	B	B	B
	<i>Odacidae</i>	B	B	B	B		B	B	B	B	B	B	B
Pemppheridae	<i>acropilus</i>	B	B	B			B	B	B	B	B	B	B
	<i>Olisthops cyanomelanus</i>	B	B	B	B		B	B	B	B	B	B	B
Pemppheridae	<i>Siphanosgrathus</i> sp.	B	B	B	B		B	B	B	B	B	B	B
	<i>Parapropacanthus elongatus</i>	B	B	B	B		B	B	B	B	B	B	B
Pinguipedidae	<i>Pemppheris</i> sp.	B	B	B	B		B	B	B	B	B	B	B
	<i>Paraperic haackei</i>	B	B	B	B		B	B	B	B	B	B	B
Pinguipedidae	<i>Paraperic ramsayi</i>		P										

**Table 2 (continued)**

Family name	Taxon name	Passive filtration										Active filtration	
		Charged					Non-charged						
		4 h	8 h	12 h	24 h	34 h	4 h	8 h	12 h	24 h	34 h		
Platycephalidae	<i>Leviprora inops</i>	P											
	<i>Platycephalus grandispinis</i>	B			B					B	B		B
Pomacentridae	<i>Cliramis</i> sp.	P				P						P	
	<i>Parma microlepis</i>	B	B							B	B	B	B
Scombridae	<i>Scombridae</i> —unknown 1									B			B
	<i>Scomber</i> sp.	B	B		B					B	B		B
Scorpaenidae	<i>Scorpaenidae</i> —									P			



# Results - Analyzing Mean Values

## Mean Taxa Detected

Ashmore -

- Charged: 3
- **Non-charged: 10**
- Active: 42

Daw -

- Charged: 8
- **Non-charged: 11**
- Active: 17

## Mean Taxa Detection Based on Submersion Time

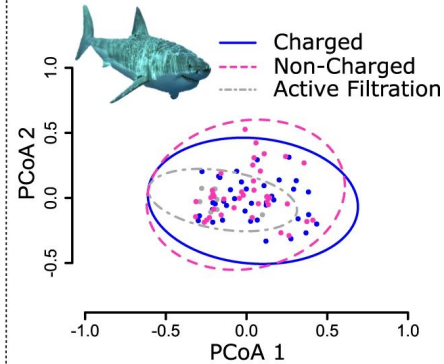
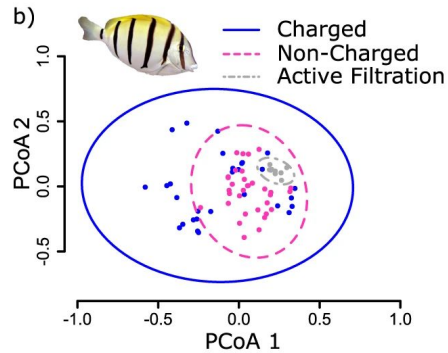
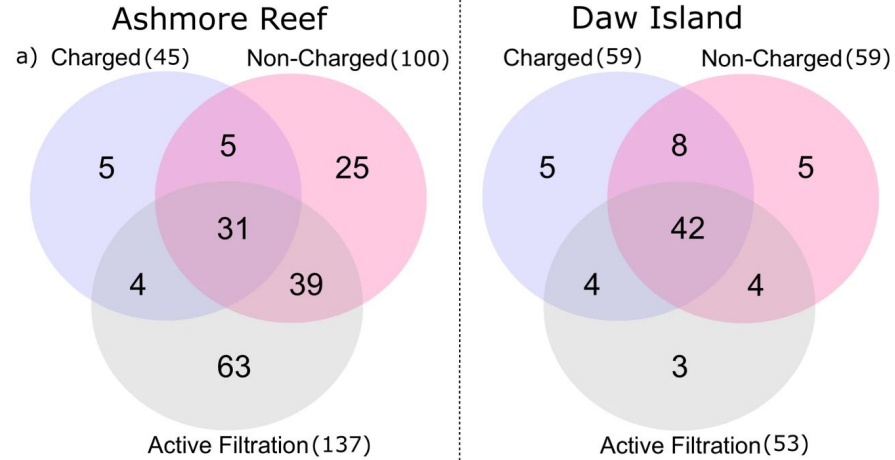
Ashmore -

- After 4 Hours: 2
- After 8 Hours: 5

Daw -

- No significant differences between any of the filters, including active

# Results - Analyzing Taxa Community



# Conclusion

Their results show **promising evidence** that it could be used to properly collect eDNA and **significantly expand the amount of environmental metabarcoding** that can be done and biodiversity that can be analyzed.

The passive solution is

- Inexpensive and scalable
  - Eliminates any need for active / manual collection and filtration
- More appropriate for temperate, but still acceptable for tropical environments
- Easily replicable for more analysis on viability as well as implementation
  - Different membrane materials, understanding physical limitations of membranes, understanding implications of varying environments