

The OceanOmics dashboard

A visualisation tool for the democratisation of eDNA data

20.2.2025



We generate all this eDNA data,
but how do we generate insights
from the data?

-> <http://edna.minderoo.org>

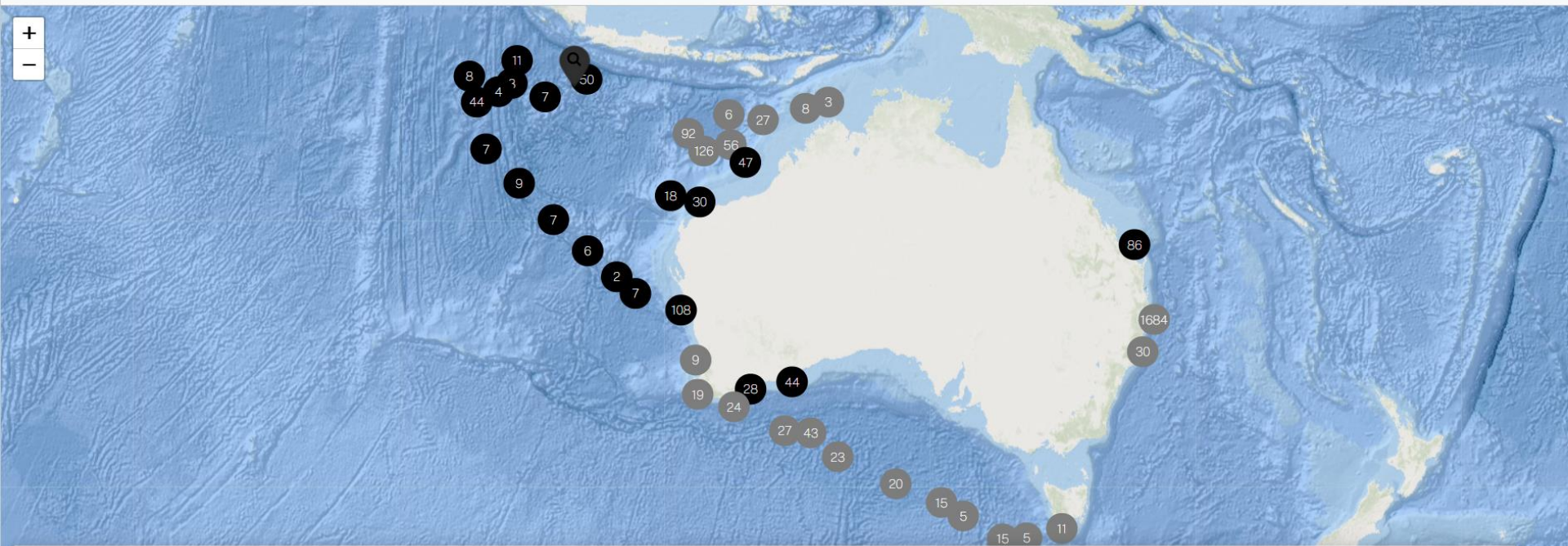


Data map

Select Year: All
Filter by assay: All
Select marine fish species: All
Expert-distribution models: Display AquaMaps occurrence model

Display Australian Marine Parks

? Info



All taxonomic annotations based on NCBI nt database downloaded on: **02/03/2024**
The data presented in this dashboard do not include IUCN species that are listed as 'endangered', 'critically endangered', or 'vulnerable'. If you would like further information or data access, please contact: oceanomics@minderoo.org

Data map

Select Year: All

Filter by assay: All

Select marine fish species: Ablabys taenianotus (Cockatoo Waspfish)


Expert-distribution models: Display AquaMaps occurrence model

Display Australian Marine Parks

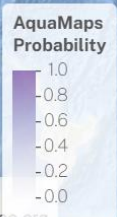
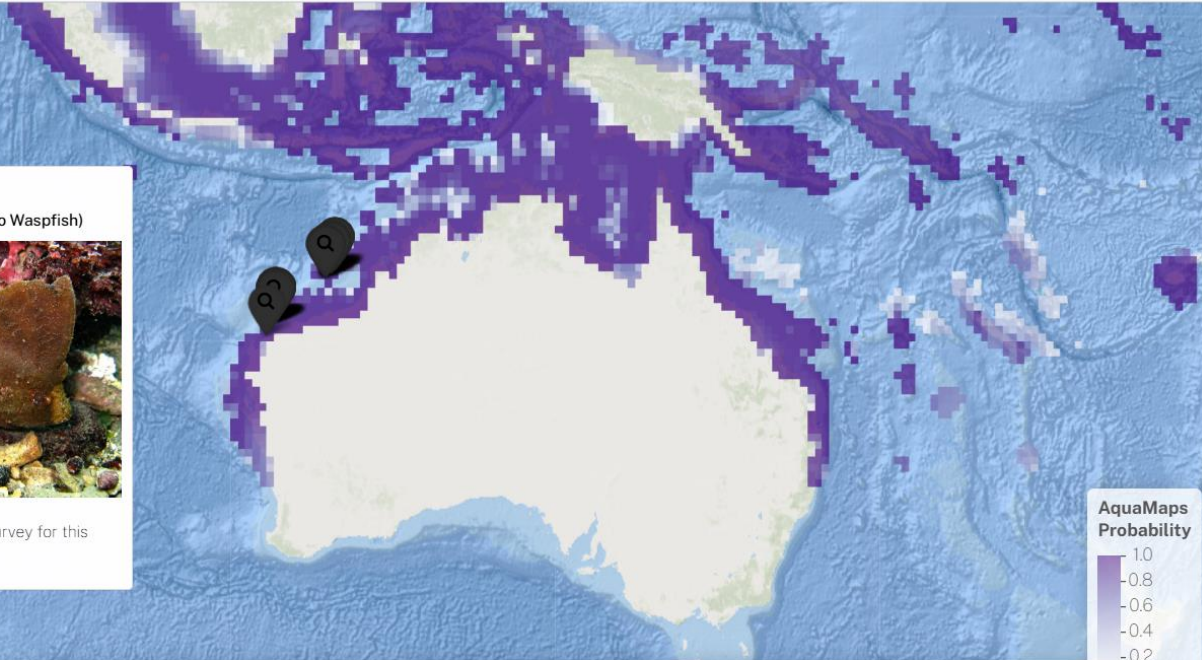
? Info



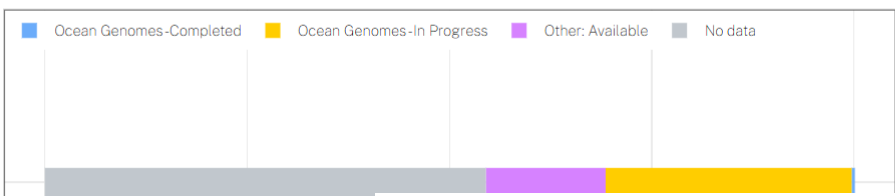
Reef Life Information
 Ablabys taenianotus (Cockatoo Waspfish)



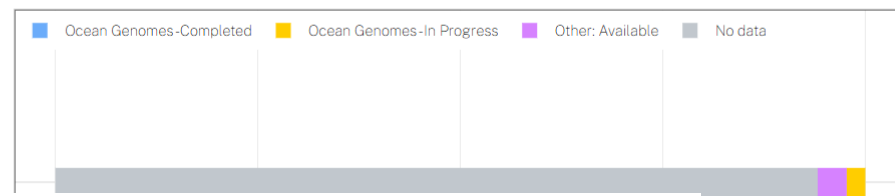
No information on Reef Life Survey for this species.



Families: Genome availability



Species: Genome Availability



Dr Shannon Corrigan, Ocean Genomes – Reference Quality Genome Resources for Marine Vertebrates, R3 (this room), 16:15 – 16:30

Genomes data

📄 COPY
📄 EXPORT CSV
📄 EXPORT CSV
📄 EXPORT EXCEL

Search:

Species	Species Common Name	High Quality Genome Status	High Quality Genome BioProject ID	Draft Genome Status	Draft Genome BioProject ID	ONT	HiFi	HiC	Illumina	Family	Family Common Name
All	All	All	All	All	All	All	All	All	All	All	All
<i>Pempheris klunzingeri</i>	Rough Bullseye	Completed	PRJNA179283	In Assembly	PRJNA1098793	Sequenced	Sequenced	Sequenced	Sequenced	Pempheridae	Bullseyes, Sweepers

Ask anything from our eDNA data!

We use Anthropic (Claude 3.5 Sonnet) and the metadata you can see on the eDNA tab. This data contains eDNA findings from all of our expeditions, all samples and fish-sightings based on amplicon sequencing variants. Here you can ask questions about this data.

Some examples: 'Are there any sharks in the data?', 'What is the southern-most fish spotted?', or 'How many distinct species of fish are in the data?'

WARNING: Do not trust the results blindly. Always verify independently. You can download the metadata in the eDNA tab and run the same code Claude writes below to verify. Consider asking the same question again: you may get a different result. For example: when you ask about sharks, sometimes Claude looks for Chondrichthyes, sometimes for Elasmobranchii, and sometimes for Carcharhiniformes.

Answer

Question: What snappers (Lutjanidae) were discovered in this dataset? For each Lutjanidae, please comment on whether you expect to find this species at these latitudes/longitudes

Answer: The following snappers (Lutjanidae) were discovered in this dataset:

1. *Aphareus furca* (Smalltooth Jobfish): Found between -22.33°S to -10.40°S and 96.00°E to 119.66°E. This distribution is expected, as it's within its known range in the Indo-Pacific region.
2. *Aphareus rutilans* (Rusty Jobfish): Found between -17.55°S to -9.98°S and 96.00°E to 119.65°E. This is within its expected range in the tropical Indo-Pacific.
3. *Aprion virescens* (Green Jobfish): Found between -23.90°S to -10.41°S and 96.00°E to 152.39°E. This wide distribution is consistent with its known range across the Indo-Pacific.
4. *Lutjanus* species: Several *Lutjanus* species were found, including *L. bohar*, *L. carponotatus*, *L. kasmira*, and others. Their distributions generally fall within the expected ranges for these species in the Indo-Pacific region.
5. *Mesolepocentrus* (Midnight Snapper) and *Mesolepocentrus* (Black and White Snapper): Both found between

Thought process

filamentosus' '*Symphorichthys spilurus*' '*Symphorus nematophorus*'] **Thought: Now that we have the list of Lutjanidae species, we need to analyze their locations. Let's get the latitude and longitude ranges for each species.**

```
Action: python_repl_ast Action Input: lutjanidae_data = df[df['family'] == 'Lutjanidae'] for species in lutjanidae_data['species']: species_data = lutjanidae_data[lutjanidae_data['species'] == species] lat_range = (species_data['Latitude'].min(), species_data['Latitude'].max()) lon_range = (species_data['Longitude'].min(), species_data['Longitude'].max()) print(f'{species}: Latitude range: {lat_range}, Longitude range: {lon_range}')
```

Aphareus furca: Latitude range: (-22.33498333, -10.404), Longitude range: (96.0, 119.6614) Aphareus rutilans: Latitude range: (-17.547918, -9.982217245), Longitude range: (96.0, 119.649689) Aprion virescens: Latitude range: (-23.90085, -10.4124), Longitude range: (96.0, 152.3922667) Caesio caerulea: Latitude range: (-28.9702, -17.06570848), Longitude range: (113.0, 152.3922667) Caesio cuning: Latitude range: (-34.11940095, -17.06570848), Longitude range: (115.4560262, 152.3922667) Caesio teres: Latitude range: (-22.33498333, -10.404), Longitude range: (95.89178333, 119.6527131) Dipterygonotus balteatus: Latitude range: (-28.8606, -17.065952), Longitude range: (113.0, 152.3922667) Etelis carbunculus: Latitude range:

Ask me anything

What snappers (Lutjanidae) were discovered in this dataset? For each Lutjanidae, please comment on whether you expect to find this species at these latitudes/longitudes

Submit Done.

Next feature:



Cocos-Keeling Transect: Replicate MF_4_3_3 report

This replicate is part of the [Cocos-Keeling Transect](#). See this dataset on [GBIF](#), on [OBIS](#), and download the data on [AWS](#).

We thank Parks Australia, NBDL, and CSIRO.



Number of ASVs

75



Families detected

16



Species detected

17

[Detected species - images](#)

[AI-based species summary](#)

[Detected species - table](#)

[Sampling map](#)

[Krona visualisation](#)

[Taxonomy-independent visualisation](#)

[Raw data](#)



Centrobranchus nigroocellatus



Chauliodus sloani



Coris aygula



Grampus griseus



Hemigymmus melapterus



Lampanyctus alatus



Notoscopelus resplendens



Anthropic Claude AI summary of species found in this replicate

The marine transect between Perth and Cocos Keeling Islands reveals an extraordinary diversity of mesopelagic lanternfish (family Myctophidae), including several species of *Diaphus* (*D. phillipsi*, *D. parri*, *D. mollis*), *Lampanyctus* (*L. nobilis*, *L. alatus*), *Notoscopelus resplendens*, and the striking *Centrobranchus nigroocellatus*. These small, bioluminescent fish play a crucial role in the ocean's daily vertical migration and food web dynamics. The region supports impressive large marine life, including the sleek blue shark (*Prionace glauca*) and the charismatic Risso's dolphin (*Grampus griseus*). Perhaps most remarkably, the transect revealed the presence of the oarfish (*Regalecus glesne*), one of the world's longest fish species and rarely encountered by humans, demonstrating the area's significance for unusual and poorly understood marine species.

Deep-sea predators are well-represented, including the viperfish (*Chauliodus sloani*) and the elongated bristlemouth (*Gonostoma elongatum*). These species are complemented by the extraordinarily long and thin slender snipe eel (*Nemichthys scolopaceus*), showcasing the unique adaptations of deep-ocean life.

The transect also includes species typically associated with reef systems and coastal waters, such as the humphead wrasse (*Coris aygula*), silver drummer (*Kyphosus sydneyanus*), and the unusual truncated sunfish (*Ranzania laevis*). Their presence alongside deep-water species highlights how this oceanic corridor connects different marine ecosystems and supports species from multiple ocean zones.

The diversity of species detected along this transect emphasizes its importance as a route for both resident and migratory species, connecting the temperate waters off Western Australia with the tropical Indian Ocean. This makes the region particularly significant for understanding connectivity between marine ecosystems and for marine conservation efforts.

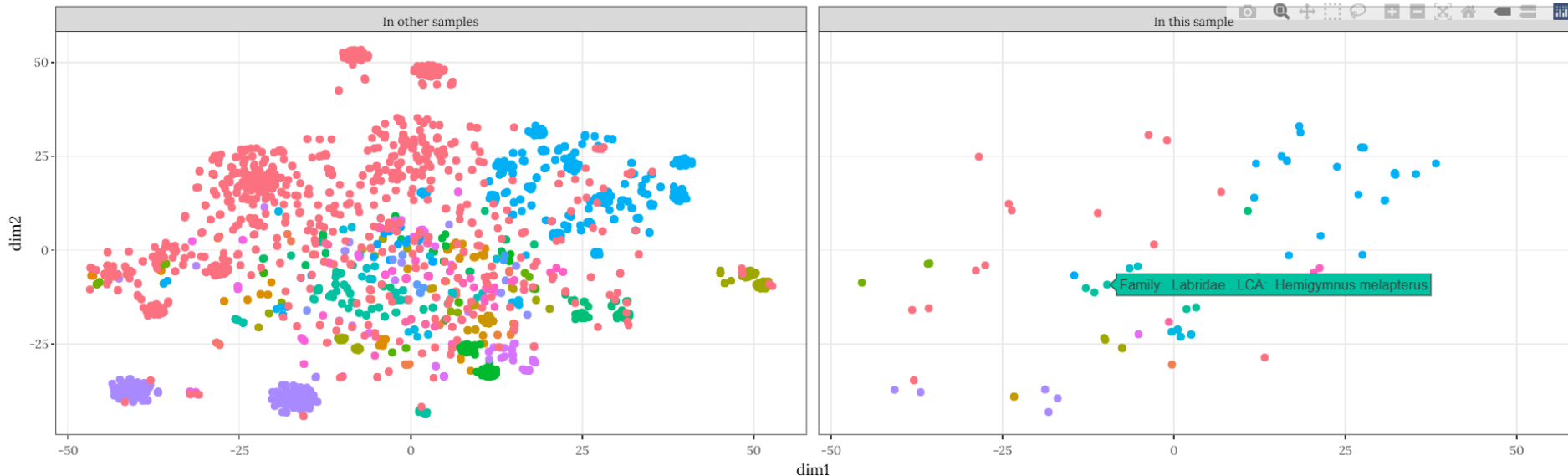
Table 1: Table of species sightings

Family	Genus	Species	Sampling depth (m)	ASV	Curation	Assay	IUCN Code	% Identity	Read count	Read count percentage (sample)	Read count per mille (voyage)
Myctophidae	<i>Lampanyctus</i>	<i>nobilis</i>	10	ASV_140	3 May be close relative	12S	LC	90.173	4808	4.6	0.0
Myctophidae	<i>Diaphus</i>	<i>phillipsi</i>	10	ASV_154	2 Plausible	12S	LC	100	5772	5.5	0.0
Myctophidae	<i>Diaphus</i>	<i>parri</i>	10	ASV_157	2 Plausible	12S	LC	100	18	0.0	0.0
Myctophidae	<i>Diaphus</i>	<i>phillipsi</i>	10	ASV_159	2 Plausible	12S	LC	100	4385	4.2	0.0
Carcharhinidae	<i>Prionace</i>	<i>glauca</i>	10	ASV_1598	1 Validated	12S	NT	100	111	0.1	0.0
Myctophidae	<i>Lampanyctus</i>	<i>nobilis</i>	10	ASV_160	3 May be close relative	12S	LC	90.173	3284	3.1	0.0
Carcharhinidae	<i>Prionace</i>	<i>glauca</i>	10	ASV_1708	1 Validated	12S	NT	100	95	0.1	0.0
Delphinidae	<i>Grampus</i>	<i>griseus</i>	10	ASV_1726	2 Plausible	12S	NA	100	9	0.0	0.0
Myctophidae	<i>Notoscopelus</i>	<i>resplendens</i>	10	ASV_174	2 Plausible	12S	LC	97.688	3	0.0	0.0
Molidae	<i>Ranzania</i>	<i>laevis</i>	10	ASV_1855	1 Validated	12S	LC	97.647	66	0.1	0.0

1–10 of 28 rows

 Previous **1** 2 3 Next

For all ASVs sampled during the Cocos Keeling voyage, where does this sample's diversity sit?



We fine-tuned DNABERT-S with all 12S and 16S sequences sequenced by OceanOmics. We then calculated embeddings for all ASVs and clustered them into two dimensions using TSNE for the above plot. The plot shows all ASVs collected during the entire voyage, colored by whether we have a hit for this ASV in our reference database, and split up showing where this sample's ASV diversity sits in comparison to all other samples' ASV diversity.



Connecting eDNA with action

It includes two dedicated modules. The first module, "Biosecurity and biodiversity" supports biodiversity surveys and biosecurity activities. For example, the identification and management of biosecurity incursions, and the discovery of new populations of native and critical endemic species. Ripple's second module, "Metrics" is focussed on water quality monitoring, including metrics for monitoring ecosystem health.



Biosecurity and biodiversity

Explore when and where species are detected. Custom searches and notifications make eDNA-based biomonitoring a breeze.

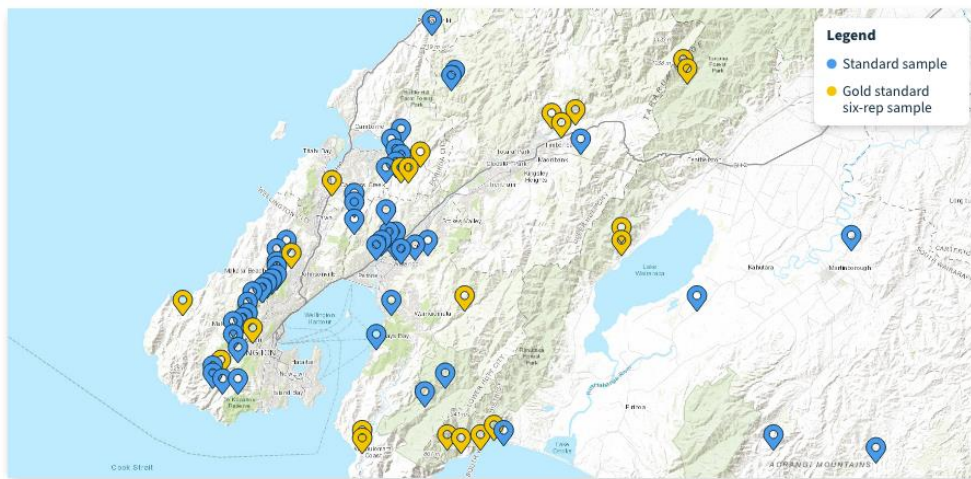


Metrics

Ut duis nibh litora proin malesuada interdum ipsum lacus tempus. Eleifend auctor erat malesuada at euismod, aptent erat.



Visualise detections in space and time



- Design and page im



Downloaded on 05 February 2025 from <https://app.rippledna.com/>



Acknowledgements

Research collaborators:

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Key partners

