Extreme weather advice fund report

Resilience beyond the storm: harnessing environmental DNA (eDNA) insights to inform post-extreme weather recovery strategies.

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Prepared by: Eddy Dowle, Gert-Jan Jeunen and Neil Gemmell

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Contents

Summary

- Cyclone Gabrielle was one of Aotearoa New Zealand's most costly natural disasters.
- Temporal datasets allow us to understand the long-term recovery of taxa and communities to the cyclone.
- Here we integrated eDNA data from three separate government monitoring programs (HBRC, MfE and NIWA).
- Data from three separate eDNA programs were combined to generate a temporal dataset covering 93 sites, sampled 277 sites with 1723 replicates.
- 91 of these sites were sampled both pre and post cyclone (the other two had multiple samples post cyclone).
- Three dashboards were developed to enable end-users to analyse and view the results.
- Dashboard one allows end-users to understand an individual taxa's response to the cyclone through time.
- Dashboard two allows end-users to undertake community level analyses as individual sites.
- Dashboard three allows end-users to explore how diversity has changed across the HB region.
- Combined these dashboards enable end-users to analyse the recovery and response of communities and taxa to Cyclone Gabrielle through time. Allowing end users to delve into how different locations and management practices have impacted recovery, and highlighting the utility and promise of eDNA approaches in biomonitoring programs.

Introduction

Tropical Cyclone Gabrielle passed over Aotearoa New Zealand in February 2023 claiming 11 lives and resulting in one of NZ's costliest disasters. The ecological impacts on freshwater systems across the Hawkes Bay (HB) and Tairāwhiti regions were extensive. Rainfall as high as 56mm per hour was recorded and the sheer volume of water overwhelmed management systems resulting in extensive flooding, stop bank breaches, land erosion, along with considerable damage to riparian plantings and stock exclusion fences across the regions (McMillan, Dymond et al. 2023, McLean 2024). The cyclones impact on biodiversity in the immediate aftermath was immense (RNZ 2023), but the long-term recovery and resilience of taxa and communities requires in-depth analyses of temporal datasets.

Environmental DNA (eDNA) or DNA that is collected from the environmental samples such as water, soil, air etc (Ruppert, Kline et al. 2019). These datasets enable swift and efficient ecosystem monitoring (Bista, Carvalho et al. 2017, Perry, Seymour et al. 2024). Despite being a relatively new survey method it is now commonly used in local government, CRI and central government monitoring programs. However, a lack of end-user accessibility due to inherent complexities in analysing and interpreting eDNA data has somewhat hindered its use and integration in management frameworks. Cyclone Gabrielle represents one of the first major ecological disasters in NZ for which we have extensive pre and post event eDNA sampling and presents a first opportunity to understand how environmental DNA (eDNA) datasets can contribute to our understanding of biodiversity changes after an extreme event.

The data analysed in this report comes from three separate agencies. Hawkes Bay Regional Council (HBRC) began routine eDNA monitoring in 2020 and has continued regular eDNA monitoring through to 2024. In addition, following Cyclone Gabrielle both the Ministry for the Environment (MfE) and NIWA ran eDNA monitoring programs in Hawkes Bay (HB). All three programs were run using the same service provider, Wilderlab. Resulting in three, independent but overlapping eDNA datasets that were yet to be integrated. Here we integrate these extensive datasets to assess how both individual taxa and communities at monitoring sites were impacted and recovered following the cyclone. We have developed a series of easy-to-use dashboards that allow for the voluminous data to be displayed in an accessible and ecologically meaningful manner to help empower local governments and communities to mitigate the ecological impacts of future extreme weather events.

Site selection

Sites were reconciled across three sources: HBRC, MfE, and NIWA. Across these three sources data was available from 112 unique sites within the HB region. Of these sites 91 had data from pre and post cyclone Gabrielle, 12 had data only pre cyclone and 9 had data only post cyclone. For the purposes of this study, we only considered the sites with pre and post cyclone sampling, along with two sites with multiple collections post cyclone only (total 93 sites). These 93 sites were sampled a total of 277 times and comprised a total of 1723 individual sample replicates. For most sites a 6-replicate approach per sample was used, however six samples had a replication number of 4 or 5 (Table 1).

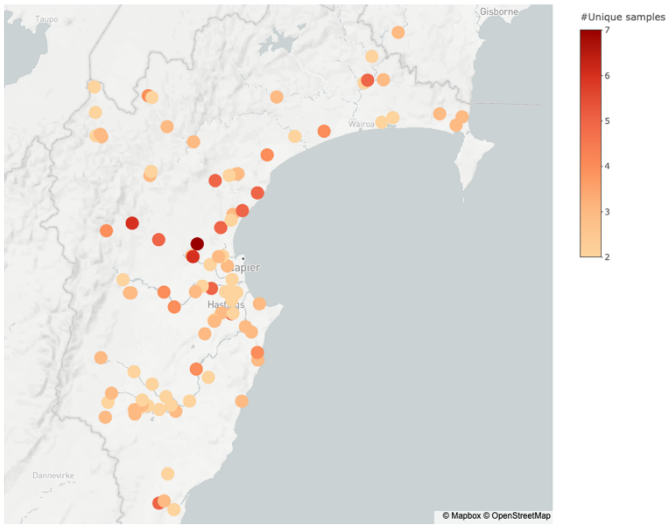


Figure 1. Map of 93 Hawkes Bay sites included in the analyses, sample number (i.e. number of unique time points sampled) per site is indicated in the colour.

HBRC SITE NAME	HBRC SITE ID	# UNIQUE SAMPLES	SAMPLING DATES	PRE & POST CYCLONE SAMPLING	LOWEST REPLICATION NUMBER PER SAMPLE	LATITUDE HBRC	LONGITUDE HBRC
AROPAOANUI AT AROPAOANUI RD	317	5	26/01/22, 19/04/23, 30/08/23, 16/11/23, 25/03/24	Yes	6	-39.26977494	176.9788611
AWANUI STRM AT FLUME	255	2	9/03/22, 20/03/24	Yes	6	-39.69101139	176.7977566
CLIVE RVR US WHAKATU	11	2	10/03/22, 20/03/24	Yes	6	-39.60194427	176.8895437
ESK RVR AT BERRY RD	303	5	24/02/22, 20/04/23, 30/08/23, 16/11/23, 24/01/24	Yes	6	-39.22872948	176.7967515
ESK RVR AT WAIPUNGA BR	9	5	6/01/22, 31/05/23, 30/08/23, 16/11/23, 24/01/24	Yes	6	-39.38553749	176.8204721
HANGAROA RVR AT DONNERAILLE PARK	337	3	2/02/22, 30/03/23, 9/01/24	Yes	6	-38.73150268	177.585286

HERE HERE AT TE AUTE RD	3121	5	9/03/22, 18/04/23, 31/08/23, 17/11/23, 6/03/24	Yes	6	-39.67221205	176.8663065
IRONGATE STREAM AT RIVERSLEA RD	257	3	22/03/22, 24/03/23, 6/03/24	Yes	6	-39.66972181	176.8235071
KAHAHAKURI STRM AT LINDSAY RD	3358	2	25/01/22, 19/03/24	Yes	6	-39.97727668	176.5061434
KAREWAREWA STRM AT PAKI PAKI BR	263	2	9/03/22, 20/03/24	Yes	6	-39.69391042	176.790851
KŌPUAWHARA STRM AT LOWER RAIL BR	330	3	3/02/22, 31/03/23, 10/01/24	Yes	6	-39.01540381	177.8606906
MAHARAKEKE AT SH2	405	2	25/01/22, 19/03/24	Yes	6	-39.9838125	176.4764944
MAHIARUHE STRM DS SANDY CREEK AT SH2	593	2	26/01/22, 25/03/24	Yes	6	-39.20814014	176.8812379
MAKARA STRM AT ST LAWRENCE RD	3360	2	21/06/22, 20/03/24	Yes	4	-39.88347977	176.767364
MAKARETU STRM AT SH 50	19	3	31/01/22, 19/04/23, 18/01/24	Yes	6	-40.01535301	176.3231461

MAKARETU US MAHARAKEKE CONFL.	3353	3	25/01/22, 24/03/23, 19/03/24	Yes	6	-39.99047658	176.4481704
MAKARORO AT BURNT BR	402	3	31/01/22, 13/04/23, 20/03/24	Yes	6	-39.81820732	176.3037635
MANGAKURI AT US MANGAKURI RD BR	2414	3	22/02/22, 12/04/23, 27/03/24	Yes	6	-39.96240315	176.9109916
MANGAMAHAKI STRM AT POURERERE RD	3359	2	28/04/22, 20/03/24	Yes	6	-39.96191712	176.6860525
MANGAMAIRE STREAM AT MANGAMAIRE	4351	2	10/05/22, 5/04/24	Yes	6	-40.3199301	176.6190724
MANGAONE RV AT DARTMOOR BR	503	3	5/09/23, 17/11/23, 27/02/24	Post only	6	-39.47966436	176.695798
MANGAONE RVR AT RISSINGTON	266	7	20/01/22, 21/03/22, 27/04/23, 2/06/23, 5/09/23, 17/11/23, 27/02/24	Yes	6	-39.44027718	176.7191712

MANGAONUKU STRM AT TIKOKINO RD	284	2	31/01/22, 20/03/24	Yes	6	-39.90571067	176.5249822
MANGAORAPA STRM AT MANGAORAPA	249	5	22/02/22, 14/04/23, 11/09/23, 13/11/23, 27/03/24	Yes	6	-40.29864299	176.55423
MANGAPOIKE RVR AT SUSPENSION BR	338	3	9/03/22, 18/04/23, 9/01/24	Yes	5	-38.89078354	177.5215811
MANGARAU STREAM AT TE AUTE RD	3120	2	17/02/22, 11/01/24	Yes	6	-39.67092448	176.8730673
MANGARUHE STREAM US WAIROA RIVER	4352	2	1/01/22, 13/03/24	Yes	6	-38.90157841	177.4382485
MANGATARATA STRM AT MANGATARATA RD	277	3	11/02/22, 14/04/23, 23/01/24	Yes	5	-39.99561382	176.6265231
MANGATUTU STRM AT MANGATUTU RD	2360	5	20/01/22, 21/03/22, 5/09/23, 17/11/23, 27/02/24	Yes	6	-39.42579212	176.5528768
MARAEKAKAHO AT KERERU RD	276	4	15/03/22, 24/03/23,	Yes	5	-39.64992856	176.6204968

			29/03/23, 16/01/24				
MARAETOTARA RVR AT TE AWANGA	12	3	3/02/22, 27/03/23, 15/03/24	Yes	6	-39.63932097	176.9869366
MARAETOTARA RVR AT WAIMARAMA RD	253	3	3/02/22, 24/03/23, 15/03/24	Yes	6	-39.7330069	176.9527047
MOHAKA D/S RIPIA RVR CONFL.	3186	3	17/03/22, 28/04/23, 14/03/24	Yes	6	-39.21184539	176.5151524
MOHAKA D/S WAIPUNGA RVR CONFL.	3182	3	17/03/22, 5/04/23, 26/03/24	Yes	6	-39.09905431	176.702962
MOHAKA DS TAHARUA	3152	3	8/03/22, 23/01/24, 21/03/24	Yes	6	-39.0821621	176.3072321
MOHAKA RV AT RAUPUNGA	3	2	13/05/22, 5/04/24	Yes	6	-39.08073426	177.1398713
MOHAKA US TAHARUA	2961	2	8/03/22, 28/03/23	Yes	6	-39.07894814	176.2828583
MOKOMOKONUI RVR AT TARTRAAKINA RD	321	3	24/02/22, 20/04/23, 24/01/24	Yes	6	-39.0482548	176.5895946

NGARURORO RVR AT FERNHILL	354	5	21/03/21, 16/03/22, 8/09/23, 17/11/23, 16/01/24	Yes	6	-39.58814184	176.7801561
NGARURORO RVR AT KURIPAPANGO OLD	298	4	22/03/21, 16/03/22, 30/03/23, 16/01/24	Yes	6	-39.39608894	176.3276692
NGARURORO RVR AT WHANAWHANA	299	2	16/03/22, 5/04/24	Yes	6	-39.55922754	176.3989022
NGARURORO RVR DS HAWKE'S BAY DAIRIES	2594	4	16/02/22, 12/04/23, 5/09/23, 12/03/24	Yes	6	-39.60051752	176.5756792
NUHAKA RV AT NUHAKA VALLEY RD	8	3	31/03/21, 3/03/22, 7/03/24	Yes	6	-39.00507633	177.7637813
OHARA STRM AT BIG HILL RD	3670	3	15/03/22, 11/04/23, 12/03/24	Yes	6	-39.60284874	176.4272281
OHIWIA AT BROUGHTONS RD BR	3476	2	16/03/22, 5/04/24	Yes	6	-39.580914	176.7408346
OPOUTAMA STRM AT SMITHS WOOLSHED	2125	3	3/02/22, 31/03/23, 7/03/24	Yes	6	-39.04310867	177.8348701

PAKURATAHI STREAM (FISHING SITE?)	NA	3	7/01/22, 2/05/23, 20/02/24	Yes	6	-39.34136164	176.8734807
PAPANUI STRM AT MIDDLE RD	285	4	26/03/21, 1/02/22, 19/04/23, 5/04/24	Yes	6	-39.85599148	176.7151363
POPORANGI STREAM AT BIG HILL RD	477	3	15/03/22, 11/04/23, 16/01/24	Yes	5	-39.6029662	176.4339317
PORANGAHAU RVR AT KATE'S QUARRY	14	3	10/05/22, 12/04/23, 5/04/24	Yes	6	-40.29143584	176.576616
PORANGAHAU US MAHARAKEKE CONFL.	3731	3	25/01/22, 24/03/23, 5/04/24	Yes	6	-40.00477991	176.4504644
POUKAWA STRM AT STOCK RD	148	3	20/01/22, 18/04/23, 6/03/24	Yes	6	-39.69704465	176.7937504
POUKAWA STRM TE MAHANGA RD	474	3	9/03/22, 18/04/23, 6/03/24	Yes	6	-39.73898846	176.7518481
PUHOKIO STRM AT TE APITI RD	394	3	27/01/22, 24/03/23, 15/03/24	Yes	6	-39.82594967	176.9806066

RAUPARE AT ORMOND RD	2393	2	9/03/22, 3/04/24	Yes	6	-39.5991706	176.8414295
RIPIA RVR U/S MOHAKA RVR CONFL.	604	2	17/03/22, 10/01/24	Yes	6	-39.19798685	176.5206221
RUAHAPIA STREAM AT SHOWGROUNDS	3119	2	22/03/22, 20/03/24	Yes	6	-39.62715633	176.8677318
RUAKITURI RVR AT DOUGHBOY BR	336	2	9/03/22, 13/03/24	Yes	6	-38.81273387	177.471836
SANDY CREEK AT GAUGE STATION	4355	3	26/01/22, 19/04/23, 11/03/24	Yes	6	-39.20594845	176.8946739
TAHARUA RVR AT HENRY'S BR	3278	2	8/03/22, 21/03/24	Yes	6	-39.00060212	176.2806762
TAHARUA RVR AT RED HUT	3151	3	8/03/22, 28/03/23, 21/03/24	Yes	6	-39.07383262	176.301812
TAHARUA RVR AT WAIRANGO	2446	2	8/03/22, 21/03/24	Yes	6	-38.91506297	176.2755079
TAIPO AT CHURCH RD	3117	3	21/03/22, 11/04/23, 14/03/24	Yes	6	-39.51370554	176.849409
TAMINGIMINGI STREAM	Fishing	2	22/12/21, 20/02/24	Yes	6	-39.36086561	176.8652367

TAUREKAITAI STRM AT WALLINGFORD	352	2	22/02/22, 27/03/24	Yes	6	-40.20222569	176.5920127
TE NGARUE STRM	81	5	26/01/22, 19/04/23, 30/08/23, 16/11/23, 25/03/24	Yes	6	-39.32887696	176.9138617
TUHARA STREAM DS TRIB	4138	2	2/02/22, 3/04/24	Yes	6	-39.03321926	177.5144462
TUKIPO RV US MAKARETU CONFL.	3357	3	25/01/22, 24/03/23, 19/03/24	Yes	6	-39.97506578	176.4814555
TUKIPO RVR AT STATE HIGHWAY 50	144	2	13/05/22, 20/03/24	Yes	6	-39.96575918	176.334306
TUKITUKI AT ONGA WAIPUK RD	20	2	25/01/22, 19/03/24	Yes	6	-39.95864468	176.4823549
TUKITUKI RV US WAIPAWA RV	3282	2	25/01/22, 19/03/24	Yes	6	-39.97602155	176.6061197
TUKITUKI RVR AT RED BR	407	3	12/01/22, 13/04/23, 18/01/24	Yes	6	-39.71535149	176.92705
TUKITUKI RVR AT SH 2 BR	17	2	28/04/22, 18/03/24	Yes	6	-39.98956806	176.5558105

TUKITUKI RVR AT SH50	356	3	31/01/22, 13/04/23, 18/01/24	Yes	6	-39.93590679	176.3498931
TUTAEKURI AT PUKETAPU	357	2	20/01/22, 3/04/24	Yes	6	-39.50894313	176.7743792
TUTAEKURI RVR AT DARTMOOR	3241	6	22/01/20, 4/05/22, 2/06/23, 5/09/23, 17/11/23, 27/02/24	Yes	6	-39.48269939	176.7010786
TUTAEKURI RVR AT BROOKFIELDS BR	13	2	4/05/22, 4/04/24	Yes	6	-39.55892941	176.8692757
TUTAEKURI RVR AT LAWRENCE HUT	272	6	21/03/22, 4/05/22, 5/04/23, 3/10/23, 13/11/23, 28/02/24	Yes	6	-39.37090216	176.4387695
TUTAEKURI-WAIMATE STRM	431	2	15/03/22, 12/03/24	Yes	6	-39.59699834	176.862999
WAIARUA STRM U/S STATE HIGHWAY 5 CULVERT	325	4	6/01/22, 30/03/23, 25/03/24, 26/03/24	Yes	6	-38.94436853	176.5081469

WAIAU RVR AT OTOI	331	3	2/03/22, 30/03/23, 9/01/24	Yes	6	-38.94859777	177.0619665
WAIHUA RV AT WAIHUA VALLEY RD	4	4	3/03/22, 13/09/23, 18/12/23, 10/01/24	Yes	6	-39.0635117	177.2657249
WAIKARI AT GLENBROOK	594	4	17/03/22, 13/09/23, 21/12/23, 10/01/24	Yes	6	-39.1428385	177.0205854
WAIKATUKU STRM OFF HARRISON RD	3472	2	2/02/22, 4/04/24	Yes	6	-39.01821145	177.5625489
WAIKOAU RV AT WAIKOAU RD BR	16	2	26/01/22, 25/03/24	Yes	6	-39.21144244	176.8568317
WAINGONGORO STRM AT WAIMARAMA RD	387	4	15/03/21, 3/02/22, 24/03/23, 15/03/24	Yes	6	-39.80101073	176.978427
WAIPAWA RVR AT SH 50	280	2	31/01/22, 20/03/24	Yes	5	-39.86462888	176.4466655
WAIPAWA RVR AT SH2 WAIPAWA	18	2	28/03/22, 20/03/24	Yes	6	-39.94739687	176.5845799
WAIPUNGA AT POHOKURA ROAD	322	2	6/01/22, 30/03/23	Yes	6	-38.95041565	176.5241655

WAIROA RIVER AT RIVERINA ROAD	4353	5	9/03/22, 18/04/23, 13/09/23, 18/12/23, 9/01/24	Yes	6	-38.89249799	177.4535763
WAITIO STRM AT OHITI RD	2591	3	16/03/22, 24/03/23, 12/03/24	Yes	6	-39.59936674	176.7112161
WHARERANGI - DAN AND LINDSAY BATES	NA	2	30/05/23, 15/06/23	Post only	6		
WHARERANGI US AHURIRI ESTUARY	3665	3	20/03/22, 11/04/23, 14/03/24	Yes	6	-39.48262665	176.8108069

Table 1. Outline of the sampling included in this analysis. Sampling includes 91 samples with pre and post cyclone samples and 2 with multiple replicates post cyclone datasets. Included here is the latitude and longitude values provided by HBRC, we note that these values differed somewhat between the HBRC datasets and the Wilderlab metadata tables.

Methods

Assays selection

The eDNA data analysed was generated by Wilderlabs. Due to the mix of sequencing approaches taken across the samples we have limited our analyses to those assays most consistently represented across the data (Table 2). These assays cover a variety of genes (mitochondrial, nuclear and chloroplast) and each have specific community targets (e.g. plants, invertebrates, vertebrates etc).

WILDERLAB ASSAY NAME	SAMPLE COUNT	% SAMPLE COVERAGE	ASSAY GENE TARGET	ASSAY COMMUNITY TARGET
BE	1710	99%	18S	General Eukaryote
BU	1723	100%	18S	General Eukaryote
CI	1718	99%	COI	Invertebrates (mostly insect)
MZ	1708	99%	Rbcl	Vascular plants
RV	1684	98%	12S	Vertebrates
TP	1717	99%	Chloroplast	Vascular plants
UM	1723	100%	16S	Microbe
WV	1713	99%	16S	Vertebrates

Table 2 – The coverage and target gene/communities of the eight assays used in the analysis.

Developed dashboards

Statistical analyses of the results have focused on two key aspects, species distribution and site diversity changes pre and post cyclone. Following input from end-user/stakeholders who wanted simple tool to evaluate species changes post cyclone we developed three interactive dashboards to explore the data. As such we have not included an extensive report outlining the impacts on individual sites but rather have chosen a few examples to highlight how to interpret the data, allowing end users to explore the data in a way that focuses on their question, species or site of interest. The dashboards enable end users to answer questions about individual taxa and community recovery pre and post cyclone. Combined these can be used to understand how management practices impacted their recovery across the Hawkes Bay region. Publicly available dashboards allow users to explore the data and download figures and taxa lists, a separate 'Site Analyses' dashboard is available to HBRC to allow them to download the raw data. Dashboards can be viewed:

Project overview: https://www.biodiscover.co.nz/our-work/current-projects
Full screen site analyses: https://ejd-biodiscover.shinyapps.io/HBRC_site_analyses/

Full screen diversity change analyses: https://ejd-biodiscover.shinyapps.io/HBRC_Diversity_change_analysis/
Full screen species change analyses: https://ejd-biodiscover.shinyapps.io/HBRC_SpeciesMaps/

Taxa filters

Prior to us accessing the data, concerns were raised regarding the level of terrestrial DNA contamination present in the datasets post cyclone Gabrielle. It is clear from photos taken in the aftermath of cyclone Gabrielle that a large amount of terrestrial material (soil, vegetation, and accompanying terrestrial species) entered the waterways and that this terrestrial contamination continued for some time post cyclone due to the high rates of erosion experienced by the surrounding landscapes. As a potential consequence of this input, the taxa counts post cyclone were at times higher than in pre-cyclone samples. To account for this effect, we collated a list of 'known freshwater animals' to ensure a curated subset of animals known to have freshwater stages could be compared pre and post cyclone. For species such as freshwater fish this list complete, and their lifecycle allows us to have some confidence in the data. However, most of the invertebrate species on this list have both a terrestrial and freshwater life stages. This means that although we are confident these species can occur in freshwater it is possible that the DNA detected in the water came from a terrestrial source rather than a freshwater source. We excluded some known freshwater taxa, such as annelids and nematodes, as we currently lack both the life history details and genetic database coverage to ensure they can be adequately separated into freshwater or terrestrial taxa. As such, the freshwater animal species filter should not be viewed as a compressive filter as many taxa groups cannot be accurately separated into freshwater and terrestrial taxa. The filtering process also requires that the taxonomic classification of ASV's is detailed enough that they can be classified into freshwater or non-freshwater taxa. For some reads this will not be possible due to the incomplete nature of genetic databases or a lack of informative sequence data (i.e. it's not possible to distinguish between some taxa with that particular marker). In these situations, if the ASV's is not classified to a low enough level they will be classified as 'non-freshwater'. The freshwater animal filter is only available for assays CI, RV and WV which have sufficient diversity to allow filtering and target primarily animal species. Currently we have not extended this list to include freshwater plants (assays MZ and TP) or microbes (assay UM).

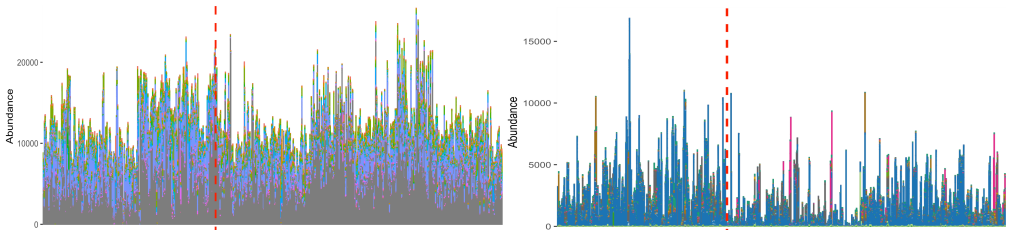


Figure 2. Read abundance across all sites for one assay (CI). On the left no filtering is applied and while on the right reads are filtered based on the freshwater species list. In this case a substantial drop in read abundances post cyclone (red) line can be seen, suggesting that a large proportion of the reads post cyclone were comprised of likely non-target terrestrial species.

In addition to general freshwater species filter we provide four other filters, that represent commonly studied freshwater groups. The first is a 'Fish' filter which filters ASV's for those classified as either the Class (Actinopteri and Hyperoartia) or Genus (Aldrichetta, Anguilla, Carassius, Cheimarrichthys, Ctenopharyngodon, Cyprinus, Galaxias, Gambusia, Geotria, Gobiomorphus, Mugil, Oncorhynchus, Retropinna, Rhombosolea, and Salmo) level for New Zealand freshwater fish,

this is available for assay RV and WV. The second is a 'EPT' filter that filters for the insect orders Ephemeroptera, Plecoptera or Trichoptera, this is available for assay CI. The third and forth are 'HB MCI-HB' and 'HB MCI-SB', both of these use the same list of macroinvertebrate species commonly assessed as part of the Macroinvertebrate Community Index (MCI). Both the MCI filters can be further filtered using a slider to focus on high or low tolerant species.

Species distribution maps

Species distribution maps are provided to show how taxa detections changed pre and post cyclone. For this analysis only the presence/absence of taxa in the eDNA dataset was considered. There is evidence that some eDNA datasets are semi-quantitative (Rourke, Fowler et al. 2022), however the relationship between reads and abundance estimates requires significant testing in natural settings (Yates, Fraser et al. 2019), and thus we have restricted these analyses to presence/absence only. The presence or absence of a taxa was determined across all eight assays and taxa can be filtered based on Family, Genus or Species. Taxa lists can be subset by 'All', 'Insecta' or 'Freshwater fish' to reduce the length of the species lists. Seasons or comparisons can be altered using the Year or Comparison drop down menu. The 'Select taxa' list can be searched, and the background map changed. The list of sites and status of the taxa is outputted as a table below the map. Note that depending on the season or comparison selected the total site number will change, reflecting the sites assessed during the selected period rather than all 93 sites. Site names can be brought up on a click and the map can be moved/resized as needed. Combined with end user knowledge about the cyclone impact and management practices at sites these maps can provide information about at which sites individual taxa were most sensitive and resilient. Below is an example of the different views available for a selected taxon (*Anguilla australis* the short-fined eel). In this example loses were seen in some sites post cyclone with some recovery in the following year. These maps are available for all freshwater taxa listed in the freshwater species list. Sampling years are defined by seasons (1st July -30th June) or a comparison (e.g. pre vs post cyclone).

Select sampling year or Comparison

2020-2021

Select taxonomic level

Species

Select taxa filter

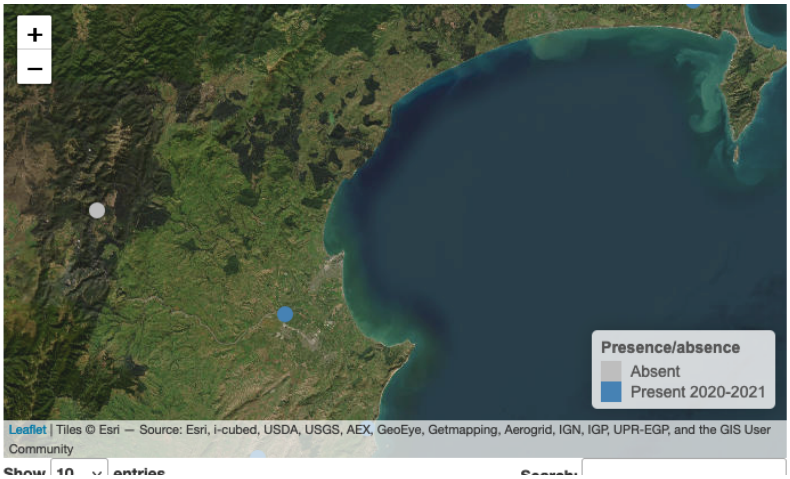
All

Select taxa

Anguilla australis

Change background

Satellite



Show 10 entries

Select sampling year or Comparison

2021-2022

Select taxonomic level

Species

Select taxa filter

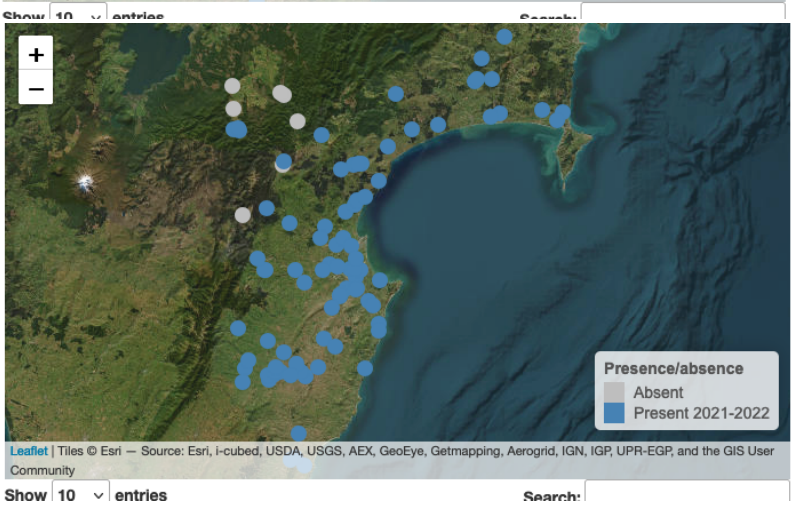
All

Select taxa

Anguilla australis

Change background

Satellite



Show 10 entries

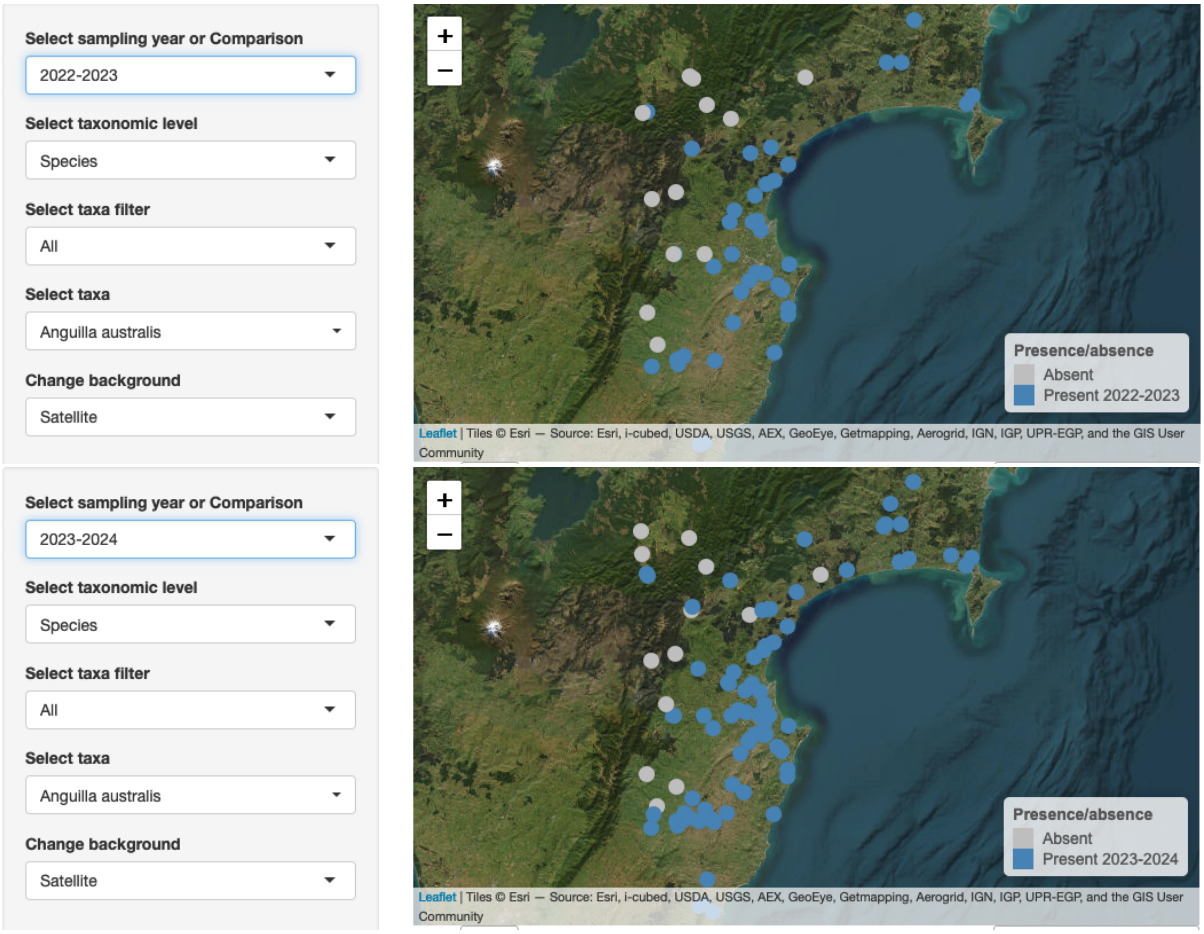


Figure 3. Presence absence maps of *Anguilla australis* in 2021 through to 2024. The total sample number changes reflecting the sampling effort undertaken in each year. A taxon can be absent (site sampled but species not present) or present. Site names can be brought up by the user clicking upon a site.

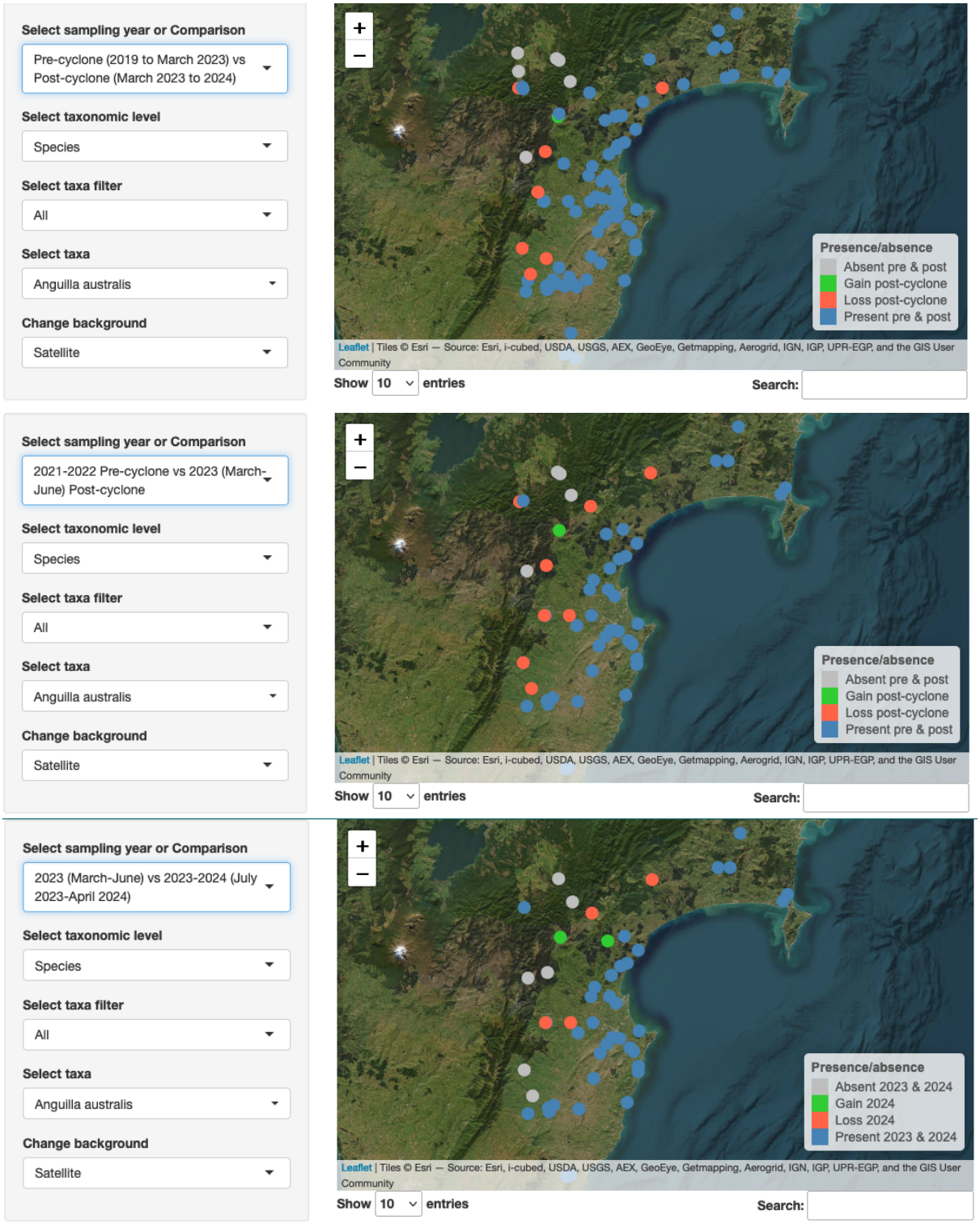


Figure 4. Presence absence maps across time periods. Contrast can be made pre and post cyclone (Precyclone (2019 – March 2023) vs Post cyclone (March 2023 – 2024)), in the season directly preceding and following the cyclone (2021-2022 Pre-cyclone vs 2023 (March -June) Post-cyclone) or 2023 (March-June) vs 2023-2024 (July 2023-April 2024) e.g. post cyclone 2023 vs 2024 seasons.

Analyses within a site

Standard quality assessment, diversity and spatial analyses are generated per site and assay. We have split these by site, and assays. With options to filter assays based on taxa (as discussed above) and recolour figures based on different classification levels (e.g. Class, Genus or Species). For abundance figures either the top ten most abundant Classes or Genera are displayed or all can be labelled (may result in a large number of taxa depending on the level chosen) with all others grouped under 'Other' (to avoid overly complicated figures). We display nine analyses per site/assay which are broken down to either 'Site Statistics' or 'Site Analyses'. Below is an overview of their function and interpretation. We note due to the large number of sites and assays (92 x 8 = 736 total analyses), we have not hand checked all results and thus they should be interpreted by the viewer using the guide below to determine whether a) the sequencing/sampling was adequate and appropriate b) whether any outlier data are likely influencing the final interpretation.

Site statistics

To assess the data quality of a site we provide three approaches to quality check the data for each site. Below is an overview of the rationale behind these assessments and their interpretation.

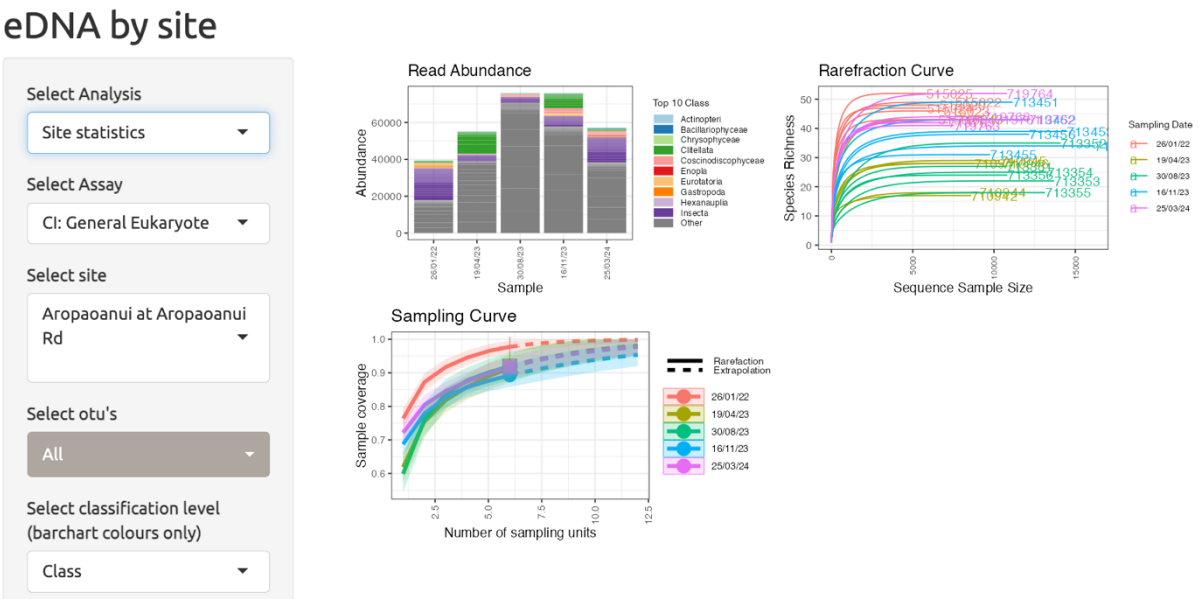


Figure 5. General overview of the 'Site statistics' analyses. Select Analysis allows the user to switch been 'Site statistics' and 'Site analysis'. Select Assay allows the user to change between the eight assays. Select site allows the user to switch been sites, Select otu's allows the user to filter the taxa list (only available for certain assays). Select classification level allows the user to change the taxa colouring in the barcharts. Figures can be downloaded as SVG's along with a table of included taxa.

Total read count per sample

Firstly, we display the total read count abundance per sample. This indicates the total read counts across all replicates for a sample. Due to sequencing variation these numbers will always vary somewhat and should be considered in conjunction with the rarefaction and sampling curves. If the read abundances vary but rarefaction and sampling curves show all replicates and samples have been sampled exhaustively the read abundance is unlikely to be influencing the data. If, however, the rarefaction curves and sampling curves have not reached asymptote in a particular sample the abundance data can be used to help assess the level of variation in the sequencing effort between

samples. If there are large variations in sequencing effort and inadequate sequencing coverage or replication (as shown by the rarefaction and sampling curves) the samples may require further sequencing or there may be more appropriate ways to analyse the data that consider the impact of sequencing read depth.

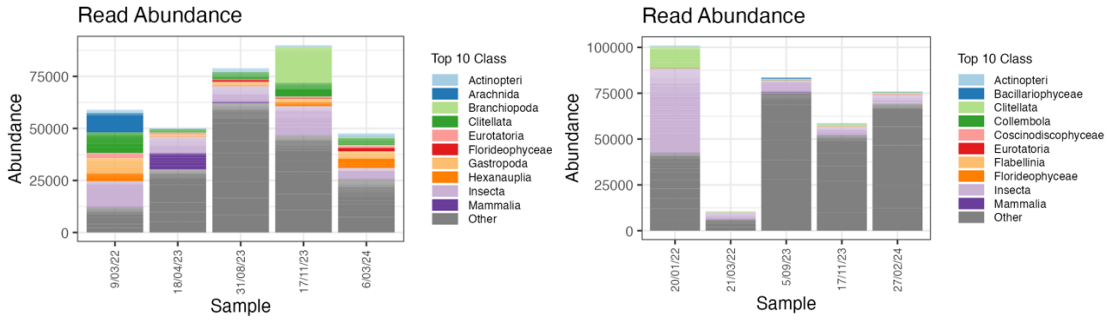


Figure 6. Read abundances per sample. Due to variation in sequencing these values will always somewhat differ but large variations in conjunction with poor rarefaction curves and/or sampling curves may suggest that sequencing effort could impact the results. In the first example read abundances within a site is relatively consistent across samples and are unlikely to impact results. In the second example abundances differ between sites and rarefaction curves should be checked to ensure adequate sequencing effort has been undertaken across the different samples.

Rarefaction curves

Rarefaction curves are generated by randomly re-sampling a sample replicates reads and counting the taxa number present in the resampled reads. A sample replicate is considered adequately sequenced when the curve reaches asymptote (has levelled of), and thus further sequencing would not add taxa. If the rarefaction curves do not reach asymptote this suggests that further sequencing is required to adequately capture the sequence diversity within a replicate.

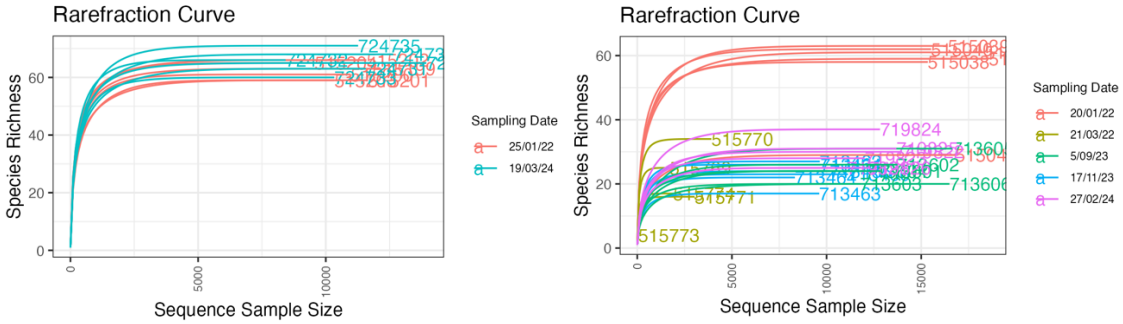


Figure 7. Rarefaction curves can be used to assess whether adequate sequence depth per replicate has been reached. In the first example all replicates have reached asymptote, and further sequencing would not change diversity estimates. In the second example replicate 515773 has not achieved adequate sequencing depth and caution should be taken with including this replicate in statistical analyses.

Sampling curves

Sampling curves appear similar to rarefaction curves but whereas before we considered each replicate as a separate entity the sampling curve considers what impact adding further replicates would have on the diversity counts for a sample. As with the rarefaction curve a sampling count is considered complete when it reaches asymptote and further sample replicates would not add

additional taxa counts to a sites sample. In this figure we display not only the rarefaction (subsampling) but also an extrapolation (addition of further samples). If a sample does not reach asymptote this suggests that further replication is needed to fully capture the diversity within a sample. This figure will not be displayed if the number of taxa is below 10 or less than 5 replicates are included per sample.

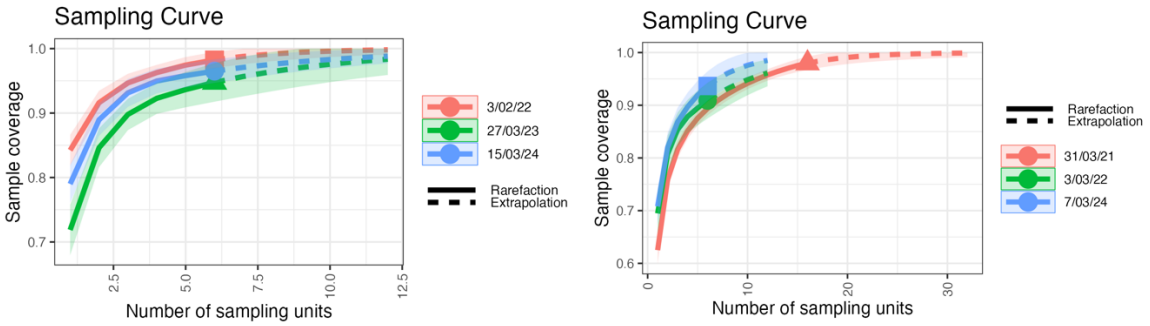
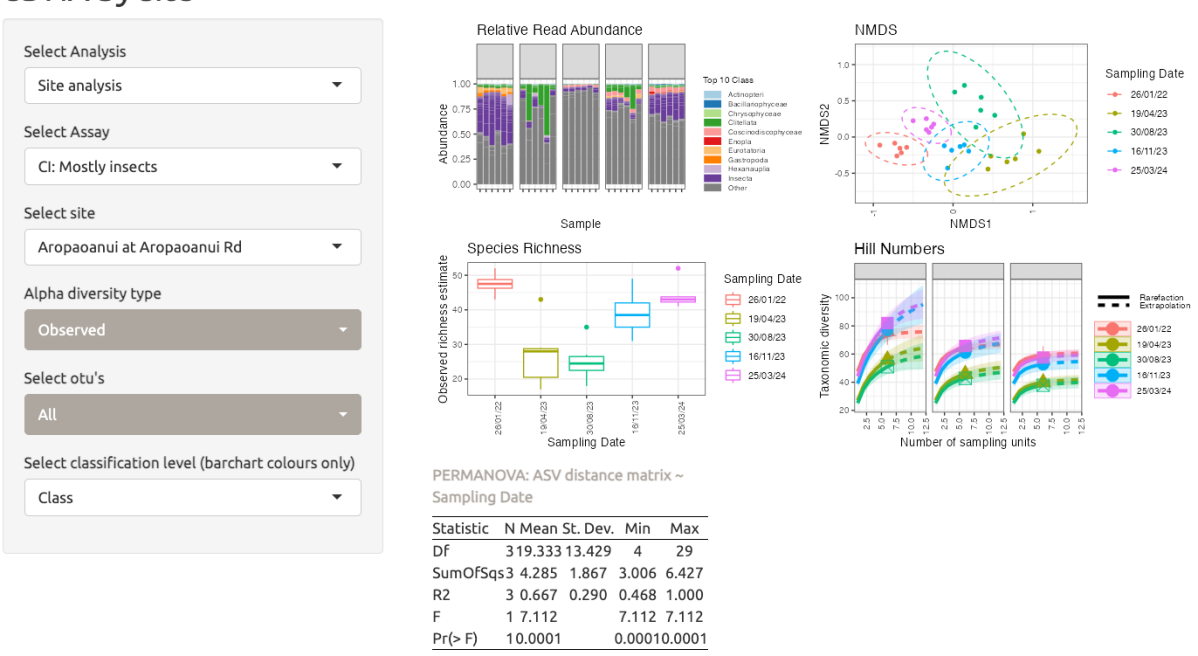


Figure 7. Sampling curves for two sites. In the first example all samples have all largely reached asymptote. In the second example blue and green samples have not quite yet reached asymptote. Whether this will impact the Site Analysis will depend on what statistics are used and how they are interpreted. For example, the rarefaction and extrapolation curves for the alpha diversity estimates (e.g. see Hill number plots below) should be examined to understand the impact of sampling on diversity estimates.

Site analyses

We provide five approaches to assess the diversity and dissimilarity at a site between samples. This allows end users to understand how different communities have recovered at a site, which in combination with end user knowledge of cyclone impact and management practices will enable a greater understanding of the temporal response and recovery at a site. Below is an overview of the rationale behind these assessments and their interpretation. As with the site statistics analyses can be restricted to taxa groups for appropriate assays.



Statistic	N	Mean	St. Dev.	Min	Max
Df	3	19.333	13.429	4	29
SumOfSqs	3	4.285	1.867	3.006	6.427
R2	3	0.667	0.290	0.468	1.000
F	1	7.112		7.112	7.112
Pr(> F)	1	0.0001		0.0001	0.0001

Figure 8. General overview of the ‘Site analysis’ dashboard.

Relative read abundances

Bar plots of relative read abundances per replicate grouped by sample is provided to visualise the main taxa differences between replicates/samples. Charts can be coloured by Class or Genus by changing the side-bar toggle. Only the top 10 taxa for are coloured with all others being grouped into ‘Other’.

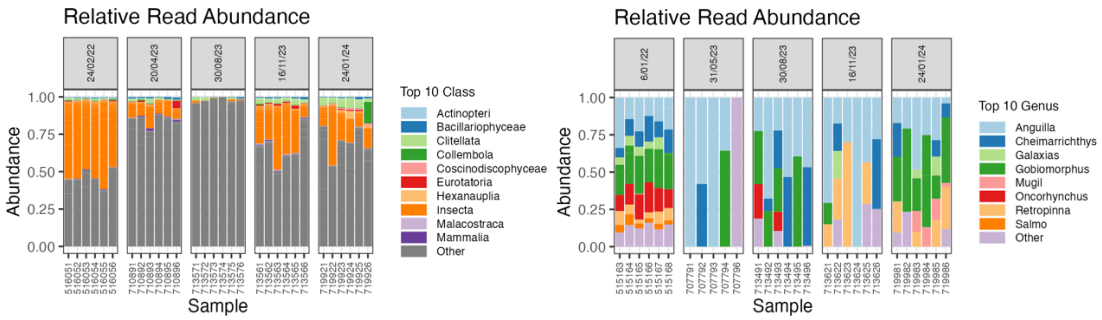


Figure 11. Relative read abundances for two assays with colouring at either the class, genus or species level depending on the assay chosen. Note that the ‘Other’ group will includes both taxa outside of the top 10 most abundant and any taxa unclassified at that level (e.g. taxa not identified to a genus level), this results in the ‘Other’ category remaining even when <10 taxa are included in the analysis (e.g. in B ‘Other’ is comprised solely of taxa unclassified at the Genus level).

MDS plots

Multidimensional scaling plots (MDS plots) visualise the similarity between all replicates at a site. Replicates are coloured by sample and 95% confidence circles are drawn for each sample. We expect that replicates within a sample should cluster together but that depending on the impact of the sampling date (e.g. pre/post cyclone, season) the samples will vary in similarity from each other.

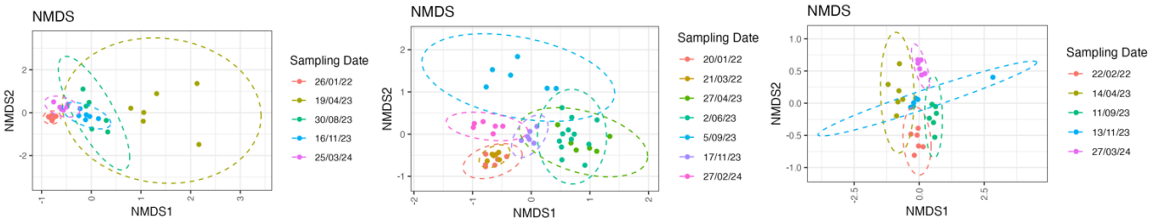


Figure 12. MDS plots for three sites. Replicates for a sample are coloured and 95% confidence interval curves drawn. We note that for many sites the samples post cyclone (2023) show higher levels of variation (less clustering) and are spatial separated from 2022 and 2024 sites in the MDS plot, indicating that these post-cyclone samples are more dissimilar (highlighted here in the first two plots). This effect seems to largely dissipate by 2024. The third plot highlights the issue that outlier points can have on data interpretation. Further examination of this site shows that the outlier replicate (in blue) has not achieved adequate sequencing depth (rarefaction curve) and care should be taken to avoid spurious interpretations.

Alpha diversity estimates

Alpha diversity estimates within samples are calculated within a sample and displayed as a boxplot. Alpha diversity estimates describe the diversity within a sample and can be calculated using several different available measures; Observed, Chao1, Shannon, Simpson and InvSimpson. The different

measures vary in how they estimate diversity. Briefly, Observed represents the raw taxa richness, Chao1 focuses on richness and corrects for low abundance taxa, Shannon considers both richness and evenness, Simpson is similar to Shannon but gives more weight to abundant or more dominant taxa (note that this is calculated as 1-D or the Gini-Simpson index) and InvsSimpson is the Inverse Simpson index or 1/D. A fixed scale can be set in the Simpson analysis. Chao1, Shannon and Simpson analyses are calculated from the raw input values (e.g. uses read proportionality), due to the nature of these datasets some caution should be used in their interpretation (use of proportionality in eDNA datasets is discussed in the map dashboard section).

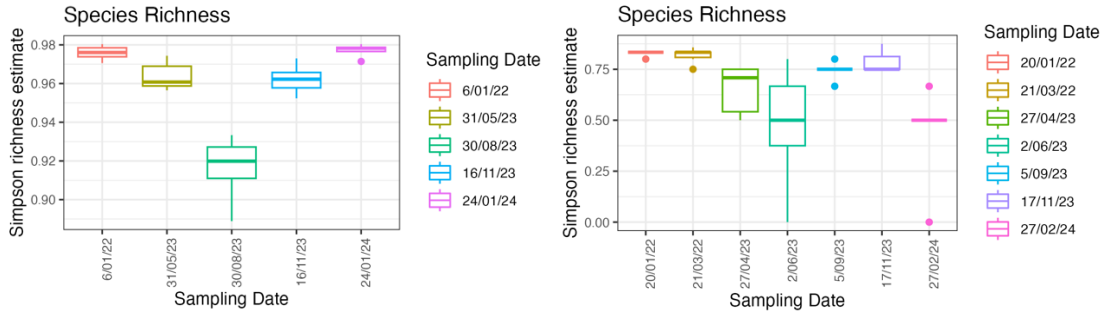


Figure 13. A-B) Shannon diversity estimates for two sites/assays. Diversity estimates are computed within a sample and displayed as a boxplot. Five alpha diversity estimates can be estimated for each assay.

Hill numbers

Coverage based diversity estimates (Hill numbers) are estimated within a sample. Hill numbers are plotted with a rarefaction and extrapolation to understand the impact of sampling and are plotted for three diversity estimates: q=0, q=1 and q=2. Detailed information on Hill numbers and their calculation can be found (Alberdi and Gilbert 2019). Briefly, q=0 is known as the species richness of taxonomic distinctness index and focuses on counting taxa without considering abundances and is useful when you want to consider the presence/absence of species without their relative abundances. q=2 corresponds to the Shannon-Wiener diversity index (Shannon entropy) and considers both the richness and evenness (abundances) of taxa and is useful if you want to give equal importance to richness and evenness. Finally, q=3 corresponds to the Simpson diversity index which emphasises the dominance of the most abundant species in a community and is useful when you want to give weight to the presence of dominant species. The Hill numbers implemented here are implemented through the iNEXT framework, which includes some variations from the original descriptions (see (Chao, Henderson et al. 2021)) for full details. Unlike the box plot values they are calculated using the incidence values (sum of presence/absence across replicates at a sample) and represent a more appropriate analysis for this type of data. This figure will not be displayed if the number of taxa is below 10 or less than 5 replicates are included per sample.

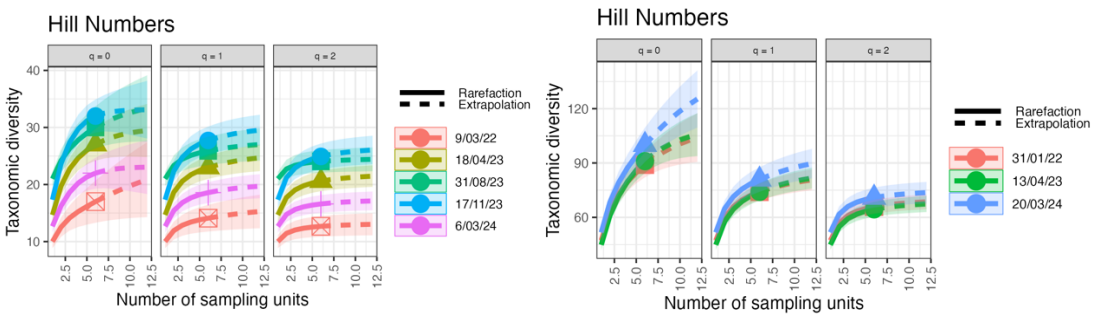


Figure 14. Coverage based diversity estimates (Hill number) for two sites. If samples have reached asymptote diversity estimates will not be impacted by the addition of more samples. Depending on the type of analysis (q=0-2) the impact of the sampling on diversity estimates will vary.

PERMANOVA

Lastly, we display a PERMANOVA table to assess whether there are statistically significant differences between the samples (e.g. collection dates). This is calculated from a dissimilarity matrix (using the presence/absence ASV table) and displayed as a table.

PERMANOVA: ASV distance matrix ~ Sampling Date

Statistic	N	Mean	St. Dev.	Min	Max
Df	3	6.667	3.512	3	10
SumOfSqs	3	0.697	0.354	0.337	1.045
R2	3	0.667	0.339	0.322	1.000
F	1	1.111		1.111	1.111
Pr(> F)	1	0.455		0.455	0.455

PERMANOVA: ASV distance matrix ~ Sampling Date

Statistic	N	Mean	St. Dev.	Min	Max
Df	3	6.667	3.512	3	10
SumOfSqs	3	0.697	0.354	0.337	1.045
R2	3	0.667	0.339	0.322	1.000
F	1	1.111		1.111	1.111
Pr(> F)	1	0.455		0.455	0.455

Figure 15. PERMANOVA tables. Two PERMANOVA analyses, mean Df, R^2, F and P-values are highlighted in the red box in the table summaries. In these examples there is a significant difference between samples (e.g. sampling dates) in first analysis.

Community analyses

To understand how communities recovered through time across the landscape we developed a dashboard to highlight how diversity changed at a site pre vs post cyclone, post cyclone vs 2024 (short term recovery) and pre cyclone vs 2024 (long-term recovery). For this analysis we only considered samples that were collected outside of June 1st – October 31st to avoid a conflation with season. We limited our analysis to the CI (insect communities), RV (freshwater fish communities) and WV (freshwater fish communities) assays as they targeted known freshwater animals and could be filtered using our freshwater species list to avoid the issue of terrestrial species contamination post cyclone. We then calculated the diversity change in freshwater taxa between three dates: pre and post cyclone, pre-cyclone to 2024 (1 year post) and post-cyclone (2023) to 2024 (1 year post). Diversity change was calculated in four different ways; observed diversity changes (calculate using the average observed diversity change at a site), incidence observed diversity changes (calculated from the summed incidence observation at a site), Shannon diversity changes (calculated from the incidence data) and Simpson diversity changes (calculated from the incidence data). As not all sites were sampled at every year not all sites are available in each comparison. These analyses allow end users to understand the spatial relationships of the temporal shifts across the region and enable a direct comparison of diversity change with other knowledge about abiotic and biotic factors at each site. Due to the timing of the GIS data availability (Dec 2024) the analyses comparing diversity changes to abiotic and biotic factors form part of an ongoing project between Biodiscover and HBRC.

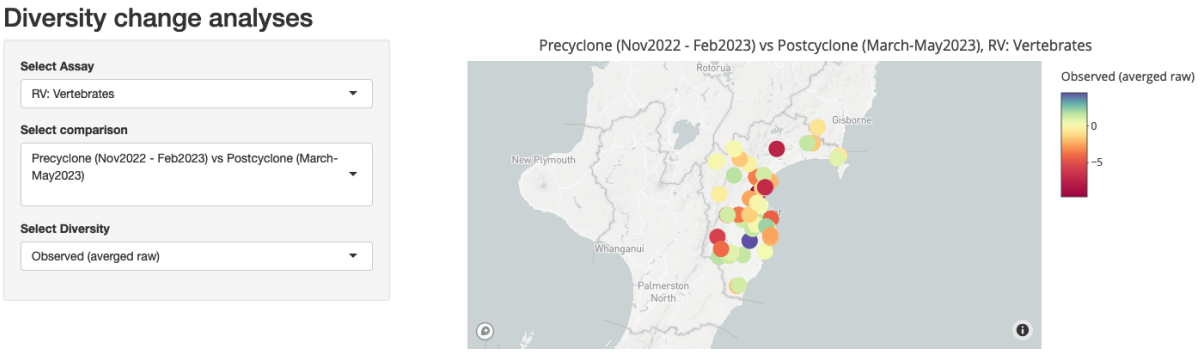


Figure 16. Dashboard overview of diversity changes pre and post cyclone. Negative values indicate a loss of observed species richness post cyclone.

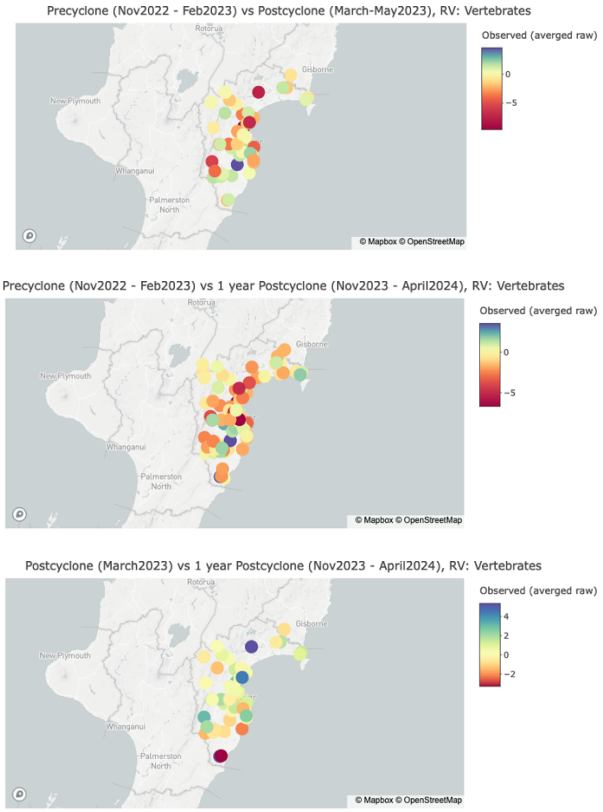


Figure 17. Diversity changes pre-post cyclone, pre cyclone vs 1 year post cyclone, and post cyclone vs 1 year later for the fish assay RV. The pre-post cyclone highlights the initial impact of the cyclone, the pre-cyclone vs 1-year post cyclone highlights the long-term recovery of a site, while the post cyclone vs 1 year post cyclone highlights the recovery immediately following the cyclone.

Discussion

Extreme weather events such as Cyclone Gabrielle are not uncommon in Aotearoa, but climate projections indicate that such devastating events will increase over the coming years (Maxwell, Butt et al. 2019). These events threaten the robustness of ecosystems and the essential services they provide. Building effective temporal tools to understand how ecosystems recover and what impact management practices have on this recovery is critical. eDNA is a swift and effective tool that are

fast becoming incorporated into monitoring programs globally. Yet their incorporation can be limited by a at times steep technical barrier, especially when datasets are fragmented and partitioned across agencies and areas. But the exploitation of these datasets is important to build our understanding of how taxa and ecosystems react to precipitation extremes, data central to land managers and end-users looking to support resilient ecosystems that can mitigate the impact of future extreme events.

Here we showcase the importance of long term eDNA datasets in understanding how individual taxa and communities recover across time following the devastating Cyclone Gabrielle. The easy-to-use dashboards developed in this report enable end-users to answer several key questions about the resilience and susceptibility of taxa and communities to Cyclone Gabrielle while ensuring that the data results is interpreted in a statistically robust manner. This approach is relevant to councils and community groups across Aotearoa.

The first dashboard highlights how species distributions change before and after an extreme event to addresses two significant questions. Firstly, what immediate impact does an event have on a taxa and secondly how does a taxa recover from an event? Both questions require consistent temporal sampling both prior to and post an extreme event. The dashboard allows end-users to understand a taxa's resilience and through the identification of sites in which susceptible taxa persisted identify management practices that may support their recovery.

Our second dashboard focuses on understanding how each site responded to and recovered from Cyclone Gabrielle. Understanding how a community responds to an extreme weather event allows us to delve into what factors (land use, riparian plantings etc) might impact a species recovery. By combing the three datasets available we were able to generate 91 sites covering a wide range of factors with pre and post cyclone sampling. This extensive dataset covers a wide range of environments. The site-by-site application allows end-users to explore site diversity changes at various scales across several analyses. These results highlight how communities were impacted by the initial event and how they have recovered in the subsequent 2024 season. Critically we have included several statistical analyses to ensure that both the robustness of the data and resulting statistical tests can be assessed easily and effectively by end-users.

Our third dashboards highlights how species diversity has recovered across the HB region. It enables the quick identification of sites or areas that have or have not recovered post cyclone, highlights how diversity has changed 1-year post cyclone and compares current diversity estimates to levels pre-cyclone for a glimpse at their long-term recovery. This dataset of diversity change can be integrated into future models of how recovery was impacted by biotic and abiotic factors.

Cyclone Gabrielle caused immense economic and environmental damage across Aotearoa. Understanding how ecosystems responded and recover from the disaster is critical to helping support resilient systems moving forward. eDNA is a swift and effective approach that can be used alongside other traditional monitoring programs. There are currently several commercial suppliers operating in Aotearoa that offer eDNA sequencing services (Wilderlab and Sequench). However, these suppliers focus on data generation and not data interpretation which can require a specialist understanding, especially when incorporating voluminous temporal datasets. As a result, despite its integration into local and central government monitoring programs eDNA datasets are at times not placed in ecologically relevant contexts, restricting our ability to exploit them to answer questions about species and community responses across temporal scales. Due to the data's complexity and sheer size, along with the variety in questions end-users have our approach in this

report has been to not give an answer to the question of how did a site or taxa respond to Cyclone Gabrielle, but rather to provide easy to interpret and use tools to enable end-users to assess their questions and taxa of interest. Our hope is that this approach will be of more long-term use than selectively reporting on some taxa and sites.

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