

Resilient Rivers, the ecosystem health monitoring program, and eDNA across Southeast Queensland: Towards scalable biotic monitoring of ecosystem condition

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Key points

- The Resilient Rivers eDNA monitoring program sampled 245 stream reaches across southeast Queensland in a single spring 2025 round.
- The survey was designed partly around long-term Ecosystem Health Monitoring Programme (EHMP) waterway monitoring stations.
- eDNA reproduces EHMP condition scores on the same scale and predicts upstream catchment context comparably to macroinvertebrate sampling, while adding species-level detections for key vertebrates and other groups.
- Findings will be strengthened by future seasonal eDNA monitoring data.

Abstract

As part of the Resilient Rivers SEQ program, comprehensive environmental DNA (eDNA) sampling was undertaken with the aim of tracking rehabilitation efforts and key species across the region. We sampled 245 stream reaches in spring 2025; half co-located with an active station from the Ecosystem Health Monitoring Programme (EHMP). We use this co-located dataset to ask two questions. First, how well does eDNA recover EHMP-derived condition scores: initial analyses here discuss SIGNAL2 (a macroinvertebrate pollution-sensitivity index) and O/E50 (the ratio of observed to expected native fish species relative to a reference condition)? Second, treating measured upstream catchment context as the best available proxy for ecosystem condition, which data source reflects that context most faithfully? A simple eDNA-derived SIGNAL2 computed from the macroinvertebrate families eDNA detected tracks EHMP SIGNAL2 across the co-located reaches with reasonable fidelity (Pearson $r \approx 0.6$). Predicting an unmonitored reach is more challenging, and under spatial cross-validation eDNA recovers SIGNAL2 at $R^2 \approx 0.54$. The same samples identify threatened natives (platypus, Australian lungfish, Oxleyan pygmy perch), invasive pests including tilapia, and declining species that are hard to survey by conventional means. We report initial findings here, which will be bolstered by a second round of sampling underway for autumn 2026.

Keywords

environmental DNA, ecosystem condition, monitoring, SIGNAL2, catchment health, predictive modelling

Introduction

The Resilient Rivers Program

The Resilient Rivers South East Queensland initiative (RRSEQ) is a multi-decade partnership between the Council of Mayors (SEQ), the region's local councils, the Australian Government, the Queensland Government, Seqwater and Healthy Land & Water. It was established following the 2011 and 2013 SEQ floods to coordinate catchment-scale investment in waterway and wetland condition (revegetation, weed management, fish-passage works and sediment-load reduction) across the catchments of Moreton Bay. The SEQ City Deal has committed to furthering these objectives, with scientific research that helps target on-ground investment and quantify ecological return a key pillar of the initiative.

Stream condition monitoring in SEQ

Stream-condition information in SEQ is currently anchored by the Ecosystem Health Monitoring Programme (EHMP), run by Healthy Land & Water. This program has sampled around 135 freshwater reaches per year over 25+ years with water-quality, macroinvertebrate and fish surveys, all contributing to a regional report card. Two EHMP metrics anchor the analyses below. SIGNAL2 (Stream Invertebrate Grade Number Average Level; Chessman 2003) scores a site by the pollution sensitivity of the macroinvertebrate families present in a standardised streambed kick-net sample. O/E50 is the ratio of observed to expected native fish species relative to a reference condition.

This kind of monitoring is powerful but resource-intensive: each visit requires a trained operator, field kick-netting or electrofishing, and expert identification. This limits data availability, both within and beyond the EHMP network. eDNA methods have been proposed to extend the spatial and taxonomic reach of monitoring at lower cost, but direct, landscape-scale comparisons of eDNA against established health metrics are required to understand power, spatial resolution, and structuring factors that influence model applicability.

This study

Wildlife Queensland collected duplicate water samples at 245 SEQ reaches in spring 2025. Of these, 133 are within 2 km of an active EHMP station (118 essentially at the same reach). This co-located design lets us calibrate eDNA against EHMP where both exist, then predict the calibrated signal to the many reaches where only eDNA was collected.

The dataset addresses several questions; two are outlined here:

1. **Alignment with existing metrics.** Across the directly co-located reaches, how closely does eDNA recover EHMP-derived condition scores (SIGNAL2, O/E50)?
2. **Which data source mirrors catchment condition best.** Treating measured upstream catchment context (land use at multiple buffer scales, riparian vegetation and canopy structure, long-term water quality, and 20-year forest-loss disturbance) as the best available proxy for actual ecosystem condition, how faithfully does each data source (the eDNA community, the EHMP macroinvertebrate community, or the summary indices derived from either) reflect that context?

Methods

- **Sampling.** Paired water samples (median 5 L per replicate) at 245 sites using Smith-Root 5µm self-preserving filters.
- **eDNA metabarcoding panel.** Eleven assays per water sample, spanning bacteria (16S), microeukaryotes (18S), algae and plants (ITS2, trnL), aquatic macroinvertebrates (COI), and fish and other vertebrates (12S, 16S). Detected sequences are assigned to taxa against reference databases.
- **Environmental data.** Upstream catchment and riparian-corridor land use at multiple buffer scales; multi-year satellite measures of vegetation greenness, surface water and elevation; satellite-lidar canopy height and cover; long-term EHMP water-quality records; and 20-year satellite-derived forest-loss disturbance.
- **Prediction and cross-validation.** Condition scores are predicted from the eDNA and environmental data with approaches varying in simplicity and power (here, we show supervised weighted averaging and random forest models. The Chessman iterative learning approach that works well across NZ fails in SEQ). To measure how well a model would score a new, unmonitored reach, we use spatial cross-validation so the model cannot simply interpolate from nearby neighbours. Reported R^2 is the fraction of variance explained on held-out reaches above a catchment-wide-mean baseline.

Results from Spring 2025

Study area

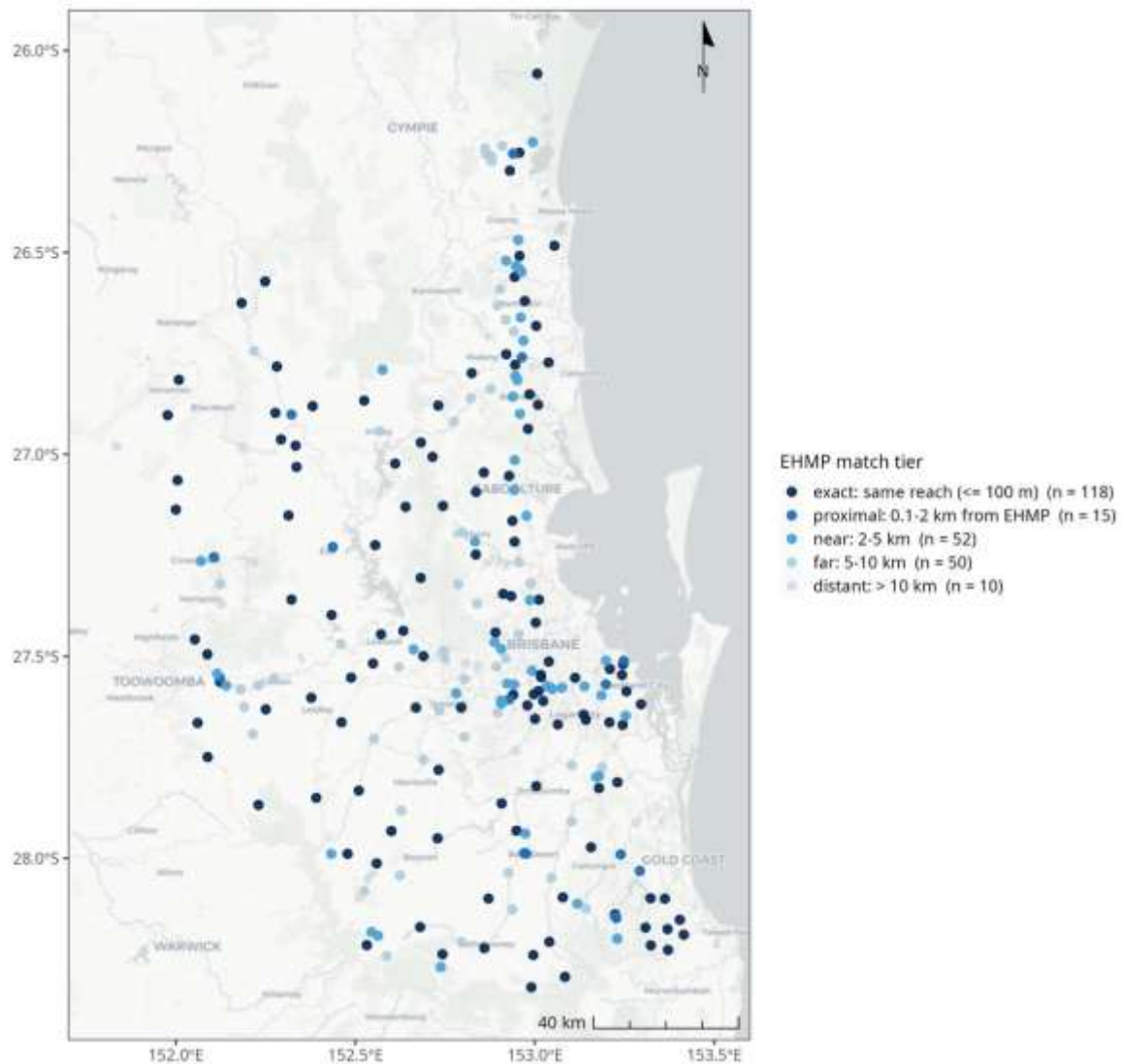


Figure 1 Spring 2025 eDNA sampling reaches across Southeast Queensland (n = 245), classified by distance to the nearest active EHMP station. The ‘exact’ and ‘proximal’ set (n = 133) is used for the eDNA-versus-EHMP comparison

How well does eDNA recover EHMP SIGNAL2?

Figure 2 shows the most simple and interpretable approaches to comparing eDNA and SIGNAL scores: directly applying Chessman (2003) grades to the macroinvertebrate families eDNA detects (A), and a supervised weighted-averaging index (B). The two approaches differ in what they do: panel A weights and fits nothing, panel B tunes a taxon-by-taxon index to the data and is then scored on the same reaches it was tuned on. Both are optimistic, because neither is asked to predict a reach it has not already seen.

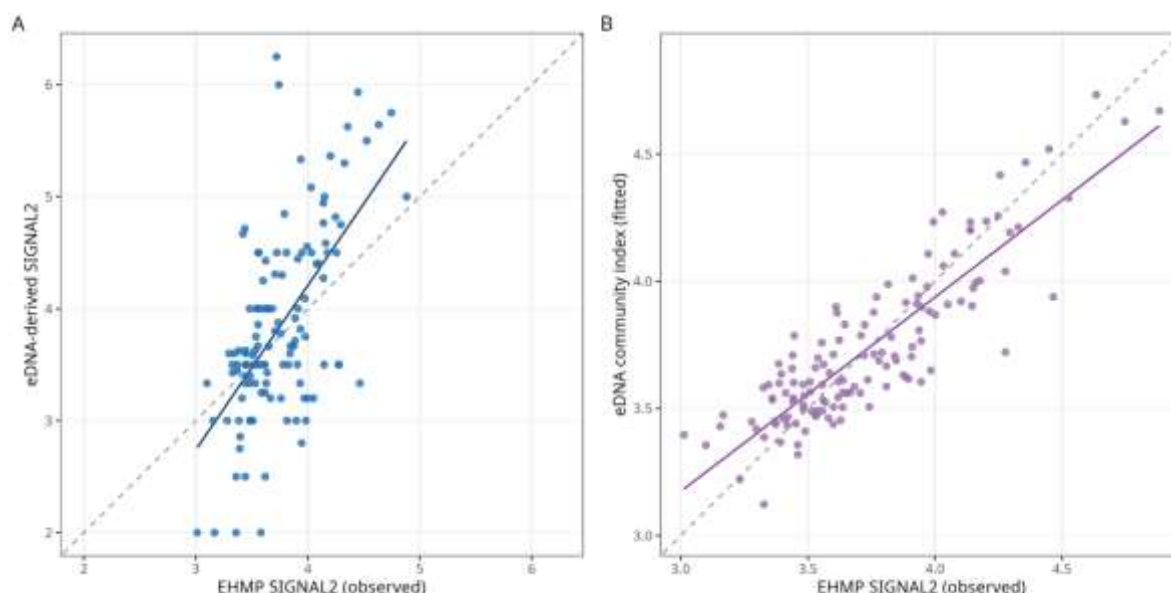


Figure 2 Two simple views of eDNA-derived SIGNAL2. (A) A direct, untrained calculation: Chessman (2003) grades applied to the macroinvertebrate families eDNA detects, versus EHMP SIGNAL2 ($r \approx 0.61$, $n = 123$). (B) A one-dimensional community index fit to, and scored on, the same reaches ($R^2 \approx 0.76$). Grey dashed lines are 1:1

The test that matters for a monitoring program is more nuanced: predict the score at a reach the model has never seen. Under a spatial cross-validated random forest model, the eDNA community recovers long-term-mean SIGNAL2 at $R^2 \approx 0.54$ (Figure 3). This forecast is relevant to extrapolation to a new catchment or region with similar stream types. For denser sampling within the existing EHMP network (interpolation within the monitored catchments) the estimate is $R^2 \approx 0.71$ within a single stream type.

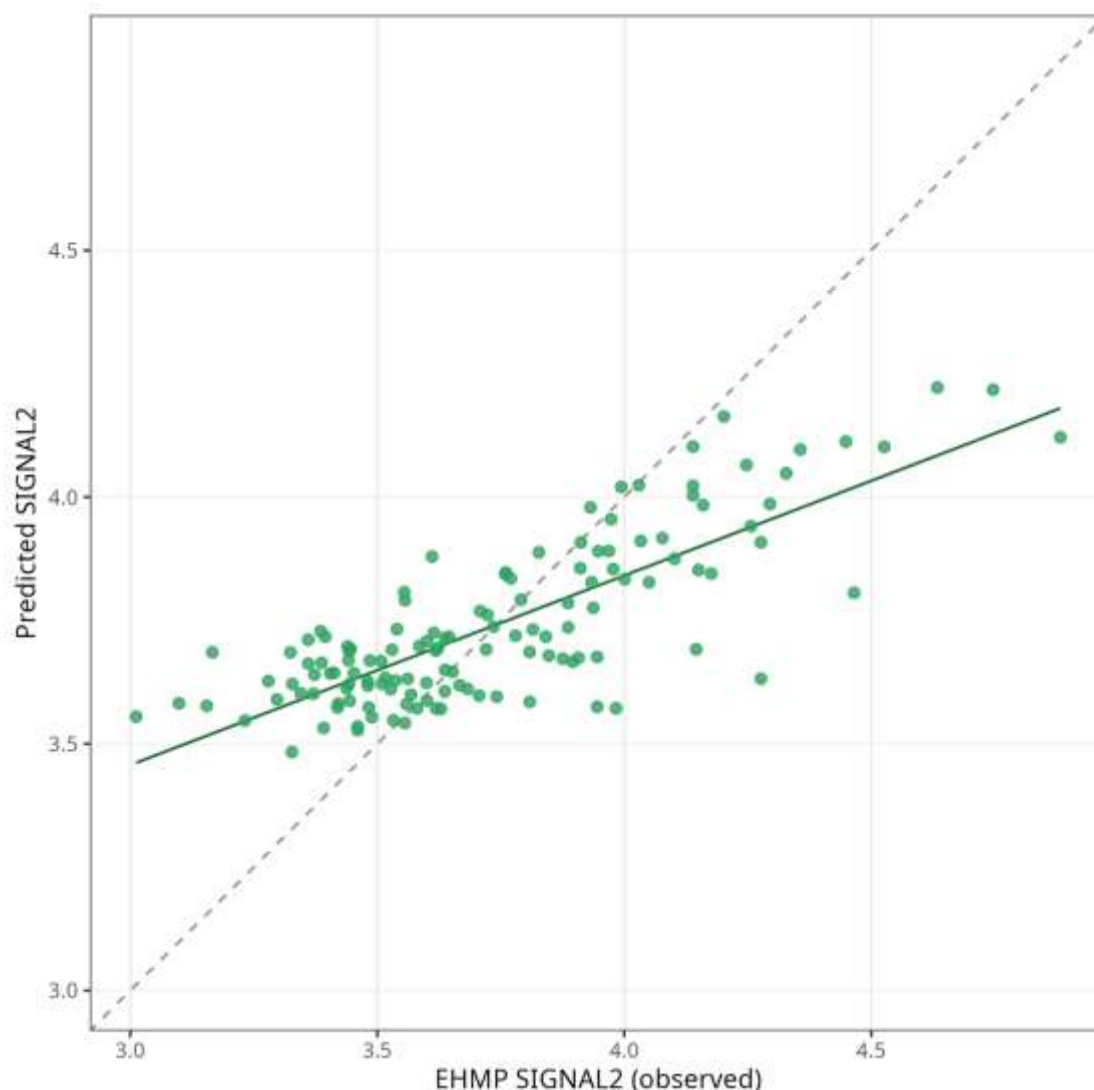


Figure 3 Predicting an unseen reach: eDNA community alone predicting EHMP long-term-mean SIGNAL2 at reaches held out under random forest with spatial cross-validation ($R^2 \approx 0.54$, $n = 132$). Each point is a reach the model was not trained on, and whose near neighbours were also withheld. Grey dashed line is 1:1

For SIGNAL2 the eDNA community and a full landscape-and-satellite model perform about equally, with SIGNAL2 strongly determined by catchment. For the native-fish O/E50 index, environmental data is essentially uninformative, while eDNA recovers it at $R^2 \approx 0.38$. As a direct biotic indicator calibrated on co-located reaches, eDNA-based predictions can be applied to every reach, including those with no EHMP station, to map predicted condition across the network (e.g. SIGNAL2 scores in Figure 4).

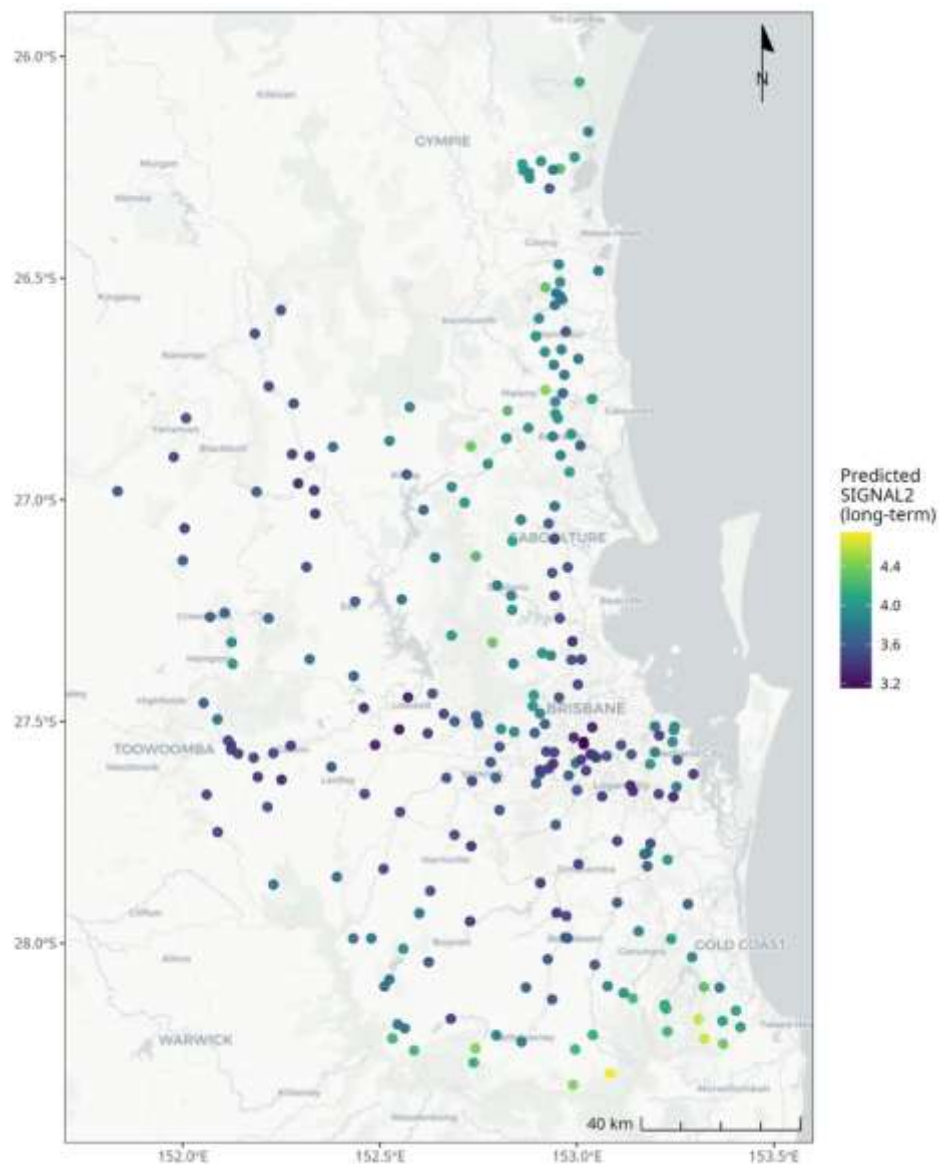


Figure 4 Predicted long-term-mean SIGNAL2 for all 245 eDNA reaches, from the eDNA model applied across the network. Higher scores (yellow, green) indicate predicted-cleaner reaches; lower scores (purple, dark) indicate predicted-degraded reaches

The eDNA model recovers biologically interpretable indicators: the strongest clean-water SIGNAL2 indicators are mayflies (*Austrophlebioides*, *Atalophlebia*), riffle beetles (*Sclerocyphon*), caddisflies (*Ethochorema*), the native shrimp *Australatya striolata* and stream frogs (*Litoria*). The strongest degraded-water indicators are the eastern mosquitofish *Gambusia holbrooki*, carp, and nutrient-associated bacteria and diatoms. For the native-fish O/E50 index, the positive indicators are native fish (Australian smelt *Retropinna semoni*, Australian bass *Macquaria novemaculeata*, rainbowfish *Melanotaenia*, eel-tailed catfish *Tandanus tandanus*), while the negatives include the DNA of cleared and weedy catchments (invasive hackberry *Celtis sinensis*, *Ruellia*, Sapindaceae) and nitrogen-cycling

bacteria (Nitrosomonadaceae, Rhodocyclaceae), a direct molecular fingerprint of nutrient enrichment and riparian clearing.

Beyond driving the condition indices, the same panel detects individual species of direct interest to catchment managers and recovery teams. Threatened and significant natives detected include the EPBC-listed Australian lungfish (8), southern barred frog (7), Oxleyan pygmy perch (2), the iconic platypus (25 reaches), and the narrow-range endemic Lamington spiny crayfish. Established pest fish were detected widely: eastern mosquitofish (144 reaches), tilapia (65 reaches, a declared noxious pest in Queensland), green swordtail (55), southern platyfish (47), the pearl cichlid (20), and common carp (7).

Which data best reflect broader catchment context

Rather than predicting EHMP from eDNA, we ask which biotic data source best predicts measured upstream catchment context (Figure 6). Two results stand out:

1. Community data beats summary indices. The full community matrix, from eDNA or EHMP, predicts upstream land use far better than the collapsed summary indices (SIGNAL2, O/E50).
2. The eDNA community predicts upstream land use similarly to the EHMP kick-net community. A single eDNA round (two replicates per site) carries roughly as much land-use information as two averaged EHMP kick-net sampling events.

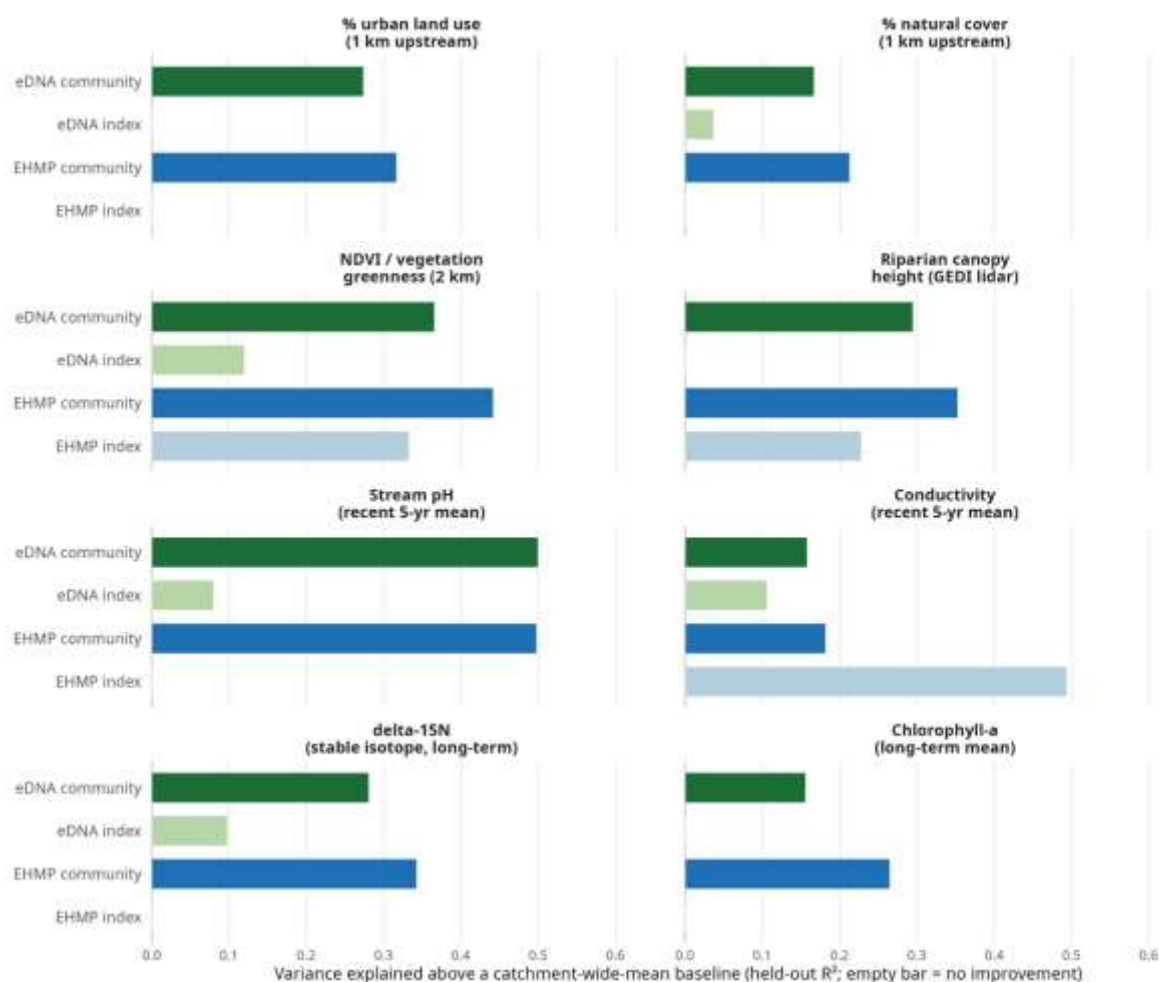


Figure 6 Predictive performance of four data sources for catchment-context and water-quality. Bars show the fraction of variance explained over a catchment-wide-mean baseline, on held-out reaches. The four sources are the EHMP summary indices (SIGNAL and O/E50), EHMP

macroinvertebrate community, eDNA summary indices, and eDNA community. Community matrices consistently outperform the summary indices in both programs

Where the eDNA model is wrong, and why

The SIGNAL2 predictions are reasonably tight (root-mean-square error, RMSE, ≈ 0.20 grade-units on the 1–10 scale), but the errors are informative. eDNA in flowing water is a cumulative, catchment-integrated signal that diverges predictably from kick-net sampling where a reach's upstream catchment differs from its local condition.

- Intact, forested reaches are under-predicted. The model sees a catchment with recent upstream disturbance and expects degradation, but both the kick-net and the eDNA panel find a community still close to reference condition; the biological community has not yet responded or the disturbance is not the limiting stressor.
- Urban reaches with clean upstream remnants are over-predicted. Here eDNA registers sensitive taxa carried downstream from upstream forest remnants, while the local kick-net community is degraded.

Current models capture part of this through multi-radius upstream land-use predictors. The more complete solution is a stream-network transport model that attributes detected eDNA to its likely upstream origin given network topology, hydrology and decay with distance, the subject of ongoing work.

Discussion and conclusions

eDNA can deliver EHMP-familiar scores wherever a sample can be taken. From one spring water sampling, a calibrated model extrapolates reasonably well to unmonitored reaches ($R^2 \approx 0.54$) and interpolates within a network strongly ($R^2 \approx 0.71$).

For questions where catchment condition itself is the target, community data is essential. The eDNA community matches the EHMP macroinvertebrate community at predicting upstream land use, and both far exceed the summary indices, a reminder that collapsing a community to a single index discards most of the landscape signal. This positions eDNA well for landscape-scale stressor mapping, where one water sample carries roughly the information of two kick-net visits.

eDNA adds data conventional programs cannot. The same samples map threatened, cryptic and declining species (platypus, lungfish, purple-spotted gudgeon) and invasive pests including tilapia, and resolve bacterial and diatom signals tied to water chemistry.

Habitat stratification is essential. Distinctive habitats such as coastal regions and acidic wallum streams have distinctive communities. These are relatively undersampled at present, and models consequently predict their condition poorly.

Although the predictive power of the eDNA models above are relatively strong against existing metrics, it's important to acknowledge the analyses here compare a single eDNA sampling event with many years of accumulated data. Incorporating data from the second sampling season here, and from other exemplary regions, will allow partitioning of temporal and spatial variation and calibrated eDNA sampling plans for other regions.

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initiative of Council of Mayors (SEQ) delivering coordinated catchment management for healthy and resilient waterways and wetlands across SEQ.

References

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