



Original Software Publication

ForamEcoQS: An analytical software suite for foraminiferal ecological quality status assessment

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ABSTRACT

ForamEcoQS is an open-source desktop application for Ecological Quality Status assessment based on foraminifera, single-celled, predominantly marine organisms that typically produce a shell. It imports species abundance matrices, resolves taxonomic names against regional ecological-group lists, calculates diversity descriptors and major foraminiferal biotic indices, converts outputs to five EcoQS classes, and exports tables and figures. The software combines an interactive Windows graphical interface with a command-line mode for reproducible batch processing. Validation against published reference datasets, independent Python and R package implementations, and a large-scale stress test of 3491 samples confirms high numerical agreement, while configurable reference lists and thresholds make methodological choices explicit for monitoring and research workflows.

Metadata

Nr	Code metadata description	Metadata
C1	Current code version	v1.0.0
C2	Permanent link to code/repository used for this code version	https://github.com/uniurb/bit/ForamEcoQS
C3	Legal code license	MIT License
C4	Code versioning system used	git
C5	Software code languages, tools and services used	C#; Microsoft .NET 6.0; Windows Forms; ClosedXML v0.102.3; ExcelDataReader v3.7.0; OxyPlot v2.1.2
C6	Compilation requirements, operating environments and dependencies	Microsoft Windows 10 64-bit or later; .NET 6.0 Desktop Runtime for Windows if compiling manually; any x64 processor; ≥4 GB RAM; ≥200 MB free disk space.
C7	If available, link to developer documentation/manual	Repository README and documentation: https://github.com/uniurb/bit/ForamEcoQS
C8	Support email for questions	m.mangiagalli@campus.uniurb.it; fabrizio.frontalini@uniurb.it; fabio.francescangeli@unifr.ch

1. Motivation and significance

Marine sediments integrate the cumulative effects of multiple

anthropogenic pressures, including contaminant inputs, organic enrichment and physical disturbance. They therefore represent valuable archives for assessing environmental change and ecosystem health. Environmental legislation such as the European Water Framework Directive and the Marine Strategy Framework Directive requires the assessment of ecological quality status (EcoQS) for marine and transitional waters through biological quality elements (BQEs) [1,2]. In this context, benthic foraminifera, single-celled organisms living on or within marine sediments, are widely used as BQEs of human-derived environmental change because they are abundant, diverse, rapidly responsive to environmental change and well preserved in sediments [3–5]. Their spatial distribution in bottom sediments is controlled by a wide range of environmental variables and ecological parameters [6–8]. More recently, ecological indices based on benthic foraminifera (e.g., Foram-AMBI, TSI-Med, exp(H'bc), Foraminiferal Stress Index) have been developed and applied for EcoQS evaluation [9–15]. Documented applications include Atlantic and Mediterranean areas [16–21], Brazilian transitional systems [22,23], Indian estuaries [24] and Arabian waters [25].

Despite this potential, routine foraminiferal EcoQS assessment remains fragmented. Users commonly combine spreadsheet calculations, regional species lists, manual taxonomic harmonisation and separate plotting tools. This increases processing time and makes results sensitive to undocumented choices in species assignment, index selection and

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threshold systems. Reviews of foraminiferal biotic indices have also emphasised that different indices and regional calibrations can produce non-equivalent classifications for the same assemblage [26].

ForamEcoQS addresses this problem by providing a single open-source desktop application for importing foraminiferal abundance matrices, matching taxa to ecological-group reference lists, calculating diversity descriptors and foraminiferal biotic indices, converting outputs to the five EcoQS classes, and exporting tables and graphics. The target users are researchers, monitoring laboratories and environmental managers who need transparent, repeatable calculations rather than a collection of manual steps. ForamEcoQS's contribution is a software-engineering integration of previously published indices and workflows rather than a new ecological method or index: every calculated index and threshold system originates from the cited primary literature.

The software contributes to scientific discovery and applied monitoring by making alternative index and threshold choices explicit. Users can compare EcoQS classifications across indices, quantify agreement among classification systems, and document the reference list used for each calculation. This supports inter-study comparability, sensitivity analysis and reproducible reporting in foraminifera-based biomonitoring.

2. Software description

ForamEcoQS is implemented in C# as a Microsoft .NET Windows Forms application (currently targeting .NET 10, a supported long-term release). The program provides both an interactive graphical user interface and a command-line mode for scripted batch processing. It runs as a self-contained Windows desktop tool and does not require R, Python or proprietary statistical software at runtime. Windows Forms was chosen because it matched the authors' existing development experience and shortened delivery time; migration to a cross-platform framework is discussed as planned future work in Section 4.

The application is organised around modules for data ingestion, reference-list management, taxonomic matching, index calculation, EcoQS classification, visualisation and export. Input can be provided as Excel workbooks (.xls, .xlsx) or as delimited CSV files; Excel input/output specifically is handled with ClosedXML and ExcelDataReader, while plots are produced with OxyPlot. All numerical calculations are performed in double precision.

2.1. Software architecture

The typical processing pipeline is shown in Fig. 1. Users load an Excel or CSV species abundance matrix, select the most appropriate biogeographic reference list, resolve species names through exact, normalised and genus-level matching, optionally apply manual ecological-group overrides, normalise abundance data, select indices and export tabular or graphical outputs. The same calculation engine is used by the GUI and CLI modes, reducing the risk of workflow-dependent numerical differences.

Species-name resolution proceeds in three steps: (i) an exact, case-insensitive match against the selected reference list; (ii) a normalised match after stripping author citations and bracketed annotations (for example, matching "Ammonia parkinsoniana (d'Orbigny, 1839)" to "Ammonia parkinsoniana"); and (iii) a genus-level fallback that assigns an unmatched species to a "Genus sp." entry when the reference list provides one. This fallback does not merge distinct named species into a single reference taxon; it only applies when no more specific match exists. A name resolved at any of the three steps inherits the ecological group of the corresponding reference taxon.

Taxa that remain unmatched can optionally be checked against the WoRMS online taxonomic database [27], which indicates whether a name is a currently accepted or considered a synonym, and if applicable provides the corresponding accepted name. However, ForamEcoQS does not automatically reassign the ecological group of a synonymous taxa;

applying this information remains a user decision and is recorded through the persistent override mechanism described in Section 2.2. All assignments are presented to the user in a colour-coded matching report, and any override entered at this point is stored and reapplied automatically in subsequent runs.

Removal of unmatched taxa and rescaling of sample abundances to 100% are optional, as is the entry of the mud percentage, which is required only when a selected metric depends on grain-size data. Results are reported as numerical values and as an EQS classification for each sample, and can be exported to an Excel workbook or as image files.

Unresolved taxa are treated differently by the two families of calculations. Diversity descriptors (Shannon H', Simpson diversity, Pielou's J, ES(100), species richness, total abundance) are computed from the complete abundance vector for a sample regardless of taxonomic matching status, so an unresolved species still contributes to these values exactly as a resolved one would. Sensitivity-based indices (Foram-AMBI, FSI, TSI-Med, BENTIX, BQI, FoRAM Index, NQIf, FIEI, Foram-M-AMBI) instead depend on ecological-group percentages: an unresolved species contributes to the total-abundance denominator but not to any group's numerator, so a high proportion of unresolved taxa dilutes these percentages towards zero rather than being silently excluded. The percentage of the assemblage actually assigned to an ecological group is tracked and displayed for FSI and FoRAM Index (Fig. 2, "FSI Assigned %"); unmatched rows are additionally highlighted in the GUI grid (Fig. 2) and listed as warnings in the CLI log.

Input files must contain species names in the first column and sample abundances in subsequent columns. An optional mud-percentage row is detected for TSI-Med calculations. Species names containing author citations or annotations are normalised before matching. Unmatched taxa are highlighted in the GUI and can be excluded, manually assigned or handled with user-supplied custom lists. The mud-percentage row, when present, is an additional row (not column), labelled "mud", "mud (%)" or "%mud", placed alongside the species rows with one value per sample column (for example: row 1 = Species, Sample A, Sample B; row 2 = mud (%), 45, 60; row 3 onward = species abundances). In the command-line workflow, taxa that do not match the selected reference list are logged as warnings and excluded from eco-group-dependent indices; passing the -worms flag additionally checks each unmatched name against the WoRMS database and reports its taxonomic status.

2.2. Software functionalities

ForamEcoQS calculates common diversity descriptors, including Shannon diversity, bias-corrected Shannon diversity and its exponentiated form, Simpson diversity, Pielou evenness, Hurlbert ES(100), species richness and total abundance [28–32]. It also implements sensitivity-based and multivariate indices used in foraminiferal EcoQS assessment, including Foram-AMBI, FSI, TSI-Med, BENTIX, FoRAM Index, FIEI, NQIf, BQI and Foram-M-AMBI [9,11,13–15,33–39]. Formula details are provided in Supplementary Materials 1; extended validation, software comparison, module descriptions, reference lists and EcoQS thresholds are provided in Supplementary Materials 2. As an illustrative example of the underlying formulae (the complete set is given in Supplementary Materials 1), Foram-AMBI is a weighted average of ecological-group proportions, $\text{Foram-AMBI} = (0 \times \text{EG1} + 1.5 \times \text{EG2} + 3 \times \text{EG3} + 4.5 \times \text{EG4} + 6 \times \text{EG5}) / 100$, where EG1–EG5 are the percentage abundances of ecological groups I (most sensitive) to V (most opportunistic) [15]; FSI is $\text{FSI} = (10 \times \text{Sen} + \text{Str}) / (\text{Sen} + \text{Str})$, where Sen and Str are the percentages of stress-sensitive and stress-tolerant taxa, respectively [14]. Because the FoRAM Index was developed for tropical reef assemblages dominated by symbiont-bearing larger foraminifera, ForamEcoQS flags FoRAM Index results with an explicit warning whenever fewer than 20% of the assemblage can be assigned to a FoRAM Index functional group (symbiont-bearing, stress-tolerant or other heterotrophic), signalling that the index is unlikely to be ecologically meaningful for that sample rather than returning an unqualified value [35].

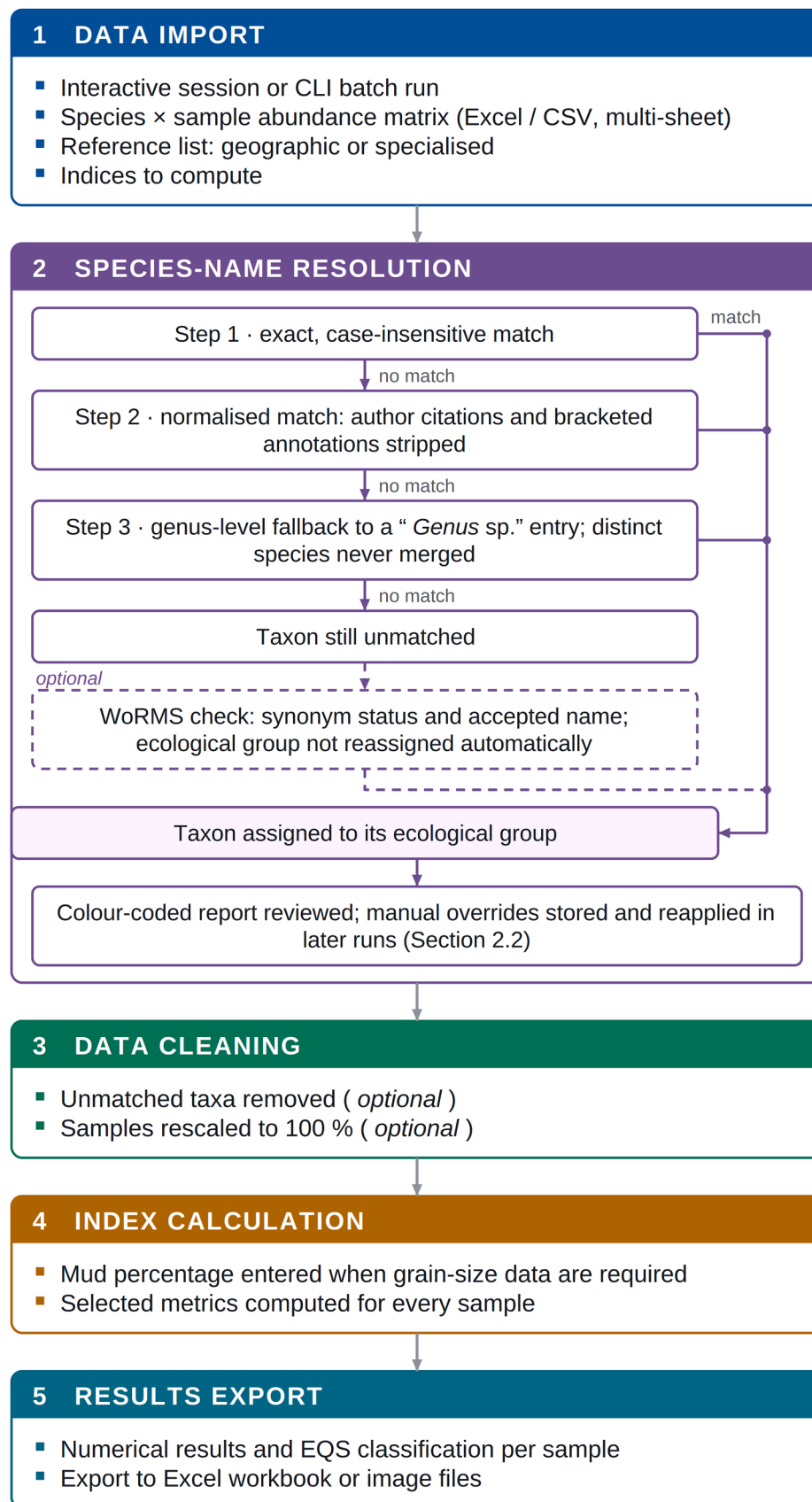
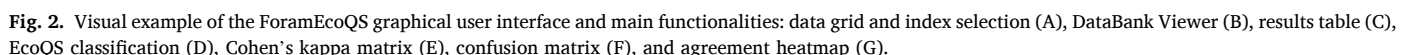


Fig. 1. Schematic workflow of the ForamecoQS processing pipeline. The pipeline is organised in five stages: data import (1), species-name resolution (2), data cleaning (3), index calculation (4) and results export (5). It can be run either as an interactive session or as a command-line batch job. Dashed outlines and dashed arrows denote optional steps.



Data cleaning (DATA CLEANING, Fig. 1). Input: the matched abundance table. Processing: optional removal of unmatched taxa and optional normalisation of sample totals to 100%, both user-selectable. Decision logic: removal and normalisation are independent toggles, so users can, for example, keep unmatched taxa in diversity calculations while excluding them from a normalised eco-group view. Output: the abundance table passed to index calculation.

Index calculation (INDEX CALCULATION, Fig. 1; BioIndicesCalculator). Input: the (optionally cleaned) abundance table, ecological-group assignments, and, for TSI-Med, the mud percentage. Processing: diversity descriptors are computed from the full abundance vector; sensitivity-based indices are computed from ecological-group percentages as described above. Decision logic: index-specific specialised reference lists (FSI, TSI-Med, FoRAM Index) are loaded automatically when those indices are selected; the FoRAM Index returns a warning instead of a bare number when fewer than 20% of the assemblage is classified into a functional group. Output: one numeric value per index per sample, plus assigned-percentage diagnostics.

EcoQS classification and agreement (Fig. 2D-G). Input: numeric index values and a user-selected threshold system (for example, Borja et al. (2003) versus Parent et al. (2021b) for ForAM-AMBI). Processing: each value is mapped to one of five EcoQS classes; weighted Cohen's kappa and confusion matrices are computed between pairs of indices. Decision logic: threshold boundaries are fixed per index/threshold-system combination and are not inferred from the data; the software does not select a single classification when systems disagree (Section 4). Output: EcoQS class labels per sample per index, plus agreement diagnostics.

Visualisation and export (RESULTS EXPORT, Fig. 1). Input: computed indices, EcoQS classes and agreement diagnostics. Processing: OxyPlot renders bar, line, box, scatter, heatmap and composite plots; ClosedXML assembles Excel workbooks with one row per index and one column per sample. Decision logic: plot type, colour scheme and export resolution (150–1200 DPI) are user-selected. Output: PNG/JPEG figures and Excel workbooks.

3. Illustrative examples

Fig. 2 illustrates the primary user-facing workflow. A user selects the desired ecological and diversity indices, inspects or edits species ecological-group assignments, computes index values by sample, visualises EcoQS classifications, and exports agreement summaries. In GUI mode this workflow is intended for interactive quality control and exploratory comparison among indices. In CLI mode the same calculations can be run in a reproducible batch command, for example: ForAMecoQS.exe -i samples.xlsx -list jorissen -o results.xlsx -index all -mud 35. ForAMecoQS is distributed as a pre-compiled Windows installer that requires no administrator privileges for ordinary use and bundles the .NET runtime; Supplementary Materials 2 gives full installation and command-line quick-start instructions.

Validation against published reference values is summarised in Table 1, cross-validation against independent Python and R implementations is summarised in Table 2, and EcoQS classification agreement is visualised in Fig. 3. The validation used published reference datasets, an independent Python implementation (scikit-bio, for general diversity descriptors) and, for indices without an existing Python package, the original R packages vegan [41] (Hurlbert rarefaction), entropart [42] (Chao-Shen bias-corrected Shannon entropy) and BBI [43] (the classic AMBI weighted-formula engine) to check the C# calculations across 237 published-value samples from Mediterranean, Adriatic, Brazilian reef, Arabian Gulf and Indian estuarine settings [21, 24, 44–46], together with a large-scale stress test of 3491 Eastern Pacific samples (BENFEP database) covering species richness from 1 to 90 per sample to evaluate low-diversity and high-diversity edge cases. Perfect or near-perfect numerical agreement was obtained for the diversity indices, ES(100), exp(H'bc), FSI and FoRAM Index. ForAM-AMBI showed high correlation but larger absolute differences when published values were generated from different ecological-group lists, which reflects list selection rather than a formula error, confirmed by exact agreement between ForAMecoQS's weighted-formula implementation and the independent BBI R package's AMBI engine on matched ecological-group compositions. Because the calculation engine is deterministic and shared between the GUI and CLI, two users running the same input file,

Table 1
Complete validation summary: ForAMecoQS vs. published reference values and BENFEP_v2 stress-test formula checks.

Index	Datasets	n	r	R2	RMSE	MAPE
exp(H'bc)	[21,24]	156	0.9992	0.9984	0.3078	0.41%
H'log2	[21]	36	1.0000	1.0000	0.0003	0.01%
FSI	[21,44] > 63 µm and >125 µm	46	0.9976	0.9952	0.2747	4.60%
ForAM-AMBI	[21,44] > 63 µm and >125 µm	46	0.9538	0.9098	0.5321	28.42%
FoRAM Index	[45]	9	0.9999	0.9998	0.0379	0.50%
Species Richness	[21,13,46]	97	0.9989	0.9978	1.0204	1.26%
H'ln	[44] > 63 µm and >125 µm, [13,46]	71	0.9880	0.9762	0.0831	1.14%
Pielou's J'	[13,46]	61	0.9959	0.9917	0.0081	0.48%
Simpson (1-D)	[46]	30	0.9925	0.9851	0.0046	0.32%
BENFEP_v2 diversity stress test	[43], Eastern Pacific BENFEP_v2 (PANGAEA); 3491 samples, 1531 taxa, richness 1–90 (median 17.0)	3491	1.0000	1.0000	≤ 3.21e-05	n.a.

Table 2
Cross-validation of ForAMecoQS against the Python package scikit-bio and the R packages vegan, entropart and BBI.

Index	n	r	RMSE	MAE
Diversity indices (Python package: scikit-bio 0.7.3)				
Shannon H'ln	237	1.0000	0.0000	0.0000
Shannon H'log2	237	1.0000	0.0000	0.0000
Simpson (1-D)	237	1.0000	0.0000	0.0000
Pielou's J'	237	1.0000	0.0000	0.0000
Species Richness (S)	237	1.0000	0.0000	0.0000
Total Abundance (N)	237	1.0000	0.0000	0.0000
Diversity indices (R packages: vegan 2.7.5, entropart 1.6.16)				
ES(100) [vegan::rarefy]	237	1.0000	0.0000	0.0000
exp(H'bc) [entropart Chao-Shen]	237	1.0000	0.0007	0.0005
ForAM-AMBI formula [R package BBI 0.3.0 AMBI engine]	5	1.0000	0.0000	0.0000

The ForAM-AMBI row reports a formula verification against five synthetic ecological-group profiles reproduced exactly by the BBI package's AMBI engine (maximum absolute difference = 0), rather than a per-sample statistical comparison. It does not validate the foraminiferal species-to-ecological-group assignment, which is instead supported by the published-value validation presented in Table 1.

reference list and settings obtain identical numerical results.

4. Impact

ForAMecoQS improves the pursuit of existing research questions by replacing dispersed manual workflows with a documented, reproducible computational pipeline. It allows users to ask how EcoQS classifications change when different foraminiferal indices, reference lists or threshold systems are applied to the same assemblage data. This is particularly important in transitional waters and regional monitoring programs, where index calibration choices can influence management interpretation.

The software also supports new comparative analyses. Because multiple indices are calculated within the same environment, users can quantify agreement among EcoQS systems and identify samples where

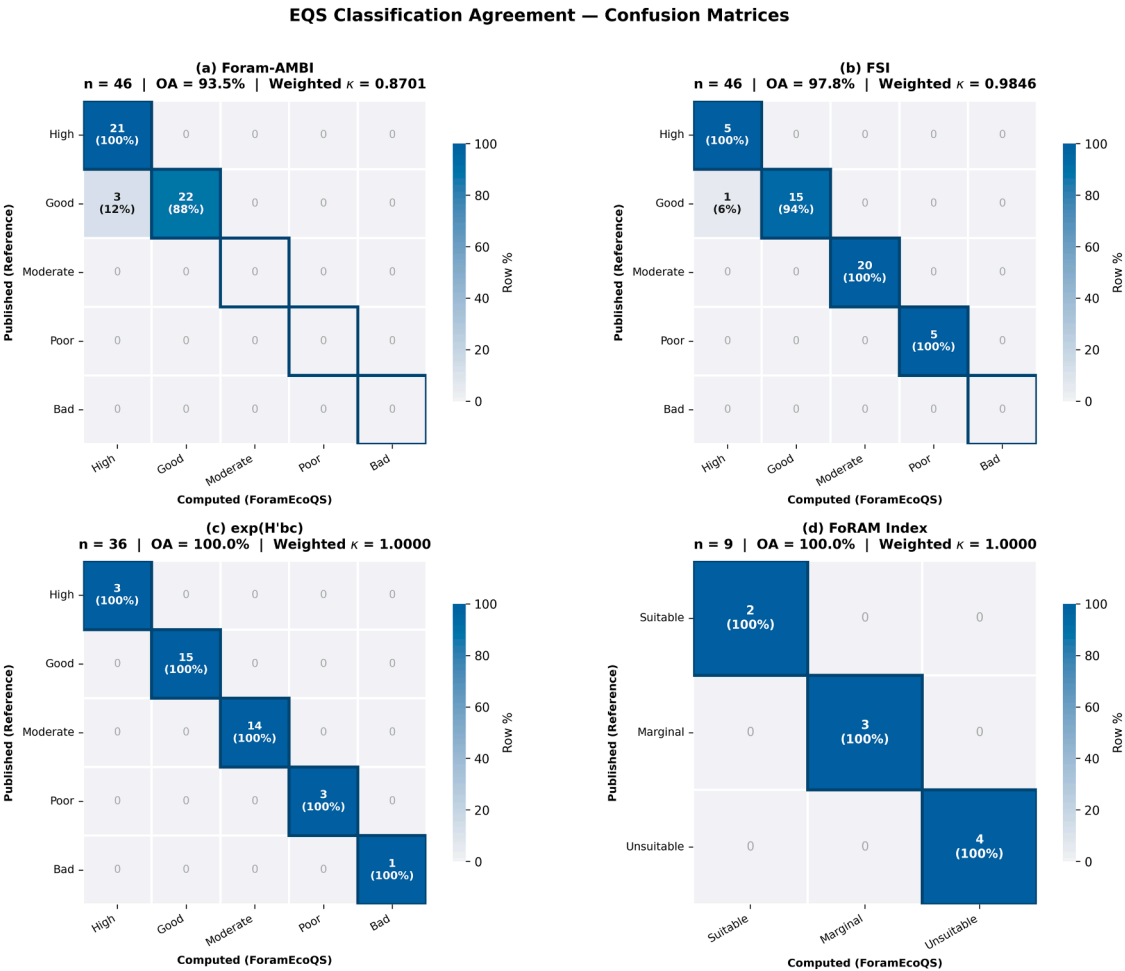


Fig. 3. EcoQS classification agreement between published reference classifications and ForAM-AMBI outputs.

classifications diverge. This helps distinguish computational uncertainty from ecological or calibration-related uncertainty. The agreement module is useful for intercalibration exercises, method comparison and transparent reporting to environmental managers.

This diagnostic role is deliberate rather than a gap: ForAM-AMBI does not select a single regulatory classification on the user's behalf, because the correct threshold system depends on region, sediment fraction and calibration dataset, choices that fall outside what the software can verify

Table 3
Comparison of ForAM-AMBI with existing software for computing benthic biotic and diversity indices. Indices listed are those relevant to ecological quality assessment; general multivariate methods (ordination, PERMANOVA) are excluded.

Software	Platform	Biotic indices	Diversity indices	ForAM-specific	GUI/CLI	Open source	EQS classification
AMBI v5.0(AZTI)	Windows	AMBI, M-AMBI	H', S	No	GUI	No (freeware)	Yes (5-class)
BENTIX Add-In (HCMR)	Excel/Windows	BENTIX	No	No	GUI	No (freeware)	Yes (5-class)
PRIMER v7	Windows	No	H', S, J', d, α , 1-D, ES(n)	No	GUI	No (commercial)	No
PAST!	Windows	No	H', S, J', d, α , 1-D, ES(n)	No	GUI	No (freeware)	No
BBi(R package)	Cross-platform	AMBI, NSI, ISI	No	No	CLI	Yes	Yes (nEQR)
ambir(R package)	Cross-platform	AMBI, M-AMBI, DKI	H'	No	CLI	Yes	Partial
benthos(R package)	Cross-platform	AMBI, ITI	H', Simpson, Margalef, ES(n), S	No	CLI	Yes	Partial
forams (R package)	Cross-platform	ForAM Index	SHE analysis	Yes	CLI	Yes	ForAM only
vegan (R package)	Cross-platform	No	H', 1-D, J', α , ES(n), S	No	CLI	Yes	No
Python BQItool	Cross-platform	BQI	No	No	CLI	Unclear	No
ForAM-AMBI	Windows	ForAM-AMBI, FSI, TSI-Med, ForAM, NQIf, ForAM-M-AMBI, FIEL, BENTIX, BQI	H'ln, H'log2, H'bc, exp(H'bc), 1-D, J', S, N, ES(100)	Yes	GUI + CLI	Yes (MIT)	Yes (5-class, multiple thresholds)

from the input data alone. In Mediterranean soft-bottom applications, different published threshold systems can assign different EcoQS classes to the same assemblage; therefore, users remain free to select in advance and report explicitly, the single threshold system that matches the region, sediment fraction and species list documented for the monitoring programme, and to use the agreement diagnostics as a sensitivity check rather than as a basis for choosing between classifications after the fact.

Compared with existing tools, ForamEcoQS is foraminifera-specific and broader in scope. AMBI [47] and BENTIX tools target macrofauna, PRIMER [48] and vegan [41] provide general community ecology functions, and the forams R package focuses mainly on the ForAM Index [49]. ForamEcoQS integrates foraminiferal diversity metrics, sensitivity-based indices, multivariate indices, EcoQS translation and graphical outputs in a single open-source application; unlike the compared R packages, it additionally combines a GUI and a CLI around the same calculation engine and reports EcoQS agreement diagnostics directly. Table 3 gives a feature-by-feature comparison against AMBI, BENTIX, PRIMER, PAST, BBI, ambiR, benthos, forams, vegan and the Python BQItool.

Current limitations are also clear. The GUI is Windows-only because it uses Windows Forms; migrating to a cross-platform framework such as .NET MAUI or Avalonia remains planned future work. Index outputs remain dependent on the completeness and regional suitability of ecological-group lists, and species that cannot be matched even after WoRMS-assisted synonym checking still require a manual override. Direct ecological validation against independent pollution or contaminant measurements, beyond agreement with published EcoQS classifications, has not yet been carried out and is identified as a priority for future work. Future development should therefore prioritise cross-platform deployment, expanded reference-list guidance for less-specialist users, additional regional calibrations, ecological (pollution-gradient) validation and standardised reporting formats for monitoring programs. A concise SWOT synthesis of these strengths, limitations, opportunities and external risks is provided in Table 4.

5. Conclusion

ForamEcoQS provides an open-source, reproducible software environment for converting benthic foraminiferal abundance data into diversity metrics, biotic indices and standardised EcoQS classifications. Its main contribution is the integration of taxonomic matching, regional reference-list selection, multi-index calculation, threshold-based classification, visualisation and agreement analysis in one workflow.

The software reduces the practical barriers to foraminifera-based biomonitoring and helps users document the methodological choices that most affect EcoQS outputs. Validation against published data and independent code supports the correctness of the implementation, while remaining discrepancies highlight expected differences caused by ecological-group lists and threshold conventions. By combining GUI usability with CLI reproducibility, ForamEcoQS is positioned as a practical tool for research, monitoring and future community extension.

CRedit authorship contribution statement

Matteo Mangiagalli: Writing – review & editing, Writing – original draft, Visualization, Software, Methodology, Formal analysis, Data curation. **Fabrizio Frontalini:** Supervision, Project administration, Methodology, Funding acquisition, Data curation, Conceptualization. **Carla Cristallo:** Visualization, Validation, Methodology, Investigation, Data curation. **Fabio Francescangeli:** Visualization, Validation, Supervision, Methodology, Investigation, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial

Table 4

SWOT analysis of ForamEcoQS.

Strengths	Weaknesses
Unified platform computing all major foraminiferal biotic indices plus a full suite of diversity descriptors.	Windows-only distribution due to the Windows Forms GUI, limiting accessibility for macOS/Linux users. Sensitivity of index values to the selected reference list and list completeness; results can be list-dependent near EQS boundaries. Optional WoRMS synonym verification is diagnostic rather than automatic: it reports the accepted name for a resolved synonym but does not itself reassign the ecological group, so manual overrides are still needed in that case.
Multi-list reference architecture with transparent species assignment and override support to handle biogeographic variability.	
Dual GUI/CLI workflows enabling both interactive use and reproducible batch processing in automated pipelines.	
Validated numerical implementation (cross-validation against independent code and published reference values) with high EQS agreement.	
Open-source (MIT) design with exportable outputs and built-in EQS agreement diagnostics (kappa/confusion matrices, heatmaps).	
Opportunities	Threats
Migration to a cross-platform framework (e.g., .NET MAUI/Avalonia/web) to broaden adoption.	Ongoing taxonomic revisions and regional calibration differences can undermine cross-study comparability without careful reporting. Regulatory threshold updates or differing national conventions may require continuous maintenance of EQS classification settings.
Extending WoRMS integration from diagnostic synonym reporting to optional automatic ecological-group reassignment when a resolved synonym is already present in the reference list under its accepted name.	Emergence of competing, cross-platform tools could reduce uptake if portability is not improved.
Extension to additional indices and environment-specific variants as they are proposed and validated in the literature.	Dependence on specific .NET and third-party library ecosystems may introduce long-term maintenance or compatibility risks.
Standardised reporting/export formats aligned with regulatory workflows and intercalibration exercises.	
Community-driven expansion of regional reference lists and broader benchmarking across habitats and sediment types.	

interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.softx.2026.102921](https://doi.org/10.1016/j.softx.2026.102921).

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