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From biodiversity to design: a phylogeny-aware, data-driven framework for biological model selection in bio-inspired design

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Supplementary material for this article is available [online](#)

Abstract

Selecting suitable biological models remains one of the most challenging and least formalised steps in biomimetic design. Existing tools support searching for biological strategies and transferring principles into engineering concepts, but provide limited guidance on which organism to prioritise once multiple plausible candidates are identified. Here we present a phylogeny-informed, data-driven framework that structures model selection as an explicit comparison. The framework computes four module scores per candidate model: data sufficiency, innovativeness, phylogenetic characteristics, and an open-ended contextual module for project-specific constraints. Users assign weights to the modules to reflect resources, timelines, and design requirements, yielding an overall compatible score and a ranked shortlist. We demonstrate the framework in a microplastic-filtration case study using 35 suspension-feeding taxa and three archetypal user scenarios. Rankings reveal a compact set of candidates that remains competitive across scenarios, while a smaller subset shifts in response to changes in priorities, thereby distinguishing robust starting points from context-dependent opportunities. Overall, the framework fills an under-supported gap in current biomimetic workflows by providing a structured decision-support layer for biological model selection.

1. Introduction

Biomimetics draws inspiration from living organisms and translates biological knowledge into solutions to practical human problems (Vincent *et al* 2006, ISO/TC266, 2015). In this paper, we use ‘biomimetics’ as an umbrella term that also encompasses the closely related concepts of biomimicry and bio-inspired design. Biomimetics has generated impactful innovations across product development, architecture, aerospace, medicine, and many other fields, yielding numerous success stories (Lurie-Luke 2014, Chirazi *et al* 2019). Yet, given Earth’s 3.8-billion-year evolutionary history and more than one million described species, biomimetics remains at an early stage of exploration (Snell-Rood 2016): fewer than one-thousandth of known species have so far been explored as sources of biomimetic inspiration (Zhang *et al* 2025a).

A persistent bottleneck lies in biological model selection—deciding which organism to prioritise once multiple plausible candidates exist. Although model choice can strongly shape downstream effort and outcomes, it remains under-formalised and often opaque in the bio-inspired design process (Fayemi *et al* 2015); explicit documentation of how teams compare candidates and converge on one organism (or a small set of organisms) to carry a project forward remains limited. As a result, practitioners face a fundamental challenge: identifying a suitable source of biological inspiration within the vast diversity of life (Willocx *et al* 2020).

Dedicated tools and frameworks already support several stages of the biomimetic workflow (Fayemi *et al* 2017, Wanieck *et al* 2017, Zhang *et al* 2025b); biological strategy platforms such as AskNature (Deldin and Schuknecht 2014) and Asteria (Asteria 2025) help users expand and retrieve candidate strategies;

algorithmic aids such as FISh (Willocx and Duflou 2023) and SEABIRD (Vandevenne *et al* 2015) help align engineering functions with biological mechanisms; knowledge-transfer tools such as BID Canvas (Nagel *et al* 2017) and BioCards (Lenau *et al* 2015) support the interpretation and abstraction of biological principles for subsequent engineering development. Together, these approaches help generate sets of potentially relevant biological models and support the translation of selected biological knowledge into technical concepts. However, a critical step remains insufficiently addressed: systematically narrowing the pool of candidate organisms to those most suitable for a specific design context. This design context matters because biological organisms are not arbitrary repositories of functions: their traits are shaped by long histories of selection within specific evolutionary contexts, producing solutions that have been tested against particular sets of conditions (Penick *et al* 2022). Model selection is therefore not only a search for functional similarity, but also an assessment of whether the biological context is relevant to the intended design context. As biological knowledge and searchable resources continue to expand, the number of organisms that potentially match a given biomimetic design challenge can be expected to increase accordingly, making model selection more and more consequential.

An illustrative filtration example highlights the problem. A practitioner defining a high-level goal such as ‘filtration’ can rapidly assemble a large and diverse set of candidate inspirations: e.g. a search for ‘filter’ on AskNature yields 289 biological-strategy entries (searched on 15 July 2025), while a query in Web of Science (WoS) returns roughly ten times more publications under ‘filter (Topic) AND biology (Topic)’ (query performed on 15 July 2025). Beyond databases, other approaches such as consultations with biologists and team brainstorming can further expand the candidate pool. At the same time, ‘filtration’ functions arise across distant lineages, e.g. filter-feeding fishes (Sanderson 2024), sponges (Leys *et al* 2011), bivalves (Riisgård and Larsen 2001, Ward and Shumway 2004), aquatic insects (Wallace and Merritt 1980, Filippov *et al* 2023), and physiological filtration in kidneys (Haraldsson *et al* 2008), yielding candidates that are heterogeneous in mechanism, scale, etc. Once the pool becomes sufficiently large, selection typically defaults to experience, disciplinary familiarity, or narrative appeal, rather than transparent, comparable evidence, because dedicated decision-support tools for this selection step remain limited (Zhang *et al* 2025b).

To address this gap, we developed an algorithmic framework for selecting biological models. By integrating decision-relevant information and allowing user-defined weighting to reflect project priorities and constraints, the framework scores and

ranks candidate organisms. Importantly, phylogenetic information is embedded by design, enabling users to identify evolutionarily diverse and often overlooked taxa that may hold substantial potential for biomimetic exploration.

2. Methodology

2.1. Framework overview and overall compatible score (F)

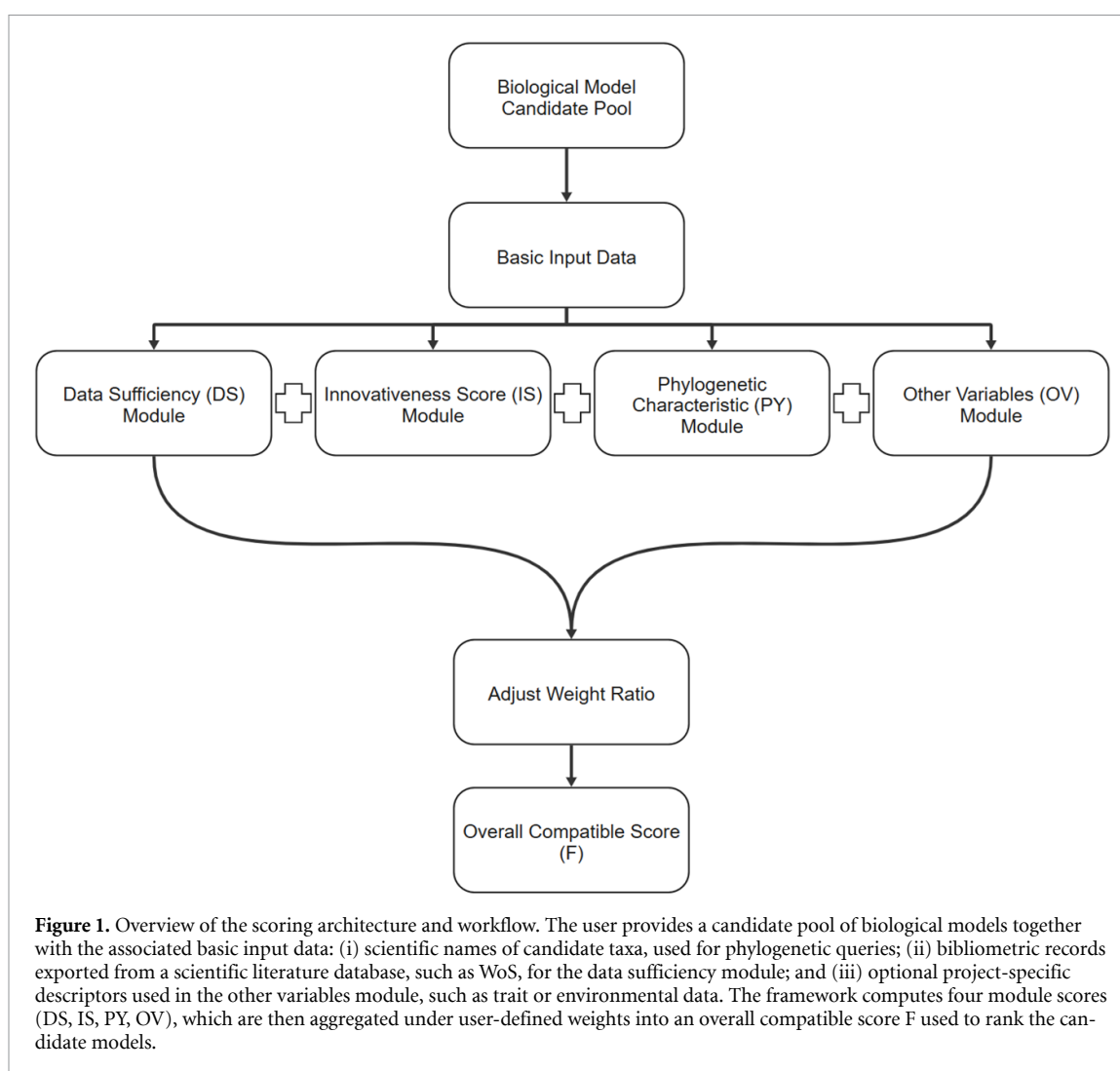
The scoring framework is designed to ensure both scalability and practical applicability. We established a four-module architecture consisting of three fixed modules and one user-defined module. The fixed modules quantify a biological model’s (i) data sufficiency (DS), (ii) innovativeness score (IS), and (iii) phylogenetic characteristic (PY) dimensions. The fourth module, other variables (OV), accommodates project-specific metrics. For any user-supplied candidate pool and associated input data, the workflow (figure 1) returns a vector of module scores for each candidate. Users then assign weights to these modules and obtain an overall compatible score (F), which can be sorted to generate a ranking of candidate biological models. Because the framework ranks the candidate pool provided by the user, candidate definition is an important input-quality step. When candidate models are defined at different taxonomic levels, users should, where possible, select the lowest taxonomic unit for which the target function is sufficiently representative and for which reliable data are available. Broad clades may be useful as early exploratory hypotheses, but if the function of interest is restricted to only a subset of a clade, the candidate should be refined to a more specific family, genus, or species before detailed prioritisation.

The four module scores are combined into a single overall score:

$$F = \alpha DS + \beta IS + \gamma PY + \delta OV \tag{1}$$

where the symbols are defined as follows:

Symbol	Meaning	Range
DS	Data Sufficiency score (Section 2.2)	0–1
IS	Innovativeness score (Section 2.3)	0–1
PY	Phylogenetic Characteristic score (Section 2.4)	0–1
OV	Other variables score (Section 2.5)	0–1
$\alpha, \beta, \gamma, \delta$	User-defined weights	0–1, with the constraint $\alpha + \beta + \gamma + \delta = 1$



Users adjust α – δ based on their case-specific requirements by translating high-level project constraints into an explicit preference over the four modules. For example, teams with limited biological capacity or short timelines may assign a larger weight to DS to prioritise models with sufficient accessible research data; teams aiming to differentiate a concept may increase IS to favour under-utilised models; teams seeking broader exploration of biological diversity may increase PY; and projects with hard contextual constraints (e.g. target particle range, habitat, manufacturability, regulatory or sustainability criteria) can encode these as OV and increase δ accordingly. Preset configurations (e.g. Exploratory, Balanced, Deep-Research) provide starting points (table 1), after which users can refine α – δ iteratively while inspecting how the ranking changes. An example of this mapping from user context to weights is demonstrated through a case study (chapter 3). In the case study, module inputs came from traceable sources: WoS records for DS, the reference corpus of prior biomimetic utilisation for IS, phylogenetic distances derived via the OpenTree-of-Life API (Open Tree of Life 2015) for PY, and the

published environmental and functional dataset of Hamann and Blanke (2022) for OV. Biological and environmental data were not AI-generated in this study; in other applications, users may provide equivalent data from scientific databases, curated trait datasets, expert assessments, patent records, or in-house measurements.

By mapping multi-dimensional information onto a single scalar F (equation (1)), the framework converts a complex, heterogeneous comparison among numerous organisms into a systematic ranking, while keeping end-users in control of strategic priorities. In the following sections, we describe how each module score is derived. All computations described in this chapter have been implemented in a Python-based prototype with a graphical user interface, which automates module-score calculation, weight adjustment, and final ranking once the candidate pool and input data are supplied; this prototype was used to produce the case study reported in chapter 3.

2.2. Data sufficiency (DS) module

The DS module quantifies ‘how much’ usable scientific evidence is available for a given biological model

Table 1. Preset weighting profiles and their target design mindsets.

Preset	Target mindset	α (DS)	β (IS)	γ (PY)	δ (OV)
Exploratory	Maximise novelty while leveraging existing knowledge	0.20	0.50	0.20	0.10
Balanced	Even consideration of all factors	0.25	0.25	0.25	0.25
Deep-research	Mechanism-focused, evidence-rich biological research	0.45	0.10	0.30	0.15

within the user-defined corpus. It serves as a proxy for the effort needed to access sufficient evidence for subsequent abstraction and technical translation. DS is computed from bibliometric indicators and optional evidence descriptors as:

$$DS = w_R R_s + w_C C_s + w_H H_s + w_Y Y_s + w_T \text{Type}_s + w_F \text{Func}_s \quad (2)$$

where the symbols are defined as follows:

Symbol	Definition	Normalisation
R	Number of relevant publications retrieved from a selected scientific literature database	$R_s = \min\left(\frac{R}{T_R}, 1\right)$
C	Total citations	$C_s = \min\left(\frac{C}{T_C}, 1\right)$
H	Model-level h-index (not author h-index), computed from citation counts of papers associated with each biological model in the filtered corpus	$H_s = \min\left(\frac{H}{T_H}, 1\right)$
Y	Median publication year	$Y_s = \frac{Y-1980}{Y_{\max}-1980}$
Type	Diversity of data types (e.g. CT, SEM, 3D models); n = number of distinct data-type categories	$\text{Type}_s = \min\left(\frac{n}{3}, 1\right)$
Func	Diversity of involved sub-functions, i.e., distinct function sub-aspects reported for the same biological strategy within the corpus. For example, the sub-functions of ‘filtration’ can include particle capture, selectivity, anti-clogging, self-cleaning, flow generation, etc.; n = number of distinct sub-function labels	$\text{Func}_s = \min\left(\frac{n}{3}, 1\right)$
$w_R \dots w_F$	User-defined weight vector	$\sum w_i = 1$ $i \in (R, C, H, Y, T, F)$
T	Dynamic threshold	$T_R = \text{median}(R)$, $T_C = \text{median}(C)$, $T_H = \text{median}(H)$

The DS score uses baseline descriptors such as publication count (R), citation number (C), h-index (H), and median publication year (Y), which is converted into a normalised publication recency

score (Y_s). These values are obtained from scientific literature databases (e.g. WoS, Scopus, or PubMed, depending on the user’s data source). The diversity-count descriptors (Type and Func) can be derived from domain-specific repositories or structured datasets when available, such as morphological/functional repositories and image archives (e.g. MorphoSource), biodiversity and taxonomy databases (e.g. GBIF), or curated bioinspiration platforms (e.g. AskNature); or approximated via automated text mining.

Instead of feeding raw counts directly into the algorithm, we apply a minimal-sufficiency principle based on a saturation logic. For each run, the algorithm examines the empirical distribution of each metric within the user’s candidate pool and defines a dynamic threshold T (typically the median, but can be manually set to specific values). Values approaching or exceeding T yield diminishing contributions to the score. This prevents, e.g. a few models having a large volume of publications from dominating the composite index and reflects practical needs, considering that once users have read a certain amount of papers on a given biological strategy and understood the mechanism, additional literature typically provides diminishing marginal value. After normalisation, users may adjust the relative weights (w_i) to reflect project priorities, for instance, emphasising literature recency or citation impact while down-weighting overall literature quantity. The final DS value is computed and passed forward to the overall compatible score calculation.

2.3. Innovativeness score (IS) module

The IS quantifies the extent to which a biological model has been previously used in biomimetic research. A corpus of 74 359 biomimetic-related publications (up to December 2024) was analysed, from which 31 776 distinct biological models were identified as having been used in biomimetic contexts (Zhang *et al* 2025a). This corpus forms a reference corpus of biomimetic prior use. This reference corpus is an integral component of the IS module, and it can be updated as the volume of biomimetic-relevant literature grows.

For each candidate i , let U_i be its occurrence count in the reference corpus. Because biological models are reported at different taxonomic ranks (species, genus, family, ...), and higher ranks

(e.g. kingdom) naturally contain larger opportunity sets (number of distinct species) than lower ranks (e.g. family), the same absolute number of uses U_i should imply weaker saturation at higher ranks. We therefore normalise U_i by a rank-specific baseline b_r , where r denotes the candidate's taxonomic rank. Here, b_r represents the typical prior-use level expected for candidates reported at rank r ; dividing U_i by b_r converts absolute prior use into a rank-normalised intensity:

$$u_i^* = \frac{U_i}{b_r} \quad (3)$$

Symbol	Meaning	Default/notes
U_i	Prior-use count of candidate i in the reference corpus	An integer ≥ 0
b_r	Rank-specific prior-use baseline used to normalise U_i at taxonomic rank r	80th percentile of positive prior-use counts at rank r (equation 4). If no positive counts exist for a rank in a given reference corpus, b_r is set to 1 by convention
u_i^*	Rank-normalised intensity	

The rank baseline b_r is generated from the global reference corpus to reflect typical exposure at the rank r :

$$b_r = Q_{\{0.80\}}(\{U_j \mid \text{rank}(j) = r, U_j > 0\}). \quad (4)$$

Within each rank r , prior-use counts are strongly right-skewed in the reference corpus (the 31 776 distinct biological models used in biomimetics). We therefore use the 80th percentile ($Q_{\{0.80\}}$) of prior-use counts as the default b_r . This provides a robust near-saturation baseline: it reflects a high but not extreme level of prior use at a given rank, while reducing sensitivity to outliers and avoiding over-penalisation of broad ranks that naturally aggregate more underlying taxa. Alternative baselines (e.g. median or p70–p90) can be selected for different project scenarios. Using the reference corpus, the resulting baselines are computed (table 2).

For non-canonical ranks (e.g. Subclass), b_r is obtained by log-linear interpolation between adjacent canonical levels (here: Class and Order):

$$\ln b_{\text{subclass}} = (1 - \alpha) \ln b_{\text{class}} + \alpha \ln b_{\text{order}}, \\ \alpha \in [0, 1] \text{ (default } \alpha = 0.5). \quad (5)$$

We then map u_i^* to the IS:

$$\text{IS}_i = \frac{1}{1 + \left(\frac{u_i^*}{s}\right)^p}, \quad s > 0, p \geq 1 \quad (6)$$

Symbol	Meaning	Default/notes
s	Decay scale in the IS mapping	Default $s = 1$
p	Decay shape (steepness)	Default $p = 1$; typical range 1–2
IS	Innovativeness Score in (0,1]	Higher means more novel (less historically used)

Equation (6) yields $\text{IS}_i = 0.5$ when $U_i = b_r$ under $s = 1, p = 1$ (an interpretable ‘half-novelty’ point at the per-rank baseline). Increasing p sharpens the transition, increasing s makes decay more gradual. Here, all ranks achieve an IS of 1 at $U = 0$; as U grows, higher ranks decay more slowly (more tolerant), reflecting their larger opportunity set. Consequently, for the same absolute use, e.g. $U = 100$, a species receives a lower IS than a phylum.

2.4. Phylogenetic characteristic (PY) module

Although biomimetic research aims to harness the full potential of living organisms, published studies still focus on a narrow subset of biodiversity, mainly charismatic mammals (Zhang *et al* 2025a). To counter this imbalance, phylogenetic information is embedded into our scoring framework through two integrated layers:

- Interactive visual layer. Based on the scientific names of candidate models, the program queries the OpenTree-of-Life API (Open Tree of Life 2015), retrieves the minimal induced subtree, and renders an interactive phylogram. Users can visualise evolutionary proximity, identify isolated branches, and inspect clustered lineages.
- Quantitative layer. From the same tree distances, two complementary sub-scores are derived:

$$\text{PY}_i = \lambda \text{PU}_i + (1 - \lambda) \text{CP}_i \quad (7)$$

where the symbols are defined as follows:

Symbol	Meaning	Range
PU	Phylogenetic Uniqueness	0–1
CP	Cluster Comparative Potential	0–1
λ	User-defined weight	0–1
PY	Phylogenetic Characteristic score	0–1

2.4.1. Phylogenetic uniqueness (PU)

For a focal taxon i , PU is defined as the mean phylogenetic (patristic) distance to all other candidates:

$$\text{PU}_i = \frac{1}{N-1} \sum_{j \neq i} d_{ij} \quad (8)$$

where the symbols are defined as follows:

Table 2. Rank-specific baselines computed from the reference corpus. ‘Distinct entries’ denotes the number of unique taxonomic entries at each rank in the reference corpus after deduplication. $\sum U$ denotes the total prior-use count summed across entries within that rank.

Rank	Number of distinct entries	$\sum U$	b_r (p80)	(median)
Kingdom	6	1972	608.0	241.5
Phylum	27	8812	109.2	7.0
Class	58	8315	61.2	11.5
Order	89	3564	38.4	4.0
Family	223	3270	15.0	3.0
Genus	511	2814	5.0	2.0
Species	1607	8182	3.0	1.0

Symbol	Meaning
d_{ij}	Branch length (patristic distance) between taxa i and j
N	Total number of candidate taxa in the current query set

The raw PU values are min-max normalised across the set (i.e. each raw PU value x is transformed to $\frac{x - x_{\min}}{x_{\max} - x_{\min}}$) to obtain $PU_i \in [0, 1]$.

2.4.2. Cluster comparative potential (CP)

While uniqueness captures evolutionary distinctness, working within a small clade can also be advantageous: closely related species often share traits that facilitate comparative analysis (Losos 2011, Penick *et al* 2022). To define clusters without relying on a single global distance threshold, we partition the tree using local, quantile-based thresholds with a mutual-neighbour condition. For each focal taxon i , let

$$T_i = Q_q(\{d_{ij} : j \neq i\}), q \in [0, 1] \quad (9)$$

where $Q_q(\cdot)$ denotes the q -quantile (default $q = 0.30$). Two taxa i and j are considered within one cluster (adjacent) if

$$d_{ij} < \min(T_i, T_j) \quad (10)$$

which yields compact, interpretable components while adapting to local distance distributions. For taxon i ,

$$CP_i = \frac{|S_i| - 1}{N - 1} \quad (11)$$

where the symbols are defined as follows:

Symbol	Meaning
S_i	Cluster size: Number of taxa within the cluster containing taxon i
N	Total candidate set size

By construction, $CP_i \in [0, 1]$ without further scaling. Users can tune the parameter $\lambda \in [0, 1]$ in equation (7) to emphasise either exploration of unique organisms (high PU) or comparative depth (high CP), while q controls clustering granularity (smaller q correspond to tighter clusters; larger q

yields larger clusters). The defaults $\lambda = 0.5$ and $q = 0.30$ provide a balanced mode. Embedding phylogeny directly in the scoring system encourages exploration beyond conventionally favoured lineages and integrates evolutionary diversity into the decision process.

2.5. Other variables (OV) module

The OV module is an optional component that provides the framework’s extensibility to project-specific decision criteria. Biomimetic design projects differ widely, and so do the data types that may be relevant for model selection (ISO/TC266, 2015). While DS, IS, and PY quantify literature evidence, prior biomimetic utilisation, and phylogenetic context, OV accommodates additional, domain-specific indicators that users may wish to impose as constraints or preferences. Examples include patent-related metrics (e.g. patent counts or patent presence linked to a model or mechanism), expert assessments (e.g., ordinal ratings of market appeal or biological feasibility), and intrinsic traits (e.g., body size, habitat, behaviour, conservation status, or any other organism-level descriptor relevant to the design context).

Operationally, OV is computed by (i) importing one or more user-defined variables for the candidate set, (ii) mapping each variable to a comparable 0–1 score per candidate, and (iii) aggregating these scores with user-assigned weights to produce an overall OV score. This mapping is intentionally flexible: a variable can be encoded as binary (meets/does not meet a criterion), ordinal (e.g. low/medium/high), or continuous (e.g., numeric ranges), provided that it is transformed into $[0, 1]$ before aggregation. A concrete implementation is demonstrated in the case study (section 3.4), where published trait data of the biological models are encoded as OV variables and propagated through the overall score to illustrate how contextual constraints reshape the final ranking.

3. Results and discussions—a case study

The operation of the proposed framework is illustrated through a representative design challenge in

the context of microplastic removal from water: selecting biological models for the development of a bio-inspired filtration device. This case is aligned with ongoing biomimetics-driven microplastic mitigation efforts within the scope of the EU-funded Nature4Nature project (Nature4Nature 2023). Because the framework produces rankings that depend on user-defined priorities, we evaluate it under three archetypal user scenarios that reflect common constraints in biomimetic projects, ranging from academically led exploration to industry-led development (table 3). These scenarios are used here as an interpretive method to demonstrate how the same candidate pool can lead to different selection outcomes, i.e. this three-scenario comparison is not intended as a prescription that projects using our framework must adopt multiple ‘personas’.

The candidate pool may originate from specialised biomimetics databases, broad literature searches, expert elicitation, or AI-generated suggestions, etc. For this case study, we adopt the 35 suspension-feeding taxa compiled by Hamann and Blanke (2022). Although many additional organisms exhibit filtration capabilities and could be considered for such a design challenge, this curated subset provides a consistent and tractable test case and allows direct comparison across the three scenarios: each begins from the same list and differs only in how priorities are expressed through weighting and optional constraints. While the present case study uses a 35-taxon pool for clarity, the computational steps in the workflow are designed to scale to substantially larger candidate sets, and such candidate sets should be refined to the lowest functionally meaningful taxonomic level whenever possible.

3.1. Data sufficiency (DS) calculation

We exported complete WoS records for the 35 candidate taxa (Supplementary Data 1) and uploaded them to the algorithm. The DS module automatically extracted bibliometric descriptors for each candidate: the number of relevant papers (R), total citations (C), h -index (H), and median publication year (Y) (figure 2).

The resulting summary table of R , C , H , and Y was generated for all candidates. Thresholds (T_R , T_C , T_H) were computed as the median value across the 35 candidates (table 4), following the minimal-sufficiency principle described in section 2.2. Normalised sub-scores (R_s , C_s , H_s , Y_s) for all candidates are provided in supplementary data 2.

To illustrate extensibility beyond bibliometric inputs, the framework supports optional evidence descriptors. In the present case study, we instead used the Hamann and Blanke (2022) dataset to represent such contextual/functional descriptors via the OV module (section 3.4) and therefore set the weights for optional evidence descriptors to 0. table 5 summarises the DS weight configurations applied for the three

user scenarios (P1–P3), consistent with their resource contexts and design priorities. The full resulting DS values are reported in Supplementary Data 2.

Despite persona-specific weighting, DS values are concentrated toward the upper range: across three scenarios, 20 of the 35 candidates scored above 0.8 (figure 3). A stable set of high-DS candidates emerges across scenarios (e.g. Mobulidae, Ephemeroptera, Porifera, and *Rhincodon typus*), reflecting consistently stronger bibliometric support in terms of publication volume, citation impact, and/or recency. In contrast, certain candidates show clear scenario dependence, with DS decreasing as the setting shifts from P1 to P3 (e.g. *Urechis caupo*, *Dendropoma maximum*, and Entoprocta). This pattern indicates that these candidates rely relatively more on recency-weighted evidence and become less competitive when impact-weighted indicators (citations and model-level h -index) receive greater emphasis. Across P1–P3, P2 typically yields intermediate DS values; while P3 produces the strongest separation among candidates, i.e. the DS spread across taxa is largest.

Practically, the outcome provides a diagnostic: candidates whose DS remains high across settings represent evidence-rich starting points, whereas scenario-sensitive candidates flag where limitations in accessible evidence may constrain downstream abstraction and translation unless additional data are collected or alternative evidence sources are incorporated.

3.2. Innovativeness score (IS) calculation

The IS quantifies how extensively a biological model has been utilised in prior biomimetic research. In our implementation, this step compares two inputs (figure 4): (i) the candidate list (the 35 suspension-feeding taxa, including scientific names, common names, and expanded synonyms), and (ii) a biomimetic utilisation corpus (section 2.3). Because IS is computed solely from historical utilisation in the reference corpus (thus not involving user-defined weights), IS values are identical across personas for the 35 candidates.

IS captures novelty relative to rank-specific opportunity. Species-level candidates are sensitive to small numbers of prior uses (e.g. in this dataset, 5–6 uses reduce IS to approximately 0.33–0.38), whereas higher-rank taxa (class/order/phylum) require much larger prior-use counts to yield comparable reductions due to their larger b_r values. Accordingly, models such as Crinoidea and Larvacea retain high IS values with only 1–2 recorded uses, whereas broadly utilised clades (e.g. Porifera, Diptera, Anura) exhibit low IS (figure 5). Candidates with $U = 0$ (e.g. *Balaenoptera physalus*, *Hypophthalmichthys molitrix*, *Urechis caupo*, and *Dendropoma maximum*) represent genuinely untapped options and therefore rank highest in IS.

Table 3. Three archetypal user scenarios used to illustrate persona-dependent weighting in the case study.

Scenario (persona)	Background & resources	Strategic goal	Time scope
P1: Early-career academic researcher	Graduate researcher (e.g. MSc/PhD or early postdoc) with strong biological/taxonomic expertise; access to advanced imaging/biomechanics tools	Explore under-studied organisms with high fundamental interest rather than relying primarily on well-established models	≈2 years
P2: Start-up team	Small bio-inspired technology venture with strong prototyping capacity but limited in-house biological expertise	Identify a relatively novel biological model to differentiate the concept and support early-stage validation and communication	≈6 months
P3: Established filter manufacturer	Large filtration company exploring biomimetics for the first time; ample budget but no in-house biologists	Prioritise low-risk, literature-supported models for the incremental improvement of an existing product line as their first step into bio-inspired design	≈1 year

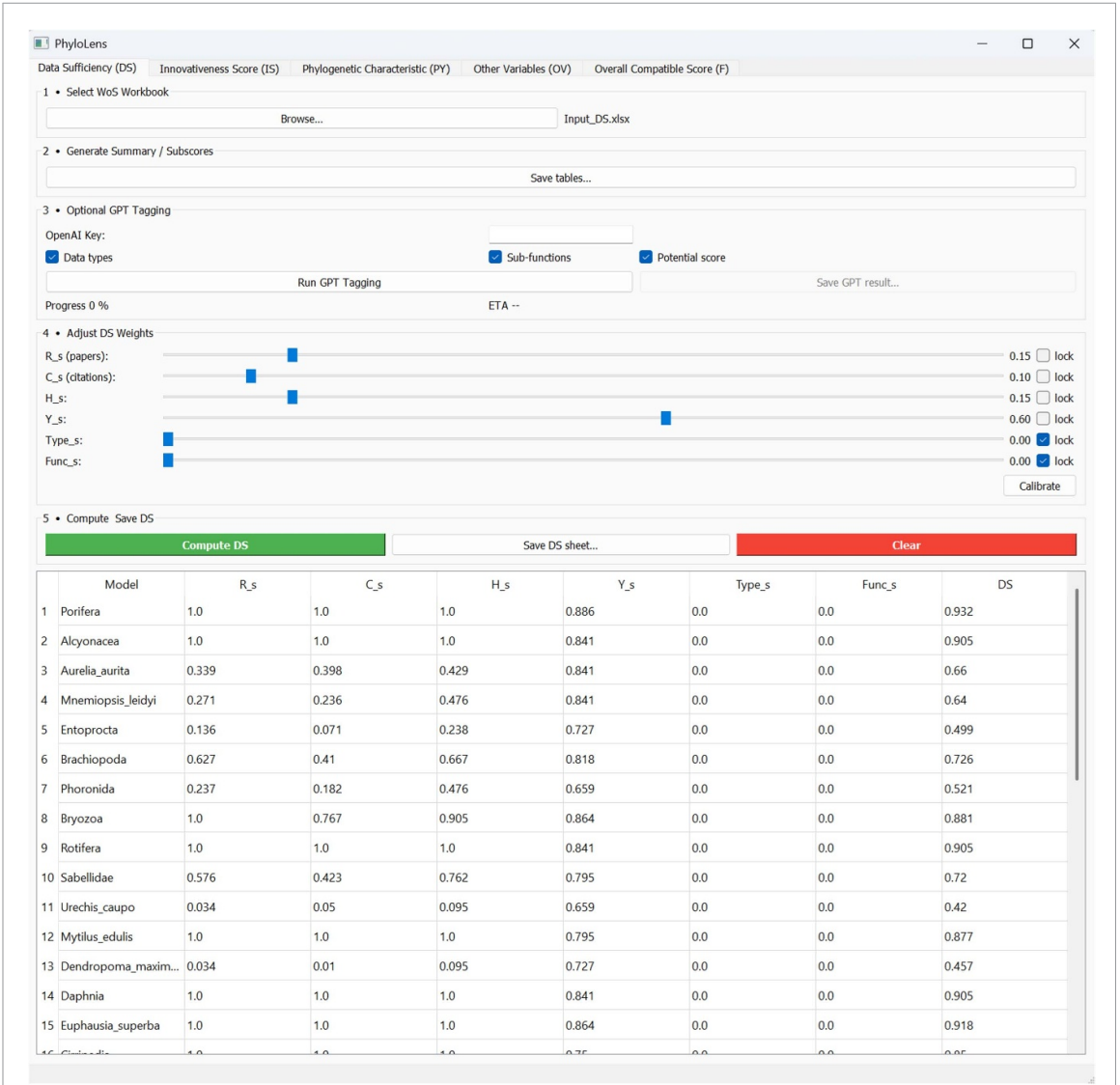


Figure 2. Data sufficiency (DS) module interface. The DS module imports WoS-exported data for the candidate pool and automatically generates a per-taxon summary table of bibliometric descriptors. The interface also provides interactive sliders to set the DS sub-score weights. Optional channels for additional evidence descriptors are available but were not used in the present DS calculation.

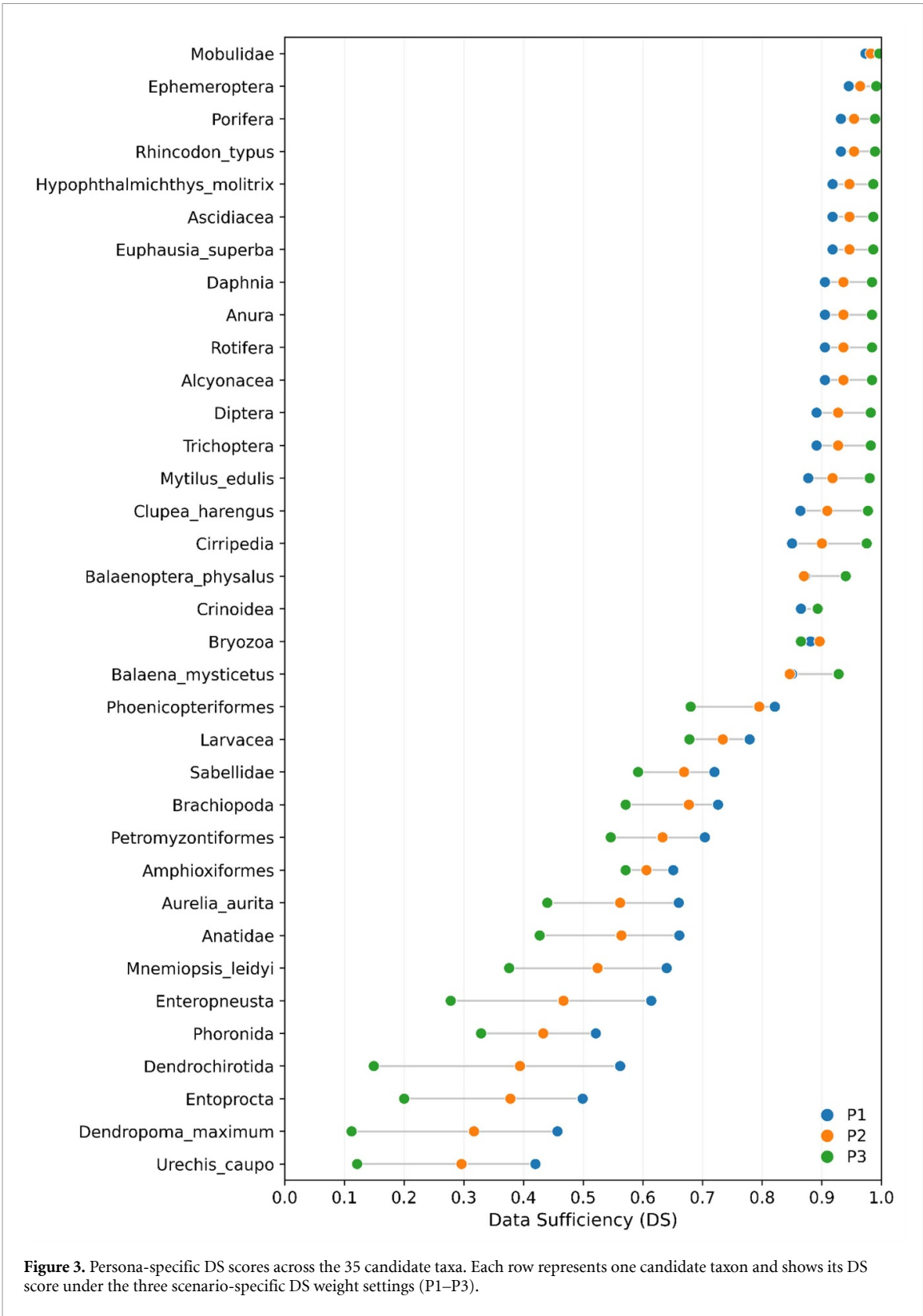


Figure 3. Persona-specific DS scores across the 35 candidate taxa. Each row represents one candidate taxon and shows its DS score under the three scenario-specific DS weight settings (P1–P3).

3.3. Phylogenetic characteristic (PY) calculation

Phylogenetic information is embedded in the framework to incorporate evolutionary context into the model selection process. Using the scientific names of the 35 candidate taxa, the pipeline queries the OpenTree-of-Life API and reconstructs the minimal induced subtree (figure 6).

Persona-specific λ (and clustering granularity q) were selected to represent contrasting strategic preferences in the case study (table 6). PY scores for all 35 taxa under each persona are reported in supplementary data 2.

Figure 7 shows that PY-based ranking shifts as the balance between PU and CP is adjusted

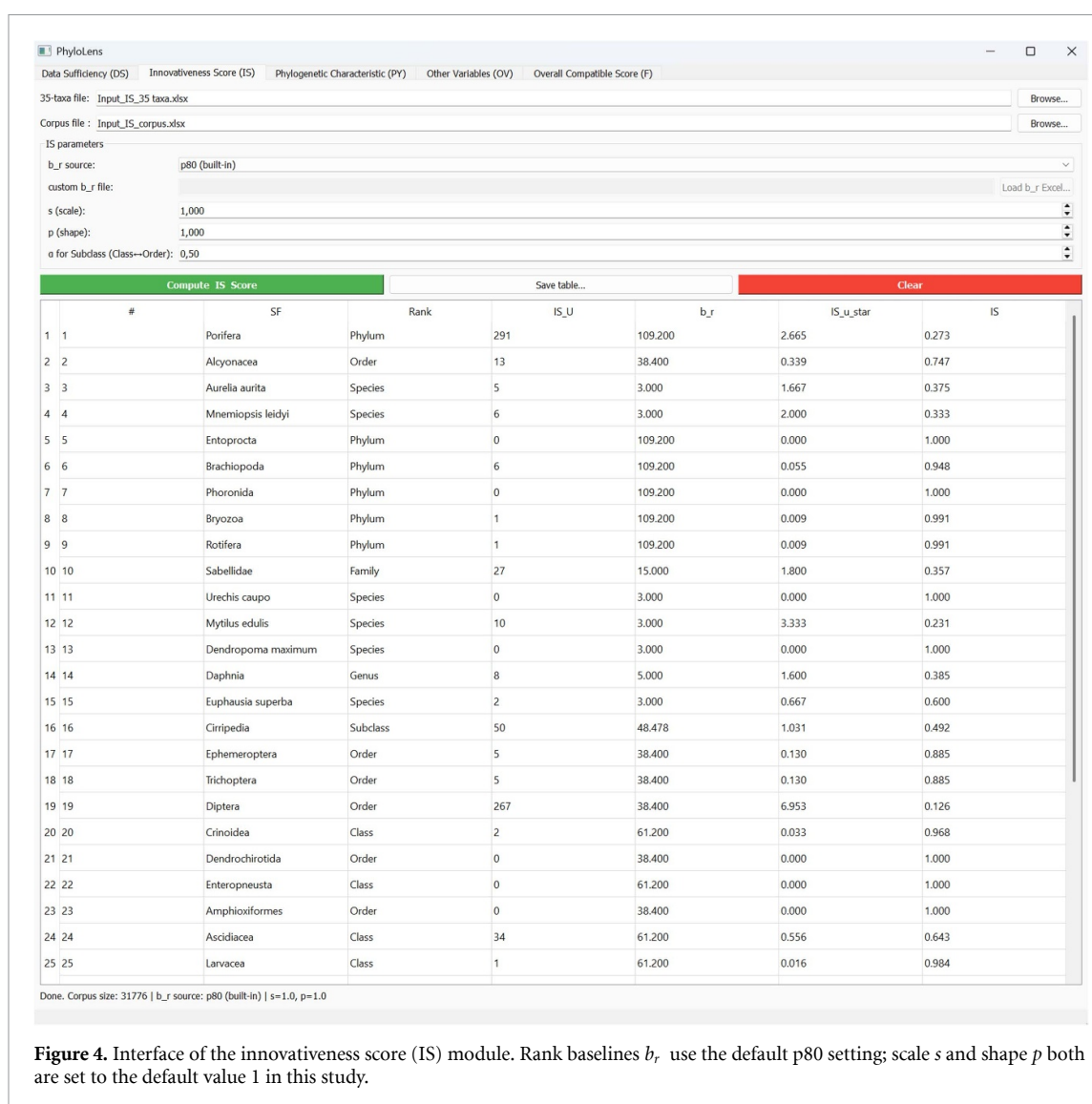


Figure 4. Interface of the innovativeness score (IS) module. Rank baselines b_r use the default p80 setting; scale s and shape p both are set to the default value 1 in this study.

Table 4. Median-based saturation thresholds used in DS normalisation.

Metric	Value
T_R	59
T_C	1719
T_H	21

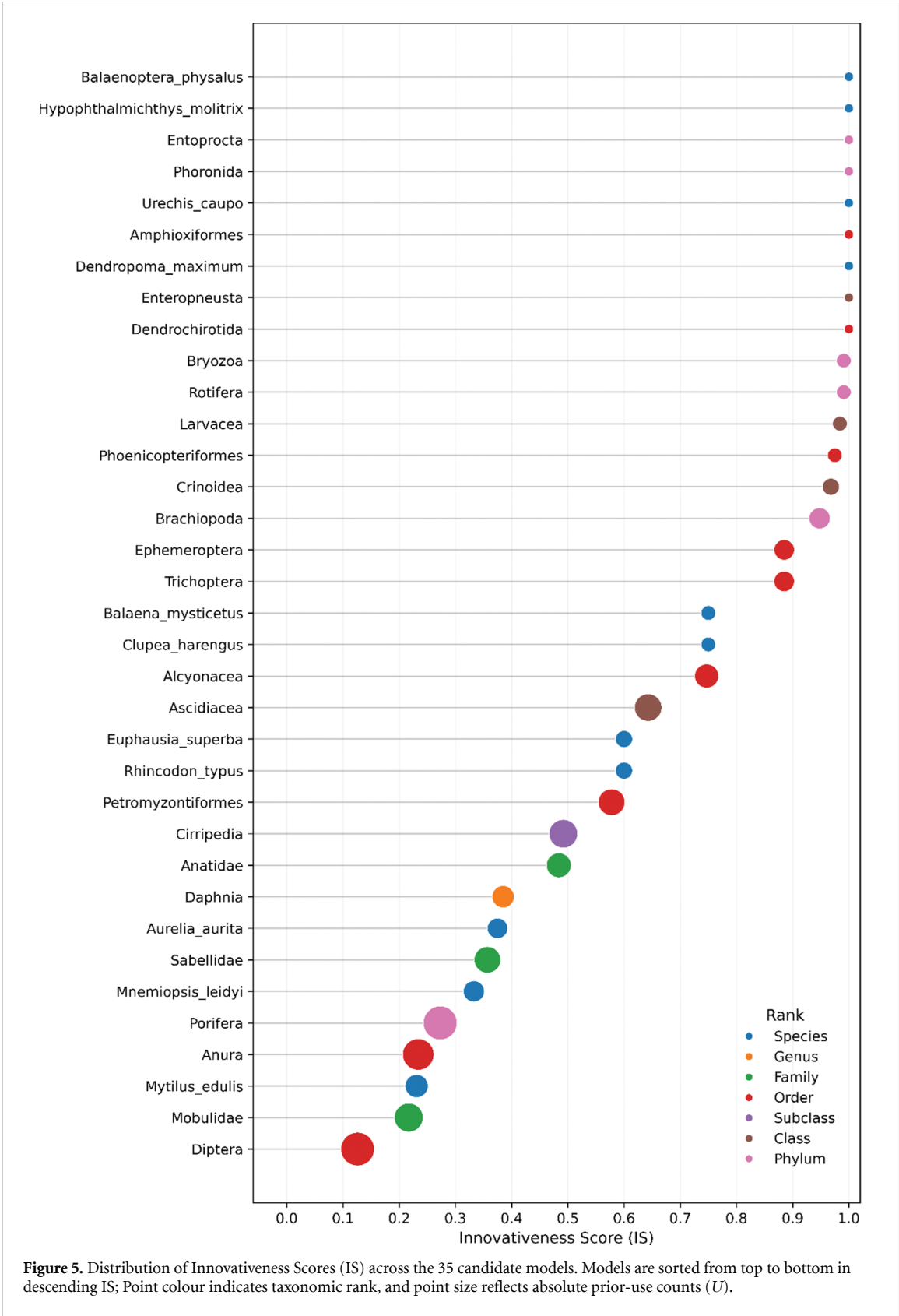
across personas. Under the uniqueness-weighted setting (P1; high λ), candidates on relatively isolated branches are favoured, and several large-bodied vertebrate lineages rise to the top (e.g. *Balaenoptera physalus* and *Balaena mysticetus* rank 1–2 in P1 but fall to 20–21 in P3), consistent with a strategy that rewards evolutionary distinctness. As λ decreases toward the comparability-weighted setting (P3), the ranking increasingly favours taxa embedded in richer neighbourhoods of close relatives (e.g. Phoenicopteriformes and Anatidae remain top-ranked under P2/P3, and candidates such as Porifera and Entoprocta move upward from P1 to

P3). The intermediate setting (P2) typically yields a compromise: for many models, ranks lie between the P1 and P3 positions. Importantly, the heatmap reveals both λ -robust and λ -sensitive candidates: some taxa remain consistently strong across settings (e.g. Phoenicopteriformes ranks 3/1/1), whereas others exhibit pronounced reversals (e.g. *Hypophthalmichthys molitrix* ranks 4/25/27). PY makes the otherwise implicit trade-off between ‘novel lineages’ and ‘comparative depth’ explicit.

3.4. Other variables (OV) calculation

To demonstrate how project-specific constraints can be propagated into model prioritisation, we implemented OV using the environmental and functional dataset adopted from Hamann and Blanke (2022) (supplementary data 3), which characterises each of the 35 filter-feeding taxa using eight categorical or ordinal variables (table 7).

After importing the dataset, the program automatically parses model names and detects which variables are present (figure 8).



For each persona, we translated its constraints into a set of OV criteria and weights (table 8), thereby expressing what ‘contextual fit’ means under different profile scenarios.

Using these parameters, OV scores were computed and compared across the three personas

(figure 9). The full list of OV scores is reported in supplementary data 2.

P3 emphasises application readiness by imposing engineering-relevant settings (e.g. capture-size ranges aligned with commercial microplastic specifications and size scales that support

Table 5. Persona-specific DS sub-score weight configurations.

Persona	w_R	w_C	w_H	w_Y	Rationale
P1: Early-career academic researcher	0.15	0.10	0.15	0.60	Minimises dependence on publication volume and citation impact while emphasising recency (Y_s). This setting down-weights ‘saturated’ models yet retains enough recent literature to initiate new studies
P2: Start-up team	0.30	0.15	0.15	0.40	Seeks recent and accessible information for rapid prototyping. Citations and h-index contribute moderately but are secondary to data availability and timeliness
P3: Established filter manufacturer	0.20	0.40	0.30	0.10	Prioritises well-established, highly cited models with a robust h-index. Publication recency is desirable but not critical

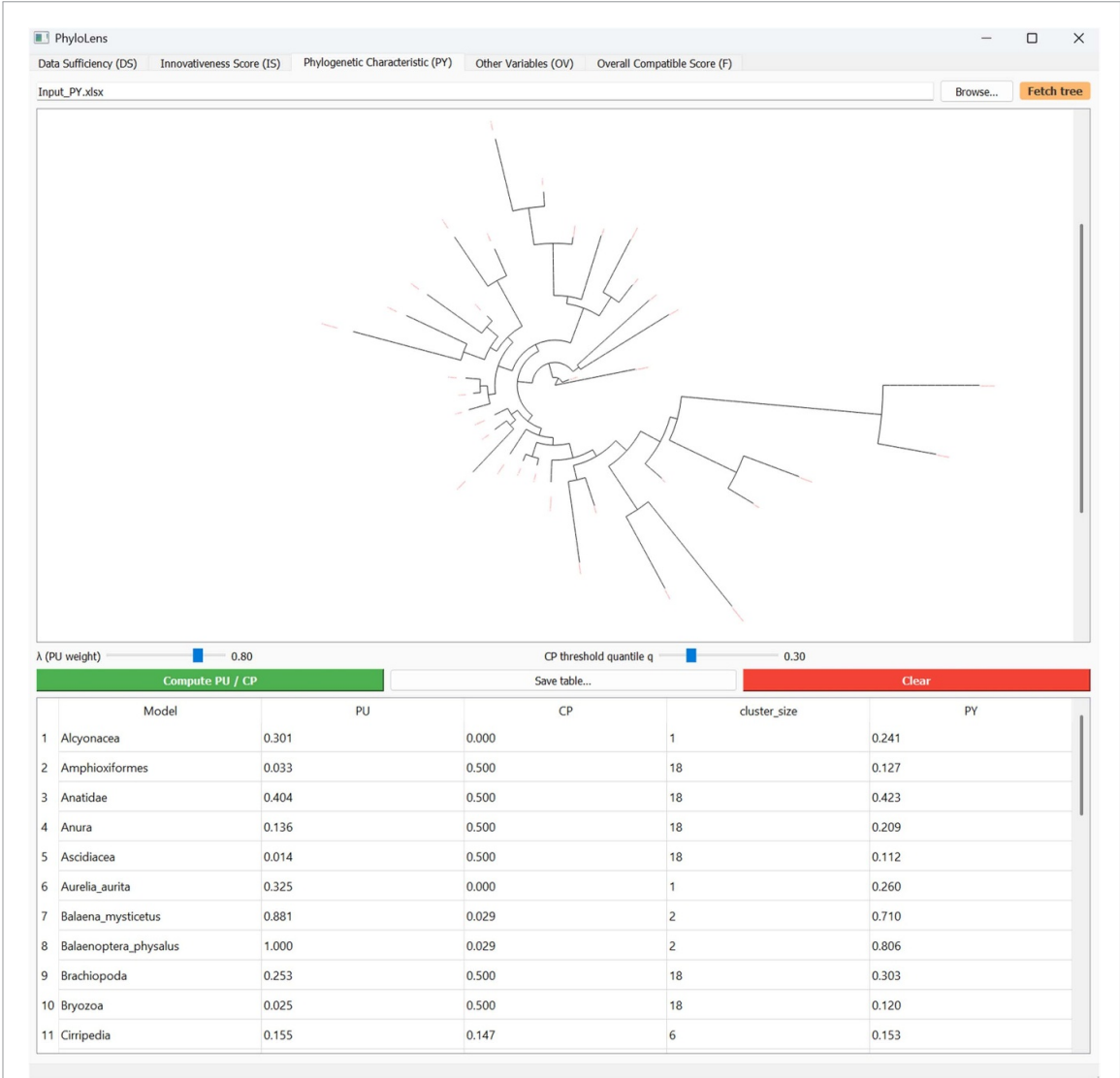
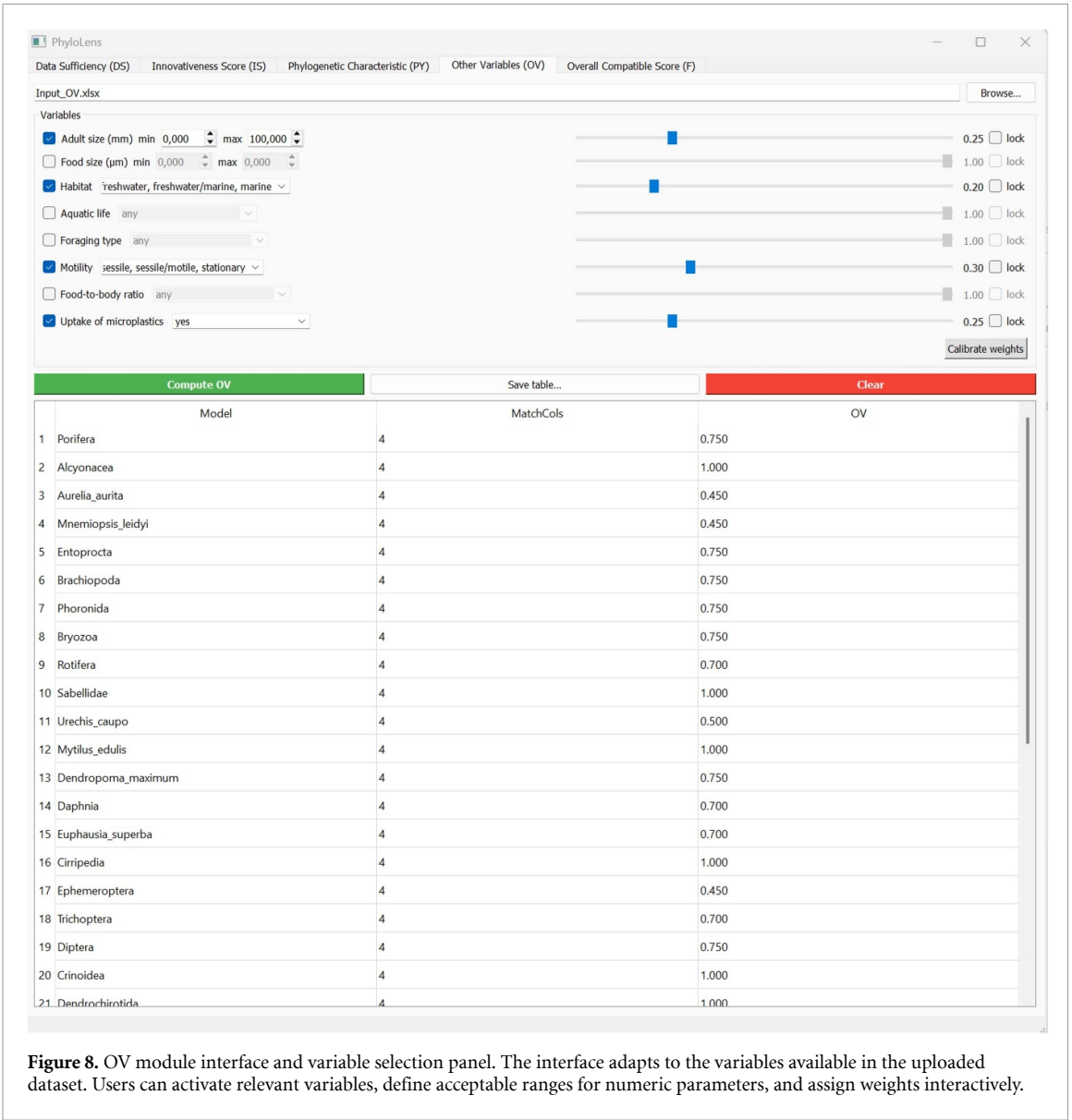


Figure 6. Interface of the phylogenetic characteristic (PY) module. An interactive phylogenetic tree of the 35 filter-feeding taxa was constructed based on OpenTree-of-Life data. Users can zoom, pan, and highlight clades to examine evolutionary proximity.



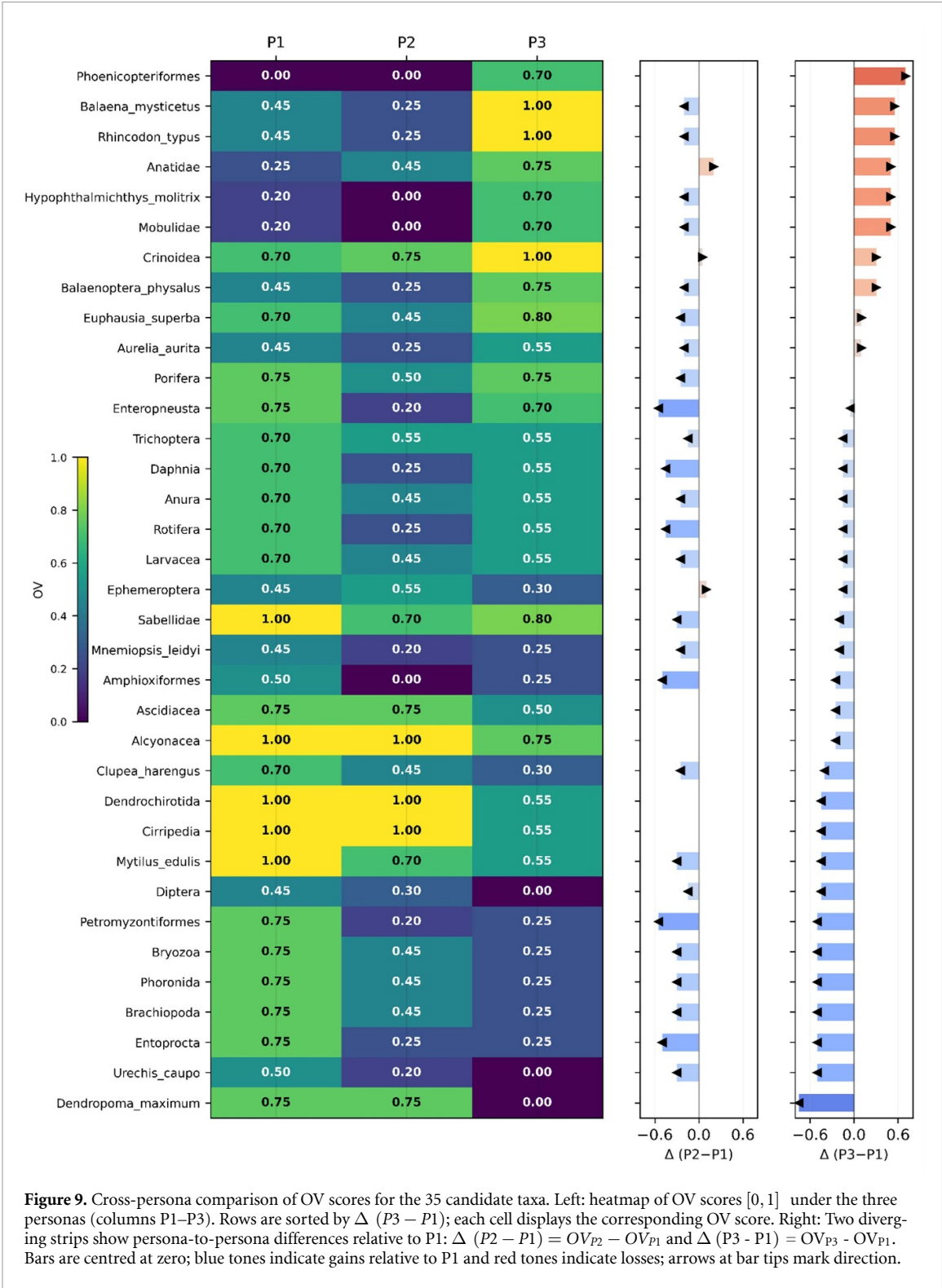
Table 6. Persona-specific PY module settings used in the case study. Persona-dependent λ values control the PU–CP trade-off, while q controls clustering granularity in the CP calculation.

Persona	λ (PU–CP trade-off)	q	Rationale
P1: Early-career academic researcher	0.80 (strong uniqueness)	0.30	Prefers evolutionarily distant models offering novel functional mechanisms
P2: Start-up team	0.50 (balanced)	0.35	Seeks originality yet values neighbouring ‘backup’ taxa for potential scalability
P3: Established filter manufacturer	0.20 (cluster-oriented)	0.25	Favours taxa with multiple close analogues, facilitating procurement, testing, and regulatory approval



manufacturable geometries). Under these constraints, several taxa increase markedly from P1 to P3, for example, Phonicopteriformes (from 0.00 to 0.70), *Balaena mysticetus* (0.45–1.00), *Rhincodon typus* (0.45–1.00), *Hypophthalmichthys molitrix* (0.20–0.70), and Mobulidae (0.20–0.70). By contrast, candidates that fit exploratory or laboratory-oriented preferences may be penalised under P3 when they fall outside the specified operational windows, for instance, *Dendropoma maximum* (from 0.75 to 0.00) and *Urechis caupo* (0.50–0.00).

P2 occupies an intermediate position. For many taxa, Δ (P2 – P1) remains closer to zero than Δ (P3 – P1), indicating that start-up constraints can preserve part of the exploratory space while



still applying basic industrial-context feasibility screens. In other cases, P2 dips below both P1 and P3 (e.g. Enteropneusta: P1/P2/P3 is 0.75/0.20/0.70; Daphnia: P1/P2/P3 is 0.70/0.25/0.55). Overall, OV functions as the framework’s mechanism for converting scenario-specific constraints into quantitative preference shifts, making the effect of ‘contextual fit’ quantitative and comparable across candidates.

3.5. Overall compatible score (F) calculation

The overall compatible score F integrates the four module outputs—DS, IS, PY, and OV—under persona-specific global weights ($\alpha, \beta, \gamma, \delta$). Users set these weights to reflect project priorities, resources, and constraints (figure 10). For illustration, the tool provides preset profiles (table 1), while allowing fully custom configurations; in this case study, each persona applied a

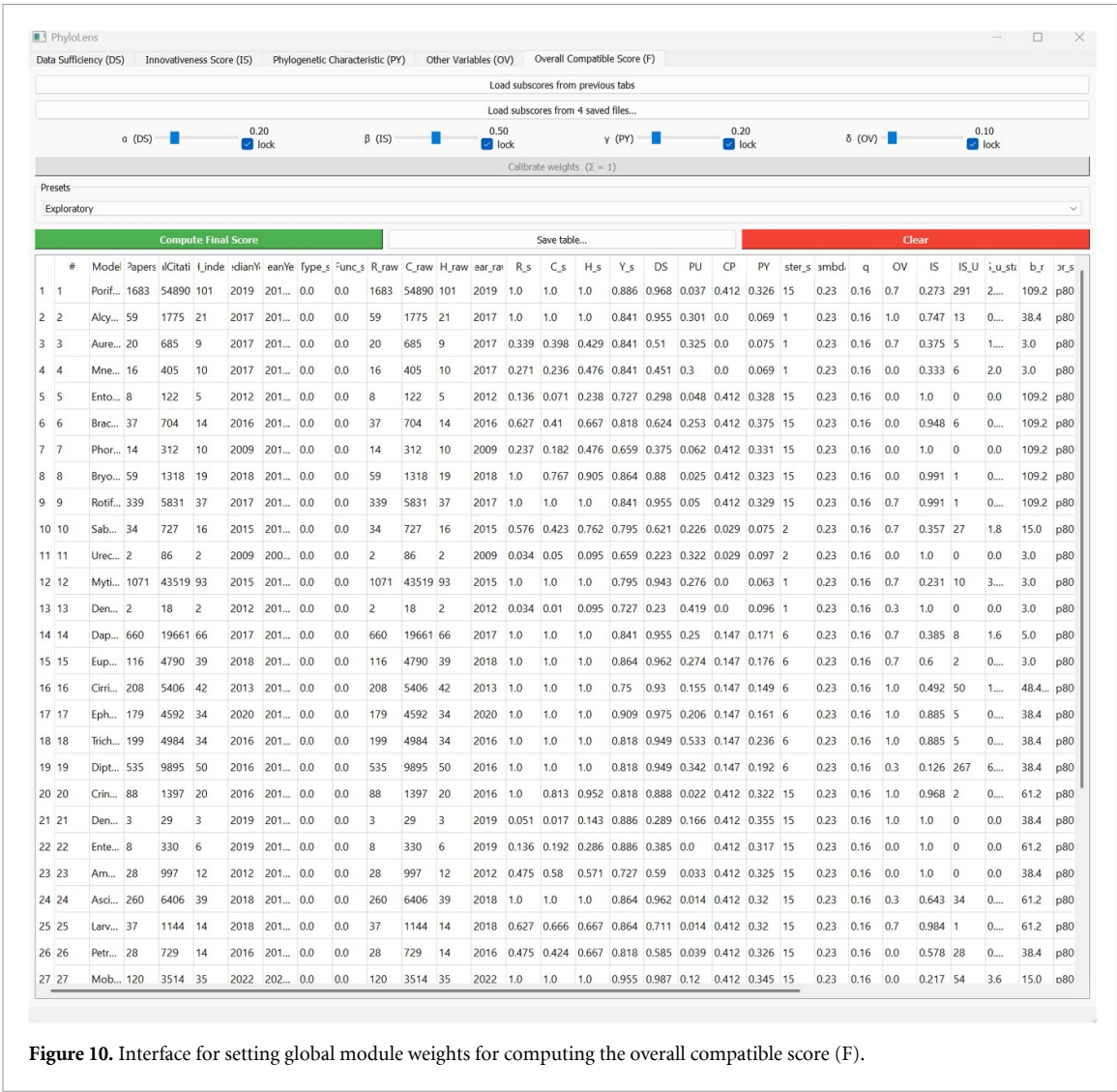


Table 7. Environmental and functional descriptors available for the 35 filter-feeding taxa. Adopted from Hamann and Blanke (2022).

Variable	Options
Habitat	marine; terrestrial; freshwater
Aquatic life zone	pelagic; benthic; terrestrial
Foraging type	active; passive
Motility	sessile; motile; stationary
Adult size (mm)	numeric (range)
Food size (μm)	numeric (range)
Food-to-body ratio	numeric
Uptake of microplastics	yes; na

distinct weighting scheme consistent with its strategic goals (table 9). The resulting compatible scores and rank orders for all three scenarios are reported in Supplementary Data 2.

Several candidates remain near the top under all three weightings, most notably *Balaenoptera physalus* (0.848/0.802/0.794), *Hypophthalmichthys molitrix* (0.701/0.752/0.790), and Trichoptera (0.696/0.751/0.746), indicating a shared signal

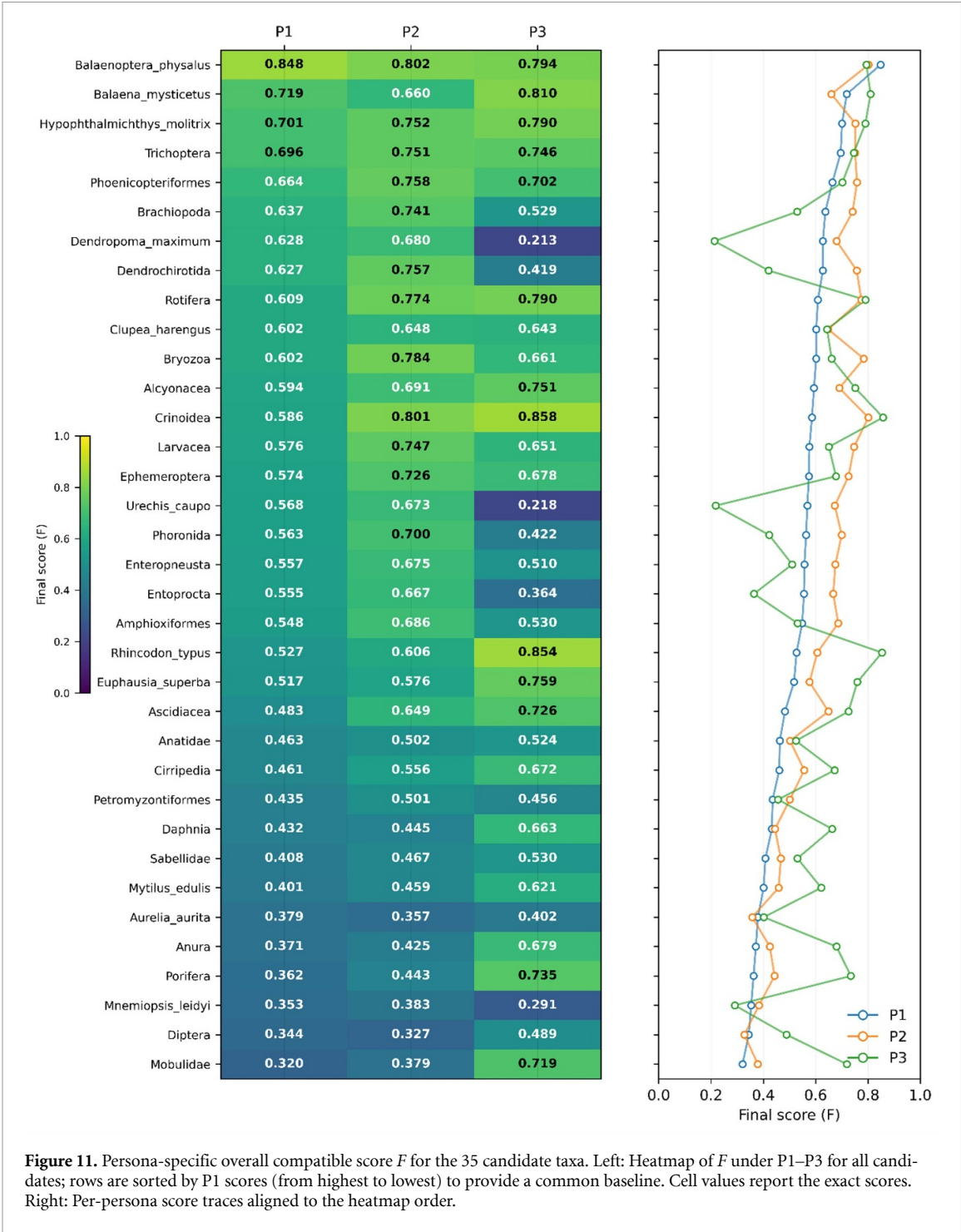
that survives varied changes in strategic emphasis (figure 11). At the same time, reweighting shifts a subset of taxa in interpretable ways: the implementation-oriented P3 profile elevates evidence- and constraint-aligned models such as Crinoidea (P1 to P3: 0.586–0.858), *Rhincodon typus* (P1 to P3: 0.527–0.854), Porifera (P1 to P3: 0.362–0.735), and Mobulidae (P1 to P3: 0.320–0.719); whereas candidates that score well when novelty/-phylogenetic exploration dominates can be strongly down-ranked when DS/OV are prioritised (e.g. *Dendropoma maximum* P1 to P3: 0.628–0.213; *Urechis caupo* P1 to P3: 0.568–0.218). The start-up profile P2 generally sits between P1 and P3, damping extremes while retaining many of P1’s high performers (7 of P1’s top-10 candidates also appear in P2’s top-10 list), consistent with a strategy that seeks differentiation without over-committing to low-evidence options. Overall, the figure makes the trade-space explicit: moving from P1 to P3 systematically shifts selection from exploration-driven candidates (IS/PY-weighted) toward deployability-driven candidates (DS/OV-weighted), while preserving a

Table 8. Persona-specific OV criteria and weighting used in the case study.

Persona	Activated variable	Target criterion/range	Weight	Rationale
P1: Early-career academic researcher	Motility	sessile OR stationary	0.30	Fixed organisms are easier to cultivate and observe over long periods in a university lab
	Adult-size (mm)	≤ 100 mm	0.25	Small/medium body size lowers cultivation costs (e.g. requires a smaller aquarium) and is easier for experimental setups
	Uptake of microplastics	yes	0.25	Ensures direct mechanistic relevance to microplastic-filtration studies
	Habitat	freshwater OR marine	0.20	Keeps options open while excluding terrestrial taxa
P2: Start-up team	Foraging type	passive OR passive/active	0.30	Passive filtration mechanisms imply simpler, low-energy devices, which is important for a cash-constrained start-up
	Motility	sessile	0.25	Sessile organisms often exhibit structurally integrated filtration architectures, which can simplify abstraction into static components
	Uptake of microplastics	yes	0.25	Ensures relevance to the target particle range; helps with pitching to investors
	Adult-size (mm)	50–500 mm	0.20	Mid-sized organisms balance manufacturability (not microscopic) with material economy (not gigantic)
P3: Established filter manufacturer	Uptake of microplastics	yes	0.30	De-risks the first bio-inspired product by starting from organisms already proven to trap microplastics
	Food-size (μm)	1–500 μm	0.25	Aligns biological capture range with commercial microplastic spec (most customer demand lies here)
	Food-to-body ratio	≥ 1000	0.25	High throughput relative to body volume indicates a potentially efficient filtration architecture
	Adult-size (mm)	≥ 500 mm	0.20	Larger organisms provide clear macro-scale filtration structures that are easier to translate into manufacturable geometries or modular industrial elements

Table 9. Persona-specific weighting schemes used to compute F.

Persona	Uses Preset	α (DS)	β (IS)	γ (PY)	δ (OV)	Rationale
P1: Early-career researcher	No	0.15	0.35	0.40	0.10	Down-weights data abundance while emphasising novelty and phylogenetic uniqueness; OV serves as a light feasibility filter
P2: Start-up company	Yes, Exploratory	0.20	0.50	0.20	0.10	Maximises innovation to attract investors; moderate DS and PY prevent over-risking or repetition; OV minimal
P3: Established filter manufacturer	No	0.45	0.15	0.15	0.25	Strongly favours literature sufficiency to reduce execution risk; OV anchors practical engineering constraints; IS and PY play less important roles



small, persona-robust shortlist that can serve as starting points regardless of persona context. To verify that these patterns are not artefacts of a particular weighting choice, we conducted module-level and global sensitivity analyses (DS sub-weight sweeps, λ sweeps in PY, and global weight (α , β , γ , δ) sweeps for F); full results are provided in supplementary note S1 and supplementary figures S1–S3.

4. Conclusions and outlook

This study contributes a practical way to make biological model selection in biomimetic design more explicit and traceable. Rather than assuming that a single ‘best’ organism exists independent of context, the framework treats selection as a data-based trade-off across four dimensions: Literature sufficiency reflects how much usable scientific

evidence is available for a candidate, signalling the effort needed to access enough material for downstream abstraction. Prior biomimetic utilisation captures how extensively a candidate has already been used as a source of inspiration, helping users distinguish well-established models from under-explored taxa. Phylogenetic context incorporates evolutionary distinctness and clade-CP, encouraging exploration beyond conventionally favoured lineages. Project-specific constraints accommodate user-defined criteria that reflect the design context. By combining these dimensions under user-controlled weights, the framework produces ranked shortlists that can be inspected, revised, and justified.

The case study highlights three practical strengths of the framework. First, it separates robust frontrunners from context-dependent opportunities. In the filtration case study, a compact set of candidates remains competitive across distinct scenario weightings, while a smaller subset shifts substantially when priorities change. Second, it makes the exploration–feasibility balance controllable: by adjusting weights, emphasis shifts from novelty-seeking to evidence- and constraint-led selection. Third, the output is auditable at the level of ‘why this organism was chosen’. Because the final score is decomposable into module contributions, teams can communicate and revisit decisions transparently as priorities, constraints, or data sources change.

From an application standpoint, the framework provides a structured decision-support layer that complements, rather than replaces, existing search and knowledge-transfer tools. Beyond its computational implementation, the framework can also serve as a qualitative scaffold in educational or workshop settings. In such contexts, the same modules can be applied qualitatively or semi-quantitatively to guide comparison, which can help students and early-stage practitioners make the criteria and trade-offs behind biological model selection explicit. The framework is intentionally modular and extensible, and this design also defines its current limitations. Outputs depend on the starting candidate pool and upstream data quality, including literature retrieval, taxonomic resolution, the biological appropriateness of the selected taxonomic level, and any datasets used for contextual variables; candidate definition is therefore a critical step before applying the ranking framework. Moreover, the case study demonstrates plausible prioritisation rather than downstream success: the framework identifies candidates that are well supported under a chosen setting, while biological interpretation, abstraction, and engineering implementation remain necessary subsequent steps outside the scope of the tool.

Future development should therefore focus on (i) developing and validating how high-level project

constraints can be accurately mapped to defensible weights and criteria settings for the algorithm; and (ii) conducting empirical evaluations of this framework across multiple domains, using measurable endpoints such as time-to-shortlist, diversity of taxa considered, stability of decisions under documented constraint changes, and downstream feasibility proxies (e.g. prototype progression). With these developments, the framework can contribute to more transparent, comparable, and context-aware biological model selection in bio-inspired design projects.

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Data availability statement

All data that support the findings of this study are included within the article (and any supplementary files).

Code and tool availability

This study describes the proposed framework in full detail, including all formulas, default parameters, rank baselines, and the operational logic required for independent reimplementations. The Python prototype used to perform the case study reported in the paper is available from the corresponding author upon request.

Supplementary Data 1 available at <https://doi.org/10.1088/1748-3190/ae7883/data1>.

Supplementary Data 2 available at <https://doi.org/10.1088/1748-3190/ae7883/data2>.

Supplementary Data 3 available at <https://doi.org/10.1088/1748-3190/ae7883/data3>.

Supplementary Note S1 available at <https://doi.org/10.1088/1748-3190/ae7883/data4>.

Supplementary Video 1 available at <https://doi.org/10.1088/1748-3190/ae7883/data5>.

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