



The LifeWatch ERIC Biodiversity
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From Aristotle to Darwin and Beyond

Revisiting the origins of marine biodiversity classification through taxonomic and functional evidence

Christos Arvanitidis, Vasilis Gerovasileiou, Eleni Voultsiadou, Leen Vandepitte, Stefanie Dekeyzer, Kostas Ganiats

10-minute oral presentation



The provocation: Darwin's sentence becomes a testable question

A historical statement is translated into a scientific hypothesis.

Linnaeus and Cuvier have been my two gods, though in very different ways, but they were mere school-boys to old Aristotle.

Scientific question

To what extent do the conceptual foundations of biological classification, and functional interpretation, trace back to Aristotle's observations of marine life?

The working hypothesis

“Echoing” is not treated as admiration, but as measurable structural resemblance.

If Aristotle’s knowledge still echoes today, then the structure of his information should be detectable in modern analytical terms.

Taxonomic echo

Ancient groupings should resemble modern taxonomic architecture in species relatedness.



Functional echo

Ancient trait descriptions should retain some correspondence with modern trait-based groupings.



Comparative evidence

Differences and similarities can be tested using the same distinctness logic.

Hypothesis in plain words: Aristotle may not have had modern taxonomy, but he may have organised marine biodiversity in ways that remain structurally recognisable.

Two evidence streams: classification and traits

The same taxa, two different kinds of information, two comparable workflows.

1 • Taxonomic data

181 marine taxa from Aristotle mapped to contemporary taxonomy; species distributed across higher ranks.

Taxonomic matrices

Aggregation matrix
Species × higher taxa matrix

2 • Biological traits

Traits extracted from Aristotle's descriptions and modern sources; species distributed in functional trait space.

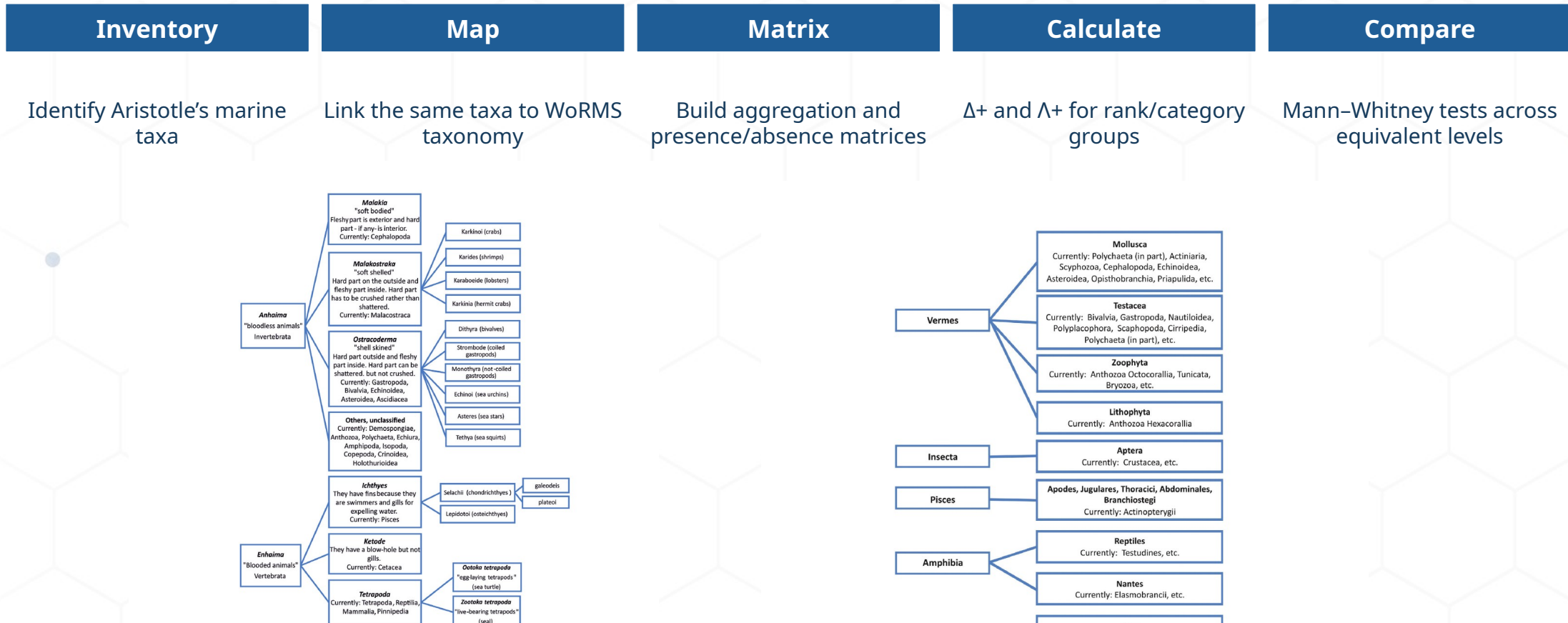
Trait matrices

Species × traits matrix
Distance matrix
Dendrogram-derived groups

Common test: $\Delta+$ and $\Lambda+$ values compared between Aristotle-derived and modern-derived structures.

Workflow A: testing the taxonomic architecture

Published comparison of Aristotle's classification with the current system.



Taxonomy asks: do the branches of Aristotle's classification resemble the branches of the modern tree?

Workflow B: testing the biological-traits architecture

The new analysis shifts the unit of comparison from taxonomic ranks to functional groupings.

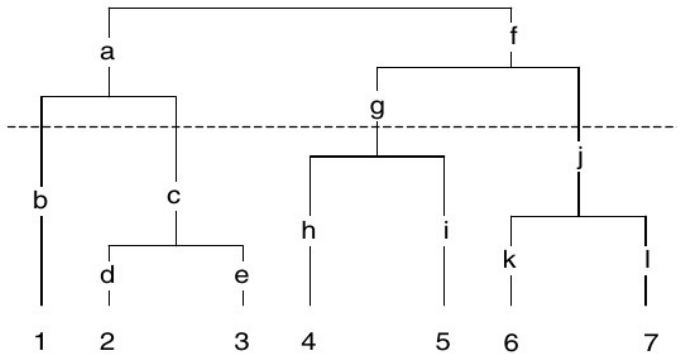
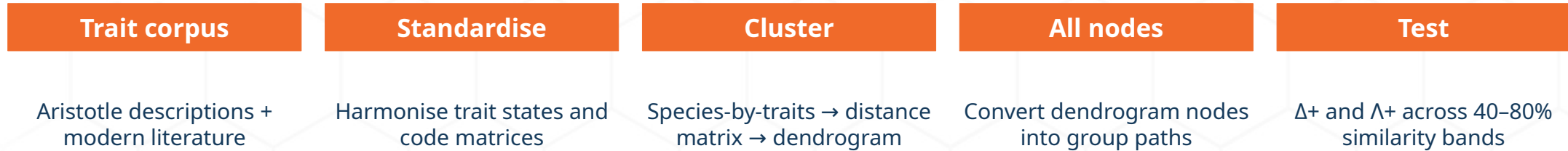


Figure 1 An example functional dendrogram of the relations between species 1–7. The dendrogram has been “cut” by the dashed line at an arbitrary level to assign species to four functional groups: {1}, {2, 3}, {4, 5}, {6, 7}. The total branch length (FD) for species 1–7 is the total length of branches *a–l*. The branch length remaining after species 6 and 7 are lost is the length of branches *a–i* (branches *j*, *k*, and *l* lost). Horizontal lines on this dendrogram do not contribute to FD.

Petchey & Gaston logic

A functional dendrogram captures trait similarity across the whole hierarchy.

For our purpose, it becomes a bridge: ancient and modern trait descriptions can be converted into comparable hierarchical structures.

Key methodological choice: all nodes of the dendrogram are used, not only a single arbitrary cut.

The actual dendrograms.



A common analytical language: Taxonomic Distinctness

The same indices make the two approaches comparable.

Average Taxonomic Distinctness ($\Delta+$)

How far apart are the species, on average, across the classification or trait-derived tree?

Taxonomic tree

**Ancient ranks
vs modern ranks**

Variation in Taxonomic Distinctness ($\Lambda+$)

How even or uneven is the distribution of species across that tree?

Functional tree

**Ancient traits
vs modern traits**

Same question: do the distributions of $\Delta+$ and $\Lambda+$ differ significantly?

Taxonomic result: Aristotle's architecture still echoes

The published analysis found similarity at meaningful hierarchical levels.

No evidence of difference

Rank 3 vs Class / Order
Rank 2 vs Order / Family

Evidence of difference

Rank 3 vs Phylum
Rank 2 vs Class

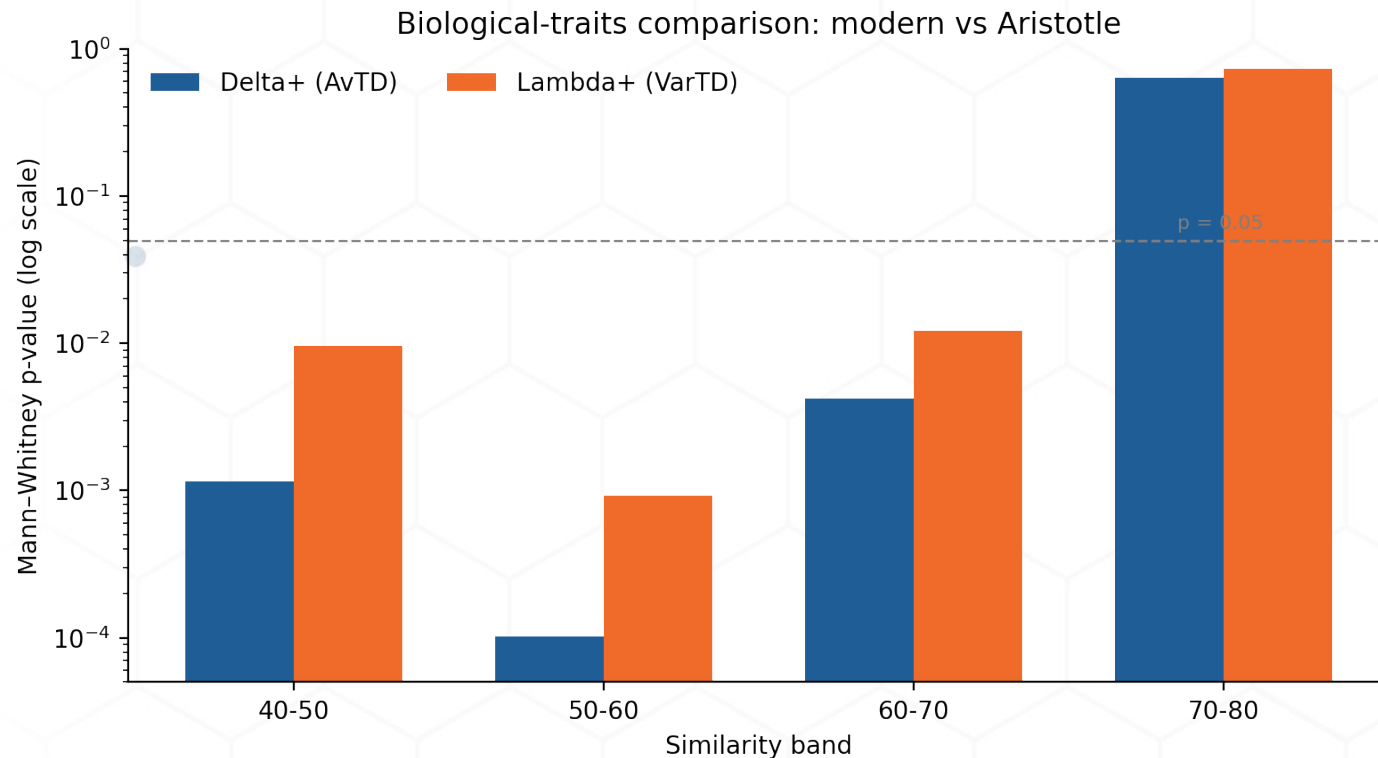
Interpretation

Aristotle's marine groupings do not simply match modern ranks, but they show a recognisable hierarchical architecture. This supports the idea that at least part of his taxonomic reasoning is still visible in current classification.

Taxonomy gives the strongest “echo”: the ancient system and the modern system are not identical, but their structure is comparable.

Biological-traits result: stronger differences, but a fine-scale convergence

The new analysis compares modern and Aristotle trait-derived dendrograms.



Main pattern

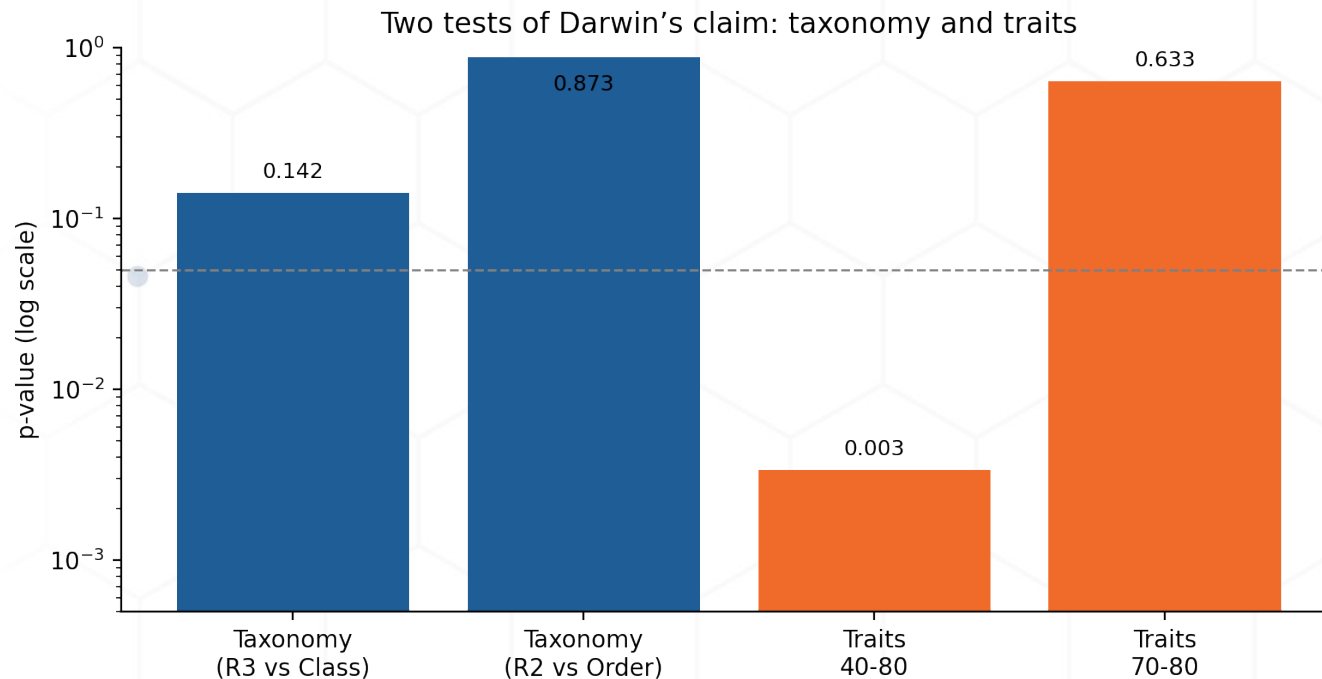
- 40–80%: significant differences for $\Delta+$ and $\Lambda+$
- 40–50%, 50–60%, 60–70%: differences are especially strong
- 70–80%: differences are not significant

Interpretation

Aristotle's descriptions do not reproduce the full modern functional trait architecture. Yet at high similarity, close to species-level functional resemblance, the two systems become more comparable.

Taxonomy and traits tell complementary stories

The same historical question becomes richer when tested through two data types.



Taxonomic approach

Strong structural resemblance at appropriate rank comparisons.

Trait approach

Broader functional differences, with convergence at the fine similarity band.

Synthesis

Darwin's claim is not simply confirmed or rejected: it becomes quantifiable and nuanced.

The ancient evidence echoes most clearly in classification, and more selectively in biological trait organisation.

Take-home message

Aristotle's observations of marine life still echo, not as modern biology, but as an early architecture of biodiversity reasoning.

What lies beyond

The workflow now turns historical natural history into reusable biodiversity informatics: datasets, matrices, dendrograms, distinctness indices and reproducible comparisons. Comparisons still need to go deeper and compare actual nodes of the dendrograms rather than similarity levels.

LifeWatch ERIC contribution

A pathway to publish the method as a reusable workflow in the LifeWatch ERIC Taxonomy VRE / my.lifewatch.eu ecosystem.

Thank you