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Unsupervised ecosystem risk assessment in the Baltic Sea reveals bottom-oxygen depletion and fishing pressure as key threats in species-abundant hotspots

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Abstract
Marine ecosystems are increasingly shaped by the combined effects of multiple environmental and anthropogenic stressors, generating non-linear, spatially heterogeneous patterns of risks to ecosystem functioning. The Baltic Sea represents a paradigmatic system where geographical constraints intersect with intense human pressures. This study presents a data-driven framework for ecosystem risk assessment, conceptualising risk as an emergent property of interacting environmental, anthropogenic, and biological stressors. The approach integrates complementary unsupervised models: a clustering-based technique (Multi K-means) and a deep learning model based on a Variational Autoencoder, to capture recurrent and anomalous stressor patterns. Model-generated risk maps are statistically analysed within an ensembled risk characterisation to ensure ecological interpretability and comparability. The framework is applied to 2020 data from the central and western Baltic Sea, integrating multi-source data with abundance information on 145 marine species, commercially relevant species, and cod. The models identify spatially concentrated ecosystem risk hotspots in species-abundant areas characterised by the concurrence of bottom-oxygen depletion, depth-related constraints, and fishing pressure, consistent with expert studies. Cross-model concordance analysis reveals consistency and complementarity between the models. By reducing subjectivity while maintaining ecological interpretability, the framework provides a scalable and transferable tool for ecosystem risk assessment and ecosystem-based management.

Keywords Ecosystem risk assessment · Baltic Sea · Cluster analysis · Deep learning · FAIR data

Introduction

Marine ecosystems worldwide are increasingly exposed to concurrent and competing pressures from multiple environmental and anthropogenic factors. Climate change, habitat alteration, exploitation of living resources, and ship traffic often interact in non-linear ways, altering ecosystem functioning, resilience, and long-term stability[1–3]. In such contexts, the risk that an ecosystem will undergo a critical transition to a new state (*ecosystem risk*, briefly) does not arise from isolated pressures — often generically referred to as *stressors* — but from their cumulative and interacting effects, which may amplify ecosystem vulnerability. This complexity has driven growing

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interest in analytical frameworks capable of integrating heterogeneous pressure factors, capturing their combined influence on ecosystem dynamics, and re-applicable across different ecosystems[4,5].

Ecosystem Risk Assessment (ERA) provides a conceptual and operational framework for identifying and representing conditions that increase the likelihood of ecosystem change, and for estimating the spatial distribution of this likelihood. Rather than focusing solely on observed degradation, ERA encompasses scenarios that predispose ecosystems to critical transitions, including biodiversity loss, reduced resilience, functional simplification, and altered ecosystem services[6–10]. Often, ERA reflects probabilistic and precautionary perspectives, oriented toward prevention, prioritisation, and risk-informed decision-making[11].

The Baltic Sea (Figure 1) represents a paradigmatic case in which natural constraints and intense human pressures co-occur and interact, shaping ecosystem structure, vulnerability and spatially heterogeneous ecosystem risk patterns[12]. As a semi-enclosed basin with limited exchange with the North Sea, the Baltic Sea contains strong salinity gradients ranging from marine to brackish waters, which are persistently stratified, making it naturally prone to low oxygen concentrations in bottom waters, a condition exacerbated by eutrophication and climate change[13,14].

These physical constraints intersect with multiple anthropogenic stressors. Fishing has long been a major driver of ecosystem change, particularly targeting demersal communities[15,16]. Cod (*Gadus morhua*) is a key demersal predator and, as a historically important commercial stock, its severe decline in stock sizes has become a classic example of ecological collapse in the North Atlantic[17,18]. The smaller cod stocks are characterised by reduced average body sizes, with worsening body condition and increasing vulnerability to ocean warming and

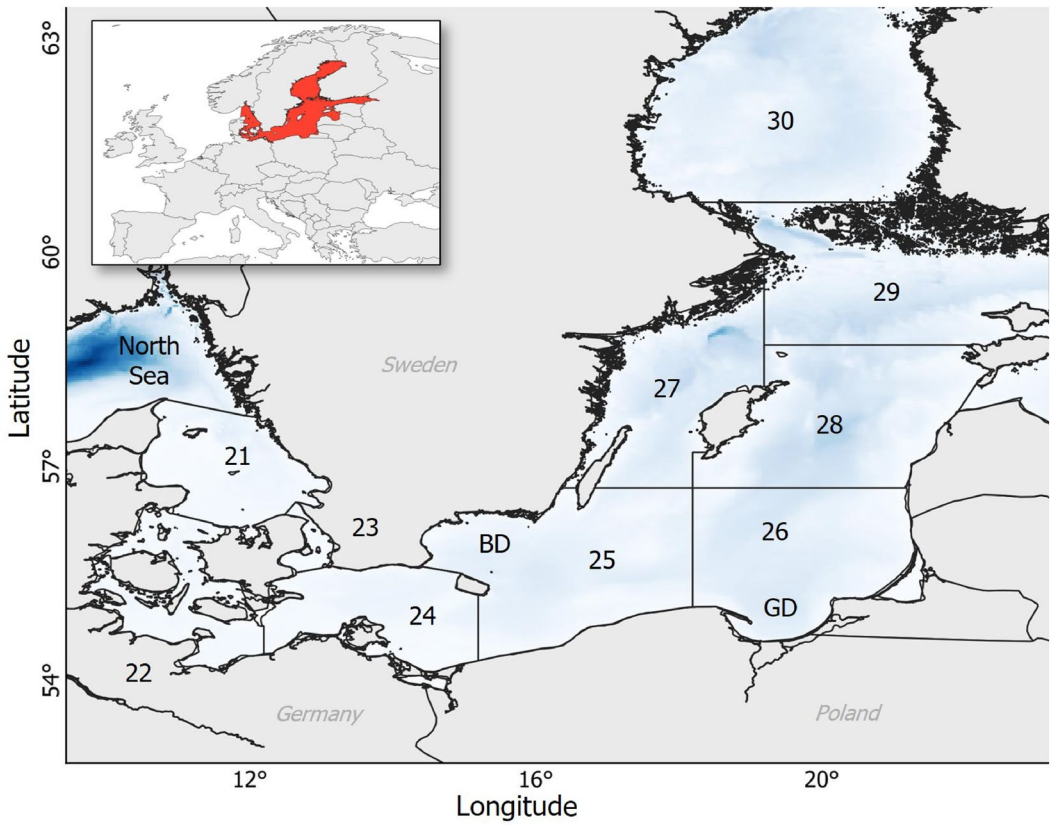

Figure 1 Baltic Sea divisions from the International Council for the Exploration of the Sea (ICES). The study reference areas comprise divisions 21–26 in the central and western Baltic Sea. The Bornholm Deep (BD) and the Gdansk Deep (GD) are indicated. The inset map (top-left) shows the location of the Baltic Sea in Europe (highlighted in red). ICES subdivisions were taken from https://gis.ices.dk/geonetwork/srv/api/records/c784a0a3-752f-4b50-b02f-f225f6c815eb. Coastal boundaries were taken from https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units/countries.

the expansion of seafloor anoxic areas, which have reduced habitat availability[19–21]. Beyond cod, other demersal species relevant to Baltic fisheries (e.g., *Limanda limanda*, *Platichthys flesus*, *Pleuronectes platessa*, and *Merlangius merlangus*) are increasingly exposed to the combined effects of exploitation, climate-driven environmental change, and bottom habitat degradation, with distributions and conditions tightly linked to benthic habitat quality[22–24]. These changing environmental conditions can further constrain reproductive success and recruitment[25,26]. In parallel, the Baltic Sea is among the most densely trafficked marine regions worldwide. Maritime traffic contributes to multiple stressors, including pollution, underwater noise, and physical disturbance of seabed habitats[27,28]. Additional disturbance arises from military activity, dumping sites, and expanding offshore.

Because of this convergence of natural constraints and intense human pressures, the Baltic Sea has long served as a natural laboratory for the development and application of ERA frameworks. Several regional initiatives, particularly within the Helsinki Commission[29] (HELCOM), have produced basin-scale spatial indices that overlay human pressure layers with ecosystem sensitivity data, providing coherent representations of cumulative impacts and supporting comparative analyses across different sub-basins[30–32]. ERA applications in the Baltic Sea have also addressed specific localised conditions - such as eutrophication, hypoxia, contaminants, and impacts related to fisheries - through sector-specific or indicator-based assessments[33–36]. Nevertheless, the operational implementation of an ecosystem-based perspective remains challenging. This limitation is particularly evident in fisheries assessment frameworks, which often remain centred on single-species dynamics, while broader ecosystem interactions and cumulative environmental pressures are treated as background conditions rather than explicitly incorporated into risk evaluations[37,38]. Collectively, however, these assessments have mainly represented cumulative pressure intensity rather than the structure, recurrence, and interactions of the stressors associated with ecosystem risk[30,31,39,40]. Many implementations have involved trade-offs between deterministic and expert-driven methods that have assumed linear dependencies among the stressors[41–45], introducing subjectivity and limiting their ability to capture non-linear interactions[46–48]. This limitation motivates the development of data-driven approaches that can identify complex, non-linear risk patterns and provide interpretable spatial assessments of ecosystem vulnerability. Recent advances in environmental monitoring and the growing availability of geospatial datasets have enabled statistical, multivariate, and machine/deep learning approaches to integrate heterogeneous variables and identify recurring ecological patterns directly from the data[48–51]. For example, integrating biotopic classes[52], environmental, and trophic heterogeneity into a spatially explicit Bayesian model has substantially improved predictions of Baltic cod biomass[53]. However, many data-driven approaches are primarily descriptive, often rely on subjective priors, and provide limited guidance on how the identified patterns relate to ecosystem risk[43,45]. Moreover, anomaly detection techniques often yield abstract deviation scores that are difficult to interpret ecologically. As a result, anomalies are rarely translated into explicit, interpretable risk categories, thereby limiting their practical relevance for ecosystem assessment and management. These approaches usually define natural and anthropogenic pressures as *stressor variables* that quantify active forces potentially associated with specific risks of ecosystem change in the area analysed[47,54]. Stressors thus become variables that contribute to an increased risk of ecosystem change, reflecting either *harmful forces* or current *fragile conditions*. Consequently, risk is conceptualised as the condition of intense concurrent and competitive exposure to these stressors.

The present paper falls within the ERA frameworks based on machine learning and deep learning. It describes a data-driven ecosystem risk assessment methodology that reduces reliance on expert-defined relationships, weights, and risk labels. It extends existing data-driven ERA approaches to provide a complementary spatial assessment of conditions associated with ecosystem risk in the central and western Baltic Sea (ICES subdivisions 21–26). The study analyses data from 2020, including 15 annually aggregated variables selected from open-access repositories, in accordance with open-science principles[55]. These variables provide an integrated description of environmental conditions, human pressures, habitats, and biological communities, including physical and biogeochemical factors (bathymetry, bottom temperature, salinity, dissolved oxygen, and primary production), anthropogenic activities (shipping, fishing, military areas, wind farms, and dumping sites), habitat characteristics (bedrock and hard-bottom sediments), and biological indicators (species richness, abundance of five key demersal commercial species, and cod abundance). Variables are selected based on their demonstrated relevance

in previous marine risk assessment studies and their capacity to represent both ecosystem vulnerabilities (e.g., biodiversity hotspots, sensitive habitats, low-oxygen areas) and anthropogenic stressors that affect ecosystem functioning and resilience in the Baltic Sea.

To address the complex interplay between the variables, this study proposes an integrated, unsupervised methodology to characterise the emergence of ecosystem risk across multiple dimensions. By combining unsupervised clustering (Multi K-means) and deep learning (a Variational Autoencoder), the methodology identifies recurrent stressor configurations and detects latent, non-linear anomalies in the multivariate stressor space. These anomalies are subsequently characterised using the original stressor variables and refined into ecologically interpretable risk profiles.

Overall, this study (1) maps spatial ecosystem risk distribution driven by multiple stressors, (2) integrates complementary unsupervised approaches into a unified assessment, and (3) highlights robust risk hotspots across different species groups. Moreover, it provides a scalable and transferable methodology for ecosystem risk assessment in complex marine systems.

Results

Cross-model concordance analysis of ecosystem risk assessment compared the outputs of two unsupervised models: one based on pure cluster analysis (Multi K-means, MKM) and another based on a deep learning model (Variational Autoencoder, VAE) refined by Multi K-means clustering (VAE+MKM). A qualitative assessment was finally performed by combining the MKM and VAE+MKM outcomes using a hierarchical combination (explained in Methods).

Cross-model concordance analysis

The ecosystem risk hotspot maps produced by MKM and VAE+MKM were quantitatively compared by examining the spatial overlap between *high*- and *lower*-risk 0.1 × 0.1 cells across the central and western Baltic Sea in 2020. Overall *similarity* was assessed using cell-by-cell pairwise similarity and agreement beyond chance (Cohen's Kappa). Comparisons were performed for four scenarios: 145 marine species (mostly including fishes, but also crustaceans, molluscs, mammals, and sponges), the five most relevant commercial demersal species (*G. morhua*, *M. merlangus*, *L. limanda*, *P. flesus*, and *P. platessa*), cod (*G. morhua*) only, and an *ensemble* obtained by merging the three species-group-specific maps (Table 1).

The comparison showed high spatial overlap between the MKM and VAE+MKM predictions, with pairwise similarity consistently exceeding 80% across all groups. Notable differences emerged when considering the agreement beyond chance. The models that considered the 145 species achieved approximately 81% pairwise similarity, with a relatively low Kappa value ($\kappa \approx 0.35$), suggesting that the predominance of non-high-risk cells in the study area may account for some of the observed similarity. In contrast, the commercial species models showed the highest level of concordance on high-risk cells, with pairwise similarity exceeding 92% and a

Table 1 Cell-by-cell pairwise similarity and agreement (as Cohen's Kappa) between the Multi K-means (MKM) and the deep learning-plus-MKM model (VAE+MKM). The comparison was conducted at a 0.1 spatial resolution using 2020 data for the central and western Baltic Sea (ICES divisions 21-26). Results are reported for three different species groups and their ensemble.

Species group	Pairwise similarity (%)	Cohen's κ
Species richness (145 species)	81.36	0.35
Commercial species (five demersal)	92.80	0.72
Single relevant species (cod)	89.30	0.48
Ensemble (all species groups)	82.24	0.59

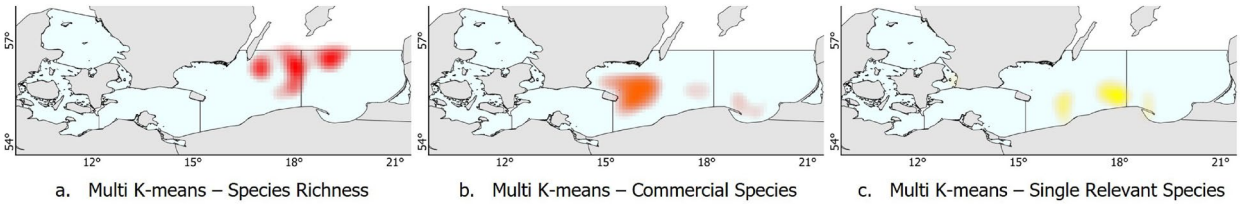

Figure 2 Ecosystem-risk hotspot maps (normalised density of high-risk cells) based on Multi K-means, across different species groups: (**a**) 145 species of general commercial and conservation importance (species richness group), (**b**) five species of high conservation and commercial importance (commercial species group), and (**c**) the cod (single relevant species). Distinct colours denote different species groups for clarity. Coastal boundaries were taken from https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units/countries.

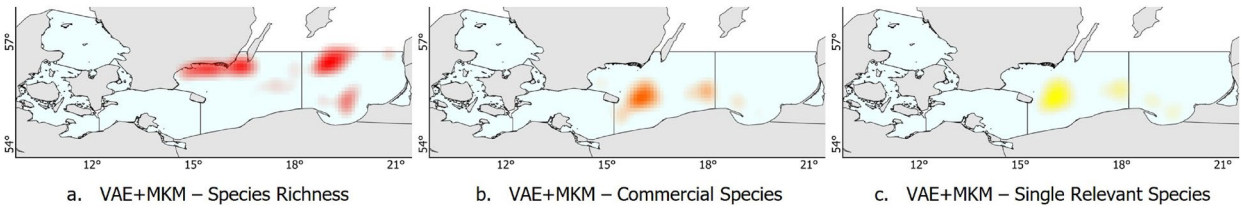

Figure 3 Ecosystem-risk hotspot maps (normalised density of high-risk cells) based on Variational Autoencoder followed by the application of Multi K-means (VAE+MKM), across different species groups: (**a**) 145 species of general commercial and conservation importance (species richness group), (**b**) five species of high conservation and commercial importance (commercial species group), and (**c**) the cod (single relevant species). Distinct colours denote different species groups for clarity. Coastal boundaries were taken from https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units/countries.

substantial agreement ($\kappa \approx 0.72$). This result indicates a strong convergence between MKM and VAE+MKM in identifying high-risk areas for relevant demersal species. The models for cod-only yielded intermediate results, with high pairwise similarity ($\approx 89\%$) but a moderate Kappa value ($\kappa \approx 0.48$), indicating reasonable agreement beyond chance but also highlighting methodological differences in how the two models captured species-specific risk patterns. At the ensemble level, the models achieved a pairwise similarity of approximately 82% and a moderate to substantial agreement ($\kappa \approx 0.59$). This result suggests that the combined risk assessments from the three species-group maps were consistent between MKM and VAE+MKM, improving agreement on individual species richness and cod assessments.

Qualitative evaluation

A qualitative assessment characterised the ecosystem risk hotspots identified by MKM and VAE+MKM across the three species-group models (Figures 2 and 3), helping to interpret the reasons underlying the assessments and to evaluate their reliability relative to previous studies. The evaluation was first conducted at the species-group level and then at the *ensemble* level (obtained by merging the three species-group maps). Moreover, the evaluation also regarded the *combined* model, obtained by merging the ensemble models from MKM and VAE+MKM. The here-reported stressor intensity interpretation as *high*/*strong*, *moderate*, and *low* derived from the stressor-wise statistical analyses performed by the models (explained in Methods).

Species richness hotspots (Figures 2a and 3a). MKM and VAE+MKM revealed different yet ecologically reliable ecosystem risks. MKM predominantly identified high-risk areas in deep to very deep offshore regions of the central and western Baltic, characterised by cold waters, a generally low salinity, low to very low bottom oxygen concentrations, and generally low surface productivity. Despite these environmentally limiting conditions, these areas consistently exhibit high species richness and abundance[56]. Risk was often associated with cumulative anthropogenic pressures, including moderate to high shipping traffic and the recurrent presence of

offshore infrastructures, while fishing ranged from moderate to strong, and military influence remained marginally important. In contrast, VAE+MKM more frequently detected high-risk areas in shallow to moderately deep waters, often near the coasts. These regions were characterised by more heterogeneous environmental conditions, including higher salinity, higher bottom-oxygen levels, and moderate to high surface productivity. Ecosystem risk matched direct human pressures, including moderate to intense fishing activity, high shipping traffic, and a pronounced presence of military areas, with wind farms and dumping sites playing a secondary role in the risk assessment. Although VAE+MKM also captured very deep and severely hypoxic areas, these regions represented a smaller fraction of the identified high-risk MKM regions. The two models produced complementary yet valid dimensions of ecosystem risk for species richness. MKM primarily emphasised offshore environments known to be exposed to chronic physical stressors, particularly persistent low-oxygen and low-salinity conditions[57–59]. Conversely, VAE+MKM captured risk associated with coastal and transitional zones where high species abundance overlapped with intense and diverse anthropogenic activities, consistent with previous studies that identified nearshore, species-rich areas in the basin as particularly vulnerable to human pressures[28,60,61].

Commercial species hotspots (Figures 2b and 3b). For the five commercial demersal species (*G. morhua*, *L. limanda*, *M. merlangus*, *P. flesus*, and *P. platessa*), more coherent spatial patterns, compared to species richness, emerged when comparing the two approaches. Both models identified deep, very cold waters as the main areas of ecosystem risk, characterised by marked to strong bottom-oxygen depletion and, by construction, very high abundance of the selected commercial species. Depth, combined with low oxygen conditions and moderate to high salinity, represented a recurring feature across nearly all hotspots detected by both MKM and VAE+MKM. MKM emphasised the most extreme conditions, identifying hotspots in very deep areas with very low bottom-oxygen levels, high salinity, and high to very high fishing intensity, accompanied by moderate-to-high shipping traffic, and the presence of dumping sites and military areas. Ecosystem risk was driven by the combination of intensive demersal fish exploitation and environmental conditions close to critical thresholds, as also highlighted by other studies[12,62–64]. VAE+MKM identified hotspots largely overlapping with those of MKM, while introducing greater variability in surface productivity and capturing some moderately deep areas. Core features found with both models remained consistent, with intense fishing and bottom oxygen depletion ranging from moderate to strong. VAE+MKM highlighted specific structural and anthropogenic factors, such as hard-bottom substrates, military areas, dumping sites, and wind farms, overall indicating that ecosystem risk was associated with multiple co-occurring stressors[65,66]. The high degree of spatial overlap between the two models indicates a robust risk assessment. MKM and VAE+MKM captured consistent ecological drivers of risk, dominated by the interaction between high abundance of commercial demersal species, intense fishing, and unfavourable physico-chemical conditions shaping the structure and spatial distribution of the demersal fishes[23,67,68].

Cod hotspots (Figures 2c and 3c). Ecosystem risks identified by MKM and VAE+MKM for cod largely overlapped. Both models highlighted high-risk areas associated with moderately to very deep conditions, cold environments, where bottom oxygen depletion ranged from moderate to strong and surface productivity was generally high. These conditions match with a known, recurrent coupling between productive surface waters, enhanced food availability, and stressful benthic conditions, under which cod is vulnerable[69]. Salinity tended to high levels, particularly in deeper offshore areas, aligning with known habitat preferences of cod[70]. The MKM model emphasised the relevance of shallower, warmer areas, characterised by very high surface productivity and only slightly reduced bottom oxygen, where cod abundance remained moderate to high, and fishing activity was moderately high. This model indicated that ecosystem risk for cod was not restricted to deep hypoxic zones but also extended to productive shallower regions subject to high exploitation. In these hotspots, ship traffic, dumping sites, military areas, and wind farms were of secondary importance compared to fisheries and were spatially limited. Similarly, VAE+MKM identified deep hotspots characterised by very low bottom-oxygen levels and intense fishing, often combined with moderate to high shipping traffic. Compared to MKM, VAE+MKM detected a greater number of areas with a stronger cumulative anthropogenic footprint, particularly the recurrent presence of military areas and dumping sites, and occasionally wind farms, suggesting greater sensitivity of this model to the co-occurrence of environmental stressors and human activities. The strong spatial agreement between MKM

and VAE+MKM indicated that ecosystem risk at the single-species level was driven by well-defined, shared mechanisms, primarily the interaction between intense fishing and oxygen-depleted bottom waters. Notably, most of the high-risk hotspots identified by both models also included the main known cod spawning areas[71].

Ensemble-level hotspots (Figure 4). Ensemble models provided a synthetic view of persistent ecosystem risk across different species groups and modelling approaches. By aggregating risk maps derived from the three species groups, both MKM and VAE+MKM highlighted a set of spatially consistent high-risk areas (Figures 4a-b), indicating that vast regions of the central Baltic exhibited elevated ecosystem vulnerability.

The strongest convergence between the ensemble models occurred for the Bornholm Basin and the Gdansk Deeps, within ICES subdivisions 25-26 (Figure 1), in agreement with other localised studies that have indicated these areas as vulnerable ecosystems[32,72]. As expected from the species-focused refinement, these areas were associated with elevated values of cod abundance, with commercial demersal species particularly concentrated in the Bornholm Basin. Their distinguishing environmental and anthropogenic characteristics included deep waters with low temperatures, moderate salinity, and strongly reduced sea-bottom oxygen in the central Baltic. Net primary production was generally low, except for the more productive coastal areas of the Gdansk Deep. Anthropogenic pressures were persistent and spatially coherent, with generally high fishing intensity and substantial shipping traffic. Dumping sites and military areas were widely represented within these hotspots, while offshore wind farms played a comparatively secondary role. Portions of these areas included hard-bottom complex habitats, indicating the co-occurrence of ecologically valuable substrates and multiple human pressures. There was, therefore, an overall agreement concerning the concurrence of high biological value, oxygen stress, and sustained anthropogenic pressure in the high-risk areas identified through ensemble modelling. These regions are known to host key ecological processes for cod[73], including spawning and nursery habitats[74,75], while also being subject to chronic bottom oxygen depletion and sustained fishing pressure[24,63].

As for the combined model, the most intense hotspots (i.e., the areas of highest density and therefore stronger colour intensity in Figure 4c) were spatially concentrated in deep offshore sectors of the central Baltic. Generally, in this model, areas with the most intense colours represented stronger spatial concordance between MKM and VAE+MKM, whereas less intense areas represented model-specific or weakly overlapping classifications. Colour intensity should therefore be interpreted as a visual indicator of cross-model agreement and risk signals that depend on specific models. The highest agreement occurred in zones with high abundances of cod and other commercial demersal species. On average, in these hotspots, waters are deep, sea-bottom temperatures are low, salinity levels tend to be high, and bottom seawater is anoxic. Moreover, net primary production in 2020 was generally low, consistent with offshore deep-basin conditions. These areas were also associated with very intense fishing and moderate maritime traffic. They frequently included military-use zones and one of the main regional dumping sites; conditions that increase the risk of pollution and contaminant release in physically constrained environments[66,76,77]. The identification of these regions was consistent with several other studies showing that similar environmental conditions and anthropogenic stressors might determine high ecosystem risk across multiple habitats and ecologically relevant species groups[72,78–81]. Overall, the HELCOM cumulative-impact assessment[40] and

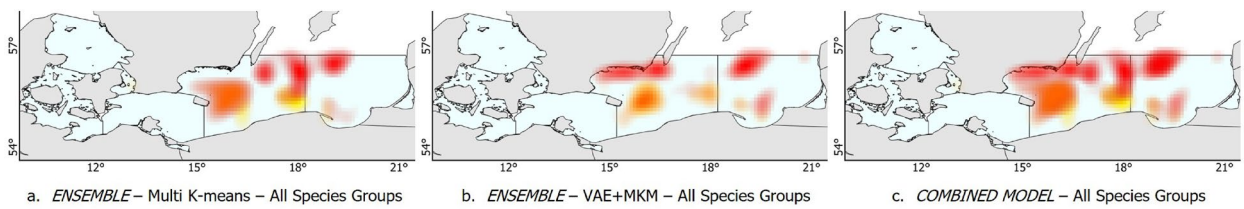

Figure 4 Ecosystem-risk multi-species-group hotspot maps (ensemble maps) from (**a**) the Multi K-means model and (**b**) the Variational Autoencoder with subsequent application of Multi K-means (VAE+MKM), and (**c**) the combination of the two models (combined model). Distinct colours denote different species groups for clarity. Stronger colour intensity indicates greater spatial overlap between the ensemble classifications. Coastal boundaries were taken from https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units/countries.

independent studies of hypoxia, demersal communities, cod spawning habitats, fishing pressure, and seabed vulnerability[57,63,69,71,72] have reported evidence for the ecological sensitivity of the principal areas identified by the models. Moreover, persistent vulnerability in these regions was evidenced by the third HELCOM Holistic Assessment[32], which covered 2016–2021 and therefore included the study year, and reported widespread adverse ecosystem conditions and cumulative pressures in the Baltic Sea.

Discussion

This study has presented a multi-model, data-driven methodology for ecosystem risk assessment, an approach designed to identify risk as an emergent property of interacting stressors rather than derived from analysing pressures in isolation. The results have demonstrated its ability to capture complex, non-linear relationships often overlooked in traditional additive or single-stressor frameworks[82,83].

Previous Baltic ERA frameworks have provided valuable cumulative assessments but have generally emphasised pressure intensity and often relied on predefined linear relationships and expert-derived weights[30,31,39–45]. This has limited their capacity to represent recurrent and non-linear stressor interactions[46–48]. Instead, the data-driven methodology presented here addresses these limitations by combining unsupervised clustering with deep learning, enabling the identification of recurring stressor patterns and latent anomalies in the multivariate stressor space. Overall, the methodology extends previous data-driven ERA approaches by integrating complementary unsupervised models with *post hoc* risk characterisation and biological refinement. It offers a reproducible, interpretable, and scalable alternative that reduces reliance on expert-defined weights and relationships.

A novel aspect of this study is the explicit characterisation of the anomalous stressor configurations identified by the VAE, followed by their clustering through Multi K-means (VAE+MKM model). This integration allowed latent and non-linear deviations in the stressor space to be characterised *post hoc* and translated into coherent, interpretable risks rather than remaining as abstract anomaly scores. Notably, the role of the VAE should not be interpreted as establishing a direct correspondence between statistical anomalies and ecosystem risk. The VAE provided candidate uncommon configurations, whereas risk interpretation arose from their subsequent characterisation in the original stressor space and from the species-abundance refinement. The combination of complementary unsupervised models enabled the exploration of multiple dimensions of ecosystem vulnerability - involving heterogeneous data and complex stressor interactions - without privileging any model. The classification did not rely on expert-assigned stressor weights or expert-labelled risk observations. The framework retained researcher-defined methodological choices concerning data selection and preprocessing. The MKM and VAE+MKM models explored complementary dimensions of ecosystem risk. MKM captured structurally persistent risk configurations associated with chronic environmental stress, particularly in deeper offshore areas characterised by stable hypoxic conditions. In contrast, VAE+MKM was more sensitive to latent processes and non-linear stressor inter-dependencies, identifying anomalous configurations often associated with cumulative anthropogenic pressures in transitional and coastal zones. This model identified ecosystem risks associated with more complex scenarios of stressor interdependency, which could otherwise remain undetected by distance-based clustering alone. Differences observed between the models reflected distinct ecosystem mechanisms rather than methodological inconsistency, reinforcing the value of a multi-model unsupervised strategy. The combined model produced a comprehensive risk assessment map that integrated two complementary views of ecosystem risk and better aligned with expert studies. It synthesised a scalable, reproducible, data-derived risk assessment, which has also been advocated by other studies[55,84,85], that captured emergent properties within a complex ecosystem. Moreover, it provided assessment gradients and a multigranular synthesis across different species- and model-specific risk assessments, in which a decrease in hotspot intensity indicated either stronger spatial concordance or species-specific conditions.

From an ecological perspective, the identified risk patterns reflected fundamental structural constraints of the Baltic Sea and revealed stressor dynamics directly from the data. The combined model showed that bottom

oxygen concentration consistently played a central role in shaping ecosystem risk. Areas characterised by low bottom oxygen coincided with high-risk conditions, highlighting hypoxia as a dominant driver of ecosystem vulnerability. Ecosystem risk was further associated with depth constraints and salinity gradients, which modulated the interactions between physico-chemical stressors and biological responses. Deep areas were typically associated with environmental stress, whereas transitional and coastal zones exhibited more heterogeneous stressor configurations. Within the species-abundant areas prioritised by the refinement, high-risk conditions were characterised by sustained fishing pressure and adverse physicochemical conditions, particularly for commercially relevant demersal species, including cod. This spatial concurrence is consistent with the hypothesis that anthropogenic exploitation may amplify vulnerability in communities already exposed to unfavourable physicochemical conditions, potentially reducing population sizes, genetic diversity, and overall resilience to environmental stress. Other anthropogenic pressures, including shipping traffic, dumping sites, military areas, and offshore infrastructure, were generally secondary but cumulatively and locally contributed to risk patterns, especially in coastal and transitional zones. These ecosystem risk drivers were consistent with existing knowledge of the Baltic Sea[57,58,63], where cumulative and interacting pressures dominate ecosystem dynamics and challenge management strategies[86,87].

Some limitations of this study should be acknowledged. The analysis was restricted to 2020, the year with the greatest simultaneous coverage of the selected heterogeneous variables. The availability of comprehensive data on fragile conditions and harmful forces was essential to our methodology, which is closely tied to the current global debate on multi-source data from open-access repositories of findable, accessible, interoperable, and reusable (FAIR) data[88–94]. The single-year design has important implications for interpretation. The resulting maps represent spatial configurations of conditions associated with ecosystem risk in 2020 and cannot guarantee that these configurations were temporally persistent. Some detected patterns may reflect chronic environmental constraints and sustained anthropogenic pressures, whereas others may have been influenced by transient conditions specific to the selected year. Although the correspondence with previous Baltic Sea studies supports the persistent vulnerability of several identified areas, it does not demonstrate the temporal stability of the model classifications. A multi-year assessment would require comparable annual snapshots with consistent variables and spatial coverage, along with procedures for handling missing years, changes in observation effort, and differences across data-definition periods. An alternative extension would involve time-dependent unsupervised machine-learning models, which remain at the technological frontier because mature VAE architectures for robustly representing temporal dependencies are not yet broadly established. These developments are outside the scope of the present spatial methodology and constitute priorities for future work.

An additional critical aspect concerns the use of species abundance proxies derived from catch-per-unit-effort (CPUE) data from the ICES trawl surveys[95]. These data were collected through fishery-oriented surveys primarily designed to characterise cod stocks. As a result, they might be subject to spatial bias, gear selectivity, and uneven coverage, and might not fully capture abundance changes across the entire fish community. Furthermore, CPUE values were spatially interpolated to obtain a harmonised grid, introducing uncertainty in areas with sparse observations. Moreover, aggregate CPUE did not capture demographic properties that may alter population vulnerability, even without corresponding changes in total abundance[53]. The hotspots should therefore not be interpreted as assessments of population demographic status. Although these factors might affect the fine-scale species-abundance representation, they do not undermine the validity of the methodology, which was designed to capture relative and spatially coherent macroscopic ecosystem risk patterns, in line with big data approaches in ecological modelling[55,96–101]. Complementary models, such as Bayesian networks, can integrate this information to explore how environmental, trophic, and fisheries dynamics interact when sufficiently consistent temporal data and prior interaction structures are available[53,102–104].

A further limitation concerns the evaluation of the risk maps. Comparison with HELCOM assessments and published ecological studies corroborated the ecological plausibility of the detected hotspots but did not constitute an independent validation of the complete spatial classification. The evaluation focused on positive hotspot detections and did not establish that cells outside the hotspots represented low-risk conditions. A spatially complete

and temporally matched independent reference assessment was unavailable for the study area. Constructing such a reference through expert elicitation would require extensive multidisciplinary knowledge of this heterogeneous ecosystem and would inevitably involve subjective choices concerning risk definitions, stressor importance, and spatial classification. Future work will explore the possibility of validating the results against independent, reproducible, and more complete indicators.

Sensitivity analysis was also limited. Hotspot aggregation can reduce the propagation of moderate clustering differences into the final hotspot maps (as explained in Methods). In the species-richness MKM model, a 15% increase or decrease in the index that regulates the selection of the optimal number of clusters yielded KDE-derived hotspot patterns with approximately 95% spatial agreement with the optimal configuration. Moreover, indirect evidence of methodological consistency comes from previous studies that have demonstrated that different clustering approaches — including Multi K-means, Fuzzy C-means, and X-means — would produce substantially overlapping ecosystem-risk patterns despite using different clustering assumptions and model-selection criteria[48,54]. Nevertheless, a more comprehensive sensitivity analysis should investigate sensitivity at multiple stages of the workflow, including alternative high-performing VAE architectures, anomaly thresholds, and input variable sets. The current study focuses on demonstrating the effectiveness of the proposed solution, whereas this analysis, which will be the focus of future work, will help distinguish uncertainty originating from the input data, model configuration, ecological-risk classification, and spatial hotspot delineation.

Finally, the data-driven nature of the methodology should not be interpreted as a complete absence of subjective decisions. The workflow reduces reliance on expert judgement during risk classification, and avoids expert-assigned stressor weights, expert-labelled training data, and manually delineated risk areas. Nevertheless, its construction involves researcher choices concerning variable selection and interpretation, spatial and temporal scope, and species-group composition. In the present study, these decisions were guided by data availability, prior ecological evidence, and established methodological procedures, and were explicitly reported to support reproducibility. Future work should systematically evaluate the sensitivity of the resulting risk maps to alternative variable sets, spatial resolutions, interpolation methods, model configurations, and classification thresholds.

Overall, our study provided a robust basis for ecosystem-level prioritisation, spatial planning, and early warning applications. The identification of ecosystem risk hotspots serves as a starting point for more detailed investigations and may support monitoring, conservation, and fisheries management in complex and vulnerable systems such as the Baltic Sea. Ecosystem risk maps can provide reproducible, data-derived priors to guide marine spatial planning and environmental assessments[105–110]. Hierarchical modelling effectively integrates multiple environmental, ecological, and anthropogenic stressors and analysis levels within a single, data-driven methodology that enables their simultaneous assessment in a rapid, reproducible, and easily adaptable manner. The methodology was also crafted to be broadly applicable. The models function independently of the Baltic Sea data, relying exclusively on the statistical characteristics and spatial patterns of the stressor variables. They were intentionally structured to support diverse spatial scales, temporal resolutions, and ecosystem types.

Conclusion

The contribution of the present work lies in extending existing data-driven ERA methodologies by integrating concurrent stressor pattern identification, anomaly detection, *post hoc* risk characterisation, and biological refinement within a multi-species-group hierarchy. The application of complementary unsupervised models, without prioritising any single approach, revealed distinct ecological mechanisms that may explain ecosystem vulnerability. The ensemble and combined approaches enhanced and synthesised the features of the individual models by integrating different rationales on ecosystem risk assessment. This unsupervised, data-driven methodology eliminated the need for subjective assumptions or expert-based weighting, making it suitable for general, large-scale evaluations involving complex data and variable interrelationships.

Methods

This section explains the steps of our methodology, following the schema in Figure 5. Generally, ecosystem risk in the central and western Baltic was contextualised by forcing the models to prioritise harmful forces acting on species-related data, under the assumption that stressor concurrence and competition were particularly critical when affecting biologically valuable or sensitive components of the ecosystem. Risk patterns were examined across different species-group perspectives, each containing an increasing number of species to reflect varying levels of granularity in the risk assessments. Models were developed independently for each species group, and an overall *ensemble* model was produced to provide a multigranular risk representation. This unified representation highlighted complementarities among the different species-group perspectives, allowing risk patterns affecting only smaller species groups to be compared with those of larger species groups.

Finally, a higher-level *combined* model was constructed by merging the outputs of two different *ensemble* models, forming a hierarchical integration that combined complementary analytical rationales and biological scales into a single, interpretable ecosystem risk synthesis, while preserving cross-model agreement.

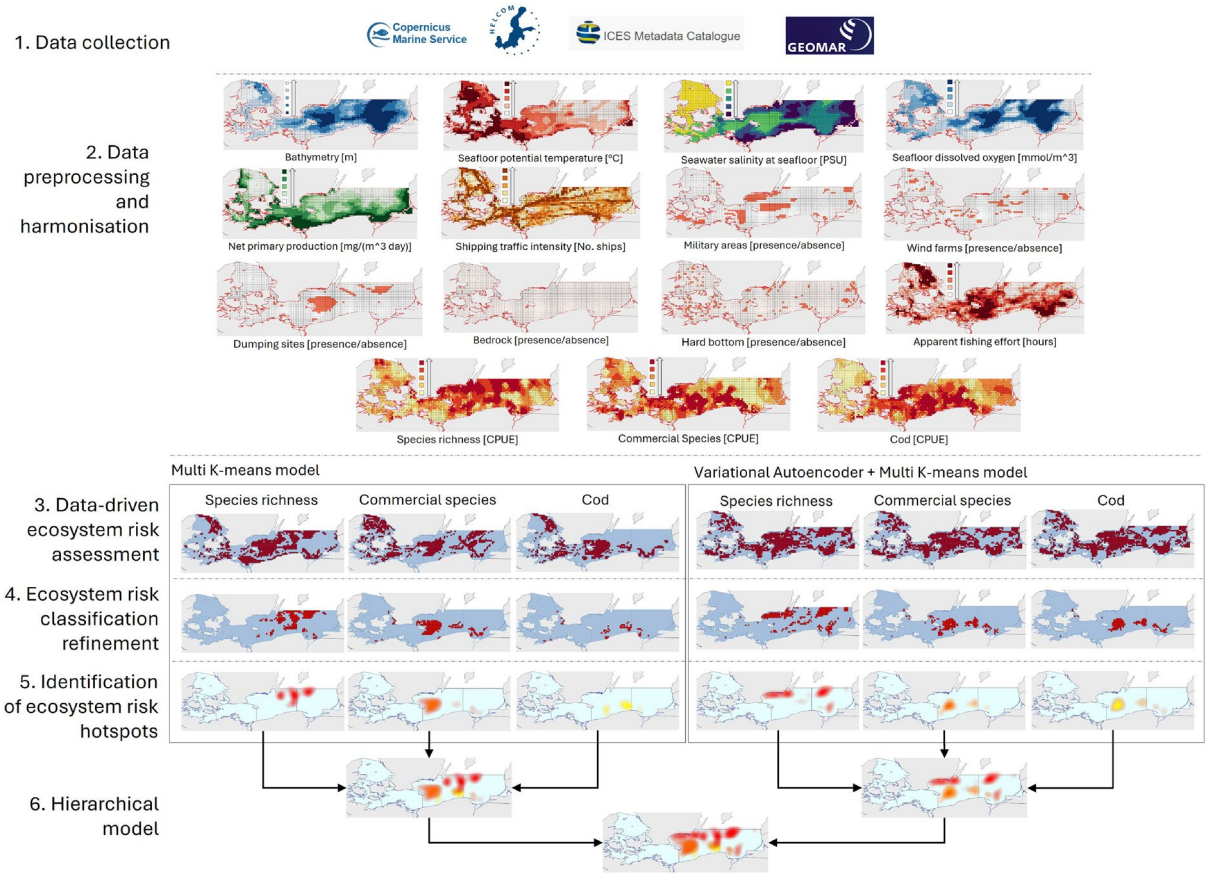

Figure 5 Schematic representation of the proposed methodology. The process begins with data collection from public repositories (step 1), followed by preprocessing and harmonisation to ensure spatiotemporal alignment of features (step 2). Ecosystem risk assessments are then conducted separately for different species groups - specifically species richness, commercial species, and cod - using Multi K-means clustering and a Variational Autoencoder (VAE), with VAE output followed by classification based on Multi K-means (step 3). To further refine the ecosystem risk classification, high-risk conditions are identified in regions with elevated species abundance (step 4). Kernel Density Estimation is then applied to highlight areas with concentrated ecosystem risk (step 5). Finally, a hierarchical model is utilised to integrate the outputs from the species-group assessments into a comprehensive overall evaluation (step 6). Coastal boundaries were taken from https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units/countries.

The final output consisted of nine spatially explicit risk hotspot maps: one for each model and species perspective ($2 \times 3 = 6$), plus two *ensemble* models, and one *combined* model. These maps reported areas where concurrent and competitive environmental and anthropogenic stressors and biological sensitivity were most likely to interact in complex manners and potentially trigger ecosystem change. Because these areas emerged from independent models and complementary biological perspectives, their spatial agreement added a further informative dimension: the hotspots produced by the *combined* model indicated stronger cross-species and cross-model consensus in the denser regions, whereas less dense regions reflected species-dependent or model-dependent assessments. These agreement patterns naturally induced a spatial gradient of risk assessment, corresponding to different levels of spatial agreement across the models.

To evaluate the results, the produced maps were verified to provide valuable and reliable *a priori* information, aligned with previous expert studies, that could be integrated into subsequent spatial planning, conservation, or ecosystem-based management analyses.

The next sections explain the details of each step of our methodology.

Data

Study area and data sources

Our study focused on the central and western Baltic Sea, encompassing ICES subdivisions 21–26, in 2020. Before selecting the study year, the temporal coverage and data-definition periods of the candidate data sources were examined. The greatest simultaneous availability of the environmental, anthropogenic, habitat, and biological variables occurred in 2020 (Supplementary Material). This year was therefore selected to maximise completeness and consistency across the heterogeneous datasets. The resulting dataset constituted a cross-sectional representation of conditions in 2020. The selected area and time frame represented the common domain for which the stressor variables were most complete, available, consistent, and reliable across the open-access primary sources available for the Baltic Sea (step 1 in Figure 5). All variables were treated as annual aggregates, providing a coherent snapshot of environmental conditions, anthropogenic pressures, and biological components of the Baltic Sea ecosystem. Variables were collected from open repositories, following an open-science oriented approach[55,111]. They described physical, biogeochemical, anthropogenic, and ecological characteristics of the Baltic Sea ecosystem (step 2 in Figure 5 and Table 2; magnified in the Supplementary Material): (1) bathymetry [m], (2) seafloor potential temperature [C], (3) seawater salinity at seafloor [PSU], (4) seafloor dissolved oxygen concentration [mmol/m³], (5) net primary production of biomass expressed as carbon per unit volume [mg/(m³ day)], (6) shipping traffic intensity [number of ship passages per cell], (7) military areas [presence/absence], (8) wind farms [presence/absence], (9) dumping sites [presence/absence], (10) sediment type: bedrock [presence/absence], (11) sediment type: hard bottom complex [presence/absence], (12) apparent fishing effort [hours], (13) species richness abundance – 145 species of commercial and conservation interest [g/minute], which included 123 ray-finned, 8 cartilaginous, and 3 jawless fishes, of which ~100 demersal or bentic, plus 7 crustaceans, 2 sponges, 1 mollusc, and 1 mammal (full list in the Supplementary Material), (14) commercial species abundance – five demersal commercial species (*Gadus morhua*, *Limanda limanda*, *Merlangius merlangus*, *Platichthys flesus*, and *Pleuronectes platessa*) [g/minute], and (15) a single relevant species abundance: cod (*G. morhua*) [g/minute].

Variables were selected based on their relevance in previous risk assessment studies and their potential to influence marine ecosystem functioning and resilience in the central and western Baltic Sea[12,25,62,80,112,113]. They provided an overall representative and integrative description of conditions that could either pose a pressure on the ecosystem or be particularly sensitive to external disturbances.

Physical and biogeochemical data were obtained from the Copernicus Marine Environmental Service (CMEMS) repository[114]. Physical conditions consisted of bathymetry, seafloor temperature, and seafloor salinity, extracted from the Copernicus Baltic Sea Physics Reanalysis[115]. Biogeochemical conditions consisted of seafloor

Table 2 Stressor variables selected for the ecosystem model in the western and central Baltic Sea, including their typologies, applied transformations, and the ecological interpretations of high values.

Variable	Stressor type	Transformation	Interpretation of high values
1. Bathymetry	Fragile condition	Direct	Deeper waters representative of open-sea environments hosting most demersal species, and areas where offshore activities are more likely to occur.
2. Seafloor potential temperature	Harmful condition	Direct	Elevated bottom temperatures potentially inducing thermal stress on benthic and demersal communities.
3. Sea water salinity at seafloor	Harmful condition	Direct	Salinity conditions potentially stressing species adapted to narrow tolerance ranges.
4. Seafloor dissolved oxygen concentration	Fragile condition	Inverse	Low oxygen availability associated with hypoxia and reduced habitat suitability.
5. Net primary production of biomass	Fragile condition	Direct	High productivity indicating biologically active and ecologically valuable areas below hypoxic conditions.
6. Shipping traffic intensity	Harmful condition	Direct	Increased maritime traffic and associated pressures (e.g., noise and pollution).
7. Military areas	Harmful condition	Direct	Presence of restricted or impacted areas due to military activities.
8. Wind farms	Harmful condition	Direct	Presence of offshore infrastructure and associated physical disturbance.
9. Dumping sites	Harmful condition	Direct	Presence of waste disposal areas and potential contamination sources.
10. Apparent fishing effort	Harmful condition	Direct	Intensity of fishing pressure exerted on species and marine ecosystems.
11. Sediment type: bedrock	Fragile condition	Direct	Presence of hard substrates supporting sensitive benthic communities.
12. Sediment type: hard bottom complex	Fragile condition	Direct	Structurally complex habitats with high ecological relevance and vulnerability.
13. Species richness: 145 species	Fragile condition	Direct/Interpolated	High biodiversity and abundance indicate areas of high ecological and conservation value.
14. Commercial species: five demersal species	Fragile condition	Direct/Interpolated	High abundance of key demersal species in ecologically sensitive habitats, subject to intense fishing pressure due to their commercial value.
15. Single relevant species: cod	Fragile condition	Direct/Interpolated	High abundance of a species with very high commercial and conservation importance.

dissolved oxygen concentration and sea surface primary production, extracted from the Copernicus Baltic Sea Biogeochemistry Reanalysis[116].

Anthropogenic pressures included maritime and offshore activities such as ship traffic[117], offshore wind farms, military areas, and dumping sites, derived from EMODnet and encoded as binary variables[118]. Fishing activity was quantified as fishing hours using the Global Fishing Watch[119]. Habitat was described using sediment type information from HELCOM[120]. The focus was particularly on hard rock and bedrock habitats, which are vulnerable to anthropogenic pressures because their degradation can reduce the suitability for spawning and the biomass of several commercial species[112]. Biological data were included by integrating relative species abundance indicators derived from fisheries survey data[121]. Catch-per-unit-effort (CPUE, measured in g/minute) was used to estimate the abundance of 145 species of commercial and conservation interest. An additional focus species group comprised five demersal species, with total CPUE used as a proxy for their total abundance. These species corresponded to stocks recognised for their economic and ecological importance[36,68]. In addition, cod was analysed separately, with its CPUE considered a standalone indicator due to its particular ecological and economic relevance[122]. All biological data were obtained from the Baltic International Trawl Survey (BITS)[123], accessed through the ICES DATRAS database[95]. Notably, these annually aggregated CPUE values represented spatial

proxies of relative abundance but did not explicitly describe population demography, including age and size structure, recruitment, mortality, growth, body condition, maturation, or migration. Moreover, because species abundances were aggregated within each biological group, they did not represent individual species as separate variables.

Data preprocessing and harmonisation

All variables were accessed in their native formats (NetCDF, CSV, raster/TIFF) and resolutions from their respective primary sources, resulting in a heterogeneous collection of spatiotemporal data across the Baltic Sea. To enable subsequent spatial risk assessment analyses and ensure spatial consistency, the variables were reprocessed. This operation included cleaning missing or inconsistent values, harmonising variable formats, and aligning spatial data within the study area using an open-source Geographic Information System (GIS) software program (step 2 in Figure 5). Point-based observations, such as the fish abundance from BITS-DATRAS, were interpolated onto a regular grid using the Bayesian Interpolation Model with Advection-diffusion Constraint (BIMAC)[99], an AI-based non-parametric model that provides a probabilistic framework for spatially interpolating marine parameter observations through the solution of the stationary advection-diffusion equation. All other environmental and anthropogenic variables were available as spatially continuous fields or gridded datasets and did not require interpolation. These variables were subsequently spatially aligned with the interpolated species-abundance layers. Finally, all variables were gridded through nearest-neighbour sampling to a common spatial resolution of 0.1×0.1 (approximately 10 km × 10 km) and merged into a single table dataset in comma-separated values (CSV) format. Each row of the final dataset represented a georeferenced spatial cell, defined by latitude and longitude, within ICES subdivisions 21–26, while columns corresponded to environmental, anthropogenic, or biological variables.

Stressor selection and definition

For the risk assessment, variables were reprocessed and interpreted as *stressors*. Stressors were defined as driving forces that contribute to an increased likelihood of ecosystem status change, either as direct *pressures* acting on the system or conditions that reflect its intrinsic *sensitivity*[47,48,54]. Numerically, a stressor is a variable whose *high values* correspond to a stronger potential influence on ecosystem status change. Depending on the ecological meaning of the original variable, this correspondence could be direct or require inversion ($\frac{1}{var.}$) to ensure that high values consistently represented high stress levels. For example, low values of seafloor dissolved oxygen concentration corresponded to high stress on the ecosystem; thus, this variable required inversion so that high values matched stressful conditions.

Stressors were classified into two complementary categories, i.e., those creating *harmful conditions*, such as anthropogenic activities or environmental factors that negatively affected habitats and biological communities; and those exposing ecosystems to *fragile conditions*, i.e., variables whose high values indicated ecosystem features sensitive to disturbance or with high ecological relevance, which required protection priority (Table 2). This distinction accounted for both external pressures and internal ecosystem susceptibility.

Ecosystem risk was defined as a condition of *intense concurrence and competition* among stressors[47,48,54]. This definition of ecosystem risk is *restricted* because it emphasises a specific selection of stressors. However, it enables scholars to examine the risks posed by the selected harmful forces to fragile conditions. In the present study, the selected variables represented key processes known to influence ecosystem functioning and resilience. Accordingly, the restricted definition of ecosystem risk based on these variables served as a realistic proxy for assessing the risk of ecosystem change.

Ecosystem risk assessment in the central and western Baltic Sea focused on the species groups formed by (1) species richness, (2) commercial species, and (3) cod. For each species group, a set of 13 variables was defined,

which included all 12 environmental variables plus one species-related variable (Table 2). At a 0.1 spatial resolution across the central and western Baltic, this variable set yielded 1904 vectors, which were reported in a table used as input for the subsequent processing steps (available in the Supplementary Material). To ensure comparability among stressors with different units and ranges, all continuous stressors were standardised using z-score normalisation (mean = 0 and SD = 1). This operation consistently assigned equal prior importance to each variable. Binary stressors (offshore wind farms, military areas, dumping sites, and sediment types) were excluded from the standardisation procedure and retained in their original (0/1, i.e., absence/presence) form.

Risk assessment methodology

Risk assessment was mostly developed in R (source code in the Supplementary material) and consisted of three main steps:

- Step 1. *Data-driven risk assessment*: Two unsupervised learning models - a cluster analysis and a deep learning-based model - are applied in combination with statistical analysis to classify risk conditions based on the stressor variables.
- Step 2. *Ecosystem risk classification refinement*: The results of each model are re-analysed to select risk conditions specifically related to species conservation.
- Step 3. *Identification of ecosystem risk hotspots*: Kernel density estimation is applied to the risk areas to highlight high-density ecosystem risk zones.

These computational steps were applied to each species group separately. An additional step was added to build a hierarchical model merging the species-group assessments and the two model outputs.

- Step 4. *Hierarchical modelling*: The species-group assessments are merged to build a unified multi-species-group view (*ensemble*) for each model. Then, these multi-species-group models are *combined* to form a single comprehensive model

Step 1: Data-driven risk assessment

Cluster analysis. Spatial patterns of ecosystem risk were identified using a Multi K-means clustering analysis applied to the standardised stressor dataset, while accounting for interdependencies among stressors through vector-distance measurements. Multi K-means is a class of algorithms that extend conventional K-means by enabling clustering across multiple K values (number of clusters); they automatically estimate the optimal solution (K^*) within a predefined range. The selection criterion varies across the implementations. In our case, Multi K-means used the $UNIF(K)$ function[47,48] to select the optimal clustering solution. This optimisation function is designed to balance model complexity and internal cluster uniformity. It compares the observed distribution of vectors across the clusters with a theoretical uniform distribution using a Chi-square test and favours solutions characterised by homogeneous and well-populated clusters. Clusterings that produce empty or sparsely populated clusters are automatically excluded, thus penalising over-segmentation. Compared with the Bayesian Information Criterion (BIC), which assumes Gaussian-distributed cluster vectors, $UNIF(K)$ imposes no constraints on cluster shape and is more suitable for ecosystem-related datasets. In addition, it generally yields a less fragmented vector space than BIC-based clustering methods (e.g., X-means[124]). In our Multi K-means application, cluster centroids – representing the mean stressor-variable vectors within each cluster – were randomly initialised and iteratively updated until convergence, using the Euclidean distance as a measure of similarity among the stressor vectors.

After clustering, statistical analysis was applied to the K^* cluster centroids to translate the clusters into *risk categories*. First, for each stressor variable, the corresponding centroid values across the clusters were compared with the empirical distribution of the variable across the entire dataset. Second, for each cluster centroid, stressor values that exceeded the 75th percentile of the related empirical distributions (upper tails) were labelled as *high*

(*H*), while the remaining variables were labelled as *non-high* (*L*). Finally, clusters were classified as *high-risk* if *H*-labelled variables predominated, and as *non-high-risk* otherwise. This classification was then assigned to the spatial cells belonging to each cluster.

Multi K-means enabled a structural analysis and preliminary classification of the stressor-variable space, translating multivariate stressor interactions into a spatially explicit classification of potential ecosystem risk. Clusters in which most stressors had high average values were classified as high-risk clusters because they indicated similar stressor composition and intensity. This classification naturally helped identify stressors associated with high risk, thereby improving the interpretability of the results.

Using the Baltic Sea data, the Multi K-means analysis identified 34 clusters ($K^* = 34$) for species richness, of which 13 were classified as high-risk and included 759 vectors. For commercial species, 36 clusters were identified, with 12 classified as high-risk (containing 696 vectors), while for cod, 31 clusters were identified, including 10 high-risk clusters (502 vectors) (step 3, left panel in Figure 5). The model output consisted of a table for each species group, reporting the risk classification of the corresponding cluster for each stressor-variable vector.

Deep learning–based model. Multi K-means clustering relies on Euclidean distance to measure similarities among vectors, a metric that cannot fully capture complex, non-linear relationships among stressors that underlie the observed data[100]. To address this limitation, a deep-learning-based model was applied as an alternative approach. This model was used to infer the latent variables that possibly generated the observed stressor-variable combinations. The selected model was a Variational Autoencoder (VAE)[125], a deep unsupervised probabilistic Artificial Neural Network (ANN) that estimates the distributions of the latent variables $\bar{z}$ that likely generated the data. The VAE simulates the distribution $p(\bar{x})$ of the input vectors $\bar{x}$, based on these latent vectors $\bar{z}$.

The VAE includes two internal ANNs: (1) an *Encoder* that maps each input vector to the means and standard deviations of a multivariate Gaussian distribution over the latent variables - the Gaussian distribution approximates the posterior distribution of the latent variables given the input vectors ($q(\bar{z}|\bar{x})$) - and (2) a *Decoder*, which can generate a reconstructed version of an input vector ($\bar{x}$) from a sample drawn from the latent space distribution ($\bar{z} \sim q(\bar{z}|\bar{x})$). The Decoder also estimates the reconstruction probability $p(\bar{x}|\bar{z})$ of $\bar{x}$ given the latent variables $\bar{z}$, which can be used to identify anomalous vectors as those inaccurately reconstructed[126–128]. The VAE training algorithm adapts the Encoder and Decoder weights to maximise the reconstruction probability of the input vectors. This optimisation requires to minimise a loss function that sums (1) the *Reconstruction Loss* (a measure of the reconstruction capability of the Decoder based on mean squared error or cross-entropy) and (2) the *Kullback-Leibler Divergence* (the distance between the learned posterior distribution $q(\bar{z}|\bar{x})$ and a multivariate Gaussian with $\bar{\mu} = (0, \ldots, 0)$, $\bar{\sigma} = (1, \ldots, 1)$, and $\dim(\bar{\mu}) = \dim(\bar{\sigma}) = \dim(\bar{z})$).

Our methodology searched for the optimal VAE architecture in terms of the number of neurons and layers using a "growing" strategy: hidden nodes (up to 200 per layer, based on previous studies[48,109]) and layers (up to 10 per ANN, spanning shallow to deep networks) were incrementally added (starting from one layer with one neuron) until the configuration with the highest total reconstruction probability over the Baltic stressor vectors was identified. Moreover, the optimal dimension of $\bar{z}$ was searched for by testing from 1 to $\dim(\bar{x})$ and selecting the one corresponding to the best reconstruction.

For the Baltic Sea data, the Encoder consisted of two hidden layers with 12 and 6 neurons, respectively, followed by a latent space with the same dimensionality as the input stressor vectors (12). The Decoder mirrored the Encoder architecture, with two hidden layers of 6 and 12 neurons, and produced the reconstructed stressor vectors at the output layer. In line with other studies[47,48,54,100,101], since no prior information about data anomalies was available, a threshold at the 50th percentile of the reconstruction probability distribution across the data was set to identify the most anomalous data, i.e., those with lower reconstruction probabilities.

The VAE identified 952 vectors as anomalous across all species groups. However, VAE anomalies alone were not sufficient for a robust assessment of ecosystem risk. They could not be interpreted directly as ecosystem-risk conditions because an anomaly indicated only an uncommon configuration in the multivariate stressor space and did not necessarily possess an ecological interpretation. Anomalous vectors thus corresponded to deviations from

typical data distributions; therefore, they required further characterisation to identify their ecological meaning and conservation relevance[129–131].

Multi K-means clustering and subsequent classification were thus applied to characterise the anomalous vectors identified by the VAE. This procedure explored variations among anomalies to identify those associated with high stressor concurrence and interaction. Among the anomalous vectors, Multi K-means identified 16 high-risk clusters ($K^* = 16$) for species richness, 14 for commercial species, and 20 for cod (step 3, right panel in Figure 5).

This two-step approach used the VAE to detect latent statistical deviations and Multi K-means to characterise the corresponding input vectors in the original stressor-variable space. It therefore provided a *post hoc* ecological characterisation of candidate risk configurations without assigning direct ecological meaning to the VAE latent dimensions.

The output of the combined VAE and Multi K-means approach consisted of a table linking each stressor vector to the risk level of its corresponding cluster.

Step 2: Ecosystem risk classification refinement

The candidate risk configurations identified by the two models (i.e., VAE and Multi K-means) constituted an intermediate stressor-based assessment, rather than a final classification of ecosystem risk. This assessment captured areas exposed to multiple interacting stressors, but it did not explicitly distinguish whether these pressures primarily affected ecologically fragile conditions or areas with limited biological relevance. A refinement step was therefore introduced to retain configurations in which concurrent elevated stressors affected areas of high biological value or susceptibility, represented here by elevated species abundance.

The abundance of key species of conservation importance is a proxy for ecosystem functioning, resilience, and service provisioning[132,133]. Areas with high key species abundance are inherently more vulnerable to cumulative stressors, as they are often accompanied by multiple functional groups that can be affected by anthropogenic disturbance and environmental change[134–138]. Consequently, the same level of stressor intensity may lead to substantially different ecological outcomes depending on the underlying species context. Priority was thus given to high-risk conditions in areas with elevated species abundance. This refinement was applied separately to the outputs of the two models for each species group. It consisted of the following steps:

1. Clusters classified as *high-risk* were selected and their associated vectors were extracted (*high-risk* clusters) (let n denote cluster abundance).
2. For each stressor variable i, the average across all *high-risk* clusters ($\bar{X}_i$) and the related standard deviation $\sigma_{\bar{X}_i}$ were calculated.
3. Each element of the *high-risk* centroid vectors ($x_{i|c_j}$, with c_j denoting *high-risk* cluster j) was compared to $\bar{X}_i$ to produce a *deviation score* (D) as follows:

   - If $x_{i|c_j} > \bar{X}_i + 2\,\sigma_{\bar{X}_i} \rightarrow D = 1$
   - Else, if $\bar{X}_i + \sigma_{\bar{X}_i} \leq x_{i|c_j} \leq \bar{X}_i + 2\,\sigma_{\bar{X}_i} \rightarrow D = 0.5$
   - Else $\rightarrow D = 0$

4. Clusters with $D \geq 0.5$ for the species-group variable were selected to identify those indicating high species abundance, which represents a proxy for fragility.
5. For these clusters, ecosystem risk was re-classified according to the following rule:
   - If $\sum_{vars} D >$ number of features/2 $\rightarrow$ *high* ecosystem risk
   - Else $\rightarrow$ *lower* ecosystem risk

Through these rules, the refinement process highlighted clusters that involved either a high deviation score ($D = 1$) for most variables or at least a significant score ($D = 0.5$) for all variables. This choice reflects the idea that even

moderate, persistent pressures on species abundance may serve as early warning signals and therefore warrant consideration in management plans. The refinement process identified clusters characterised by moderate to strong anthropogenic and environmental stressor intensities in areas of high species abundance. Accordingly, the classifications should be interpreted as areas where selected pressures and adverse environmental conditions co-occurred with elevated abundance of the focal biological group. Instead, they cannot be interpreted as evidence that the methodology independently discovered an association between high abundance and ecosystem risk.

In the Multi K-means outputs, this process identified four high-risk clusters for species richness (220 vectors), four clusters for commercial species (192 vectors), and two clusters for cod (58 vectors) (step 4, left panel in Figure 5). In the VAE plus Multi K-means outputs, this process identified four high-risk clusters for species richness (271 vectors), three clusters for commercial species (170 vectors), and three clusters for the cod (130 vectors) (step 4, right panel in Figure 5).

This process produced an updated risk assessment table for each model and species group, with refined classifications (*high risk* vs. *lower risk*) for each stressor vector and its corresponding cluster. Cells associated with vectors from the high-risk clusters were considered at *high risk*.

Step 3: Identification of ecosystem risk hotspots

To spatially aggregate and visualise areas of elevated ecosystem risk, the cell-wise classifications obtained in Step 2 were processed using Kernel Density Estimation (KDE)[139]. For each model output, the coordinates of cells belonging to *high* ecosystem risk clusters were used as input to a Quartic Kernel function. The interpolation radius was set according to the spatial autocorrelation of the cell coordinates ($\sim$0.1). This procedure generated a normalised Kernel Density Map (*heatmap*) where regions of higher density corresponded to concentrated risk hotspots (step 5 in Figure 5). To enhance visualisation and identify the highest-risk areas more precisely, density values below the 75th percentile were excluded from the heatmaps, while only values over the 75th percentile, empirically identifying *high* values, were retained for methodology evaluation.

Using KDE-derived high values likely increased solution stability and reduced sensitivity to the number of clusters identified by Multi K-means. For example, in the species-richness Multi K-means model, $K^* = 34$ was progressively reduced until the associated $UNIF(K)$ reached 85% of the optimum (i.e., a 15% reduction). The new clustering corresponded to $K = 27$, resulting in approximately 21% fewer clusters. This led to a roughly 15% increase in the number of high-risk cells detected. However, the KDE-derived high-value hotspot locations increased only by about 5% in extension, indicating approximately 95% overall spatial agreement. Similarly, a 15% increment in $UNIF(K)$ corresponded to a roughly 15% reduction in the number of high-risk cells detected, but only a 5% decrease in the high-value hotspot extension. Therefore, although the cell-level classification demonstrated some sensitivity to cluster granularity, the principal KDE-derived hotspot pattern was comparatively stable under the tested reduction in K.

Step 4: Hierarchical model

A hierarchical model was developed to synthesise the outputs of the six species-group models (3 species groups $\times$ 2 models) into a coherent assessment that maintained biological interpretability while enhancing the robustness of hotspot identification (step 6 in Figure 5). This hierarchy incorporated two dimensions of variability in ecosystem risk mapping: (1) the species groups used to represent biological sensitivity (i.e., species richness, commercial assemblages, and cod), and (2) the models used for delineating multi-stressor risks (i.e., Multi K-means and Variational Autoencoder coupled with Multi K-means).

First, for each model, an *ensemble* species model was generated by merging the three species-group hotspot maps into one multigranular risk representation (the first aggregation level of step 6 in Figure 5). The aggregation was achieved by treating the hotspots from the species-group maps as object sets and computing their union across the species groups. At regions of intersection, hotspot classification was assigned by giving precedence

to the map with the greatest number of species. The merging was thus obtained through a stacked overlap, prioritising the species-richness map, then the commercial-species map, and lastly the cod map: Regions where all hotspot maps intersected were classified as species-richness hotspots to prioritise this group. In areas where commercial species and cod hotspots overlapped, the commercial species classification was adopted. In areas where only one species-group map reported hotspots, the corresponding species-group was assigned to those hotspots. This ensemble methodology facilitated a synthetic representation of multigranular risks while providing complementary insights from species-group perspectives.

Second, a *combined* model was built by merging the two ensemble species models (final aggregation level of step 6 in Figure 5). The combined model initially treated species groups as distinct levels and calculated the union set for each group from the two models. Then it applied the previously described merging process to these merged species groups to allocate higher classification priority to species-richer hotspots. Through this process, the combined model valorised the complementary characteristics of the two unsupervised models: the structurally similar stressor configurations identified by Multi K-means and the latent, non-linear anomalous conditions captured by VAE plus Multi K-means. Consequently, the combined hotspot map effectively illustrated the convergence and divergence among the two independent model rationales. It overall produced a descriptive *cross-model concordance gradient*. Areas jointly identified by MKM and VAE+MKM appeared with greater colour intensity, whereas areas identified by only one approach appeared less intense. The gradient thus visualised spatial agreement between the two modelling approaches.

Evaluation

The evaluation of the methodology first focused on measuring the agreement among maps produced by each model (Multi K-means and VAE plus Multi K-means) for the three species groups analysed and their ensembles (*cross-model concordance analysis*). As a second step, the consistency of the ecosystem risk hotspots identified by the different models was evaluated against central and western Baltic expert studies (*qualitative* evaluation).

Cross-model concordance analysis

Cross-model concordance assessment was performed through pairwise, cell-by-cell comparisons of binary spatial classifications derived from the Kernel Density maps. These comparisons quantified the degree to which the two independently constructed unsupervised approaches identified similar spatial patterns.

Each cell in the hotspot map exceeding the 75th percentile of the KDE distribution (upper tail) was assigned a value of 1 (high-density cells), while all other cells were assigned 0. Comparisons were carried out on the same 0.1×0.1 grid. Pairwise similarity between two maps was defined as the proportion of cells classified in the same category by both maps (1 or 0). Agreement beyond chance was quantified using Cohen's Kappa statistic[140]. Pairwise comparisons were conducted between the Multi K-means and the VAE plus Multi K-means models for each species group and for the ensemble species models. For the ensemble models, a cell was assigned 1 if it was classified as *high* ecosystem risk location at any of the three levels, and 0 otherwise. No numerical comparison was conducted for the combined model, as it inherently matched the two ensemble species models. The pairwise comparisons highlighted the complementary and similar assessments made by the two modelling approaches for each species group and determined whether the ensemble species models changed the concordance level while providing a multigranular risk view. Therefore, agreement between the models was interpreted as consistency across modelling approaches. The ecological plausibility of the resulting classifications was instead explored in the subsequent qualitative evaluation.

Qualitative evaluation

Qualitative evaluation sought to characterise the primary high-risk hotspots extracted at all levels of the hierarchical model. This goal was achieved by analysing the stressor variables exhibiting the highest deviation scores within the hotspots. It offered ecological insight into model-identified high-risk hotspots and the likely drivers of ecosystem risk from interacting stressors. The reliability of the detected hotspots and their associated stressor configurations was assessed by checking whether they were consistent with independent ecological evidence from the Baltic Sea, including HELCOM regional assessments and published studies of hypoxia, cumulative human pressures, fish distributions, spawning habitats, and seabed vulnerability. Moreover, historical evidence was used to assess whether the identified locations exhibited persistent vulnerability.

This analysis offered ecological support for the hotspot classifications. Importantly, this approach was necessitated by the lack of an independent, comprehensive, and consistent reference classification of ecosystem risk for the study area. As a result, there was no ground truth available for areas beyond the identified risk hotspots.

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Data availability All geospatial data and results are available on the following Zenodo data collection as a QGIS project: https://doi.org/10.5281/zenodo.18493558 The code of the ecosystem risk assessment scripts, and the input and output tables are available on GitHub at the following link: https://github.com/cybprojects65/BalticEcosystemRiskAssessment The list of 145 species used for the species-richness models is available in the GitHub Repository: https://github.com/cybprojects65/BalticEcosystemRiskAssessment/blob/main/List_of_species.txt

Declarations

Competing interests The authors declare no competing interests.

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