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MULTIMODAL DEEP LEARNING FOR *CHELONIA MYDAS* CONSERVATION GENOMICS: ARCHITECTURES, FUSION APPROACHES, AND RESEARCH DIRECTIONS

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ABSTRACT

Modern deep learning approaches have enhanced predictive capability in conservation genomics beyond what is achievable with conventional statistical models. For *Chelonia mydas* (green sea turtle), DL is promising for genomic-enabled prediction of conservation-relevant traits (e.g., disease susceptibility, growth, hatchling success), but conventional unimodal approaches often underuse the rich ecological and health context surrounding genomic data. Multimodal deep learning (MMDL) addresses this limitation by integrating multiple information sources, including genomic sequences and variants, environmental drivers (sea-surface temperature, salinity, storm exposure), and phenotypic or health indicators, to increase predictive capacity. In this review, we introduce the core concepts of MMDL, outline widely used neural architectures (Multilayer Perceptron [MLP], Convolutional Neural Network [CNN], temporal RNNs/Transformers, autoencoders), and describe strategies for fusing heterogeneous modalities (early, intermediate, late fusion). We also summarize practical computational resources for implementing MMDL in turtle genomics. Finally, we surveyed applications and cross-domain evidence relevant to *C. mydas*, providing a meta-level view of when and why MMDL performs well, as well as the capacity of these techniques to handle multifaceted conservation challenges. In general, multimodal deep learning achieves superior prediction accuracy compared with single-modality deep learning and conventional machine learning approaches, albeit with increased computational demands, due to its ability to capture cross-modal relationships. In *C. mydas*, effective implementation relies on aligning model architectures and data fusion schemes with both the nature of the datasets and the targeted biological questions. Given its predictive edge over traditional approaches, MMDL is a valuable addition to the toolkit for genomic-driven conservation and long-term population resilience in *C. mydas*.

***Keywords*:** *Chelonia mydas*, Multimodal deep learning, Conservation genomics, Genomic prediction, Data fusion, Disease susceptibility.

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1. INTRODUCTION

Genomic breakthroughs that will help unlock the effects of genetic variation on health and survival have a critical role in the conservation of *C. mydas* (Gammon et al., 2023). As with the Green Revolution and food security, current genomic and Deep Learning (DL) technologies can now be used to address biodiversity and disease issues in this endangered species (Satam et al., 2023; Meier et al., 2025). With sequencing pipelines now offering trimming (fastp), alignment (BWA-MEM, Bowtie2), and variant calling (DeepVariant, GATK, FreeBayes, VarScan, BCFtools, Clair3), it is now possible to correlate genomic variation with the adaptive phenotype (Poplin et al., 2018). Both DL and multitrait Bayesian models are more effective than traditional methods and combine ecological and environmental information to predict disease susceptibility in *C. mydas* (Chan et al., 2026; Abdullah et al., 2026).

In a comparative analysis of Convolutional Neural Network (CNN), Multilayer Perceptron (MLP), and Ridge Regression Best Linear Unbiased Prediction (RR-BLUP), both Deep Learning (DL) approaches surpassed Ridge Regression Best Linear Unbiased Prediction (RR-BLUP), yielding 0–5% gains in predictive accuracy (Wang et al., 2023). In the context of *C. mydas*, such Deep Learning (DL) models may provide greater sensitivity for detecting short variants (SNVs and small indels) linked to stress tolerance and immune responses, when incorporated into pipelines involving trimming with fastp, alignment with BWA-MEM, and variant calling with DeepVariant, GATK, FreeBayes, VarScan, and BCFtools (Mussmann et al., 2020). Benchmarking showed GPTransformer to be

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a strong BLUP alternative for disease resistance, with potential to reveal associations with fibropapillomatosis in *C. mydas* (Stanojević et al., 2024). Comparisons showed DNNGP matched or exceeded GBLUP, LightGBM, SVR, DeepGS, and DLGWAS, with runtimes close to GBLUP and far faster than DeepGS, highlighting its potential for *C. mydas* disease risk prediction using multimodal data (Ning et al., 2023). Deep Learning (DL) methods are increasingly applied in genomic prediction, though they do not consistently surpass GBLUP or other ML frameworks. For instance, CNN and Multilayer Perceptron (MLP) models have been competitive with BayesB and Bayesian Ridge Regression (BRR) in predicting complex traits, but Deep Learning (DL) did not consistently provide superior performance (Montesinos-López et al., 2025).

In the case of *C. mydas*, this underscores the need to integrate Deep Learning (DL) techniques with existing statistical models to explain constraints in the availability of training data (Bellot et al., 2018). Other studies have found that Deep Learning (DL) models do not provide any benefit over linear methods unless nonlinear interactions among epistatic factors are evident (Li et al., 2025). Bayesian approaches, such as BL and BRR, were occasionally much more accurate, and Deep Learning (DL) networks failed to outperform Gradient Boosting, RF, or GBLUP, highlighting that the ability to capture nonlinear patterns is not sufficient to yield predictive benefits (Tan et al., 2025). Most studies rely on genotypic data and ignore environmental or phenotypic data; MMDL addresses this by combining multiple data types (Mora-Poblete et al., 2026). In the case of *C. mydas*, this implies that environmental variables (e.g., sea surface temperature, pollution indices), transcriptomic expression patterns or epigenomic marks can be added as genomic variant data. MMDL combines modalities via data fusion, thereby enhancing predictive power and accuracy (Yang et al., 2022). For example, environmental integration can enhance disease prediction, transcriptomic fusion can reveal immunopathway regulation, and epigenomic fusion can provide information on regulatory mechanisms under stress conditions (Khan et al., 2025). In this context, multi-omics data fusion can provide a holistic approach to characterizing the biological systems of endangered species such as *C. mydas* (Aslam & Aplop, 2025). By combining genomic, transcriptomic, and ecological data, conservation is enhanced through the prediction and understanding of mechanisms. This review discusses MMDL in genomic prediction, highlighting its benefits over linear and nonlinear ML (Kang et al., 2022). We present the principles of neural networks, describe major architectures, multimodal integration techniques, and tuning design, with a focus on *C. mydas* conservation genomics (Goodwin et al., 2016).

2. Machine Learning Approaches to Genome-Driven Prediction

In *C. mydas*, genomic prediction involves constructing models to forecast key biological traits, including vulnerability to disease or adaptive potential from genotypic data, typically derived from short variants (SNVs and small indels) (Wang et al., 2022). These predictions can indicate how endangered species such as *C. mydas* can survive environmental stress and inform conservation strategies. Classical methods like Ridge Regression Best Linear Unbiased Prediction (RR-BLUP) are popular in genomic studies and are effective at modeling additive effects (Hays et al., 2025). However, as data complexity increases, more elastic approaches are required to capture complex interactions. Traditional approaches are inferior to ML models, such as Deep Learning (DL), which account for nonlinear genotype-phenotype relationships, integrate genomic, phenotypic, and environmental data, and improve predictions of turtle health and survival (Aslam & Aplop, 2025).

2.1. RR-BLUP Model for Genomic Prediction

The RR-BLUP model can be represented mathematically as:

$$y=1b+Xg+e$$

Where y represents the phenotypic observations, 1 is a vector of ones associated with the intercept b, X denotes the genotype matrix containing minor allele counts, g is the vector of marker effects assumed to be normally distributed with mean zero and variance σ_g^2, and *e* captures the residual variation (Puglisi et al., 2026). One of the major shortcomings of Ridge Regression Best Linear Unbiased Prediction (RR-BLUP) is that it is applicable only to linear genotype-phenotype relationships. To overcome it, other ML algorithms like random forests, SVM and gradient boosting have been implemented, but they are explicit on feature engineering. Conversely, neural networks derive features from direct training data (Feltes et al., 2025). Traditional ML models cannot effectively scale to large datasets, whereas NNs tend to require large amounts of data. In the case of *C. mydas*, little genomic information is still a weakness, but the NNs are capable of learning on a large scale when a large amount of inputs is present. They are thus the most promising for use in future conservation genomics pipelines that combine fastp for trimming, BWA-MEM for alignment, and variant detectors such as Deepvariant, GATK, FreeBayes, VarScan, and BCFtools (Lin et al., 2022).

2.2. Artificial Neuron Architecture

The artificial neuron (AN), the basic building block of neural networks, mimics biological neural activity by

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receiving signals from other units or external sources and conveying information through weighted connections. Its mathematical formulation is shown in Fig. 1 (Eraslan et al., 2019):

y=φ (∑_(i=1)^m▒ 〖w_i x_i 〗 +b)=φ(w^T x+b)

Where y is the predicted output, such as a phenotypic trait in *C. mydas* (e.g., disease status or growth response);X=(x_1,…,x_m)^T are the input features, for example, genotypic variants represented as short variants (SNVs and small indels);w=(w_1,…,w_m)^T are synaptic weights; b is the bias term; and φ is the activation function. With the identity as the activation function, the artificial neuron reduces to a linear regression expectation (Eraslan et al., 2019). In turtle genomics, such models can be applied to large-scale datasets generated from sequencing pipelines that include trimming with fastp, alignment with BWA-MEM, and variant calling using DeepVariant, GATK, FreeBayes, VarScan, and BCFtools (Poplin et al., 2018). With the availability of the high-quality *C. mydas* reference genome (rCheMyd1.pri.v2) from the Vertebrate Genomes Project, AN-based models can be trained on comprehensive variant data to study disease associations, including fibropapillomatosis and other stress-related conditions (Roden et al., 2023).

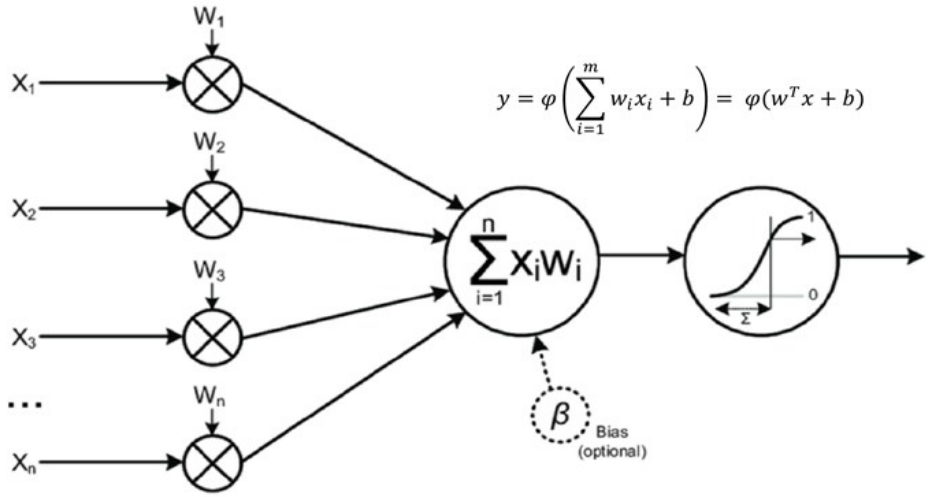

Fig. 1: Artificial Neuron: Structure and Working Principle.

2.3. Activation Functions

Activation functions introduce nonlinearity into neural network frameworks, allowing them to represent complex patterns. Frequently used variants comprise linear, rectified linear unit (ReLU), Leaky ReLU, step, sigmoid, hyperbolic tangent, exponential, and softmax functions, as summarized in Table 1 (Jubair & Domaratzki, 2023). A brief review with usage guidelines is provided. For example, Convolutional Neural Networks (CNNs) employing ReLU have been useful for modeling genomic features in endangered species (Pimpalkar et al., 2024), while softmax layers are commonly applied in classification tasks, such as distinguishing disease-affected from healthy turtles from integrated genomic–phenotypic data. For deeper technical exploration, readers are referred to comprehensive texts on Deep Learning (DL) (Bharadwaj et al., 2021).

Table 1: Widely applied activation functions and their mathematical expressions

Function	Formula
Linear	$\varphi(x) = x$
Threshold	$\varphi(x) = 1$ for $x > 0$, 0 otherwise
Sigmoid	$\varphi(x) = \frac{1}{1+e^{-x}}$
Hyperbolic tangent	$\varphi(x) = \tanh(x) = \frac{e^{x}-e^{-x}}{e^{x}+e^{-x}}$
Rectified Linear Unit (ReLU)	$\varphi(x) = \max(0, x)$
Leaky ReLU	$\varphi(x) = x$ for $x \geq 0$, αx for $x < 0$
Exponential	$\varphi(x) = e^{x}$
Softmax	$\varphi(z_i) = \frac{e^{z_i}}{\sum_{j=1}^{C} e^{z_j}}$

3. Multimodal Deep Learning and Fusion Approaches

3.1. Concept of Multimodal Deep Learning (MMDL)

The concept of MMDL rests on integrating multiple data modalities into one neural network system, similar to how different human senses provide complementary perspectives of the world. With advances in sequencing and computational technologies, such approaches can now also be applied to large-scale genomic datasets (Jabeen et al., 2023). In the context of genomic prediction for *Chelonia mydas*, MMDL enables the integration of multiple modalities, including genomic data from short variants (SNVs and small indels), phenotypic traits such as disease status, ecological variables like sea surface temperature, and other omics layers such as transcriptomic or proteomic profiles (Subramanian et al., 2020). Indicatively, recent papers on population genomics of sea turtles

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have emphasized the need to combine genomic and ecological evidence to quantify adaptive potential during climate change. Likewise, transcriptomic studies of turtles with fibropapillomatosis have identified differences in gene expression associated with tumor development, underscoring the importance of integrating multimodal data in disease studies (Barbanti et al., 2025). Through integration of these numerous inputs, researchers will be able to develop more valid models in predicting disease vulnerability, climate change resilience and adaptive capacity at population levels.

3.2. Advanced Deep Learning Applications in Genomic Prediction of *Chelonia mydas*

RNNs, ResNets, Transformers, GNNs, and Autoencoders are deep learning models that have high potential for genomic predictive success in *C. mydas*, and in conservation, the questions of their application and suitability to practice arise (Ghosh et al., 2025). These complicated models suggest several broader implications onto *C. mydas*. They improve prediction accuracy, since they succeed in modeling complex genetic organisms that are responsible in influencing traits such as exposure to fibropapillomatosis or climate-related adaptation (Zhu et al., 2025). They are also characterized by high performance and efficiency, with support for feature extraction and representation learning, which enable efficient predictions in genomic workflows that use fastp, BWA-MEM, and variant-calling packages (DeepVariant, GATK, FreeBayes, VarScan, and BCFtools) (Chen et al., 2018). More importantly, both neural network architectures can be scaled to particular problems: RNNs can model temporal ecological variables such as seasonal foraging or migration, and Convolutional Neural Networks (CNNs) and ResNets can learn hierarchical features in genomic data, such as short variants (SNVs and small indels). Transformers are trained on large-scale genomic datasets such as rCheMyd1.pri.v2 reference genome (Zhu et al., 2025), and GNNs can capture events. The combination of these models facilitates advanced models of high-dimensional turtle genomic data, which help expose nonlinear interactions among genotype, phenotype, and environment and ultimately improve the predictive accuracy of conservation genomics, as the relationships among genomic variation, ecological resilience, and disease phenotypes are being established in *C. mydas*.

3.3. Factors to Consider When Choosing a Deep Learning (DL) Architecture

Guidance on selecting an appropriate architecture should include consideration of the gradient vanishing (GV) problem, which reduces trainability. Although certain architectures alleviate GV, it is also influenced by the choice of activation function: e.g., the sigmoid function can cause gradients to disappear at non-zero points, but ReLU can overcome that, because its nonzero response is linear (Ntambwe & Ntambwe, 2025). GV is often tackled using residual networks and LSTM models, but LSTMs have many synaptic connections and therefore are more computationally expensive. Multilayer perceptions (MLPs) are beneficial for *C. mydas* genomic analyses, in which characteristics of short variants (SNVs and small indels), sea surface temperature, or seagrass abundance can be analyzed as independent features (Aslam & Aplop, 2025). Recurrent neural networks (RNNs)/LSTMs, on the contrary, are designed to handle sequential data, i.e., longitudinal health records or migrations. Convolutional neural networks (CNNs) are well-suited to genomic sequences, and transformers can also learn the structure of DNA sequences, although too many layers can lead to gradient degeneration (Choi & Lee, 2023).

3.4. Multimodal Data Fusion Strategies

A key challenge in multimodal analysis is deciding how best to combine diverse data sources. MMDL models address this by merging modalities at different stages of the learning process early, intermediate, or late fusion. Each strategy is independent of network type and data structure (Sucre et al., 2025). For *C. mydas*, genomic data, environmental indicators, and phenotypic disease information can be integrated at these stages to improve predictions of health and conservation outcomes.

***3.4.1. Early Fusion Approach*:** Here, multimodal data are fused at the first stage by concatenating them into a common vector or matrix that functions as the DL model's input layer (Fig. 2). Early fusion leverages multimodal inputs through a shared input layer, with recurrent or convolutional layers applied when sequence structure matters (Montesinos-López et al., 2024). In *C. mydas* studies, SNVs and short indels can be fused with methylation or transcriptomic data into a 2 × p matrix, enabling simultaneous cross- and intra-modality learning. Genomic and transcriptomic matrices can also be transposed, multiplied, and input to the network, preserving cross-modality correlations throughout training (Mohammed, 2026). Early fusion struggles when modalities differ in dimension or importance. In *C. mydas* research, genomic variant vectors contrast with ecological data like sea surface temperature or seagrass maps. This approach is best for structurally similar, complementary modalities; otherwise, it risks spurious correlations and should be replaced with more suitable fusion strategies (Iqbal et al., 2025). Attention mechanisms and modality-specific transformations help manage discrepancies in multimodal data. By focusing on the most relevant features, attention greatly improves the accuracy and efficiency of deep learning models in complex prediction scenarios (Ghosh et al., 2025). Encoders reduce raw dimensionality but add

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parameters. For fusing 1D genomic with 2D or 3D ecological data, features must first be reshaped into 1D vectors. In *C. mydas* studies, limited sample sizes versus high feature counts increase the computational burden. Early fusion further expands synaptic connections, prolonging training (Ntambwe & Ntambwe, 2025).

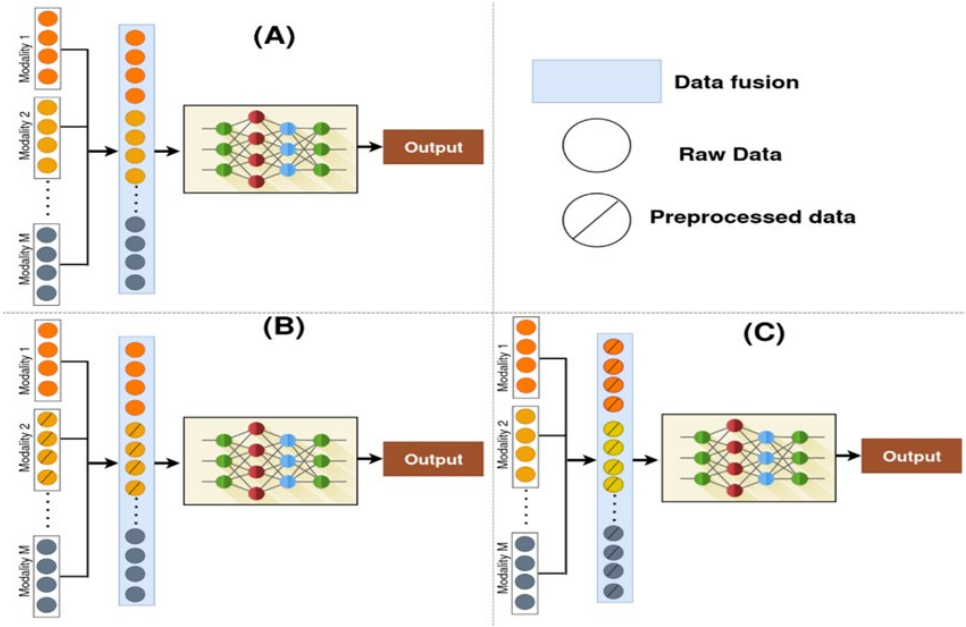

Fig. 2: Schematic representation of early fusion strategies: (a) direct integration of raw inputs from all modalities; (b) fusion of individually preprocessed selected modalities; (c) joint preprocessing followed by early integration of all modalities.

Early Fusion Struggles with Heterogeneous Inputs or Relevance, Addressed through the Following Techniques

(1) Dimensionality reduction: Techniques such as PCA, autoencoders, or t-SNE can be applied to project high-dimensional modalities into a shared lower-dimensional space prior to fusion (Ntambwe & Ntambwe, 2025).

(2) Modality-specific processing: All modalities are initially modeled with their own branches of NNs, which allows them to have optimized representations. Contributions can then be dynamically varied by attention mechanisms or adaptive fusion layers (Sucre et al., 2025).

(3) Feature engineering: Domain-specific features or operations (e.g., normalization, scaling) may be used to align heterogeneous modalities before they are fused (Ghosh et al., 2025).

(4) Attention mechanisms: How to use cross-modal or modality-specific attention modules to emphasize features of relevance and downplay noise in fusion (Parvizi Omran et al., 2025).

(5) Ensemble methods: Predict and combine predictions across modality-specific models with either averaging or weighted voting to obtain more balanced and reliable predictions (Aslam & Aplop, 2025). *C. mydas* genomic prediction has the capability to combine genomic short variants, phenotypic traits, and environmental data. The intermediate scores of each modality are fused to predict disease risk, survival, and climatic resilience using a fusion layer, averaging, or neural networks.

***3.4.2. Intermediate Fusion Approach*:** Joint fusion integrates modalities after latent features are learned with a Convolutional Neural Network (CNN) or LSTMs (Fig. 3). The fused output is processed by a Multilayer Perceptron (MLP) or a statistical model for prediction. Dimensional variation across modalities can be managed by sub-models, though reducing higher-dimensional data too strongly may remove essential information (Liang et al., 2022). Intermediate fusion allows flexible design of layers and fusion order, improving the capture of both modality-specific and joint latent factors. While marginal factors summarize patterns within single modalities, joint factors integrate across them. Deep learning architectures excel here, as they connect these features into shared representations. In *C. mydas*, combining SNVs, transcriptomic data, and environmental variables such as sea surface temperature illustrates this strength (Ramachandram & Taylor, 2017). For *C. mydas* data with missing modalities, multitask networks enable learning by pairing unimodal inputs with task-specific outputs. Each task is tied to the available data types. Though limited to multitask setups, this approach can be reformulated for genomic prediction, with traits such as disease, growth, and survival serving as output tasks while multiple modalities act as inputs.

***3.4.3. Late Fusion Approach*:** In ensemble (decision-level) fusion, each modality is modeled separately, and their predictions are aggregated using methods such as averaging, majority voting, weighted voting, or meta-classifiers to yield the final decision (Fig. 4). Late fusion generally applies empirical aggregation rules, with averaging of sub-model probabilities being the most common (Sucre et al., 2025). This assumes equal influence

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across modalities, which can obscure important genomic environmental interactions in *C. mydas* (Arantes et al., 2025). The method can be used to place greater emphasis on modality-specific reliability by weighting outputs according to predictive performance. In the case of *C. mydas* genomic prediction, late fusion is used, which combines several modalities at the output phase (Toor et al., 2025). Separate models examine genomic variants, environmental factors, and phenotype characteristics, and generate sub-products that are aggregated in the fusion layer (Hilgers & Hiller, 2025). It is a strategy that leverages the strengths of either modality to obtain more precise and robust predictions. The study of *C. mydas* could model genomic differences in health or stress (through short variants) combined with climate adaptation predictors. Late fusion takes such inputs and fuses them together to form a single prediction, which is also effective when the data are partially available. Although framed as the model aggregation, ensemble methods can be compared with data fusion in the case of combining predictions of models that rely on other modalities and can be used to support better genomic predictions in *C. mydas* (Richard Albert et al., 2023).

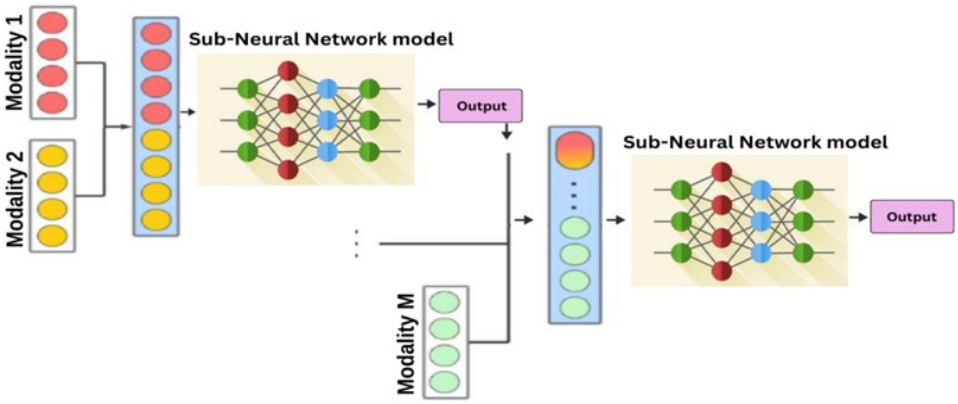

Fig. 3: Intermediate data fusion model. Modality-specific sub-outputs (marginal latent factors) are merged in the fusion module, and a final sub-model generates the complete output.

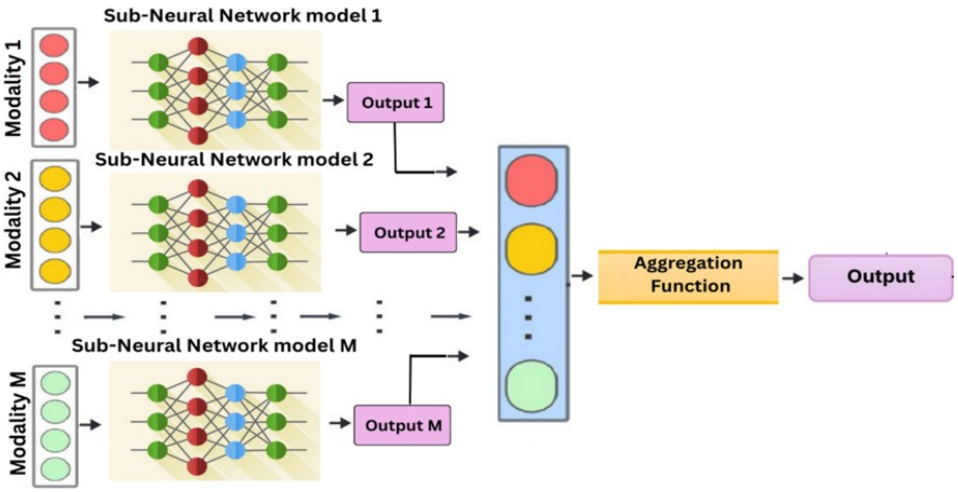

Fig. 4: Conceptual illustration of late fusion in multimodal deep learning, where each data modality is processed by a dedicated model and the resulting outputs are aggregated to generate the final prediction.

3.5. Assembly Assessment and Truth-Set Generation

Selecting Fusion Strategies for *C. mydas* Genomic Prediction. The choice of fusion approach is determined by four main factors: the modality type, complementarity, correlation, and computational cost. Key points for selecting an appropriate strategy and a summary of their features are presented in Table 2 (Sagi & Rokach, 2018). While correlations between modalities can be quantified with measures like Pearson's or Spearman's coefficients, the structural nature of the data is equally important (Bharadwaj et al., 2021). Genomic data on short variants (SNVs and small indels) may align closely with transcriptomic expression levels, favoring early fusion. In contrast, in *C. mydas* disease studies, genomic data and viral load may require independent modeling before being integrated at an intermediate fusion stage (Liang et al., 2022). At times, only some features of a modality correlate with another, while others remain independent. To manage this, modalities may be split into sub-modalities. For *C. mydas*, sea surface temperature, seagrass density, and nesting beach conditions all fall under environment, though nesting beaches could be modeled separately. To aid readers, we outline the main characteristics of each fusion strategy as follows:

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Table 2: Comparative evaluation of data fusion techniques.

	Early Fusion Approach	Intermediate Fusion Approach	Late Fusion Approach
Description	All modality-specific features are concatenated into one representation without source differentiation.	Each modality runs in its own sub-model, and their outputs merge into one prediction.	Each modality is processed independently, and the outputs are combined at the decision stage
Pros	Captures cross-modality interactions with minimal complexity by fusing at the input layer.	Balances cross- and within-modality interactions with optimized parameters; moderately complex but robust, flexible, and more effective than early fusion at handling noisy, incomplete, or high-dimensional data.	Simple, low-cost, and robust—independent processing of modalities ensures resilience to noise and missing data.
Cons	Expensive, parameter-heavy, prone to spurious correlations, and fragile to noise or missing data at input fusion	Risk of losing cross-modality information.	Loss of cross-modality information and longer training times than early fusion.

3.6. Hyperparameter Tuning

Hyperparameter tuning based on the dataset is required to achieve precise genomic prediction for Chelonia mydas. The parameters, including neurons, layers, kernels, and activations, need to be optimized by grid, random, or Bayesian search to avoid underfitting or overfitting (Kalleberg et al., 2025).

3.7. MMDL frameworks and Tools

Keras/TensorFlow, PyTorch, and Chainer support implementation of MMDL, where PyTorch is commonly preferred due to efficiency. Keras offers a comparatively easy point of entry into predictive disease and ecological adaptation in *C. mydas* genomics, although it needs parameter optimization. MMDL has become more accessible through open-source frameworks (Niemczynowicz & Kycia, 2025). Fastai and MultiZoo build upon these features, simplifying preprocessing, training, and multimodal benchmarking (Albert et al., 2020). However, data scarcity remains a bottleneck. Transfer learning is a viable approach in which a model trained in one modality is applied to another without labeled data (Montesinos-López et al., 2025). For example, genomic-environmental models can also be used to impute missing phenotypic records to improve prediction in *C. mydas* (Aslam & Aplop, 2025). Existing practical libraries, such as Optuna, can be incorporated into these frameworks to automate tuning (Akiba et al., 2019).

4. Applications and Research Directions

4.1. Literature on MMDL used in Genomic Studies

Table 3 presents a subset of multimodal deep learning (MMDL) literature with either direct or conceptual applications to genomic prediction in *Chelonia mydas*. Such studies combine short variants (SNVs and small indels) with other modalities like environmental, phenotypic, or imaging data, and in others are contrasted with unimodal deep learning models. Table 3 has been categorized to present the contexts of *C. mydas*, model overviews, anticipated traits, and comparison holders. Other work with multi-omics or other environmental data streams is also included because of its possible flexibility. The overview highlights the model's structure and predictive performance.

4.2. Summary of Genomic Prediction Studies

Table 3 presents a curated set of multimodal deep learning (MMDL) studies with direct or transferable relevance to genomic prediction and conservation research in Chelonia mydas. The listed works demonstrate how heterogeneous data sources, including genomic variants, phenotypic traits, environmental variables, multispectral imagery, and temporal sensor data, can be integrated using neural architectures such as LSTMs, transformers, CNN-LSTM hybrids, and neural network–based mixed models. Each study is summarized by its application context, model template, data modalities, response variable, and baseline methods used for comparison. Together, these examples illustrate the methodological diversity of MMDL frameworks and provide a practical foundation for adapting multimodal genotype, phenotype, and environment modeling strategies to disease risk assessment, habitat evaluation, and population resilience analysis in *C. mydas*.

4.3. Genomic Prediction Performance Using Multimodal Deep Learning in *Chelonia mydas*

Multimodal deep learning architectures are highly effective at combining heterogeneous data sources, including genomic, phenotypic, environmental, telemetry, and population-level information, by capturing relationships across modalities. A hypothetical *C. mydas* example is outlined below that integrates (1) genomic data (short variants,

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SNVs and small indels) representing standing genetic diversity; (2) phenotypic/health observations such as fibropapillomatosis tumor load, growth, or survival; (3) environmental variables such as sea surface temperature, chlorophyll-a, pollution indices, and nesting beach metrics; and (4) population/rookery assignment or kinship (a proxy for pedigree). The MMDL framework uses modality-specific encoders: a genomic encoder (e.g., DNN/CNN) for variant data; a phenotypic encoder for clinical and morphometric features; an environmental encoder (e.g., RNN/attention) to capture temporal–spatial structure; and a graph-based encoder for population/rookery relationships. With intermediate data fusion, encoded representations are combined in a fusion layer (e.g., concatenation, attention, or tensor fusion) to capture interactions among genomic, phenotypic, environmental, and population modalities (Tsai et al., 2019). A final prediction head outputs targets such as disease probability, survival, or migration success under specified environmental conditions.

Table 3: Genomic prediction studies and model templates adapted for *C. mydas* research.

No.	References	Study Context	Model Template	Modalities	Response Variable	Baseline Methods
1	(Putra et al., 2025)	Marine wildlife health forecasting	LSTM (± temporal attention)	Weather/ocean time series + clinical phenotypes	Disease/tumor risk; survival	SVR–RBF; Lasso; simple data-driven baselines
2	(Papazekou et al., 2024)	Nesting/foraging site monitoring	Tab-DNN + Spectral-DNN fusion	Genomic variant summaries + management + UAV multispectral	Early-season performance; site suitability	Unimodal Tab-DNN; RF; XGBoost
3	(Abdelwahab & Torkamaneh, 2026)	Large-scale variant + environment	Performer-based transformer	Genomic (SNVs and small indels) + weather/ocean features	Health or migration outcomes	Kernel baselines; CNN-MLP; ResNet-MLP
4	(Luo et al., 2024)	Multi-omics integration with missing data	NN-MM	Genomic + epigenomic + transcriptomic + proteomic	Composite health index; growth	Single-step mixed model
5	(Chang et al., 2025)	Habitat quality prediction	CNN + LSTM	Multispectral imagery + in situ sensors	Survival probability; habitat risk	Unimodal LSTM
6	(Wang et al., 2023)	Genotype × Environment modeling	DeepG2P-style	Genomic + environment + management	Location holdout performance; resilience	GEBLUP; CNN variants; Auto-models
7	(Jiang et al., 2022)	Remote sensing fusion at scale	CropYieldNet-style	Reflectance bands + soil/sediment + meteorology (add genomics)	Population performance index	CNN; CNN+GP; CNN+LSTM
8	(Kick et al., 2023)	Comprehensive multimodal integration	based on DNN architectures employing CO and SO strategies	Integration of genomic, climatic, edaphic, and management-related data	Robust yield-analog → health/survival	Linear fixed effects; K-NN/RNR; RF/SVR
9	(Baltrusaitis et al., 2019)	Imagery + time + genomics	Multimodal PheGeMIL-style (attention)	Genomic + multispectral/thermal + DEMs	Health status; rookery risk	Lasso; RF; multimodal ablations

For *Chelonia mydas*, multimodal frameworks can shorten conservation decision cycles by guiding early triage such as allocating rehabilitation efforts or identifying threatened rookeries and by producing more accurate assessments of resilience and vulnerability than unimodal methods. This highlights the strength of MMDL in modeling genotype–phenotype–environment relationships. Its benefits include capturing nonlinear interactions, combining diverse data sources, scaling to high-dimensional inputs, adapting as new data arrive, and extracting informative representations of gene–environment dynamics. The following section outlines representative approaches, adapted for *C. mydas*, that illustrate these capacities in health and ecological prediction. Developed two LSTM-based models for health-risk prediction (e.g., tumor burden) in marine wildlife, with and without temporal attention. Compared against support vector regression and Lasso baselines using RMSE, MAE, and R^2. The multimodal versions (weather + ocean state + clinical variables) matched or exceeded unimodal time-series models across metrics, suggesting direct transferability to *C. mydas* disease-risk forecasting (Yang et al., 2022).

Introduced an MMDL to predict early-season performance by fusing multispectral UAV imagery of nesting beaches/foraging grounds with management/rehabilitation metadata and genotype summaries. A tabular DNN (management/genotype) plus a spectral DNN (imagery) outperformed either stream alone; scaling/weighting learned during training yielded the highest accuracy, an approach readily adaptable to *C. mydas* nesting-site monitoring (Zhu et al., 2025).

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Presented a performer-based transformer that replaces softmax attention with linear-time attention for efficiency, combining genomic variants with weather/ocean features. Performer-based models outperformed CNN/ResNet hybrids and kernel baselines and were well-suited to large C. mydas variant panels and long environmental sequences (Choromanski et al., 2020). Introduced a neural network–based mixed model (NN-MM) extending linear mixed models to integrate intermediate omics (epigenomics, transcriptomics, proteomics) with genotypes and phenotypes. Especially effective when some omics are missing, useful for *C. mydas* where complete multi-omics per individual is rare (Camacho et al., 2018). Combined multispectral imagery (e.g., satellite/UAV) with in situ sensor time series (temperature, turbidity) via CNN + LSTM; the fused model improved prediction over unimodal time-series baselines translatable to turtle habitat-quality and survival modeling (Chang et al., 2025). Introduced a multimodal genotype-environment management model (DeepG2P-style) that excelled on environmental holdouts and generalized to new locations; ablations confirmed the importance of genomic inputs and cross-attention between genotypes and environment, highly relevant for rookery-level forecasting in *C. mydas* (Ramachandram & Taylor, 2017).

Proposed a CropYieldNet-style architecture with surface reflectance, soil, and meteorology streams; although genomics was absent, the design shows how remote sensing + climate can be fused with a genomic branch for *C. mydas* population performance or habitat-risk indices (Pelletier et al., 2019). A comprehensive multimodal deep learning framework based on CO/SO-style DNN architectures was developed to integrate genomic, climatic, substrate, and management inputs; the multimodal configuration exceeded single-stream performance and matched classical benchmarks, indicating comparable advantages for *C. mydas* through joint analysis of genetic variants, oceanographic conditions, and husbandry practices (Aslam & Aplop, 2025). Applied an MMDL to integrate genomic data, vegetation/NDVI proxies (as habitat productivity surrogates), and time factors; results showed mixed but often improved performance versus GBLUP/GBM/SVR, indicating value in adding environmental imagery to *C. mydas* genomic prediction (Pelletier et al., 2019). As previously emphasized, MMDL frameworks are well-suited to integrating genomic, phenotypic, environmental, movement, and population information for *C. mydas*, capturing complex relationships that unimodal genomic models often miss. Specialized encoders (DNN/CNN for variants, RNN/attention for environmental sequences, GNN for population structure) connect via a fusion layer to learn interactions, followed by a final prediction head that outputs clinically or ecologically relevant targets (Tsai et al., 2019). Developed two LSTM-based models for health-risk prediction (e.g., tumor burden) in marine wildlife, with and without temporal attention. Compared against support vector regression and Lasso baselines using RMSE, MAE, and R^2. The multimodal versions (weather + ocean state + clinical variables) matched or exceeded unimodal time-series models across metrics, suggesting direct transferability to *C. mydas* disease-risk forecasting (Wilkinson et al., 2022).

Introduced an MMDL to predict early-season performance by fusing multispectral UAV imagery of nesting beaches/foraging grounds with management/rehabilitation metadata and genotype summaries. A tabular DNN (management/genotype) plus a spectral DNN (imagery) outperformed either stream alone; scaling/weighting learned during training yielded the highest accuracy, an approach readily adaptable to *C. mydas* nesting-site monitoring (Aslam & Aplop, 2025).

Presented a Performer-based transformer that replaces softmax attention with linear-time attention for efficiency, combining genomic variants with weather/ocean features. Performer-based models outperformed CNN/ResNet hybrids and kernel baselines, which are well suited to large C. mydas variant panels and long environmental sequences (Vaswani et al., 2017a). Proposed a neural-network mixed model (NN-MM) extending linear mixed models to integrate intermediate omics (epigenomics, transcriptomics, proteomics) with genotypes and phenotypes. Especially effective when some omics are missing, useful for *C. mydas* where complete multi-omics per individual is rare (Camacho et al., 2018). Combined multispectral imagery (e.g., satellite/UAV) with in situ sensor time series (temperature, turbidity) via CNN + LSTM; the fused model improved prediction over unimodal time-series baselines—translatable to turtle habitat-quality and survival modeling (Pelletier et al., 2019).

Introduced a multimodal genotype–environment–management model (DeepG2P-style) that excelled on environmental holdouts and generalized to new locations; ablations confirmed the importance of genomic inputs and cross-attention between genotypes and environment—highly relevant for rookery-level forecasting in *C. mydas*. Proposed CropYieldNet-style architecture with surface reflectance, soil, and meteorology streams; although genomics was absent, the design shows how remote sensing + climate can be fused with a genomic branch for *C. mydas* population performance or habitat-risk indices (Zhu et al., 2025). A comprehensive multimodal deep learning framework (CO/SO-oriented DNN architecture) was developed to integrate genomic, climatic, substrate, and management inputs; the multimodal models surpassed single-stream approaches and performed competitively against classical baselines, indicating comparable advantages for *C. mydas* through joint modeling of genetic variants, oceanographic conditions, and husbandry practices (Camacho et al., 2018). Applied an MMDL to integrate genomic data, vegetation/NDVI proxies (as habitat productivity surrogates), and time factors; results showed mixed

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but often improved performance versus GBLUP/GBM/SVR, indicating value in adding environmental imagery to *C. mydas* genomic prediction (Zhu et al., 2025).

Introduced a Phenotype–Genotype Mutual Information Learning (PheGeMIL-style) framework using attention over multispectral, thermal, elevation, and genetic variant channels; multimodal integration yielded the strongest correlations transferable to *C. mydas* by substituting turtle health, habitat, and variant data (Vaswani et al., 2017). As previously emphasized, MMDL frameworks are well suited to integrate genomic, phenotypic, environmental, movement, and population information for *C. mydas*, capturing complex relationships that unimodal genomic models often miss. Specialized encoders Deep Neural Network (DNN)/Convolutional Neural Network (CNN) for variants, RNN/attention for environmental sequences, GNN for population structure) connect through a fusion layer to learn interactions before a final prediction head outputs clinically or ecologically relevant targets (Baltrusaitis et al., 2019).

4.4. An Illustrative Multimodal Deep Learning Example for *Chelonia mydas*

Conceptual Framework of a Multimodal Deep Learning Model Integrating Environmental and Genotypic Factors in *Chelonia mydas*. In this context, health-related phenotypic data such as fibropapillomatosis tumor presence, growth rate, or survival can be modeled alongside environmental variables, including sea surface temperature, salinity, pollution indices, and nesting beach quality, as well as genotypic data derived from short variants (SNVs and small indels). Genotypic data would be processed using established workflows, including quality trimming with fastp, read alignment with BWA-MEM, and variant detection with DeepVariant, GATK, FreeBayes, VarScan, or BCFtools, followed by filtering based on minor allele frequency and missing-data thresholds (Danecek et al., 2021).

4.5. Key Considerations for Practical Deployment

For *Chelonia mydas*, MMDL offers superior predictive capacity by integrating genomic, phenotypic, and environmental modalities. Convolutional Neural Networks (CNNs), Deep Neural Networks (DNNs), and Long Short-Term Memory (LSTM address specific data types, while ResNets help overcome gradient vanishing (Montesinos-López et al., 2024). Resource-intensive optimized frameworks are more efficient, and performance gains depend on the fusion strategy, dataset completeness, and architectural design. Notably, MMDL is not necessarily more effective than unimodal methods, and the computational cost must be weighed against potential gains (Baltrusaitis et al., 2019).

4.6. Trends and Future Outlook

Future trends are to become more interpretable in MMDL models, as the black-box nature commonly constrains uptake in conservation genomics. Interpretable frameworks focus on improving transparency by clarifying the contributions of genomic, phenotypic and environmental modalities to predictions. Attention mechanisms, feature visualization and saliency mapping are some of the tools that can be used to show the relative importance of a particular locus, ecological variable, or phenotypic feature, thus making its output more actionable in conservation decision-making (Tsai et al., 2019). In turtle genomics, recent advances to MMDL will focus on the incorporation of a wide range of types of data up to now: genomic variants, transcriptomic data, disease phenotypes, oceanographic data, and location features of nest sites to produce robust health, survival and population dynamics predictions. The model-free efficiency of genomic prediction in non-model marine organisms, including Chelonia mydas, is projected to be even further enhanced by Deep learning architectures (Eraslan et al., 2019). Transfer learning will also be of great interest. Initialization or fine-tuning of turtle-specific multimodal architectures can be obtained from pretrained models trained on related genomic or environmental datasets. This will aid in reducing the dependence on massive, labeled datasets- which are typically scarce in cases of endangered species, such as *C. mydas* and enhance predictive accuracy of diverse types of data. Nevertheless, unimodal models also present certain challenges not associated with the application of MMDL. The broader data acquisition methods, intensive preprocessing, complex architecture, and high computational cost require careful planning when using multimodal frameworks for conservation and disease studies of *C. mydas* (Aslam & Aplop, 2025).

5. CONCLUSION

Multimodal Deep Learning (MMDL) offers a promising direction for advancing the genomics of *C. mydas* by integrating environmental, phenotypic, and genomic data into a unified prediction framework. Similar to unimodal Deep Learning (DL), multimodal approaches require large, high-quality datasets; however, they have the potential to offer greater predictive power than traditional methods. Although computational costs remain high, advanced fusion strategies can capture complex cross-modal interactions, thereby improving predictive accuracy and overall model robustness. Hyperparameter optimization is particularly important for datasets associated with endangered

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species such as *C. mydas*, where sample sizes are often limited. Overall, multimodal techniques may provide an effective framework for disease prediction, population assessment, and long-term conservation planning under increasing environmental pressures.

Declarations

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Author's Contribution: AN conceived and designed the review, conducted the literature search and synthesis, and prepared the original draft, tables, and figures. FA (corresponding author) supervised the work, contributed to conceptualization and methodology, and critically revised the manuscript for intellectual content. FA (Fahad Aslam) assisted with literature curation, validation of the surveyed methods, and manuscript review and editing. All authors read and approved the final version of the manuscript.

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