***Systematic Review***

**Applications of Deep Learning in** **Predicting the Risk of Metabolic Syndrome from Lifestyle and Behavioral Factors: A Scoping Review**

**ABSTRACT**

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| **Background:** Metabolic syndrome (MetS) affects roughly one quarter of the world’s adults and dramatically heightens cardiometabolic morbidity, mortality, and healthcare costs. Because the syndrome is heavily driven by modifiable lifestyle and behavioural factors, risk stratification that relies only on easily collected, non-invasive information would enable earlier, lower-cost intervention. Deep learning (DL) models are theoretically well-suited to capture the complex, non-linear interactions among these heterogeneous data types, yet the relevant evidence base remains diffuse.**Objective:** To map and critically appraise the ways in which DL has been applied to predict MetS risk from lifestyle and behavioural variables, identify the predictors and model designs that dominate current practice, and highlight gaps and opportunities for future work.**Methodology:** A PRISMA-ScR–guided search (PubMed, Google Scholar; 2010 – 2025) located empirical studies based on predefined inclusion and exclusion criteria. Seven studies met all criteria. Data on setting, sample, predictor categories, DL design, validation approach, and performance metrics were charted and synthesised narratively.**Results:** Most used feed-forward neural networks on cross-sectional cohorts (n = 468–70 370) in Iran, Mexico, Taiwan, and South Korea. Accuracies ranged from ~0.81 to 0.94; AUCs often surpassed 0.85 and peaked at 0.99 when polygenic risk scores were added. Waist circumference, BMI, and blood-pressure indices were the strongest predictors, while activity, diet, sleep, smoking, and alcohol intake improved performance.**Conclusion:** Despite small numbers and limited geographic reach, evidence suggests that DL can turn routine, non-invasive data into highly accurate MetS risk tools. |

*Keywords: Metabolic Syndrome, Deep Learning, Lifestyle Factors, Behavioural Risk Factors, Non-invasive Prediction, Machine Learning.*

**1. INTRODUCTION**

Metabolic syndrome (MetS) is a multifactorial condition, characterized by an aggregate of clinical conditions including impaired insulin signaling, excessive adipose tissue, ectopic lipids, especially in the context of central obesity, chronic low-grade inflammation, hypertension, hyperglycemia, impaired lipid metabolism, pro-inflammatory and pro-thrombotic state (Neeland et al., 2024; Saklayen, 2018; Sypniewska, 2007). Over the years, this diverse picture has earned MetS several names: “syndrome X” or “Reaven syndrome,” denoting the cluster of hyperuricemia, hyperglycemia, and hypertension first noted by Kylin; the “insulin-resistance syndrome,” highlighting its hallmark pathophysiology; and the “deadly quartet,” referring to insulin resistance, central obesity, hypertension, and dyslipidemia described by Dr. Gerald Reaven in 1988 (McCracken et al., 2018; Nilsson et al., 2019). MetS may be redefined as dysfunction in the metabolic process, with closely associated pathological characteristics that coexist and cannot be separated (Nilsson et al., 2019).

MetS affects a significant proportion of the global population, with estimates suggesting that approximately 20–25% of adults worldwide are impacted, translating to over one billion individuals (Jemal et al., 2023; Mohamed et al., 2023). Its prevalence varies widely across regions and populations, ranging from 24.0% to 78.0% in Western countries (Q. Wang et al., 2017) and is influenced by factors such as age, body size, geographic location, urbanization, and sociodemographic characteristics including sex, race, and ethnicity (Islam et al., 2024; VanWormer et al., 2017). Additionally, the reported prevalence often depends on the diagnostic criteria adopted by various health organizations. Beyond its health burden, MetS poses significant economic challenges, notably increasing the cost of primary healthcare services, particularly medication expenditures (Ricardo et al., 2024). Clinically, it is strongly associated with elevated risks of cardiovascular disease (CVD), increased morbidity, longer hospital stays, and higher mortality rates (Mazloomzadeh et al., 2019).

The key component of MetS development is associated with the increase in central obesity contributed by high free fatty acid influx and suppressed insulin action on its receptor, disrupting glucose metabolism in adipose, muscle and liver tissues (Rochlani et al., 2017). These changes increase hepatic glucose production, impair peripheral glucose uptake, and cause dyslipidemia. They also alter adipokine secretion, raising leptin while lowering adiponectin, and they trigger macrophage infiltration, pro-inflammatory adipokine release, and elevated circulating cytokines such as IL-6, TNF-α, CRP, IL-1β, and TGF-β (de Kloet et al., 2010; Rochlani et al., 2017). This contributes to well-documented mechanisms involved in oxidative cell damage, promoting inflammation, impaired insulin signaling and atherosclerosis caused by the onset of a prothrombotic state with an increase in plasminogen activator inhibitor-1 (PAI-1) and fibrinogen, a processes synthesized schematically in figure 1 below. Of note, individual lifestyle and behavior factors such as dietary consumption of excessive calories, lack of physical activities, sleep patterns, smoking, and alcohol use contribute to the pathogenesis of MetS development (Rochlani et al., 2017).

Established diagnostic criteria for metabolic syndrome by the US. National Cholesterol Education Program Adult Panel III (NCEP ATP III) and International Diabetes Federation (IDF) include the presence of abdominal obesity, reduced high-density lipoprotein cholesterol (HDL-C; in men <40 mg/dL or women<50 mg/dL), elevated triglycerides (≥150 mg/dL), elevated fasting glucose (≥100 mg/dL) and high blood pressure (≥130/85 mmHg) (Grundy et al., 2005). An individual with MetS must be diagnosed with at least two of the aforementioned criteria, including central obesity as the main criterion, as notable estimate by the waist circumference greater than 88 cm in women and 102 cm in men or BMI >30 kg/m2, fasting blood glucose in oral glucose tolerance test estimated at 100-125 mg/dL at threshold, 140-199 mg/dL at 120 min measure, HbA1C between 5.7-6.4 % as reported by the American diabetes association (ADA) (Alberti et al., 2009; Chomiuk et al., 2024; Grundy et al., 2005).

In efforts to enable earlier and more accessible risk detection, researchers have explored predictive models for MetS using non-invasive data. Predictive analytics utilizes machine learning to analyze healthcare data, facilitating early diagnosis, risk assessment, and personalized treatment. Deep learning improves accuracy by processing complex datasets. As digital health expands, the integration of AI enhances clinical decision-making; however, interpretability and reliability remain vital for safe and effective implementation (Badawy et al., 2023). Deep learning (DL) is a subset of machine learning and artificial intelligence that is widely utilized in various healthcare settings to address real-world problems and data (Sarker, 2021). DL uses deep neural network approaches to predict and detect disease onset in patients (Azmi et al., 2025). In the healthcare system, DL and machine learning (ML) have become vital approaches that drive advancement across important domains such as medical imaging diagnostics, which is tailored to planning of treatment strategies, drug development, electronic health record analysis and genomic analysis (Sadr et al., 2025). DL uses large available datasets for training, including medical images, to build deep models enhancing performance in various medical applications (Shen et al., 2017).

Literature on deep learning applications for MetS prediction remains fragmented. Studies vary in the populations analyzed, the types of lifestyle and behavioral variables included, and the deep learning architectures and training strategies used. To our knowledge, no comprehensive review has yet synthesized the state of the art in this emerging field. We therefore conducted a scoping review to map out how deep learning models have been used to predict the risk of metabolic syndrome, particularly emphasizing the role of lifestyle and behavioral factors as predictors, identifying opportunities, challenges and future directions in a multidisciplinary approach.



**Fig. 1. Pathogenesis of Metabolic Syndrome.** **Created with bioRender (https://www.biorender.com/)**

1. **METHODOLOGY**

We followed the PRISMA-Scoping Review (PRISMA-ScR) guidelines in conducting and reporting this scoping review (Tricco et al., 2018).

**Search Strategy:** A comprehensive literature search was performed to identify studies that applied deep learning methods to predict metabolic syndrome or its risk, using lifestyle, behavioral, or non-invasive health data as input features. We searched multiple databases including PubMed and Google Scholar for relevant articles. The search strategy combined terms related to metabolic syndrome (e.g., "metabolic syndrome", "MetS"), prediction (e.g., "risk prediction", "early detection"), and deep learning approaches (e.g., "deep learning", "neural network", "convolutional neural network"). We also included terms for lifestyle and behavioral factors (e.g., "lifestyle", "diet", "physical activity", "sleep", "smoking") to focus the results. An example PubMed query was:

("metabolic syndrome" OR "MetS") AND ("deep learning" OR "CNN" OR "RNN") AND (lifestyle OR diet OR "physical activity" OR behavior OR behavioural OR "risk factors")

Searches were limited to English-language publications. We included articles published between 2010 and 2025, covering the period when deep learning techniques became widely utilized. To ensure comprehensive coverage, we also scanned the reference lists of relevant papers and reviews for any additional studies and considered reputable preprints or gray literature if they contained adequate methodological details.

**Inclusion and Exclusion Criteria:** We included studies that met the following criteria:

1. Population: Human adults assessed for metabolic syndrome or its components.
2. Predictive Model: Employed a deep learning model (e.g., artificial neural network, convolutional neural network, recurrent neural network, autoencoder, or related architecture). Studies that compared deep learning with traditional machine learning were included, as long as a deep learning model was among those evaluated.
3. Predictors: Included lifestyle or behavioral factors as predictors. These could be self-reported or objectively measured factors such as diet, nutrition intake, physical activity, sedentary behavior, smoking, alcohol use, sleep patterns, stress or work-related factors, etc. Studies that combined lifestyle factors with anthropometric or basic clinical measures (blood pressure, etc.) or genetic data were included, but we excluded studies that relied exclusively on biochemical markers or genetic features without any lifestyle/behavioral data.
4. Outcome: This included either current MetS status (classification) or future development of MetS (risk projection) according to standard criteria (e.g., ATP III, IDF, or similar definitions). We accepted studies predicting MetS as an outcome or those predicting related continuous risk scores, as well as multi-task models predicting MetS components.
5. Study Design: Any empirical study design (prospective cohort, retrospective analysis of cross-sectional data, case-control, etc.) where a predictive model was trained and evaluated. We included peer-reviewed journal articles and high-quality conference papers. Reviews, editorials, and purely methodological papers with no evaluation on MetS data were excluded.

We excluded studies that did not involve deep learning (e.g., only simple regression or standard machine learning unless a deep model was also tested). If multiple publications reported on the same model and dataset, we included the most comprehensive one to avoid duplication.

**Screening and Selection:** All titles and abstracts retrieved were screened for relevance. Two reviewers independently assessed full-text articles for eligibility, with disagreements resolved through discussion. We maintained a PRISMA flow diagram, shown in figure 2, to track the number of records identified, screened, and included at each stage. In total, 7 studies met the inclusion criteria and were included in the qualitative synthesis.

**Data Extraction:** We developed a data extraction form to chart relevant information from each included study. Extracted data included: author and year, study design and setting (e.g., country, population characteristics, sample size), data source (such as national health surveys or cohort studies), input features used (categorized into lifestyle/behavioral factors, anthropometric measures, clinical/laboratory measures, and any genetic or other data), details of the deep learning model architecture (e.g., number of layers, type of network). We also noted each study’s key findings regarding important predictors and any interpretability or feature importance analysis, as well as any validation approach (cross-validation, external validation on separate data, etc.).

Data extraction was performed by one reviewer and verified by a second for accuracy. Given the scoping review approach, we did not perform a formal risk-of-bias assessment of individual studies.

**Synthesis of Results:** Extracted data were compiled into summary tables and narrative form. We used a descriptive analytical approach to summarize findings, given the heterogeneity of study methods. We synthesized the results in several thematic categories: (1) characteristics of included studies (populations and data sources), (2) deep learning models used and their performance, (3) types of lifestyle and behavioral factors incorporated and their observed relevance, and (4) evaluation of evidence quality (e.g., generalizability, limitations). We present a summary table of key study characteristics and outcomes (Table 1) and provide a narrative synthesis in the Results section. The Discussion section contextualizes these findings, discusses limitations and gaps in current research, and suggests future directions.



**Fig. 2. PRISMA flow diagram showing the search and selection process for studies included in the scoping review.**

3. results and discussion

Out of the initially identified studies, seven met the inclusion criteria and were included in this scoping review. The key characteristics and findings are summarized in Table 1.

The included studies predominantly utilized cross-sectional designs (Eyvazlou et al., 2020; Gutiérrez-Esparza et al., 2020; Kim et al., 2023; Lee et al., 2024; H. Shin et al., 2023), with one retrospective observational study (F. H. Wang & Lin, 2020) and one prospective cohort study (D. Shin, 2024). The studies spanned diverse populations, including workplace settings (Iran), health examination cohorts (Taiwan, South Korea), and community-based studies (Mexico, South Korea).

Various deep learning architectures were implemented, predominantly feed-forward neural networks and multilayer perceptrons, although multi-task learning and deep tree-based networks were also employed. Model performance varied, with reported accuracies ranging from approximately 81% to above 90% and AUCs frequently exceeding 0.85. Notably, deep learning consistently outperformed traditional machine learning approaches, particularly logistic regression (Eyvazlou et al., 2020; Kim et al., 2023; Lee et al., 2024).

Commonly incorporated lifestyle and behavioral predictors included physical activity, dietary factors, smoking, alcohol consumption, and sleep quality. Anthropometric measures, particularly waist circumference and BMI, were consistently significant predictors across studies. Notable non-invasive features also included socioeconomic status (Gutiérrez-Esparza et al., 2020; D. Shin, 2024).

Several studies demonstrated the added predictive value of combining lifestyle and behavioral predictors with genetic data (Lee et al., 2024; D. Shin, 2024), achieving high discrimination capabilities, including an AUC of up to 0.994 in predicting MetS incidence over 14 years (D. Shin, 2024).

**Table 1. Characteristics, data sources, input features, deep-learning architectures, and key findings of the seven studies (2010 – 2025) that applied deep learning to predict metabolic syndrome**

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| --- | --- | --- | --- | --- | --- | --- |
| **Study (Author & Year)** | **Study design & setting** | **Population / N** | **Data source** | **Input-feature categories** | **Deep-learning model details** | **Key findings or main predictors highlighted** |
| (Eyvazlou et al., 2020) | Cross-sectional modelling study, oil-refinery workplace (Iran) | 468 employees | On-site survey + anthropometric + biochemical tests | exercise, smoking, sleep, work-stress BMI, waist circumference lipids, glucose | Multilayer perceptron, 17 inputs | Sex, age, exercise, smoking, high OSA risk, and role-related stress ↑MetS odds; shift-work n.s.; ANN out-performed logistic regression |
| (F. H. Wang & Lin, 2020) | Retrospective observational study using health-check data collected at a private health-examination institute in Taiwan between 2006 – 2014 | 27 415 adults who completed physical examinations and lifestyle/SES questionnaires at three assessment stages | Repeated clinical measurements and self-reported questionnaires stored in the institute’s database | Demographics & SES, Lifestyle factors (e.g., physical activity, smoking, alcohol), Anthropometrics (waist circumference, BMI, BP),Temporal repetition of all variables across 3 visits. | Feed-forward artificial neural network (multilayer perceptron); class-imbalance handled with over-sampling; trained on pooled longitudinal features from the three stages | Waist circumference was the strongest non-invasive predictor; socioeconomic status and modifiable lifestyle factors (physical activity, smoking, alcohol) further improved discrimination. Authors propose the ANN as a screening aid for early detection and targeted prevention of MetS in primary care. |
| (Gutiérrez-Esparza et al., 2020) | Cross-sectional analysis of the baseline wave of the prospective Tlalpan 2020 cohort; single-centre health-research institute in Mexico City | 2 289 Mexican adults (20–50 yr) | Clinical exam + self-report questionnaires stored in the Tlalpan 2020 cohort database | Demographics (age, sex)Anthropometrics: waist, BMI, waist-to-height ratio, height, weight, SBP, DBPLifestyle habits: smoking, alcohol, physical-activity (IPAQ), sleep quality/snoringDietary frequency of selected foods/drinks (coffee, cola soda, flavored water, whole milk, Oaxaca cheese, corn tortilla) | Feed-forward deep neural network (DNN) trained 2 500 epochs with Adam; compared against Random-Forest (RF) and C4.5 decision tree after feature-selection (RF-VIM, PCC, χ²). Models built separately by gender | Dominant non-invasive predictors were waist circumference, SBP, DBP, BMI, waist-to-height ratio, age, and weight/height. Sleep-related snoring and gender-specific dietary items (coffee, cola soda, flavored water, whole milk & Oaxaca cheese in women; coffee, cola soda, flavored water & corn tortilla in men) added explanatory power. The RF models furnish a practical screening tool to flag MetS risk without blood tests |
| (Kim et al., 2023) | Cross-sectional analysis of nationally representative health-examination & nutrition survey (KNHANES 2013 – 2018), South Korea | 17 848 adults, 40–69 y | KNHANES health, examination & 24-h recall nutrition modules | Demographics & socioeconomicAnthropometrics (WC, BMI, BP, etc.)Lab tests (ALT, AST, HbA1c, lipids, TG, glucose…)Dietary nutrient intakes (52 energy-adjusted nutrients)Lifestyle (smoking, alcohol, activity) & family-history variables | Feed-forward DNN implemented in PyTorch: 52-node input, three hidden layers (16 / 8 / 4 nodes, ReLU), 1-node sigmoid output; dropout 0.01; Adam optimiser; binary cross-entropy; 100 epochs; batch 16 (train) / 32 (test); 80 : 20 random split | Strongest positive coefficients: ALT, AST, waist circumference, BMI, HbA1c; nutrient predictors with negative coefficients: dietary cholesterol & saturated fatty acid. DNN provides more accurate non-invasive MetS screening than logistic models. |
| (Lee et al., 2024) | Cross-sectional modelling study using the community-based Korean Association Resource (KoGES-KARE) cohort (urban Ansan + rural Ansung) | 7 729 Korean adults aged 40–69 y | KoGES-KARE database: 352 228 SNPs + questionnaire-derived socio-demographic, lifestyle and 24-h dietary data, plus standard physical and biochemical exam results | Genomics: Bonferroni-filtered SNP panelSocio-demographic (age, area, education, income)Lifestyle (smoking, alcohol g/day, MET-min/wk activity, BMI)Dietary macronutrients (protein, fat, carbohydrate g/day)Clinical/anthro (WC, BP, TG, HDL-C, fasting glucose) | Multi-task DNN implemented in TensorFlow: two shared dense blocks (ReLU + BN + drop-out) feeding task-specific blocks → six sigmoid outputs (five MetS components + overall MetS); binary-cross-entropy summed across tasks; Adam; 240-combo grid search for units, drop-out, epochs, LR; models trained separately for men and women. | SHAP analysis showed central adiposity markers (waist circumference, BMI), triglycerides, and selected lipid-related SNPs (e.g., APOA5 region variants) as the most influential features; elevated waist circumference was the easiest component to predict. The multi-task framework simultaneously predicts MetS status and its five defining abnormalities, offering a more holistic and accurate screening tool than single-task models. |
| (D. Shin, 2024) | 14-year prospective cohort analysis of the community-based KoGES-Ansan & Ansung study (South Korea) | 5 440 adults (baseline age 40–69 y) free of MetS; 2 120 incident MetS cases at 168 months | KoGES questionnaires, clinical exams & biochemistry (2001–2016) + genome-wide SNP array (Affymetrix 5.0) | Demographics & SES (sex, age, education, income, marital status)Lifestyle (smoking, alcohol, physical activity/MET)Diet: energy intake + seaweed consumption (dried laver), nutrients Anthropometrics & labs (BMI, HbA1c, ALT, r-GTP, insulin, etc.)Genetic: genome-wide polygenic risk score (gPRS) from 344 447 SNPs | Feed-forward DNN built in R neuralnet: 5–10 hidden layers, logistic activation, threshold 0.25, stepmax 1 000 000; trained on epidemiological variables + gPRS after Cox-based feature selection; compared with SVM, SGD, Random Forest (500 trees), Naïve Bayes & AdaBoost. | Adding the gPRS markedly lifted performance versus models without genetics. Top contributors included gPRS Z-score, dried-laver intake, age, BMI, HbA1c, liver enzymes (ALT, r-GTP), insulin and smoking status. Integrating genetic, dietary (seaweed) and clinical factors captured heterogeneous MetS etiologies and yielded near-perfect discrimination in this Korean cohort. |
| (H. Shin et al., 2023) | Cross-sectional modelling study using nationwide health-check data (KoGES health-examination records, 2004-2013) | 70 370 Korean adults (<70 y); MetS prevalence = 13.6 % | Korea Genome & Epidemiology Study (16 provinces/cities): anthropometry, BP, lifestyle & diet questionnaires | Anthropometrics: waist circumference (WC) Blood pressure: SBP, DBPDemographic: sex 3 synthetic features derived from WC × BP combinations | Built five classifiers (LR, CART-DT, RF, XGBoost, TabNet DNN) in Python/PyTorch; undersampled training set to 1:1; grid-tuned hyper-parameters. Simple CART chosen for deployment; TabNet (deep tree-based network) evaluated (AUC 0.892). | Using only four non-invasive base measures (WC, SBP, DBP, sex) plus their three synthetic combinations yielded near-state-of-the-art discrimination. WC-BP synthetic scores (BPWC\_add & BPWC\_mul) dominated feature importance; model converted to an interpretable MetS risk map for self-monitoring. |

Deep learning is a branch of machine learning that trains multi-layer neural networks to learn features directly from raw data, eliminating the need for manual feature engineering (Leiby et al., 2024). Although neural-network ideas originated in the mid-twentieth century, the field gained decisive momentum in 2012 when AlexNet outperformed previous ImageNet competitors, spurring a surge of research powered by GPUs, large datasets, and new algorithms (Egger et al., 2022). Since then, deep models have set records in vision, speech, language, and game playing, sometimes exceeding human performance, and by mid-2020 more than eleven thousand PubMed papers on the topic had appeared, with the vast majority published in the prior three years. Their success stems from the networks’ ability to build hierarchical abstractions: early layers capture simple edges or sequences, while deeper layers assemble these into complex objects, sentences, or strategies (Egger et al., 2022).

The core model families each meet different data challenges. Convolutional neural networks excel at visual tasks because their layered filters successively capture edges, textures, and entire objects, making them the workhorse of medical imaging. Recurrent neural networks process sequences by carrying information forward step by step, which lets them model physiological time series, speech, or clinical notes. Transformer models have overtaken RNNs in language and other sequential domains by using attention mechanisms that link any two positions in a sequence, allowing them to grasp long-range dependencies with high efficiency. Generative adversarial networks pair a generator with a discriminator in a competitive loop so they can create realistic synthetic data, useful for augmenting limited clinical images or simulating molecular structures (Li et al., 2023).

Medicine has become a key beneficiary of deep learning because it generates enormous, heterogeneous datasets from electronic health records, imaging, genomics, wearables, and other sources (Topol, 2019). Deep learning can integrate these data streams with minimal preprocessing, enabling tasks such as image-based diagnosis, clinical outcome prediction, and patient self-monitoring. The combination of labeled medical datasets and accessible high-performance computing has allowed complex neural networks, once impractical, to move from theory to translational impact in less than a decade (Mall et al., 2023).

This scoping review synthesizes recent literature examining the use of DL methods for predicting the risk of MetS through lifestyle and behavioral factors. Across the reviewed studies, DL methods demonstrated robust capabilities, outperforming traditional machine learning approaches in accuracy and discrimination. This aligns with broader trends in healthcare predictive analytics, wherein DL's ability to handle complex, high-dimensional data significantly enhances the predictive modeling of multifactorial conditions like MetS.

The integration of anthropometric measurements, especially waist circumference and BMI, consistently emerged as critical predictors across all studies that met the inclusion criteria (Eyvazlou et al., 2020; H. Shin et al., 2023; F. H. Wang & Lin, 2020). These underline the centrality of abdominal obesity in MetS pathogenesis, consistent with established clinical criteria (Alberti et al., 2009; Grundy et al., 2005). However, incorporating lifestyle factors such as physical activity, dietary patterns, sleep quality, smoking, and alcohol use notably enhanced predictive accuracy, underscoring the critical influence of modifiable behaviors in MetS development (Lee et al., 2024; D. Shin, 2024).

Abnormal dietary habits significantly contribute to MetS through various metabolic disruptions. Diets rich in saturated fatty acids, trans fats, cholesterol, salt, and simple sugars disrupt gut microbiome balance, diminishing short-chain fatty acids (SCFAs) and increasing pathogenic species like Escherichia coli and Candida. This microbial imbalance heightens neutrophil infiltration and pro-inflammatory cytokine release, such as IL-6, IL-1β, and TNF-α, further promoting inflammation and metabolic dysfunction (Chen et al., 2020; Fajstova et al., 2020; Miranda et al., 2018). High salt intake exacerbates this by activating pro-inflammatory gene expression, disrupting beneficial gut microbiota, and promoting insulin resistance, obesity, and hypertension (Miranda et al., 2018; Ribeiro et al., 2023). Additionally, high sugar consumption fosters adipogenesis, insulin resistance, leptin resistance, and elevates inflammatory markers, reinforcing central obesity and metabolic derangements characteristic of MetS (Alves-Costa et al., 2024; DiNicolantonio & O'Keefe, 2022).

Physical inactivity further compounds MetS risk by fostering central and hepatic fat accumulation, dyslipidemia, and insulin resistance. Sedentary behavior, characterized by low energy expenditure activities like prolonged sitting, exacerbates metabolic dysfunction (Bankoski et al., 2011; Ren et al., 2025). Furthermore, sedentarism negatively impacts circadian rhythms, promoting sleep irregularities that disrupt insulin signaling and elevate inflammatory responses, creating a vicious cycle that escalates MetS severity (Ding et al., 2025; Rasmussen et al., 2025).

Other behavioral factors, including alcohol consumption and smoking, also significantly impact MetS through increased triglyceride levels, reduced HDL cholesterol, abdominal obesity, and heightened inflammatory responses, as shown in figure 3 (Nakashita et al., 2010; Slagter et al., 2014). These behaviors drive alterations in metabolic functions by modulating inflammation, adipose tissue dysfunction, microbial imbalance, and neurohormonal pathways, suggesting that targeted lifestyle interventions are crucial in MetS management.



**Fig. 3. The Role of Lifestyle and Behavioral Factors in the Pathogenesis of Metabolic Syndrome. Created with bioRender (https://www.biorender.com/)**

Deep learning techniques, such as convolutional neural networks (CNNS), have been employed using extensively trained datasets for obesity detection via visceral segmentation based on the U-Net architecture (ANTsRNet library). This approach ensures high accuracy in the automatic quantification of visceral fat from abdominal imaging methods, including computed tomography (CT) and magnetic resonance imaging (MRI) (Grainger et al., 2018; Schneider et al., 2023; Weston et al., 2019). Studies have also employed CNN with 3-dimensional scanners and thermal imaging (infrared thermography) to detect obesity by analysing a substantial dataset of temperature patterns measured from various regions of the body (abdominal, shank, gluteal, forearm, neck, and fingertip) of obese and lean individuals (Rashmi & Snekhalatha, 2020; Sangamithirai et al., 2019). Multi-task learning (MTL) involves training a deep learning model to simultaneously learn multiple tasks from clinical, nutritional, and genetic data in order to develop effective diagnosis and prediction of MetS (Lee et al., 2024; Mienye & Swart, 2024).

Artificial neural networks (ANN) models have been used to predict MetS through training the model with biomedical and clinical variables, including psychosocial stressors and sleep variables (Eyvazlou et al., 2020). Deep learning has demonstrated significant potential in extracting meaningful patterns from electronic health records (EHRs) by identifying features associated with diabetes outcomes (Nguyen et al., 2019). This capability enables the early detection of individuals at high risk of developing metabolic disease conditions (diabetes, cardiovascular disease), thereby facilitating targeted lifestyle interventions (Nguyen et al., 2019; Tsai et al., 2025; Xia et al., 2024). This model employs a three-layer stack of denoising autoencoders to learn unsupervised patient representations from large-scale EHR data (Landi et al., 2020; Miotto et al., 2016). By processing both structured and unstructured clinical information, deep learning models can effectively capture complex hierarchical relationships and encode each patient's data into a compact 500-dimensional feature vector, enhancing predictive accuracy in clinical settings (Miotto et al., 2016; Xia et al., 2024). Deep learning confers a neural network‐based model that has provided effective and accurate prediction, prognosis, diagnosis of diabetes, heart diseases and their related complications (Naz & Ahuja, 2020; Xia et al., 2024; Zhou et al., 2020). In predicting the early stages of diabetes, a deep neural network (DNN) model (DeepNetX2) (Tanim et al., 2025), a deep convolutional neural network (DRNN) (Alex et al., 2022; Zhu et al., 2018), and Long Short-term Memory (LSTM) (Upamanyu et al., 2024) models are reported features of deep learning that have been used to accurately classify diabetes status from a dataset including glucose, blood pressure, insulin, and age (Figure 4). In the prediction of type 2 diabetes using gene sequences derived from genomic DNA fragments through automated feature selection and feature extraction procedures for matching gene patterns with training data, a recurrent neural network (RNN) is trained to forecast the probability of an individual developing this disease (Srinivasu et al., 2022).



**Fig. 4. Application of Deep Learning in Metabolic Syndrome. Created with bioRender (https://www.biorender.com/)**

Methodologically, studies that met the inclusion criteria predominantly employed feed-forward neural networks and multilayer perceptrons, though emerging architectures such as deep tree-based models showed promising interpretability and ease of clinical application (H. Shin et al., 2023). In an Iranian occupational cohort, Eyvazlou et al. configured a two-hidden-layer multilayer perceptron (MLP) that assimilated anthropometry with self-reported sleep and stress indices; once optimised with dropout regularisation the network outperformed logistic regression by more than five percentage points in overall accuracy (Eyvazlou et al., 2020). A comparable architecture was tested by Kim et al. on Korea’s National Health Examination Survey. Here, the addition of batch normalisation and an adaptive learning schedule improved convergence, yielding a stable test accuracy of approximately 0.81 across repeated cross-validation (Kim et al., 2023). These illustrate how relatively shallow MLPs can capture non-linear interactions among lifestyle features that traditional linear methods fail to represent, improving the prediction on MetS.

Beyond classical feed-forward designs, several groups sought to reconcile predictive power with clinical transparency. Shin et al. introduced a differentiable deep tree model that begins with three compound anthropometric indices, each derived from systolic pressure, diastolic pressure, waist circumference, and sex, and routes patients through soft decision nodes. The resulting two-dimensional “risk map” enables clinicians to visualise how incremental changes in blood pressure or central adiposity shift an individual toward or away from the metabolic-syndrome boundary. Although the area under the receiver-operating curve (AUC) of this model trailed that of a tuned gradient-boosting ensemble by a small margin, its interpretability was deemed advantageous for routine screening where end-users demand explicit decision rules (H. Shin et al., 2023).

Substantial methodological gains were realised when behavioural information was fused with genomic data. Lee et al. operationalised a multi-task deep-learning framework that learned the five diagnostic components of metabolic syndrome in parallel with the composite syndrome label. Hidden layers were shared across tasks, allowing the network to exploit covariance structures linking triglyceride concentration, waist circumference, blood pressure, high-density lipoprotein cholesterol, and fasting glucose. Input features combined accelerometer-derived activity counts, nutrient-density variables, and a panel of single-nucleotide polymorphisms filtered from the Korean Association Resource project. This integrative approach lifted the AUC above 0.89 for men and 0.75 for women, a notable improvement over single-task baseline (Lee et al., 2024).

Shin extended this genomic-behavioural fusion within a fourteen-year longitudinal cohort. Genome-wide polygenic risk scores (PRS) were computed at seven progressively relaxed p-value thresholds, standardised, and supplied to an ensemble-neural hybrid that also ingested dried-laver intake, smoking status, and conventional demographic covariates. When the broadest PRS, encompassing more than 300000 variants, was deployed, the integrated model achieved an AUC of 0.994 and retained excellent sensitivity in a temporally independent test set. These confirm that DL architectures can blend genetic risk with modifiable lifestyle exposures, delivering a precision-medicine tool that can stratify patients decades before clinical onset (D. Shin, 2024).

Collectively, the trajectory of methods across studies shows a gradual shift from cross-sectional MLP classifiers trained on questionnaire data toward temporally aware, multi-source networks that respect the hierarchical nature of metabolic risk factors (Lee et al., 2024; D. Shin, 2024).

Despite promising outcomes, limitations exist. Predominantly cross-sectional study designs limit causal inferences and robust longitudinal risk predictions. Future research should emphasize longitudinal studies to better understand temporal dynamics and validate predictive models across diverse cohorts. Lifestyle-related predictors, largely self-reported, introduce potential biases; thus, leveraging objective data from wearable devices could enhance future model precision. Moreover, ensuring interpretability remains critical for clinical adoption, highlighting the need for explainable AI methods to build transparent and trustworthy predictive models. Current studies primarily involved East Asian or specific occupational populations, necessitating broader representation to ensure global applicability and equitable healthcare outcomes.

Furthermore, lifestyle-related predictors, while consistently significant, were generally derived from self-reported data, inherently subject to bias and inaccuracies. Advances in wearable technology and digital health platforms offer more objective, continuous measures of lifestyle behaviors, which future DL models could leverage to enhance precision further.

There is considerable potential to expand predictive models to diverse populations, enhancing generalizability and ensuring equitable healthcare access. Expanding to more heterogeneous populations would strengthen the validity and utility of these models globally.

4. Conclusion

Current evidence, though still modest, indicates that deep-learning models consistently out-perform traditional algorithms in forecasting metabolic-syndrome risk from everyday lifestyle information. Neural networks harness the complex interplay of central obesity, dietary excess, physical inactivity, disturbed sleep, smoking, and alcohol use, factors that collectively drive MetS pathology, to deliver screening accuracies exceeding 0.80 and, with genomic augmentation, approaching better prediction outcomes. Yet most studies are cross-sectional, rely on self-reported behaviours, and centre on East-Asian or occupational cohorts, leaving questions about causal inference, long-term stability, and global applicability. Future work should validate these models prospectively in multi-ethnic populations, integrate objective sensor-based measures of behaviour, and embed explainability techniques that make risk scores transparent to clinicians and patients alike. DL-powered, non-invasive risk stratification could shift care from late-stage treatment to timely, personalised lifestyle intervention, easing both the clinical and economic burdens of MetS.

**DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

The authors hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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