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MOLECULAR-NET: Graph-Based Representation of Molecular Networks and Interactions

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Abstract

Complex molecular systems contain multiple structural and interaction patterns that are difficult to interpret using conventional descriptive approaches. This study proposes MOLECULAR-NET, a graph-based framework for representing molecular networks and interactions within the scope of chemical graph theory. In the proposed model, molecular entities, atoms, functional groups, or interaction sites are treated as vertices, while chemical bonds, associations, or interaction pathways are represented as edges. The study aims to explore how graph parameters such as degree, connectivity, distance, clustering, centrality, and topological indices can support the visualization and analysis of complex molecular relationships. Through literature review and network-based analysis, the paper highlights the relevance of graph modeling in identifying hidden structural patterns, interaction strength, and relational behavior in molecular systems. The proposed approach is applicable to systems chemistry and bioinformatics, offering a mathematical basis for molecular interpretation, comparison, and future computational prediction studies and broader graph-oriented chemical data analysis applications.

Keywords: Chemical graph theory, molecular network, graph modeling, topological indices

1. Introduction

Chemical graph theory has emerged as an important mathematical approach for representing molecular structures through graph-based models, where atoms, bonds, functional groups, and interaction sites can be interpreted as vertices and edges [1]. This representation allows complex chemical systems to be studied using discrete mathematical tools rather than relying only on conventional structural descriptions [2]. In molecular graph models, the connectivity pattern of a molecule provides valuable information about its stability, reactivity, similarity, and interaction behaviour [3], [4]. Therefore, graph-based molecular representation provides a useful mathematical foundation for studying complex chemical structures.

In recent years, molecular networks have gained attention in systems chemistry, cheminformatics, bioinformatics, and computational molecular analysis [5]. Molecular interactions are often not isolated events, as they form interconnected networks involving multiple chemical entities, pathways, bonds, and association patterns [6]. Traditional visualization methods may not fully reveal hidden molecular relationships, especially when the interaction network contains many nodes and edges [7]. Graph theory provides useful measures such as degree, connectivity, shortest path, clustering coefficient, centrality, and distance-based indices to understand molecular network behaviour [8]. These graph parameters help researchers examine molecular systems beyond simple structural visualization.

The study of molecular networks through graph modeling is particularly relevant because many chemical and biological behaviours depend on interaction patterns rather than individual molecular units alone [9], [10]. Molecular recognition, reaction pathways, protein-ligand association, drug-target interaction, and biochemical signalling can be better understood when the system is represented as a network [11], [12]. In this context, chemical graph theory supports both qualitative visualization and quantitative analysis by converting molecular information into mathematical structures [13], [14]. Hence, graph modeling supports both theoretical interpretation and applied analysis of molecular interactions.

Although graph-based molecular analysis has developed significantly, complex molecular interactions remain difficult to visualize, compare, and interpret in a unified manner [15], [16]. Many existing approaches focus either on individual molecular graphs or on computational prediction models, while less attention is given to a structured framework that combines chemical graph theory with molecular network analysis [17], [18]. This creates a need for a graph-oriented model that can represent molecular entities and their interactions clearly while also allowing mathematical analysis through topological and network-based parameters [19], [20]. Addressing this gap can improve the interpretation of molecular systems in both theoretical and applied chemical research.

Therefore, the present study proposes MOLECULAR-NET: Graph-Based Representation of Molecular Networks and Interactions as a conceptual and analytical framework for understanding molecular systems through graph models. The objective of the study is to explore how molecular interaction networks can be represented, visualized, and analyzed using graph-theoretic concepts. The proposed approach is based on literature review and network analysis, with emphasis on molecular network construction, graph parameters, topological indices, and interaction interpretation. The study is expected to contribute to chemical graph theory by providing a mathematical basis for analyzing complex molecular relationships and supporting future applications in systems chemistry, bioinformatics, cheminformatics, and molecular data analysis.

1.1 Contributions

The novel contributions of this study are:

- The study proposes MOLECULAR-NET as a graph-based framework for representing molecular networks and interactions.
- The study applies graph parameters such as degree, connectivity, centrality, clustering, and topological indices to analyze molecular relationships.
- The study supports the visualization and interpretation of hidden molecular patterns for applications in systems chemistry and bioinformatics.

2. Literature Review

This section deals with existing studies on chemical graph theory, molecular graph representation, and graph-based analysis of molecular networks and interactions. Table 1 shows summary of research gaps.

Rottach et al. (2025) [21] analyzed the topology of molecular representations and showed that representation structure strongly influences the performance and interpretation of machine learning models in chemical prediction tasks.

Chen et al. (2025) [22] introduced knowledge-aware contrastive heterogeneous molecular graph learning and represented molecules through molecular, elemental, and pharmacological graph views to improve molecular property and interaction analysis.

Hakeem et al. (2025) [23] applied topological modeling and QSPR prediction to bioactive polyphenols and demonstrated that graph-based molecular descriptors can effectively represent physicochemical properties.

Sorgun and Ullah (2025) [24] developed a Python-based vertex-edge-weighted molecular graph framework and showed that weighted molecular graph models improve QSPR analysis of cardiovascular and diabetes drug molecules.

Zhang et al. (2025) [25] investigated tricyclic graphs using the inverse sum indeg index and demonstrated the relevance of topological index analysis for octane isomers and benzenoid hydrocarbons.

Ahmed et al. (2025) [26] examined bone cancer drug molecules through topological indices and machine learning, showing that neighborhood degree-based graph descriptors support molecular property prediction.

Pradeepa and Arathi (2025) [27] studied degree-based topological indices for QSPR/QSAR modelling of cardiovascular antihypertensive agents and confirmed the importance of graph descriptors in pharmaceutical molecular analysis.

Fazal et al. (2025) [28] explored entropy measures with topological indices for colorectal cancer drugs and showed that graph-based descriptors can be linked with physical properties through regression and machine learning approaches.

Akhbari et al. (2026) [29] developed a QSPR model for Alzheimer's drugs using topological indices and M-polynomial, highlighting the role of degree-based descriptors in computational molecular interpretation.

Mufti et al. (2026) [30] conducted QSAR analysis of drugs using graph-based degree-based topological indices and regression models, confirming the usefulness of chemical graph theory in molecular property analysis.

Table 1. Summary of Research Gaps

Ref.	Authors	Main Focus of the Study	Identified Research Gap
[21]	Rottach et al. (2025)	Analyzed the topology of molecular representations and its influence on machine learning performance.	Limited focus on a unified graph-based framework for molecular network visualization and interpretation.
[22]	Chen et al. (2025)	Developed knowledge-aware heterogeneous molecular graph learning for molecular property and interaction analysis.	More clarity is needed in connecting multiple molecular graph views with chemical graph theory concepts.
[23]	Hakeem et al. (2025)	Applied topological modeling and QSPR prediction to bioactive polyphenols.	Limited application of topological descriptors to broader molecular interaction network representation.
[24]	Sorgun and Ullah (2025)	Proposed a vertex-edge-weighted molecular graph framework for QSPR analysis.	Further work is needed to simplify weighted graph models for general molecular network interpretation.
[25]	Zhang et al. (2025)	Studied tricyclic graphs using the inverse sum indeg index for chemical applications.	The study focuses mainly on specific graph classes and needs extension to complete molecular network systems.
[26]	Ahmed et al. (2025)	Predicted bone cancer drug properties using topological indices and machine learning.	Computational prediction is emphasized more than transparent graph-based relationship visualization.
[27]	Pradeepa and Arathi (2025)	Used degree-based topological indices for QSPR/QSAR modelling of antihypertensive agents.	Limited focus is given to hidden molecular pathways, central nodes, and clustered interaction regions.
[28]	Fazal et al. (2025)	Explored entropy measures and topological indices for colorectal cancer drugs.	The integration of entropy, topology, and molecular network-level visualization remains limited.
[29]	Akhbari et al. (2026)	Developed a QSPR model for Alzheimer's drugs using topological indices and M-polynomial.	The study focuses on drug property modelling rather than a general molecular network interpretation framework.
[30]	Mufti et al. (2026)	Conducted QSAR analysis of drugs using graph-based degree-based topological indices and regression models.	Existing analysis remains prediction-oriented and needs stronger emphasis on graph-based molecular interaction patterns.

2.1 Research Gaps

The reviewed studies show that chemical graph theory, molecular graph representation, topological indices, molecular dynamics networks, and graph learning models have been widely applied to molecular analysis. However, most existing studies focus either on individual molecular structures, topological descriptors, molecular property prediction, or computational graph learning, while limited attention is given to a simple and unified framework for representing complete molecular networks and interactions. There is also a gap in connecting chemical graph theory with practical molecular network visualization, where atoms, bonds,

functional groups, and interaction pathways can be analyzed together using graph parameters such as degree, connectivity, centrality, clustering, shortest path, and topological indices. Therefore, the present study addresses this gap by proposing MOLECULAR-NET as a graph-based framework for representing, visualizing, and interpreting complex molecular relationships.

2.2 Problem Statement

Complex molecular interactions are difficult to visualize and analyze because they involve multiple atoms, bonds, functional groups, pathways, and interaction patterns within a single molecular system. Existing studies in chemical graph theory and molecular representation provide useful topological descriptors and computational models, but they often focus on individual molecular structures or prediction-based analysis rather than a unified network-level interpretation. As a result, hidden molecular relationships, influential nodes, strong interaction pathways, and structural clusters may not be clearly identified. Therefore, there is a need for a graph-based framework that can represent molecular networks and interactions in a simple, structured, and mathematically interpretable form.

3. Research Objectives

The novel objectives of this study are:

- To develop MOLECULAR-NET as a graph-based framework for representing molecular networks and interactions.
- To analyze molecular relationships using graph parameters such as degree, connectivity, centrality, clustering, and topological indices.
- To support the visualization and interpretation of hidden molecular interaction patterns in systems chemistry and bioinformatics.

4. Proposed Methodology

The proposed methodology is designed as a review-based analytical and graph-modeling approach. It uses existing studies as the foundation for constructing the MOLECULAR-NET framework and then applies graph-theoretic measures to represent, analyze, and interpret molecular networks and interactions. The methodology is organized into eight stages, beginning with research design and literature selection and ending with visualization and interpretation of molecular interaction patterns.

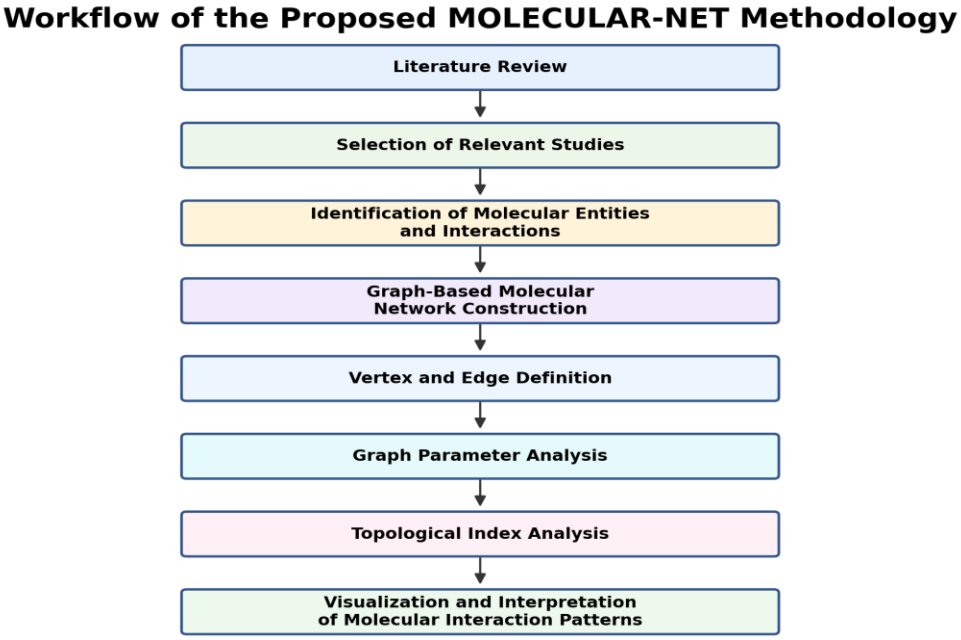

Figure 1. Workflow of the proposed methodology (MOLECULAR-NET)

Figure 1 presents the workflow of the proposed MOLECULAR-NET methodology for graph-based representation and analysis of molecular networks and interactions. The process begins with a literature review of studies related to chemical graph theory, molecular networks, graph parameters, and topological indices. Relevant molecular entities and interactions are then identified, followed by graph-based molecular network construction. In this framework, vertices represent atoms, functional groups, or molecular entities, while edges represent bonds, associations, or interaction pathways. The constructed network is analyzed using graph parameters such as degree, connectivity, centrality, clustering coefficient, and shortest path, followed by topological index analysis. Finally, the results are used to visualize and interpret hidden molecular interaction patterns.

4.1 Research Design

This study follows a review-based analytical research design with a proposed graph-theoretic framework. It is not limited to a conventional literature review; instead, it develops MOLECULAR-NET as a structured model for representing molecular networks and interactions. In this framework, a molecular system is converted into a mathematical graph, where vertices represent molecular entities and edges represent bonds, associations, or interaction pathways. The general molecular network is defined as:

$$G_m = (V, E, w) \quad (1)$$

where G_m denotes the molecular graph, V denotes the set of vertices, E denotes the set of edges, and w denotes the weight function assigned to the interaction strength or relational importance of each edge. This design helps in converting complex molecular relationships into a measurable and interpretable graph structure.

4.2 Data Sources and Literature Selection

The data source for this study is secondary literature related to chemical graph theory, molecular graph representation, molecular networks, graph parameters, topological indices, systems chemistry, cheminformatics, and bioinformatics. Relevant studies are selected from standard scientific databases and publisher platforms such as Scopus, ScienceDirect, SpringerLink, Wiley Online Library, MDPI, Hindawi, PubMed, and Google Scholar. The selected studies are screened based on relevance to molecular networks, graph modeling, topological descriptors, and interaction analysis. The literature set can be represented as:

$$L = \{l_1, l_2, l_3, \ldots, l_n\} \quad (2)$$

where L represents the set of selected studies and l_i represents each individual study included for methodological review and framework development. Studies that do not focus on graph theory, molecular representation, molecular interactions, or network analysis are excluded from the review base.

4.3 Molecular Entity Identification

In this stage, molecular entities and interaction components are identified from the selected literature and conceptual molecular systems. The molecular entities may include atoms, functional groups, molecular substructures, molecules, proteins, ligands, or interaction sites depending on the application area. These entities are mapped into graph vertices using a transformation function. The mapping process is expressed as:

$$\varphi : M \rightarrow V \quad (3)$$

where M represents the set of molecular entities and V represents the corresponding set of graph vertices. Similarly, molecular interactions such as bonds, associations, reaction pathways, or biochemical links are mapped into graph edges as:

$$\psi : I \rightarrow E \quad (4)$$

where I represents the set of molecular interactions and E represents the corresponding set of graph edges. This step provides the basic foundation for converting molecular information into graph-based network form.

4.4 Graph-Based Network Construction

After identifying molecular entities and interactions, the molecular network is constructed as a graph. Each vertex denotes a molecular component, and each edge denotes an interaction between two components. The

graph may be undirected when the interaction is mutual, directed when the interaction has direction, and weighted when interaction strength is considered. The adjacency matrix of the molecular network is defined as:

$A = [a_{ij}],\ a_{ij} = 1 \text{ if } (v_i, v_j) \in E; 0 \text{ otherwise}$ (5)

where A is the adjacency matrix and a_{ij} indicates whether an interaction exists between vertex v_i and vertex v_j. For weighted molecular networks, the edge weight is defined as:

$w_{ij} = f(v_i, v_j)$ (6)

where w_{ij} represents the strength, frequency, stability, or importance of the interaction between two molecular entities. This construction allows molecular systems to be analyzed using standard graph-theoretic tools.

4.5 Vertex and Edge Definition

The vertex set and edge set are formally defined to maintain consistency in the MOLECULAR-NET framework. Vertices may be classified as atom vertices, functional group vertices, or molecular entity vertices. Edges may be classified as bond edges, association edges, or pathway edges. The complete vertex and edge sets are represented as:

$V = V_a \cup V^f \cup V_m$ (7)

$E = E^b \cup E^a \cup E^p$ (8)

where V_a represents atom vertices, V^f represents functional group vertices, V_m represents molecular entity vertices, E^b represents bond edges, E^a represents association edges, and E^p represents pathway edges. This classification helps the model represent different levels of molecular structure and interaction.

4.6 Graph Parameter Analysis

The constructed molecular graph is analyzed using graph parameters that describe the structural and relational properties of the network. The degree of a vertex measures the number of direct connections associated with a molecular entity and is defined as:

$d(v_i) = \Sigma_{j=1}^{n} a_{ij}$ (9)

The density of the molecular network shows how strongly the molecular entities are interconnected and is expressed as:

$\rho(G_m) = 2|E| / \{|V|(|V| - 1)\}$ (10)

Degree centrality identifies highly connected molecular entities and is defined as:

$C^D(v_i) = d(v_i) / (n - 1)$ (11)

Closeness centrality measures how close one molecular entity is to all other entities in the network and is expressed as:

$C^c(v_i) = (n - 1) / \Sigma_{j \neq i} \text{dist}(v_i, v_j)$ (12)

Betweenness centrality identifies molecular entities that act as bridges between interaction pathways and is defined as:

$C^B(v_i) = \Sigma_{s \neq i \neq t} \sigma_{st}(v_i) / \sigma_{st}$ (13)

The clustering coefficient measures the local grouping tendency of molecular entities and is expressed as:

$C_i = 2e_i / \{k_i(k_i - 1)\}$ (14)

where $d(v_i)$ is the degree of vertex v_i, $\text{dist}(v_i, v_j)$ is the shortest distance between two vertices, σ_{st} is the total number of shortest paths from s to t, $\sigma_{st}(v_i)$ is the number of shortest paths passing through v_i, e_i is the number of links among neighbouring vertices, and k_i is the degree of vertex v_i. These parameters help identify influential nodes, strong interaction regions, and hidden molecular relationship patterns.

4.7 Topological Index Analysis

Topological indices are used to describe the structural properties of molecular graphs in numerical form. These indices help compare molecular networks, identify structural patterns, and support chemical interpretation. The Wiener index is used to measure distance-based structural information and is defined as:

$$W(G_m) = 1/2 \sum_{i=1}^{n} \sum_{j=1}^{n} dist(v_i, v_j) \quad (15)$$

The Randić index is used to describe branching and connectivity properties of molecular graphs and is expressed as:

$$R(G_m) = \sum_{vivj \in E} 1 / \sqrt{(d_i d_j)} \quad (16)$$

The first and second Zagreb indices are degree-based topological descriptors and are given as:

$$M_1(G_m) = \sum_{i=1}^{n} d_i^2 \quad (17)$$

$$M_2(G_m) = \sum_{vivj \in E} d_i d_j \quad (18)$$

where $W(G_m)$ represents the Wiener index, $R(G_m)$ represents the Randić index, and $M_1(G_m)$ and $M_2(G_m)$ represent the first and second Zagreb indices. These indices provide a mathematical basis for interpreting molecular structure, connectivity, branching, and interaction complexity.

4.8 Visualization and Interpretation

In the final stage, the constructed graph and computed parameters are used to visualize and interpret molecular interaction patterns. Vertices with high degree or centrality are interpreted as influential molecular entities, while highly clustered regions indicate possible functional groups, active interaction zones, or structural communities. The overall molecular network interpretation score can be expressed as a normalized weighted form:

$$S_m = \alpha C^D + \beta C^c + \gamma C^B + \delta C_i + \lambda T^I \quad (19)$$

where S_m is the molecular network interpretation score, C^D, C^c, C^B, and C_i are normalized graph parameters, T^I represents normalized topological index information, and α, β, γ, δ, and λ are assigned weights. The final interpretation helps reveal hidden molecular relationships, important interaction pathways, highly connected molecular components, and structurally significant regions within the molecular network.

5. Results and Discussion

5.1 Overview of Molecular Network Representation

The molecular network representation in the proposed MOLECULAR-NET framework converts complex molecular systems into graph-based structures for systematic analysis. In this representation, atoms, functional groups, molecular entities, and interaction sites are considered as vertices, while bonds, associations, reaction links, and interaction pathways are considered as edges.

Table 2. Overview of Molecular Network Representation in MOLECULAR-NET

Network Component	Molecular Meaning	Graph-Based Representation	Analytical Purpose
Atom	Basic chemical unit in a molecule	Vertex	Identifies individual molecular components
Functional group	Chemically active molecular group	Vertex or subgraph	Represents reactive or structurally important regions
Molecular entity	Complete molecule or molecular unit	Vertex	Supports network-level molecular comparison

Chemical bond	Connection between atoms	Edge	Shows direct structural linkage
Molecular association	Interaction between molecular units	Edge	Represents relational or interaction strength
Interaction pathway	Route of molecular interaction	Path	Helps analyze molecular communication routes
Interaction strength	Stability, frequency, or importance of interaction	Edge weight	Supports weighted network analysis

Table 2 presents the basic components used for representing molecular systems in the MOLECULAR-NET framework. It explains how atoms, functional groups, molecular entities, chemical bonds, molecular associations, interaction pathways, and interaction strengths are converted into graph-based elements such as vertices, edges, paths, and edge weights. This table helps clarify the relationship between molecular meaning and graph-theoretic representation, thereby providing a clear foundation for molecular network construction and further analysis using graph parameters and topological indices.

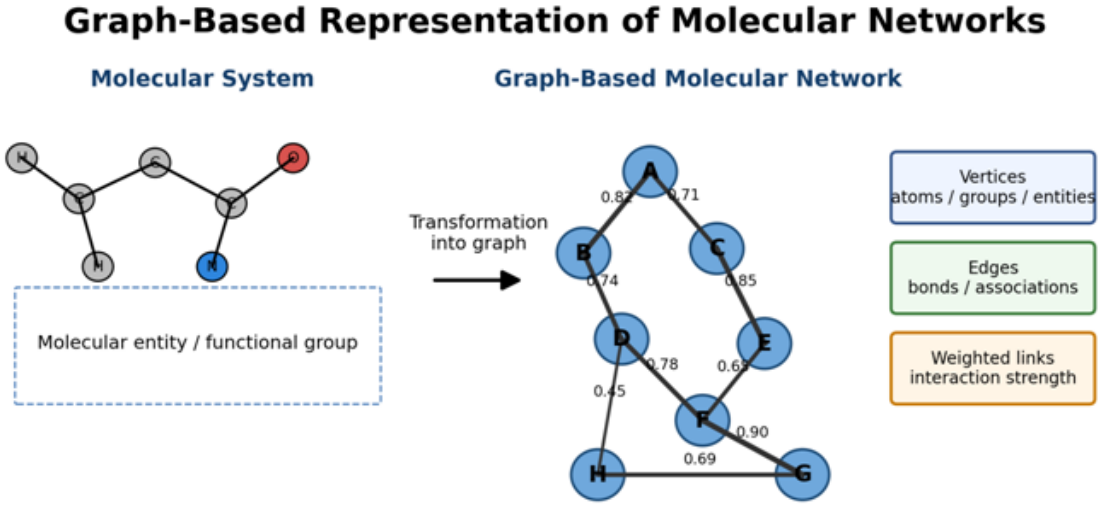

Figure 2. Graph-Based Representation of Molecular Networks

Figure 2 illustrates the graph-based representation of molecular networks in the MOLECULAR-NET framework. The molecular system is transformed into a network model in which atoms, functional groups, molecular entities, and interaction sites are represented as vertices, while bonds, associations, reaction links, and interaction pathways are represented as edges. Weighted links indicate the strength, stability, frequency, or importance of molecular interactions. This representation provides a clear visual structure for understanding molecular relationships and supports further analysis using graph parameters and topological indices.

5.2 Graph-Based Construction of Molecular Networks

Graph-based construction of molecular networks in the MOLECULAR-NET framework involves converting molecular information into a structured graph model. In this construction, the molecular system is represented as G = (V, E), where V denotes the set of vertices and E denotes the set of edges. Vertices represent atoms, functional groups, molecular entities, or interaction sites, while edges represent bonds, associations, and interaction pathways.

Table 3. Graph-Based Construction of Molecular Networks in MOLECULAR-NET

Construction Step	**Description**	**Graph-Theoretic Representation**	**Purpose**
Molecular data selection	Selection of molecular structures, interaction data, or network information	Input molecular dataset	Provides the basic information for network construction
Entity identification	Identification of atoms, functional groups, molecules, or interaction sites	Vertex set V	Defines molecular components as graph nodes
Interaction identification	Identification of bonds, associations, or interaction pathways	Edge set E	Defines relationships among molecular entities
Graph formation	Construction of the molecular network using vertices and edges	G = (V, E)	Converts molecular information into a graph model
Edge weighting	Assignment of interaction strength, stability, frequency, or importance	Weighted edge w_{ij}	Supports weighted molecular network analysis
Matrix representation	Representation of interactions using adjacency or weighted matrices	A = $[a_{ij}]$, W = $[w_{ij}]$	Enables mathematical and computational analysis
Network validation	Checking connectivity, isolated vertices, and meaningful interaction paths	Connected or partially connected graph	Ensures the constructed network is suitable for analysis

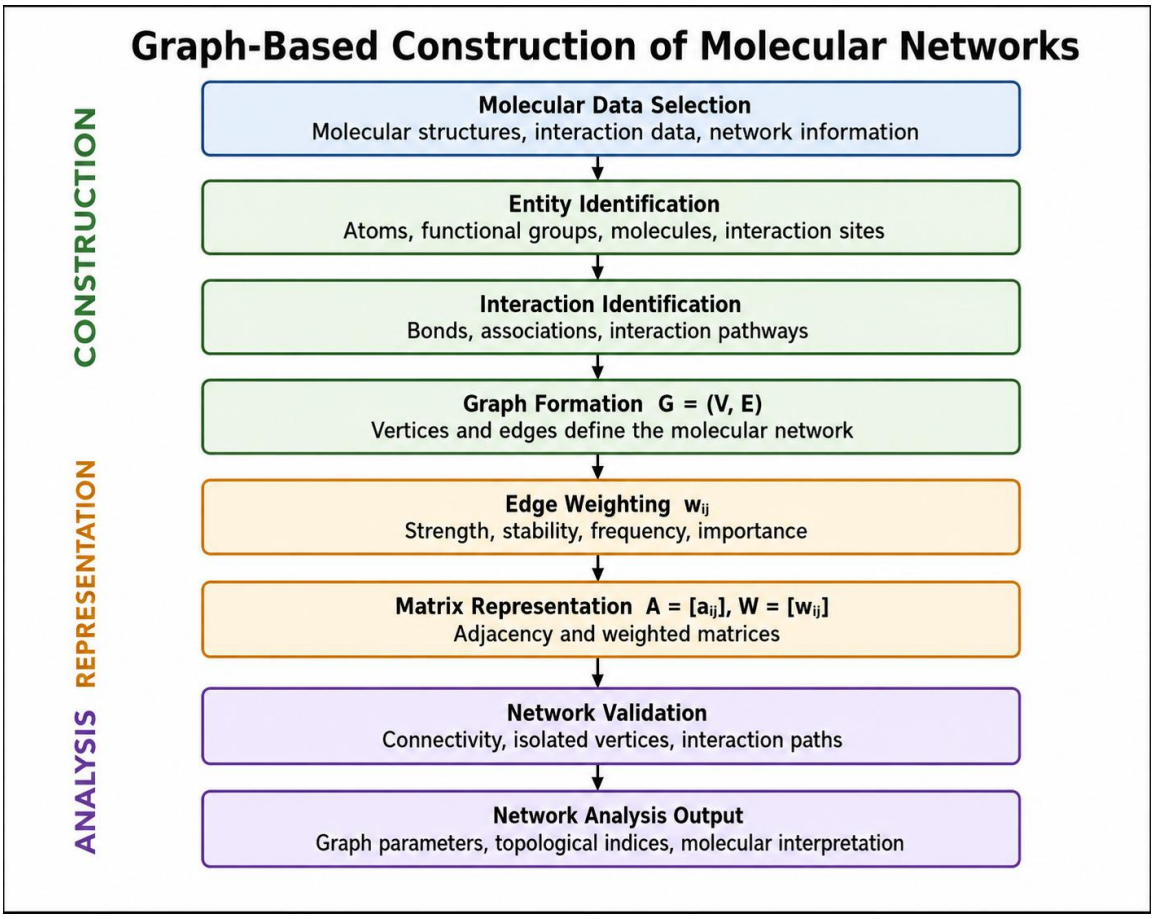

Figure 3. Graph-Based Construction of Molecular Networks

Table 3 summarizes the major steps involved in constructing molecular networks through the proposed graph-based approach. It begins with molecular data selection and continues through entity identification, interaction identification, graph formation, edge weighting, matrix representation, and network validation. Each step explains how molecular information is transformed into a mathematical graph structure such as vertex set, edge set, weighted edge, adjacency matrix, and weighted matrix. This table supports the systematic construction of molecular networks and prepares the data for graph parameter analysis, topological index calculation, and interpretation of molecular interaction patterns.

Figure 3 illustrates the construction process of molecular networks in the MOLECULAR-NET framework. The process begins with molecular data selection, followed by the identification of molecular entities and interactions. These entities are converted into vertices, while bonds, associations, and interaction pathways are converted into edges. The graph is then represented as G = (V, E), and interaction strength is included through weighted edges. The constructed graph model forms the basis for adjacency matrix representation, graph parameter analysis, topological index calculation, and interpretation of molecular network behaviour.

5.3 Analysis of Vertex and Edge Characteristics

The analysis of vertex and edge characteristics helps explain the structural role of molecular entities and their interactions within the MOLECULAR-NET framework. Vertices represent atoms, functional groups, molecular entities, or interaction sites, while edges represent bonds, associations, and interaction pathways. Table 4 summarizes the major vertex and edge characteristics used for molecular network interpretation. These characteristics support the identification of highly connected molecular components, important interaction links, isolated regions, and structurally significant pathways within the molecular network.

Table 4. Analysis of Vertex and Edge Characteristics in MOLECULAR-NET

Characteristic	Graph Element	Molecular Interpretation	Analytical Significance
Vertex identity	Vertex	Atom, functional group, molecular entity, or interaction site	Identifies molecular components in the network
Vertex degree	Vertex	Number of direct molecular connections	Shows highly connected molecular units
Vertex centrality	Vertex	Importance of a molecular entity in the network	Identifies influential molecular components
Isolated vertex	Vertex	Molecular entity with no direct connection	Indicates disconnected or weakly linked components
Edge identity	Edge	Bond, association, or interaction pathway	Defines molecular relationships
Edge weight	Edge	Strength, stability, frequency, or importance of interaction	Supports weighted interaction analysis
Edge direction	Edge	Direction of reaction or interaction flow	Explains pathway-based molecular behaviour
Path connection	Edge/path	Sequence of molecular interactions	Helps trace molecular communication routes

Figure 4 illustrates the vertex and edge characteristics used in the MOLECULAR-NET framework. The figure represents molecular entities as vertices and molecular interactions as edges, with highly connected vertices indicating important molecular components and weighted edges showing interaction strength. Isolated or weakly connected vertices represent less influential molecular entities, while connected paths indicate possible interaction routes within the molecular network. This representation supports the interpretation of molecular structure, connectivity, and interaction behaviour in a clear graph-based form.

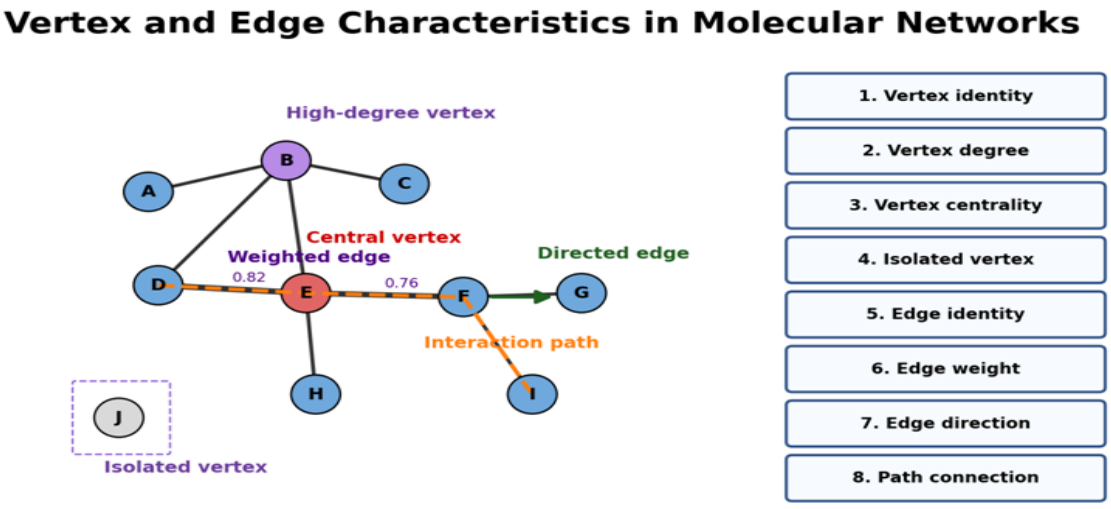

Figure 4. Vertex and Edge Characteristics in Molecular Networks

5.4 Graph Parameter Analysis

Graph parameter analysis is used to examine the structural behaviour of molecular networks in the MOLECULAR-NET framework. The constructed molecular network is analyzed using degree, connectivity, closeness centrality, betweenness centrality, clustering coefficient, shortest path, and edge weight. These parameters help identify highly connected molecular entities, influential interaction sites, strong molecular pathways, and locally clustered molecular regions. Table 5 summarizes the major graph parameters used for molecular network analysis and their interpretation in chemical graph theory.

Table 5. Graph Parameter Analysis in MOLECULAR-NET

Graph Parameter	Mathematical Meaning	Molecular Interpretation	Analytical Purpose
Degree	Number of edges connected to a vertex	Number of direct interactions of a molecular entity	Identifies highly connected atoms, groups, or molecular units
Connectivity	Relationship among vertices in the network	Linkage strength among molecular components	Shows whether the molecular network is connected or fragmented
Closeness centrality	Average shortest distance of a vertex to others	Accessibility of a molecular entity within the network	Identifies entities that can quickly connect with other molecular units
Betweenness centrality	Frequency of a vertex in shortest paths	Mediating role of a molecular entity	Detects important bridge nodes and interaction control points
Clustering coefficient	Local grouping tendency around a vertex	Formation of local molecular clusters	Reveals closely connected structural or functional regions
Shortest path	Minimum distance between two vertices	Minimum interaction route between molecular entities	Helps trace efficient molecular interaction pathways
Edge weight	Strength or importance of an edge	Stability, frequency, or strength of interaction	Supports weighted analysis of molecular relationships

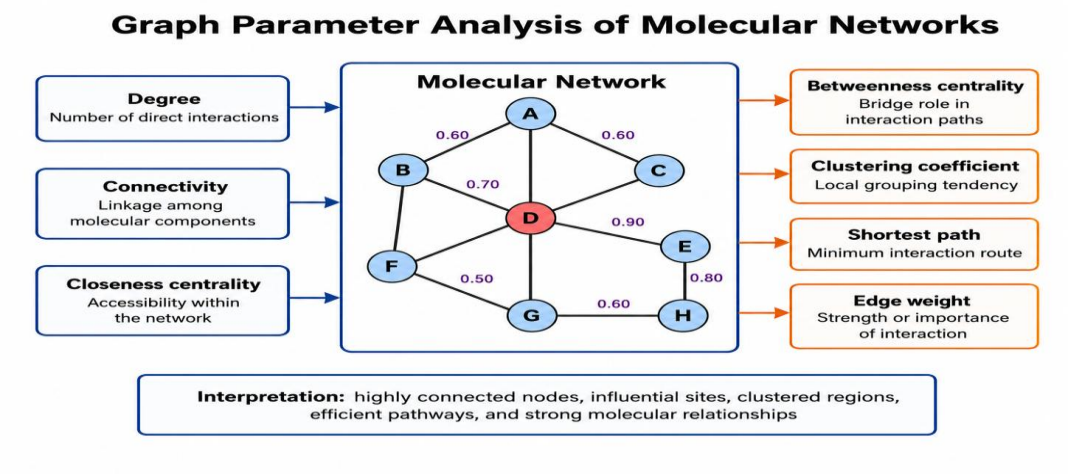

Figure 5. Graph Parameter Analysis of Molecular Networks

Figure 5 presents the graph parameter analysis process used in the MOLECULAR-NET framework. The constructed molecular network is examined through degree, connectivity, centrality, clustering coefficient, shortest path, and edge weight measures. Highly connected vertices indicate important molecular components, central vertices reveal influential interaction sites, clustered regions represent closely related molecular groups, and weighted edges show the strength or importance of molecular interactions. This figure explains how graph parameters support the interpretation of hidden molecular relationships and structurally significant regions within the molecular network.

5.5 Topological Index Analysis

Topological index analysis is used to describe the structural and interaction properties of molecular networks through numerical graph descriptors. In the MOLECULAR-NET framework, topological indices help quantify molecular size, branching, connectivity, interaction strength, and structural complexity. These indices convert the graph structure of molecular networks into measurable values that support comparison, interpretation, and classification of molecular systems. Table 6 presents the major topological indices used in the proposed framework and explains their molecular significance.

Table 6. Topological Index Analysis in MOLECULAR-NET

Topological Index	**General Expression**	**Molecular Interpretation**	**Analytical Purpose**
First Zagreb index	$M_1(G) = \sum_{vi \in V} d(v_i)^2$	Measures the contribution of vertex degrees	Identifies highly connected molecular structures
Second Zagreb index	$M_2(G) = \sum_{vivj \in E} d(v_i)d(v_j)$	Measures degree interaction between connected vertices	Explains bond-based structural strength
Randić index	$R(G) = \sum_{vivj \in E} 1 / \sqrt{(d(v_i)d(v_j))}$	Describes molecular branching and connectivity	Supports molecular structure comparison
Wiener index	$W(G) = \sum_{i<j} d(v_i, v_j)$	Measures total shortest path distance	Represents molecular compactness and distance pattern
Harary index	$H(G) = \sum_{i<j} 1 / d(v_i, v_j)$	Measures inverse distance relationship	Indicates closeness among molecular components
Sombor index	$SO(G) = \sum_{vivj \in E} \sqrt{(d(v_i)^2 + d(v_j)^2)}$	Measures degree-based edge strength	Supports analysis of structural complexity
Weighted topological index	$T^I = \sum_{vivj \in E} w_{ij} f(d(v_i), d(v_j))$	Includes edge weight and vertex degree information	Interprets weighted molecular interaction networks

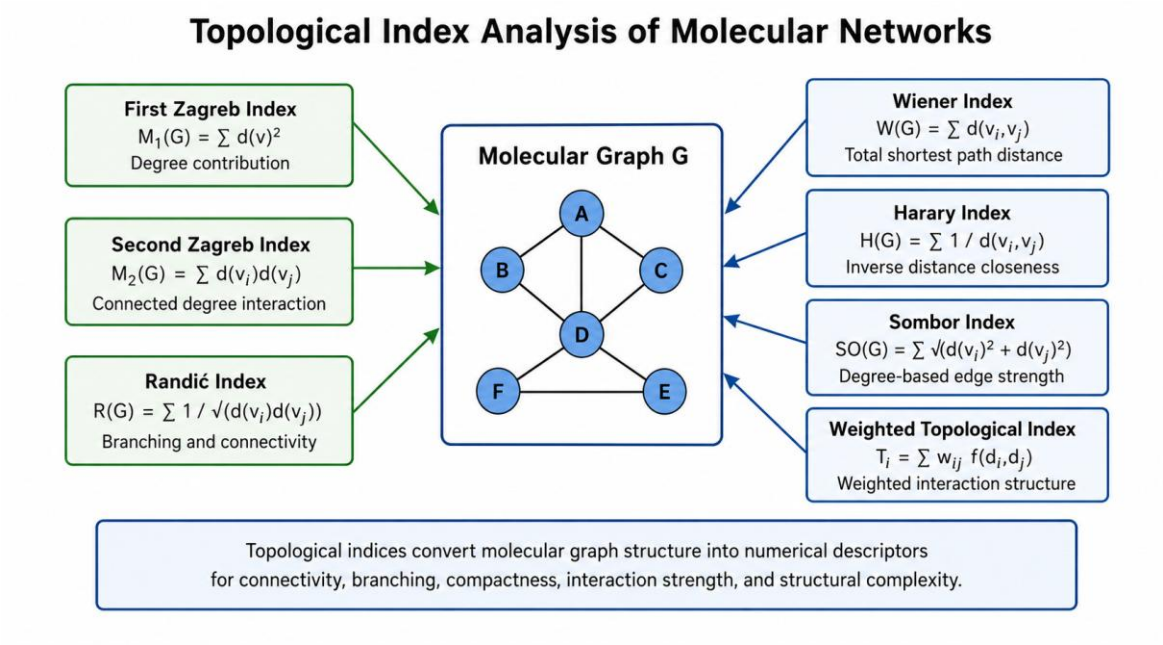

Figure 6. Topological Index Analysis of Molecular Networks

Figure 6 presents the topological index analysis process in the MOLECULAR-NET framework. The constructed molecular graph is analyzed using degree-based, distance-based, and weighted topological indices to obtain numerical descriptors of molecular structure and interaction behaviour. Degree-based indices such as Zagreb, Randić, and Sombor indices explain connectivity, branching, and structural complexity, while distance-based indices such as Wiener and Harary indices describe molecular compactness and closeness. Weighted topological indices include interaction strength and support the interpretation of strong molecular pathways and structurally significant regions.

5.6 Identification of Hidden Molecular Interaction Patterns

Identification of hidden molecular interaction patterns is an important part of the MOLECULAR-NET framework because complex molecular systems may contain indirect connections, strong interaction pathways, clustered regions, and influential molecular components that are not easily visible through simple structural observation. Graph-based analysis helps reveal these hidden patterns by examining connectivity, centrality, clustering, shortest paths, edge weights, and topological index values. Table 7 summarizes the major hidden molecular interaction patterns identified through the proposed framework and explains their analytical significance in molecular network interpretation.

Table 7. Identification of Hidden Molecular Interaction Patterns in MOLECULAR-NET

Hidden Interaction Pattern	Graph-Based Indicator	Molecular Meaning	Analytical Significance
Highly connected molecular entity	High vertex degree	Atom, group, or entity with many direct interactions	Identifies important molecular components
Influential interaction site	High centrality value	Molecular unit with strong control over network flow	Reveals key interaction points
Bridge molecular entity	High betweenness centrality	Entity connecting different molecular regions	Detects mediator or linker components

Strong interaction pathway	High edge weight or repeated path	Stable or frequent molecular interaction route	Shows dominant molecular interaction channels
Local molecular cluster	High clustering coefficient	Group of closely connected molecular entities	Identifies functional or structural regions
Short interaction route	Low shortest path value	Efficient connection between molecular entities	Explains rapid interaction transfer
Weakly connected region	Low degree or low edge weight	Less interactive or isolated molecular component	Indicates marginal or inactive molecular regions
Structurally significant zone	High topological index contribution	Region contributing strongly to molecular complexity	Supports structural interpretation and comparison

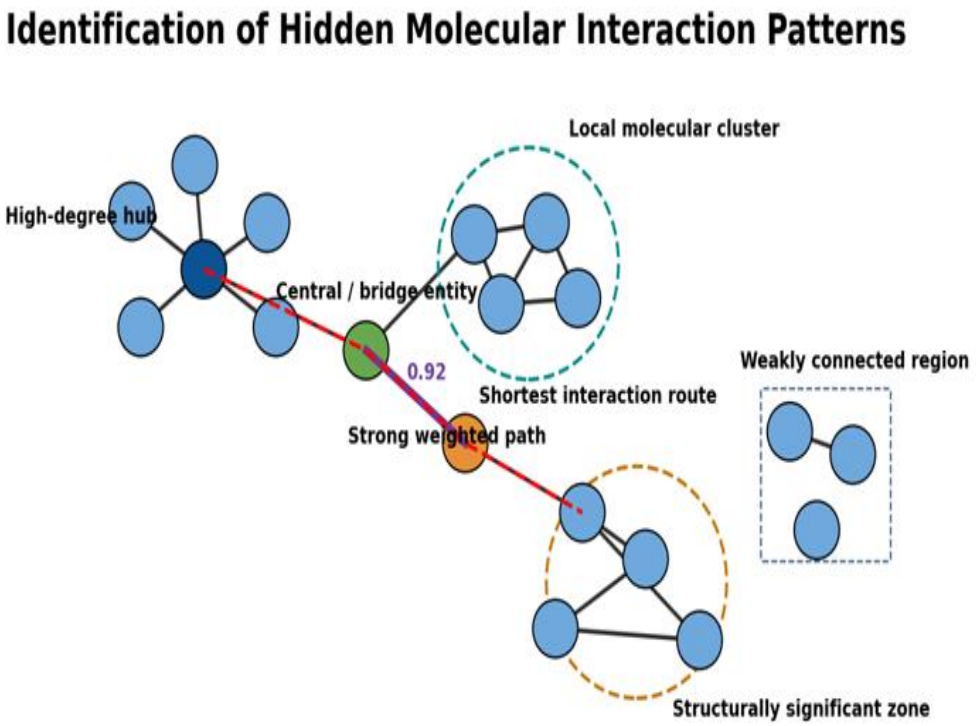

Figure 7. Identification of Hidden Molecular Interaction Patterns

Figure 7 illustrates the hidden molecular interaction patterns identified through the MOLECULAR-NET framework. The figure represents highly connected vertices, bridge nodes, clustered regions, strong weighted edges, weakly connected regions, and shortest interaction pathways within a molecular network. These visual elements show how graph-based analysis reveals molecular relationships that are not directly visible in conventional structural representation. The figure supports the interpretation of important molecular entities, dominant interaction pathways, and structurally significant regions within complex molecular networks.

5.7 Visualization of Molecular Network Relationships

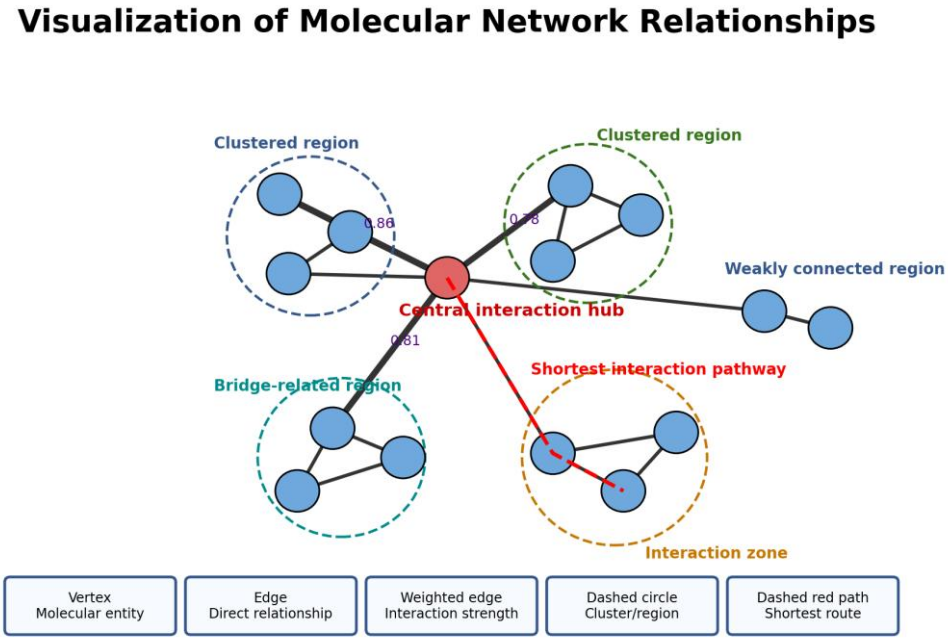

Figure 8. Visualization of Molecular Network Relationships

Figure 8 illustrates the visualization of molecular network relationships in the MOLECULAR-NET framework. The figure shows how molecular entities are connected through direct edges, weighted interaction links, clustered regions, bridge molecular entities, central interaction hubs, shortest interaction pathways, and weakly connected regions. This visualization helps explain the overall relationship pattern within the molecular network by identifying highly connected components, strong interaction routes, dense molecular clusters, and less active regions. It supports the interpretation of molecular connectivity, interaction strength, and network-level molecular behaviour in a clear graph-based form.

5.8 Discussion of Graph-Based Molecular Interpretation

The findings of the present study indicate that molecular systems can be interpreted more clearly when they are represented as graph-based networks. In the MOLECULAR-NET framework, molecular entities are represented as vertices, while bonds, associations, and interaction pathways are represented as edges. This interpretation aligns with Rottach et al. (2025), who showed that the topology of molecular representations strongly influences chemical prediction and interpretation. The present study also supports Chen et al. (2025), who emphasized the value of heterogeneous molecular graph learning for representing molecular information through multiple graph-based views. Similarly, Hakeem et al. (2025) demonstrated that graph-based molecular descriptors can effectively represent physicochemical properties, which supports the use of molecular graph models for structured chemical interpretation.

The graph parameter analysis in the present study confirms that molecular networks can be examined through degree, connectivity, centrality, clustering coefficient, shortest path, edge weight, and topological index values. This finding is consistent with Sorgun and Ullah (2025), who developed a vertex-edge-weighted molecular graph framework and showed the importance of weighted graph structures in molecular analysis. Zhang et al. (2025) also highlighted the relevance of topological indices in chemical graph applications involving tricyclic graphs, octane isomers, and benzenoid hydrocarbons. In the same direction, Ahmed et al. (2025) and Pradeepa and Arathi (2025) showed that topological indices and graph descriptors are useful for molecular property prediction, pharmaceutical interpretation, and QSPR/QSAR modelling. These studies support the present finding that graph parameters can reveal highly connected nodes, influential interaction sites, and structurally important molecular regions.

The identification of hidden molecular interaction patterns in this study further confirms the usefulness of combining graph visualization, topological descriptors, and network-based interpretation. Fazal et al. (2025)

showed that entropy measures and topological indices can be connected with physical properties of drug molecules, while Akhbari et al. (2026) demonstrated the role of topological indices and M-polynomial in computational drug property modelling. Mufti et al. (2026) also confirmed that degree-based topological indices and regression models support QSAR analysis of drug molecules. Compared with these studies, the present study extends the discussion from prediction-oriented analysis to a unified graph-based interpretation framework. Therefore, MOLECULAR-NET contributes by integrating molecular representation, graph parameter analysis, topological index interpretation, and visualization of hidden molecular interaction patterns into a single analytical model.

5.9 Theoretical and Practical Implications

5.9.1 Theoretical Implications

- The study strengthens chemical graph theory by presenting a structured framework for representing molecular networks and interactions.
- The study extends graph-based molecular analysis by integrating vertices, edges, graph parameters, and topological indices into a single interpretative model.
- The study provides a mathematical basis for identifying hidden molecular relationships, influential nodes, and structurally significant regions.

5.9.2 Practical Implications

- The proposed MOLECULAR-NET framework can help researchers visualize complex molecular systems in a simple graph-based form.
- The framework supports applications in systems chemistry, cheminformatics, bioinformatics, and molecular interaction analysis.
- The use of graph parameters and topological indices can assist in comparing molecular structures, interaction strength, and network-level molecular behaviour.

6. Conclusion

The present study proposed MOLECULAR-NET as a graph-based framework for representing and analyzing molecular networks and interactions through chemical graph theory. The framework converts molecular entities such as atoms, functional groups, interaction sites, and molecular units into vertices, while bonds, associations, and interaction pathways are represented as edges. Through graph parameters such as degree, connectivity, centrality, clustering coefficient, shortest path, edge weight, and topological indices, the study provides a structured method for identifying hidden molecular relationships, strong interaction pathways, influential molecular components, and structurally significant regions. The findings show that graph-based molecular representation can support both visualization and mathematical interpretation of complex molecular systems in systems chemistry, cheminformatics, and bioinformatics. Limitation: The study is based on review-supported graph modeling and does not include experimental validation. Future work: Future studies can apply MOLECULAR-NET to real molecular datasets and validate the framework using computational or experimental molecular interaction data.

Data Availability Statement

This study uses review-supported graph modeling and publicly available molecular information for conceptual network construction. No human or animal subject data were used in this study. The molecular structure and interaction information used for demonstration can be obtained from open-access chemical and bioinformatics databases such as PubChem, ChEMBL, and related molecular network repositories. Future studies may extend the MOLECULAR-NET framework using larger experimentally validated molecular interaction datasets.

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