

000 PARADIGM SHIFT OF GNN EXPLAINER FROM LABEL 001 SPACE TO PROTOTYPICAL REPRESENTATION SPACE 002 003 004

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007 008 ABSTRACT

009 Post-hoc instance-level graph neural network (GNN) explainers are developed to
010 identify a compact subgraph (i.e., explanation) that encompasses the most influen-
011 tial components for each input graph. A fundamental limitation of existing meth-
012 ods lies in the insufficient utilization of structural information during GNN ex-
013 plainer optimization. They typically optimize the explainer by aligning the GNN
014 predictions of input graph and its explanation in the graph label space which inher-
015 ently lacks expressiveness to describe various graph structures. Motivated by the
016 powerful structural expression ability of vectorized graph representations, we for
017 the first time propose to shift the GNN explainer optimization from the graph label
018 space to the graph representation space. However, the paradigm shift is challeng-
019 ing due to both the entanglement between the explanatory and non-explanatory
020 substructures, and the distributional discrepancy between the input graph and the
021 explanation subgraph. To this end, we meticulously design **IDEA**¹, a universal
022 dual-stage optimization framework grounded in a prototypical graph representa-
023 tion space, which can generalize across diverse existing GNN explainer architec-
024 tures. Specifically, in the Structural Information Disentanglement stage, a graph
025 tokenizer equipped with a structure-aware disentanglement objective is designed
026 to disentangle the explanatory substructures and encapsulate them into explana-
027 tory prototypes. In the Explanatory Prototype Alignment stage, IDEA aligns the
028 representational distributions of the input graph and its explanation unified in the
029 prototypical representation space, to optimize the GNN explainer. Comprehensive
030 experiments on real-world and synthetic datasets demonstrate the effectiveness
031 of IDEA, with the average improvements of ROC-AUC by 4.45% and precision
032 by 48.71%. We further integrate IDEA with diverse explainer architectures and
033 achieve an improvement by up to 10.70%, which verifies its generalizability.

034 035 036 1 INTRODUCTION

037 Post-hoc instance-level graph neural network (GNN) explainer (Ying et al., 2019; Luo et al., 2020;
038 Schlichtkrull et al., 2021; Wang et al., 2021; Chen et al., 2023; Wang et al., 2023b; Zhang et al.,
039 2023; Zhao et al., 2023; Chen et al., 2024) is a prominent research line to reveal the opaque decision-
040 making mechanism of GNNs utilized in different domains (Fan et al., 2019; He et al., 2020b; Wu
041 et al., 2023b; Liu et al., 2021; Yang et al., 2024b; Li et al., 2020; Mao et al., 2020). For each input
042 graph, post-hoc instance-level GNN explainer aims to identify a compact explanation subgraph that
043 is the most influential to the prediction made by the target GNN model.

044 Most existing GNN explainers are developed under the *label preserving framework* (Zhao et al.,
045 2023; Zhang et al., 2023) as illustrated in Figure 1(a). Within this framework, a variety of explainer
046 architectures have been proposed. For example, GNNExplainer (Ying et al., 2019) determines the
047 importance of edges and nodes through optimizable soft masks. PGExplainer (Luo et al., 2020) in-
048 troduces a parametric graph generator to capture global explanatory structures. D4Explainer (Chen
049 et al., 2023) combines the explanation search process with the denoising diffusion model (Ho et al.,
050 2020). V-InFoR (Wang et al., 2023b) and ProxyExplainer (Chen et al., 2024) incorporate the varia-
051 tional graph auto-encoder (Kipf & Welling, 2016) to improve the robustness of GNN explainer.

052 053 ¹Our code and datasets are available at <https://anonymous.4open.science/r/Idea-2736>

Despite promising achievements, the label preserving framework exhibits a fundamental limitation in utilizing structural information to identify the explanation subgraphs, thus restricting the performance of GNN explainers. As shown in Figure 1(a), the label preserving framework optimizes the explainer by aligning the GNN predictions of the input graph and the explanation subgraph in the graph label space. Nevertheless, the graph label inherently lacks expressiveness to capture the characteristics of topological structures (Yang et al., 2024a; Wang et al., 2023a). During the GNN explanation process, the topological structures are critical, especially for complex graph domains such as molecular property prediction (Kazius et al., 2005; Agarwal et al., 2023; Wu et al., 2023a; Funke et al., 2023), where multiple distinct substructures can correspond to the same label.

In order to mitigate the limitation of label preserving framework, we advocate, for the first time, to shift the GNN explainer optimization framework from the graph label space to the graph representation space. Compared with discrete graph labels, the continuous graph representations can provide fine-grained descriptions of topological structures (Sun et al., 2020; Thakoor et al., 2022; Tian et al., 2022; Yang et al., 2024a). Consequently, developing a graph representation space based optimization framework is promising to facilitate the GNN explainer to sufficiently utilize structural information during explanation process. As shown in Figure 1(b), a straightforward implementation of this blueprint is the *direct alignment framework*, which optimizes the explainer by aligning the GNN encoded representations of the input graph and the corresponding explanation. However, the direct alignment framework is far from an effective optimization framework for GNN explainers, due to the following two critical challenges.

The first challenge lies in the entanglement between the explanatory and non-explanatory substructures of the input graph. As revealed by causal inference theory (Wu et al., 2022; Sui et al., 2022), the explanatory substructure causally determines the GNN prediction, while the non-explanatory counterpart merely exhibits statistical correlations. Due to the message passing mechanism (Kipf & Welling, 2017; Veličković et al., 2018; Xu et al., 2019), the GNN encoded representation of the input graph inevitably aggregates explanatory and non-explanatory substructures. Directly aligning the representations of the input graph and the explanation risks misleading the GNN explainer to non-explanatory substructures. The second challenge arises from the distributional discrepancy between the input graph and its explanation subgraph within the GNN encoded representation space. Since the explanation subgraph is a structurally reduced version of the input graph, the explanation representation naturally follows a deviated distribution in the GNN encoded representation space (Zhang et al., 2023; Chen et al., 2024). Simplistically enforcing the representation similarity within the GNN encoded space tends to obscure the most influential subgraph rather than reveal it.

To overcome the challenges above, we propose **IDEA**, a universal dual-stage GNN explainer optimization framework grounded in a prototypical graph representation space, which is generalizable across various existing GNN explainer architectures. Specifically, IDEA consists of a Structural Information Disentanglement stage and an Explanatory Prototype Alignment stage. In the structural information disentanglement stage, we design a hierarchical graph tokenizer equipped with a customized structure-aware disentanglement objective, to disentangle the explanatory substructures from confounding non-explanatory counterpart and then cluster them into prototypical representations. In the explanatory prototype alignment stage, IDEA first unifies the GNN encoded representations of the input graph and the explanation in the prototypical representation space, to mitigate the distributional discrepancy. Subsequently, IDEA aligns the unified representational distributions to optimize the GNN explainer, enabling accurate identification of GNN explanations.

The main contributions of this work are summarized as follows.

- 108 • We propose, for the first time, the paradigm shift of GNN explainer optimization framework from
109 the graph label space to the graph representation space. Furthermore, we design IDEA, the first
110 graph representation space based GNN explainer optimization framework.
- 111 • We propose a hierarchical graph tokenizer equipped with a structure-aware disentanglement ob-
112 jective, to disentangle the explanatory substructures and encapsulate them into prototypical rep-
113 resentations. We formulate a novel explanation identification strategy based on the prototypical
114 representation space, which aligns the unified representational distributions of the input graph and
115 the explanation, to circumvent the deviated distribution of the explanation subgraph.
- 116 • Extensive experiments conducted on real-world and synthetic datasets validate the effectiveness
117 of IDEA compared with SOTA GNN explainers, with the average improvements of ROC-AUC
118 by 4.45% and precision by 48.71%. Meanwhile, the consistent superiority of the collaboration
119 between IDEA and various explainer architectures demonstrates the generalizability of IDEA.

121 2 NOTATION AND PROBLEM FORMULATION

123 **Notation.** We use $G = (A, X)$ with the adjacency matrix $A \in \mathbb{R}^{N \times N}$ and the feature matrix
124 $X \in \mathbb{R}^{N \times D}$ to denote a graph data of N nodes, where D represents the graph feature dimension.
125 If node v_i and node v_j are connected, the element in the i -th row and the j -th column $A_{ij} = 1$,
126 and 0 otherwise. Without losing generality, in this work, we focus on the *graph classification* task
127 (Hu et al., 2022), since node classification can be converted into a computation graph classification
128 problem (Chen et al., 2024). For graph classification, each graph G is associated with a label $y \in$
129 $\mathbb{R}^{1 \times C}$ where C denotes the total number of classes. The target graph neural network model $f(\cdot)$
130 has been well-trained to predict the class of any given graph G . Generally, the to-be-explained
131 GNN model consists of the following three modules, the feature encoder $f_e(\cdot)$, the pooling function
132 $\text{Pool}(\cdot)$ (e.g., mean pooling and max pooling) (Ying et al., 2018), and the task predictor $f_p(\cdot)$. The
133 GNN prediction procedure can be represented as follows,

$$134 H_N = f_e(G), H_G = \text{Pool}(H_N), \hat{y} = f_p(H_G), \quad (1)$$

135 where $H_N \in \mathbb{R}^{N \times d}$ is the matrix of d -dimensional node representations, $H_G \in \mathbb{R}^{1 \times d}$ is the pooled
136 graph representation, and \hat{y} is the predicted label. Refer to Appendix A for notation summary.

138 **Problem Formulation.** Given a well-trained GNN model $f(\cdot)$ to be explained and an input graph
139 G , the post-hoc instance-level GNN explainer $\psi(\cdot, \cdot)$ aims to identify a compact subgraph $g^* =$
140 $\psi(G, f) \subset G$, which retains the most influential components during the GNN predicting procedure.
141 Within the label preserving framework, the identified subgraph is reinforced to maintain the original
142 prediction of G . Typically, the optimization objective of the label preserving framework is defined
143 as the mutual information between the predictions of the input graph and the explanation subgraph,
144 i.e., $\text{MI}(f(g), f(G))$. In this work, we shift the GNN explainer paradigm from the label space to the
145 graph representation space, to sufficiently utilize the structural information for GNN explanations.

146 3 METHODOLOGY

148 Procedurally, **IDEA** consists of two successive stages, the Structural Information Disentanglement
149 and the Explanatory Prototype Alignment, centered on the hierarchical graph tokenizer (HGTokenizer). To
150 tackle the structural entanglement problem, in the first stage, we design a structure-aware
151 disentanglement (SAD) objective for HGTokenizer to stratify the explanatory and non-explanatory
152 substructures. During the disentanglement process, the explanatory substructures are clustered into
153 a collection of explanatory prototypes. In the second stage, based on the HGTokenizer and the
154 prototypes, we first unify the representations of the input graph and the explanation subgraphs into the
155 prototypical representation space, to circumvent the distribution discrepancy problem. Afterwards,
156 the GNN explainer is optimized by aligning the two unified representational distributions.

158 3.1 STRUCTURAL INFORMATION DISENTANGLEMENT

160 In Figure 2, we outline the overview of structural information disentanglement, which empowers the
161 HGTokenizer with the ability to decouple the explanatory substructures from the non-explanatory
counterpart. Technically, the HGTokenizer is consist of two cascade-connected graph quantizers

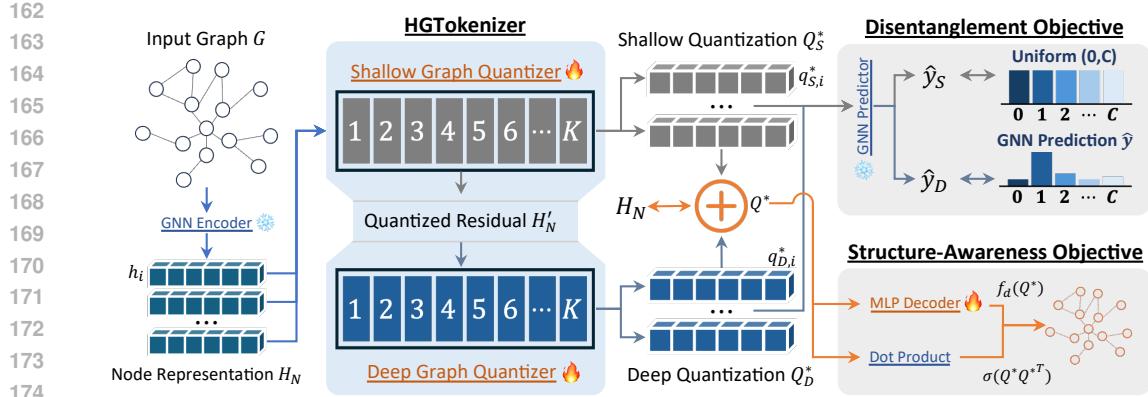


Figure 2: Overview of the Structural Information Disentanglement in IDEA. The node representation H_N is decomposed into two quantization representations Q_S^* and Q_D^* , by the cascade-connected graph quantizers in HGTokenizer. The two quantizers aim to capture the explanatory and non-explanatory substructures respectively, following the guidance of the SAD objective.

(Zeghidour et al., 2021) which take insights of the semantic tokenization (Rajput et al., 2023; Yin et al., 2025), to compactly represent the structural information with discrete codebooks.

Given the node representation matrix H_N , HGTokenizer approximates it based on the shallow and the deep graph quantizers. For the representation to be quantized, the graph quantizer looks up the nearest codeword in the codebook. Since the codebook scale K is significantly smaller than the total number of nodes, it can serve as a collection of prototypes (Dai & Wang, 2025; Zhu et al., 2025) that succinctly summarizes the input representations. Using the representation h_i of node v_i as an example, the cascade quantization procedure of HGTokenizer is formulated as follows,

$$q_{S,i}^* = \text{GQ}_S(h_i) = \arg \min_{q \in \mathcal{C}_S} \mathcal{D}(h_i, q), \quad h'_i = h_i - q_{S,i}^* \quad (2)$$

$$q_{D,i}^* = \text{GQ}_D(h'_i) = \arg \min_{q \in \mathcal{C}_D} \mathcal{D}(h'_i, q), \quad q_i^* = q_{S,i}^* + q_{D,i}^*, \quad (3)$$

where $\text{GQ}_S(\cdot)$ and $\text{GQ}_D(\cdot)$ denote the shallow graph quantizer and the deep graph quantizer, \mathcal{C}_S and \mathcal{C}_D denote the codebooks of quantizers, q denotes the codeword inside, and $\mathcal{D}(\cdot, \cdot)$ is the distance metric for quantization. The deep graph quantizer takes the residual of the shallow one, in order to spontaneously dichotomize the fused representations encoded by the target GNN model.

The SAD objective utilized to optimize the HGTokenizer consists of three terms, i.e., the structure-awareness objective, the disentanglement objective, and the standard quantization objective. The *structure-awareness objective* \mathcal{L}_S aims to recover the topological structures and node features based on the quantized node representations, enhancing the ability of HGTokenizer to capture the graph structural characteristics. Formally, \mathcal{L}_S is defined as follows,

$$\mathcal{L}_S = \left\| A - \sigma(Q^*Q^{*T}) \right\|_2^2 + \left\| X - f_d(Q^*) \right\|_2^2, \quad (4)$$

where Q^* is the matrix of quantized node representations q_i^* , $\sigma(\cdot)$ is the sigmoid function, and $f_d(\cdot)$ is a linear decoder. The *disentanglement objective* \mathcal{L}_D enforces the prediction of the non-explanatory substructures towards a uniform distribution, and guides the prediction of the explanatory substructures towards the original prediction. Formally, \mathcal{L}_D is defined as follows,

$$\mathcal{L}_D = \text{KL}[\hat{y}_S \| \mathcal{U}_C] + \text{CrossEntropy}(\hat{y}_D, \hat{y}), \quad (5)$$

where \hat{y}_S and \hat{y}_D denote the GNN predictions of the shallow and deep quantized representations, respectively. \mathcal{U}_C denotes the uniform distribution in the graph label space.

By minimizing the Kullback-Leibler divergence between \hat{y}_S and \mathcal{U}_C , IDEA reinforces the shallow graph quantizer to capture non-explanatory substructures that are unable to determine the GNN decision-making process. Meanwhile, the second term instructs the deep graph quantizer to encapsulate the explanatory substructures that are more influential. Consequently, the codebook \mathcal{C}_D inside

216 G_{QD} can not only maintain the GNN prediction of the input graph, but also recover the graph topo-
 217 logical structures along with \mathcal{C}_S . IDEA regards \mathcal{C}_D as a collection of explanatory prototypes which
 218 naturally induces a prototypical representation space for the GNN explainer optimization.

219 In addition, following the standard vector quantization process (van den Oord et al., 2017; Zeghidour
 220 et al., 2021), the *quantization objective* \mathcal{L}_Q below is adopted for the basic quantization ability,
 221

$$\mathcal{L}_Q = \|H_N - Q^*\|_2^2. \quad (6)$$

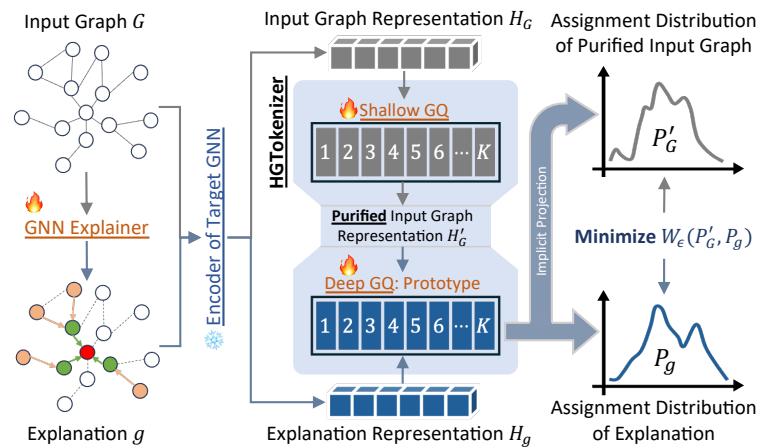
222 Hence, the structure-aware disentanglement objective is defined as follows,
 223

$$\mathcal{L}_{SAD} = \mathcal{L}_D + \lambda_S \cdot \mathcal{L}_S + \lambda_Q \cdot \mathcal{L}_Q, \quad (7)$$

224 where λ_S, λ_Q are the weighted hyper-parameters. We present a hyper-parameter analysis on the
 225 weights λ_S and λ_Q of the structure-aware disentanglement objective in Appendix C.1.

226 3.2 EXPLANATORY PROTOTYPE ALIGNMENT

227 Following the guidance
 228 of the SAD objective, the
 229 HGTokenizer can disen-
 230 tangle the explanatory in-
 231 formation from the fused
 232 graph representation en-
 233 coded by the target GNN.
 234 The deep quantizer fur-
 235 ther encompasses a col-
 236 lection of prototypes to
 237 describe the explanatory
 238 information. To circum-
 239 vent the deviated distri-
 240 bution of the explana-
 241 tion subgraphs, we for-
 242 mulate a novel explana-
 243 tion identification strat-
 244 egy on the basis of the
 245 prototypical represen-
 246 tation space. The overview
 247 of the explanatory proto-
 248 type alignment is illus-
 249 trated in Figure 3.



250 Figure 3: Overview of the Explanatory Prototype Alignment in IDEA.
 251 The input graph representation H_G is first purified by the shallow graph
 252 quantizer, to eliminate the non-explanatory information. Then, the ex-
 253 planation representation H_g and the purified input graph representation
 254 H'_G are implicitly projected into the prototypical space. At last, IDEA
 255 aligns the assignment distributions P'_G and P_g to optimize the explainer.

256 Given the target GNN model $f(\cdot)$ to be explained and an input graph G , the explanation subgraph
 257 g is generated by $\psi(G, f)$, where ψ denotes the GNN explainer. In our implementation, a typical
 258 probabilistic generator, which is well-investigated among the GNN explanation community (Luo
 259 et al., 2020; Wang et al., 2021; 2023b; Wang & Shen, 2023), is adopted as the GNN explainer
 260 backbone. The implementation details are elaborated in Appendix B.3. Formally, we denote the
 261 GNN encoded representation of the input graph as H_G and that of the explanation subgraph as H_g .

262 To filter out the non-explanatory information from the input graph representation, we feed H_G to
 263 the HGTokenizer (i.e., the cascade of GQ_S and GQ_D), formulated as follows,

$$H_{S,G} = \text{GQ}_S(H_G), \quad H'_G = H_G - H_{S,G}, \quad H_{D,G} = \text{GQ}_D(H'_G), \quad (8)$$

264 where $H_{S,G}$ is the non-explanatory fraction of the input graph representation and H'_G is the purified
 265 input graph representation after removing $H_{S,G}$. For the explanation representation H_g , we directly
 266 feed it into the deep graph quantizer GQ_D, formulated as follows,

$$H_{D,g} = \text{GQ}_D(H_g). \quad (9)$$

267 Based on the quantization procedure of GQ_D, we can implicitly unify the purified representation
 268 of the input graph H'_G and the explanation representation H_g into the prototypical representation
 269 space, instead of explicit representation projection. To be more specific, the assignment distribution

270 of the to-be-quantized representation (i.e., H'_G or H_g) over the explanatory codebook $\mathcal{C}_D \in \mathbb{R}^{K \times d}$
 271 is able to indicate its location within the prototypical representation space. Formally, the assignment
 272 distributions corresponding to H'_G and H_g are measured as follows,
 273

$$274 \quad \mathcal{P}'_G = \text{Norm}(\mathcal{D}(H'_G, \mathcal{C}_D)), \quad \mathcal{P}_g = \text{Norm}(\mathcal{D}(H_g, \mathcal{C}_D)), \quad (10)$$

275 where \mathcal{P}'_G and \mathcal{P}_g denote the assignment distributions and $\text{Norm}(\cdot)$ normalizes the quantization distance
 276 to the probability value. Theoretical justification for this practice is presented in Appendix G.
 277 Since the assignment distributions \mathcal{P}'_G and \mathcal{P}_g are identically measured over the implicit prototypical
 278 representation space, the distribution discrepancy of the explanation subgraph in the GNN encoded
 279 space is ingeniously circumvented.

280 Subsequently, IDEA adopts the entropy-regularized Wasserstein distance (Reshetova et al., 2024)
 281 between \mathcal{P}'_G and \mathcal{P}_g as the optimization objective of the GNN explainer ψ . The Wasserstein distance
 282 not only encourages the consistency between the two assignment probabilities \mathcal{P}'_G and \mathcal{P}_g , but also
 283 is insensitive to the sparsity issue of probabilistic distributions. For the stability of the explainer
 284 optimization, IDEA adopts the symmetric variant defined as follow,

$$285 \quad \mathcal{L}_{\text{IDEA}} = W_\epsilon(\mathcal{P}'_G, \mathcal{P}_g) + \frac{1}{2} \left(W_\epsilon(\mathcal{P}'_G, \mathcal{P}'_G) + W_\epsilon(\mathcal{P}_g, \mathcal{P}_g) \right). \quad (11)$$

$$287 \quad W_\epsilon(\mathcal{P}'_G, \mathcal{P}_g) = \min_{\gamma \in \Pi(\mathcal{P}'_G, \mathcal{P}_g)} \sum_{i,j} \gamma_{ij} S_{ij} + \epsilon \sum_{i,j} \gamma_{ij} \log \gamma_{ij}. \quad (12)$$

289 $\Pi(\mathcal{P}'_G, \mathcal{P}_g)$ denotes the transport polytope and S denotes the cost matrix defined as follows,
 290

$$291 \quad \Pi(\mathcal{P}'_G, \mathcal{P}_g) = \{ \Pi \in \mathbb{R}_+^{K \times K} | \Pi \mathbf{1} = \mathcal{P}'_G, \Pi^T \mathbf{1} = \mathcal{P}_g \}, \quad S_{ij} = (\mathcal{P}'_{G,i} - \mathcal{P}_{g,j})^2. \quad (13)$$

292 We implement IDEA as a dual-stage framework in order to avoid the counteraction between the
 293 optimization terms within \mathcal{L}_{SAD} and $\mathcal{L}_{\text{IDEA}}$. In Appendix F.2, we further investigate a variant of
 294 IDEA where the two stages are conducted jointly.

296 4 EXPERIMENT

298 To comprehensively validate the practicality of IDEA, we conduct extensive experiments which are
 299 designed to investigate the following research questions.
 300

- 301 • **RQ1:** How effective is IDEA compared to the label preserving based SOTA baselines?
- 302 • **RQ2:** How generalizable is IDEA collaborated with different explainer architectures?
- 303 • **RQ3:** How does each component of IDEA influence the overall explanation performance?

305 Furthermore, we present the hyper-parameter analysis, the explanation visualization, and the time
 306 complexity analysis in Appendix C, D, and E, respectively.

308 4.1 EXPERIMENTAL SETUP

310 **Dataset.** We evaluate IDEA and baselines on both real-world and synthetic datasets. The evaluated
 311 real-world datasets include Mutagenicity (Kazius et al., 2005), Benzene (Sanchez-Lengeling
 312 et al., 2020), Fluoride-Carbonyl (Sanchez-Lengeling et al., 2020), and Alkane-Carbonyl (Sanchez-
 313 Lengeling et al., 2020). The synthetic datasets is BA-2Motifs (Luo et al., 2020).

314 **Baseline.** The baselines include SOTA post-hoc instance-level GNN explainers based on various
 315 techniques, i.e., GNNExplainer (Ying et al., 2019), PGExplainer (Luo et al., 2020), GraphMask
 316 (Schlichtkrull et al., 2021), ReFine (Wang et al., 2021), V-InFoR (Wang et al., 2023b), D4Explainer
 317 (Chen et al., 2023), MixupExplainer (Zhang et al., 2023), ProxyExplainer (Chen et al., 2024).

318 **Evaluation.** Following the standard experimental settings (Luo et al., 2020; Chen et al., 2024),
 319 we train a 3-layer Graph Convolutional Network (GCN) model (Kipf & Welling, 2017) on each
 320 dataset, as the target model to be explained. To evaluate the explanation quality, we reformulate
 321 the explanation task as an edge binary classification task. Edges that belong to the expert-notated
 322 ground truth are labeled as positive, and negative otherwise. Hence, we adopt the ROC-AUC score
 323 as the main metric to evaluate the explanation performance (Ying et al., 2019; Luo et al., 2020).
 Refer to Appendix B for the experimental details.

324
 325 **Table 1: Explanation performance (ROC-AUC \uparrow) of IDEA and eight SOTA post-hoc instance-level**
 326 **GNN explainers on five datasets, in the form of $\text{mean} \pm \text{std}$. Average** reports the mean result over all
 327 **the evaluated datasets. Improvement** is defined as $(\text{IDEA} - \text{Best-Baseline}) / \text{Best-Baseline}$. The
 328 **superscript *** indicates the improvement is statistically significant with the p -value less than 0.01.
 329 **Bold font and underline** highlight the best and the runner-up performance, respectively.

Model	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs	Average
GNNEExplainer	0.6155 \pm 0.0087	0.6863 \pm 0.0126	0.6884 \pm 0.0055	0.5399 \pm 0.0102	0.5619 \pm 0.0162	0.6184 \pm 0.0103
PGExplainer	<u>0.7016</u> \pm 0.0201	<u>0.8855</u> \pm 0.0023	0.7446 \pm 0.0086	0.8091 \pm 0.0209	0.8594 \pm 0.0072	0.8000 \pm 0.0115
GraphMask	<u>0.6377</u> \pm 0.0083	<u>0.5523</u> \pm 0.0062	0.6311 \pm 0.0139	0.5843 \pm 0.0028	0.6119 \pm 0.0035	0.6035 \pm 0.0068
ReFine	0.6833 \pm 0.0052	0.8720 \pm 0.0262	0.7293 \pm 0.0077	0.5600 \pm 0.0117	0.6115 \pm 0.0027	0.6912 \pm 0.0104
V-InfoR	0.6075 \pm 0.0149	0.6642 \pm 0.0112	0.6507 \pm 0.0162	0.6437 \pm 0.0169	0.7755 \pm 0.0243	0.6683 \pm 0.0156
D4Explainer	0.5467 \pm 0.0279	0.7239 \pm 0.0165	0.7736 \pm 0.0059	0.7484 \pm 0.0099	0.7478 \pm 0.0174	0.7081 \pm 0.0128
MixupExplainer	0.5428 \pm 0.0074	0.5399 \pm 0.0020	0.7385 \pm 0.0043	0.5400 \pm 0.0002	0.8355 \pm 0.0129	0.6393 \pm 0.0035
ProxyExplainer	0.6948 \pm 0.0035	0.8593 \pm 0.0127	<u>0.9334</u> \pm 0.0033	<u>0.8804</u> \pm 0.0126	<u>0.8717</u> \pm 0.0028	<u>0.8479</u> \pm 0.0068
Direct-Align	0.6567 \pm 0.0068	0.8809 \pm 0.0008	0.3562 \pm 0.0160	0.7988 \pm 0.0042	0.8653 \pm 0.0060	0.7116 \pm 0.0056
IDEA	0.7379* \pm 0.0084	0.9138* \pm 0.0002	0.9355 \pm 0.0030	0.8868 \pm 0.0018	0.9541* \pm 0.0107	0.8856* \pm 0.0047
Improvement	5.17%	3.20%	0.22%	0.73%	9.45%	4.45%

341
 342 **Table 2: Explanation performance (Precision \uparrow) of IDEA and SOTA baselines across five datasets.**

Model	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs	Average
GNNEExplainer	0.0736 \pm 0.0030	0.1901 \pm 0.0024	0.0104 \pm 0.0013	0.0652 \pm 0.0019	0.1373 \pm 0.0034	0.0953 \pm 0.0022
PGExplainer	0.1038 \pm 0.0067	0.4484 \pm 0.0041	0.0761 \pm 0.0077	0.3253 \pm 0.0176	0.6072 \pm 0.0016	0.3122 \pm 0.0072
GraphMask	0.0748 \pm 0.0070	0.1373 \pm 0.0075	0.0104 \pm 0.0082	0.0443 \pm 0.0029	0.2337 \pm 0.0043	0.1001 \pm 0.0036
ReFine	0.0833 \pm 0.0058	0.1951 \pm 0.0272	0.1304 \pm 0.0123	0.3027 \pm 0.0117	0.5054 \pm 0.0033	0.2434 \pm 0.0119
V-InFoR	0.1230 \pm 0.0075	0.3195 \pm 0.0134	0.1304 \pm 0.0010	0.2374 \pm 0.0019	0.1380 \pm 0.0161	0.1897 \pm 0.0075
D4Explainer	0.2087 \pm 0.0299	0.3538 \pm 0.0107	0.0109 \pm 0.0061	0.3685 \pm 0.0003	0.3153 \pm 0.0173	0.2514 \pm 0.0106
MixupExplainer	0.0682 \pm 0.0083	0.1385 \pm 0.0018	0.0652 \pm 0.0038	0.2929 \pm 0.0034	0.3194 \pm 0.0105	0.1768 \pm 0.0034
ProxyExplainer	<u>0.3365</u> \pm 0.0058	<u>0.5908</u> \pm 0.0135	<u>0.3261</u> \pm 0.0035	0.1486 \pm 0.0032	<u>0.6229</u> \pm 0.0089	<u>0.4050</u> \pm 0.0067
Direct-Align	0.0805 \pm 0.0050	0.5443 \pm 0.0009	0.0109 \pm 0.0057	0.4890 \pm 0.0028	0.5872 \pm 0.0054	0.3424 \pm 0.0025
IDEA	0.4020* \pm 0.0063	0.7523* \pm 0.0003	0.4565* \pm 0.0161	0.6119* \pm 0.0183	0.7885* \pm 0.0201	0.6022* \pm 0.0119
Improvement	19.47%	27.34%	39.99%	25.13%	26.59%	48.71%

354 355 4.2 EXPLANATION PERFORMANCE (RQ1)

356
 357 The evaluation result of IDEA and SOTA post-hoc instance-level GNN explainers is presented in
 358 Table 1, in terms of the ROC-AUC score. *Direct-Align* corresponds to the direct alignment frame-
 359 work in Figure 1(b), which optimizes the GNN explainer by directly aligning the GNN encoded
 360 representations of the input graph and the explanation.

361
 362 The result sufficiently demonstrates the effectiveness of IDEA, which can consistently achieve the
 363 supreme performance on all the evaluated datasets. On average, the improvement of IDEA over the
 364 best baseline is 4.45%. For the Mutagenicity dataset, which is a complex molecular property prediction
 365 dataset, IDEA advances the explanation quality by up to 5.17%, compared to the benchmark-
 366 leading baseline PGExplainer (Luo et al., 2020). Despite the primitive explanation identification
 367 strategy, *Direct-Align* achieves the second-tier performance among the evaluated explainers, show-
 368 casing the considerable potential of GNN explainer optimization framework based on the graph
 369 representation space. On the other hand, the inferiority of *Direct-Align* to the top-tier explainers, in-
 370 cluding PGExplainer, ProxyExplainer (Chen et al., 2024), and IDEA, justify the necessity of further
 371 advance on the direct alignment framework.

372
 373 In light of the critical importance of precision in the GNN explanation evaluation, we further report
 374 the result of IDEA and SOTA baselines in Table 2. In general, the average precision of IDEA is
 375 0.6022, achieving a significant improvement by 48.69% over the runner-up ProxyExplainer. Specif-
 376 ically, for the Alkane-Carbonyl dataset, whose ground-truth explanation is the union of an alkane
 377 chain (C_nH_{2n+2}) and a carbonyl group ($C=O$), the improvement of IDEA is the highest over the five
 378 evaluated datasets, by up to 39.99%. This advancement demonstrates the ability of IDEA to explain
 379 graphs from complex domains. Similarly, the naive contestant *Direct-Align* maintains the moderate
 380 position among the evaluated GNN explainers.

378

379

Table 3: Explanation performance (ROC-AUC \uparrow) of IDEA with different explainer architectures.

Model	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs	Average
PGExplainer +IDEA Improvement	0.7016 \pm 0.0201	0.8855 \pm 0.0023	0.7446 \pm 0.0086	0.8091 \pm 0.0209	0.8594 \pm 0.0072	0.8000 \pm 0.0115
	0.7379\pm0.0084	0.9138\pm0.0002	0.9355\pm0.0030	0.8868\pm0.0018	0.9541\pm0.0107	0.8856\pm0.0047
	5.17%	3.20%	25.64%	9.60%	11.02%	10.70%
ReFine +IDEA Improvement	0.6833 \pm 0.0052	0.8720 \pm 0.0262	0.7293 \pm 0.0077	0.5600 \pm 0.0117	0.6115 \pm 0.0027	0.6912 \pm 0.0104
	0.7832\pm0.0028	0.8759\pm0.0197	0.8428\pm0.0018	0.5809\pm0.0094	0.6861\pm0.0016	0.7538\pm0.0067
	14.62%	0.45%	15.56%	3.73%	12.20%	9.05%
V-InfoR +IDEA Improvement	0.6075\pm0.0149	0.6642 \pm 0.0112	0.6507 \pm 0.0162	0.6437 \pm 0.0169	0.7755 \pm 0.0243	0.6683 \pm 0.0156
	0.5734 \pm 0.0057	0.6713\pm0.0103	0.6776\pm0.0008	0.6483\pm0.0111	0.7772\pm0.0058	0.6696\pm0.0059
	-5.61%	1.07%	4.13%	0.71%	0.22%	1.38%
ProxyExplainer +IDEA Improvement	0.6948 \pm 0.0035	0.8593 \pm 0.0127	0.9334 \pm 0.0033	0.8804 \pm 0.0126	0.8717 \pm 0.0028	0.8479 \pm 0.0068
	0.7215\pm0.0134	0.8864\pm0.0099	0.9509\pm0.0099	0.8931\pm0.0104	0.8930\pm0.0047	0.8690\pm0.0081
	3.84%	3.15%	1.87%	1.44%	2.44%	2.48%

4.3 GENERALIZABILITY ACROSS EXPLAINER ARCHITECTURE (RQ2)

We scrutinize the generalizability of IDEA by integrating various leading GNN explainer architectures and the evaluation result in terms of ROC-AUC is presented in Table 3. In detail, PGExplainer (Luo et al., 2020) adopts a well-investigated subgraph generator based on the concrete distribution (Maddison et al., 2017). ReFine (Wang et al., 2021) implements a subgraph generator for each graph class to capture the contrastive information. V-InFoR (Wang et al., 2023b) introduces a graph variational auto-encoder (GVAE) to refine the GNN encoded representations for robustness to structural corruptions. ProxyExplainer (Chen et al., 2024) merges a GAVE and a standard graph auto-encoder as the proxy generator to resist distribution discrepancy caused by the explanation subgraph.

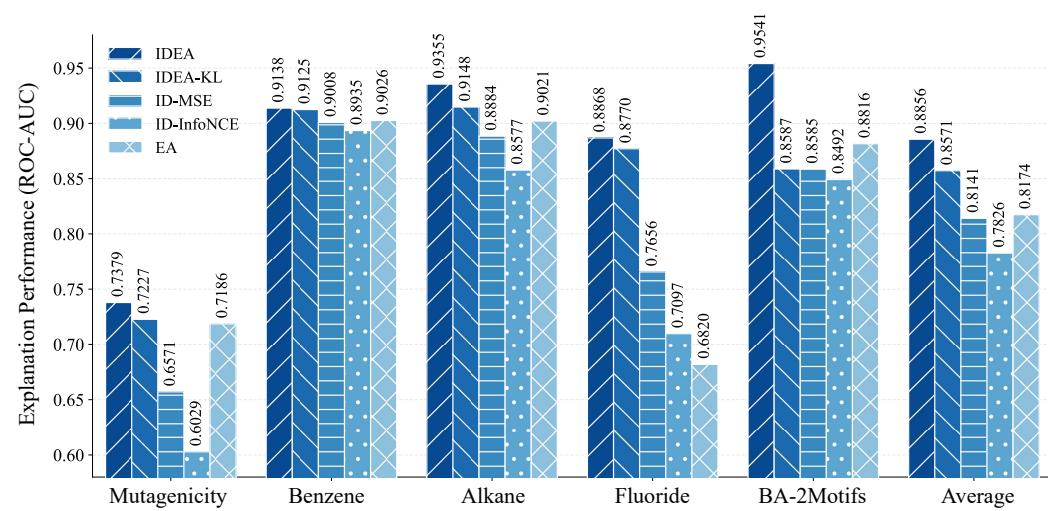
The evaluation result sufficiently demonstrates that IDEA is generalizable across four different GNN explainer architectures, with the average improvement by 10.70%, 9.05%, 1.38%, and 2.48%, respectively. The greatest advancement is achieved by the IDEA-enhanced PGExplainer, whose average performance (0.8856) even slightly exceeds the counterpart of the current leading baseline ProxyExplainer (0.8690). For ProxyExplainer that already exhibits strong performance, IDEA can further advance its explanation capacity. The IDEA-enhanced ProxyExplainer provides the best explanations for the Alkane-Carbonyl and Fluoride-Carbonyl datasets, among all the evaluated explainers. The sole exception occurs with the IDEA-enhanced V-InFoR on the Mutagenicity dataset, where the explanation performance drops by 5.61%. The possible reason for the degradation and the marginal improvement of IDEA-enhanced V-InFoR is that V-InFoR is specialized for structurally corrupted graphs, while the evaluated graphs are uncorrupted.

4.4 ABLATION STUDY (RQ3)

In this section, we probe into the influence of each component in the IDEA framework. First, we replace the Wasserstein distance in Eq.11 with the Kullback-Leibler divergence $KL[P_g || P'_G]$ and denote the variant as *IDEA-KL*. Afterwards, to validate the effectiveness of the Explanatory Prototype Alignment stage, we implement two variants, *ID-MSE* and *ID-InfoNCE*, which optimize the GNN explainer by aligning the purified representation of input graph H'_G and the explanation representation H_g . *ID-MSE* adopts the mean square error $MSE(H_g, H'_G)$ as the loss function, and *ID-InfoNCE* adopts the InfoNCE loss function (He et al., 2020a) for in-batch contrastive learning. At last, we omit the Structural Information Disentanglement stage and denote the variant as *EA*. The evaluation result of IDEA and four variants is presented in Figure 4.

We can draw the following conclusions according to the ablation result. First, the distributional discrepancy caused by the explanation subgraph deteriorates the explanation performance. By unifying the representations of the input graph and the explanation subgraph, IDEA and *IDEA-KL* significantly surpass the two variants *ID-MSE* and *ID-InfoNCE* that straightforwardly align the disunified representations. Second, although *EA* is a competitive baseline, structural information disentanglement can further boost the explanation performance. *EA* is inferior to the unabridged IDEA, with an average performance gap by 0.0682. Third, compared with KL divergence, Wasserstein distance is more suitable for GNN explainer optimization in the prototypical representation space. IDEA consistently outperforms *IDEA-KL*, with an average improvement of 3.33%.

In Appendix F, we investigate the cooperation of IDEA and the label preserving framework, where the optimization objective is defined as the convex combination of \mathcal{L}_{IDEA} and $MI(f(g), f(G))$.

Figure 4: Explanation performance (ROC-AUC \uparrow) of IDEA and its four variants.

5 RELATED WORK

Post-hoc Instance-level GNN Explainers have become a primary approach to explain GNN models, with various methods proposed to identify the critical substructures responsible for predictions. GNNExplainer (Ying et al., 2019) perturbs graph components to estimate their importance. PGExplainer (Luo et al., 2020) introduces a parametric generator to capture global explanatory signals. GraphMask (Schlichtkrull et al., 2021) and ReFine (Wang et al., 2021) advance explanations through edge selection and multi-grained analysis, respectively. D4Explainer (Chen et al., 2023) adopts diffusion models to generate explanations from random noise. MixupExplainer (Zhang et al., 2023) leverages data augmentation to resist distribution shift. V-InFoR (Wang et al., 2023b) and ProxyExplainer (Chen et al., 2024) employ variational autoencoders to enhance explanation robustness.

Prototype-based GNN explanation methods aim to improve the intrinsic interpretability of GNN models. ProtGNN (Zhang et al., 2022) introduces prototype learning into GNNs, enabling class-specific prototypical subgraphs to serve as intuitive analogical explanations. PAGE (Shin et al., 2024) extends this idea to model-level interpretability by constructing a global prototype dictionary in latent space, offering explanations of the overall decision boundary. Ragno et al. (2024) refine prototype separability and semantic consistency through enhanced architectures and training strategies. Dai & Wang (2025) further integrates prototype learning with self-explaining mechanisms, jointly optimizing prediction and interpretability.

Vector Quantization (VQ) techniques provide a powerful way to discretize continuous embeddings into discrete codewords. Since the number of the codewords tends to be significantly smaller than that of the embeddings to be quantized, VQ thereby clusters similar embeddings into a collection of prototypes. Early successes in domains such as audio (Zeghidour et al., 2021) highlight the capacity of VQ to encode complex signals into compact tokens. Combined with large language models, VQ facilitates the revolution of generative recommender systems (Rajput et al., 2023; Yin et al., 2025). Recent advances in graph community (Yang et al., 2024a) extend this principle to graph data, developing the structure-aware codebooks by tokenizing local substructures.

6 CONCLUSION

We for the first time propose the paradigm shift of GNN explainer optimization framework from the graph label space to the graph representation space, and we design IDEA, the first GNN explainer optimization framework grounded in a prototypical graph representation space. IDEA consists of a structural information disentanglement stage, which disentangles and encapsulates the explanatory substructures into prototypes, and an explanatory prototype alignment stage, which aligns the representational distributions of input graph and explanation unified in the prototypical space. Extensive experiments demonstrate the effectiveness and generalizability of IDEA.

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A NOTATION704
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In Table 4, we summarize the notations used throughout this manuscript and their descriptions.
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Table 4: Notations and corresponding descriptions.
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709 Notation	710 Description
G	711 Graph instance
A, X	712 Adjacency matrix, node feature matrix
N	713 Number of graph nodes
D	714 Node feature dimension
v_i	715 The i -th node
A_{ij}	716 Element at the i -th row, j -th column of adjacency matrix A
y, \hat{y}	717 Graph label, GNN prediction
C	718 Number of graph classes
f, f_e, f_p	719 Graph neural network model, encoder of f , predictor of f
H_N, H_G	720 Node representation matrix, graph representation vector
h_i	721 Node representation of v_i
ψ	722 Post-hoc instance-level GNN explainer
g, g^*	723 Explanatory subgraph (i.e., explanation)
\mathcal{L}_ψ	724 Label preserving loss of ψ
Ω	725 Regularization term
λ_Ω	726 Weighted hyper-parameter of Ω
GQ_S, GQ_D	727 Shallow graph quantizer, deep graph quantizer
$\mathcal{C}_S, \mathcal{C}_D$	728 Codebook of GQ_S , codebook of GQ_D
\mathcal{D}	729 Distance metric of vector quantization
q, q^*	730 Codeword, the nearest codeword
q_S^*, q_D^*	731 The nearest codeword in GQ_S , the nearest codeword in GQ_D
h'_i	732 Residual representation after GQ_S quantization
$\mathcal{L}_Q, \mathcal{L}_S, \mathcal{L}_D$	733 Quantization objective, structure-aware objective, disentanglement objective
Q^*	734 Quantization matrix
σ	735 Sigmoid function
f_d	736 Linear decoder
\hat{y}_S	737 GNN prediction of GQ_S quantized representation
\hat{y}_D	738 GNN prediction of GQ_D quantized representation
\mathcal{U}_c	739 Uniform distribution
\mathcal{L}_{SAD}	740 Structure-aware disentanglement objective
λ_Q, λ_S	741 Weighted hyper-parameter of \mathcal{L}_Q and \mathcal{L}_S
H_G, H_g	742 Representation of original graph, representation of explanation
H'_G	743 Residual representation of H_o after GQ_S quantization
$\mathcal{P}'_G, \mathcal{P}_g$	744 Assignment probability of H'_o and H_e representation of explanation
W_ϵ	745 Entropy-regularized Wasserstein distance
Π, S	746 Transport polytope and cost matrix of W_ϵ
\mathcal{L}_{IDEA}	747 IDEA optimization objective
\mathcal{L}_{Mix}	748 Weighted combination of \mathcal{L}_ψ and \mathcal{L}_{IDEA}
α	749 Weighted parameter in \mathcal{L}_{Mix}

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B EXPERIMENTAL DETAIL751
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Here, we elaborate the details of the evaluated datasets, baselines, and IDEA implementation.
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B.1 DATASET755
The dataset details are introduced as follows and the dataset statistics are summarized in Table 5.
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• **Mutagenicity** (Kazius et al., 2005) is a collection of molecular compounds labeled for their ability
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to cause mutations (i.e., mutagenic vs. non-mutagenic), widely used in cheminformatics and
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toxicology for developing predictive models. Mutagenicity contains 4,337 molecule graphs with
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NO2 and NH2 chemical groups notated as ground truth explanations.

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Table 5: The statistics of the evaluated datasets.

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Statistic	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs
Graphs	4,337	12,000	4,326	8,671	1,000
Average Nodes	30.32	20.58	21.13	21.36	25.00
Average Edges	30.77	43.65	44.95	45.37	50.90
Node Features	14	14	14	14	10
GNN Accuracy	0.8300	0.9054	0.9620	0.9340	1.0
GT Explanation	NO ₂ , NH ₂	Benzene	Alkane + C=O	F ⁻ + C=O	Motif

• **Benzene** (Agarwal et al., 2023) is a binary classification dataset of 12,000 molecular graphs sampled from ZINC15 (Sterling & Irwin, 2015). The goal is to decide whether a molecule contains at least one benzene ring. Within this dataset, the atoms that constitute the benzene ring serve as the ground-truth explanation. Multiple disjoint benzene rings are treated as separate explanations.

• **Alkane-Carbonyl** (Agarwal et al., 2023) is a binary classification set of 4,326 molecular graphs. A positive label marks a molecule that simultaneously contains an unbranched alkane chain and a carbonyl (C=O) group. The ground-truth explanation is defined as the arbitrary union of these two functional fragments present in the structure.

• **Fluoride-Carbonyl** (Agarwal et al., 2023) contains 8,671 molecular graphs. A molecule is labeled positive only if it contains both a fluoride atom (F) and a carbonyl group (C=O). The explanation is defined as the arbitrary union of these two functional units found in the structure.

• **BA-2Motifs** (Ying et al., 2019) is a synthetic binary class dataset designed to benchmark GNN explanation methods. Each graph is labeled by the presence of either a house or a cycle motif, and the respective motif itself provides the ground truth explanation for that class.

We present the accuracy of the to-be-explained GNN model for each dataset in Table 5 as well.

B.2 BASELINE

The evaluated baselines include eight SOTA post-hoc instance-level GNN explainers based on various search strategies. The details are introduced as follows.

• **GNNExplainer** (Ying et al., 2019) is a GNN explainer based on data perturbation that jointly masks edges and node features, then scores their contribution by searching for a subgraph G_S that maximizes the mutual information with the model’s overall prediction \hat{y} .

• **PGEExplainer** (Luo et al., 2020) masks graph topology and uses a learnable neural network to assign edge importance scores, optimizing the same mutual-information objective.

• **GraphMask** (Schlichtkrull et al., 2021) learns an amortized classifier that predicts whether the edge can be dropped (replaced by a learned baseline) for every edge in every GNN layer, without changing the model output, yielding a sparse post-hoc explanation.

• **ReFine** (Wang et al., 2021) adopts a pre-train and fine-tune strategy to probe GNN decisions, delivering multi-granularity insights into the model’s reasoning process.

• **V-InfoR** (Wang et al., 2023b) is a robust GNN explainer specialized for the structurally corrupted graphs, which employs the variational inference to learn the robust graph representations and generalizes the GNN explanation exploration to a graph information bottleneck (GIB) optimization task without any predefined rigorous constraints.

• **D4Explainer** (Chen et al., 2023) a generative explainer for counterfactual and model-level explanations based on a discrete denoising diffusion model, which frames the explanation problem as a distribution learning task for more reliable explanations with better in-distribution property.

• **MixupExplainer** (Zhang et al., 2023) addresses the distribution shifting issue by mixing up the explanation with a randomly sampled base graph structure.

• **ProxyExplainer** (Chen et al., 2024) extends the GIB by innovatively including in-distributed proxy graphs and derives a tractable objective function for practical implementations, where two graph auto-encoders are utilized to generate proxy graphs.

810 B.3 IDEA IMPLEMENTATION
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812 Within the main experiment, we adopt a well-investigated subgraph generator as the backbone im-
813 plementation of the IDEA framework. According to the Gilbert random graph theory, an arbitrary
814 graph G can be represented as a random graph variable, and each edge of G is associated with a
815 binary random variable r to reveal its existence. Additionally, the existence of one edge is con-
816 ditionally independent of the other edges. $\varepsilon_{ij} = 1$ means there is an edge (i, j) from v_i to v_j ,
817 otherwise $\varepsilon_{ij} = 0$. Hence, an arbitrary graph G can be represented as follows,

$$818 \quad p(G) = \prod_{(i,j)} p(\varepsilon_{ij}). \quad (14)$$

821 A common instantiation of the binary variable ε_{ij} is the Bernoulli distribution $\varepsilon_{ij} \sim \text{Bern}(\varrho_{ij})$,
822 where $\varrho_{ij} = p(\varepsilon_{ij} = 1)$ is the probability of edge (i, j) existing in the random graph G . Since
823 the Bernoulli distribution cannot be directly optimized, we introduce categorical reparameterization
824 (Jang et al., 2017) to ε_{ij} . The continuous relaxation of ε_{ij} can be formulated as follows,

$$825 \quad \varepsilon_{ij} = \sigma\left(\frac{\log \mathcal{U} - \log(1 - \mathcal{U}) + \mu_{ij}}{\tau}\right), \quad \mu_{ij} = \log \frac{\varrho_{ij}}{1 - \varrho_{ij}}, \quad \mathcal{U} \sim \text{Uniform}(0, 1). \quad (15)$$

826 where τ controls the approximation between the relaxed distribution and $\text{Bern}(\varrho_{ij})$. When τ ap-
827 proaches 0, the limitation of Eq.(15) is $\text{Bern}(\varrho_{ij})$.

828 According to Eq.(15), the Bernoulli parameter ϱ_{ij} is associated with the parameter μ_{ij} . To enable
829 end-to-end optimization, we use a multi-layer perceptron (MLP) to compute μ_{ij} . The MLP takes
830 the GNN node representation as input and concatenates the representations of two nodes v_i, v_j as
831 the representation of the corresponding edge (i, j) , which can be formulated as follows,

$$832 \quad \mu_{ij} = \text{MLP}([h_i \| h_j]), \quad (16)$$

833 where $[\cdot \| \cdot]$ is the concatenation operator. Based on $\mu = \{\mu_{ij} | i, j = 1, 2, \dots, N\}$ and Eq.(15), we
834 obtain the probability matrix M_μ whose elements indicate the existence of the corresponding edges.
835 Afterwards, we can sample the explanation g based on the probabilities in the matrix M_μ as follows,

$$836 \quad g = (X_S, A_S = M_\mu \odot A). \quad (17)$$

837 So far, we have derived the optimizable representation of g utilized in IDEA. All experiments are
838 finished on a machine with 4 NVIDIA GeForce RTX 3090 24GiB GPUs.

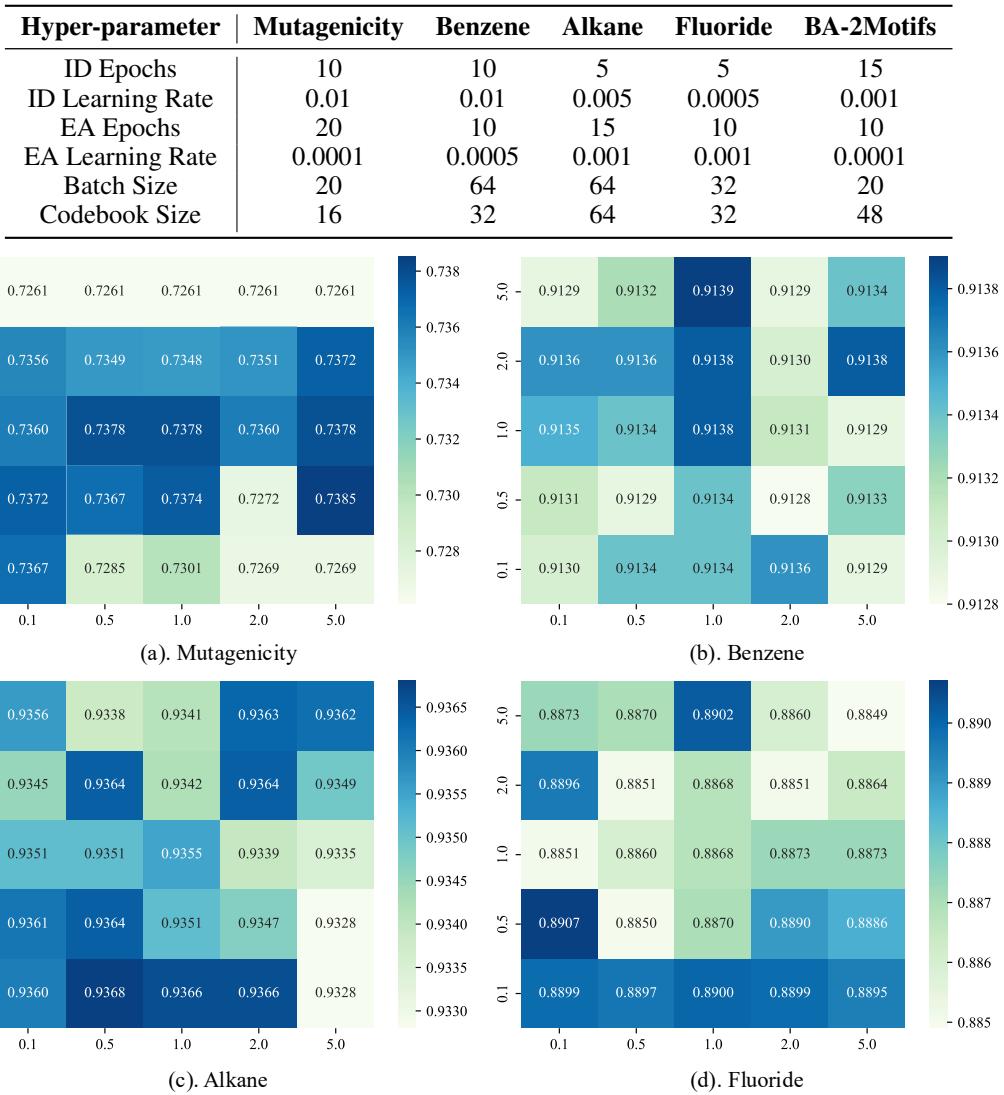
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841 B.4 STEP-BY-STEP BREAKDOWN OF HGTOKENIZER
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843 Given the input embedding $h_i \in \mathbb{R}^{1 \times d}$, the shallow codebook $\mathcal{C}_S \in \mathbb{R}^{K \times d}$, and the deep codebook
844 $\mathcal{C}_D \in \mathbb{R}^{K \times d}$, the details of HGTokenizer process are elaborated as follows.

- 845 • Step 1. Feed the input embedding h_i into the shallow quantizer. The shallow quantizer first
846 calculates the pair-wise distance between h_i and each codeword $q \in \mathbb{R}^{1 \times d}$ within the shallow
847 codebook \mathcal{C}_S . Afterwards, the shallow quantizer select the closest codeword to h_i according to
848 the K -dimensional distance vector. Step 1 is formulated by the formula $q_{S,i}^* = \text{GQ}_S(h_i) =$
849 $\arg \min_{q \in \mathcal{C}_S} \mathcal{D}(q, h_i)$ in Equation 2.
- 850 • Step 2. Calculate the quantization residual of the shallow quantizer, which is formulated by the
851 formula $h'_i = h_i - q_{S,i}^*$ in Equation 2.
- 852 • Step 3. Feed the residual embedding h'_i into the deep quantizer, the detailed quantization
853 process in the same the that in Step 1. The deep quantizer will select the closest codeword
854 $q_{D,i}^* = \text{GQ}_D(h'_i) = \arg \min_{q \in \mathcal{C}_D} \mathcal{D}(q, h'_i)$, as shown in Equation 3.

855 Subsequently, the quantized representations $q_{S,i}^*$ and $q_{D,i}^*$ provide by the shallow and deep quantizers
856 are used to compute the disentanglement loss \mathcal{L}_D . The sum of them, i.e., $q_i^* = q_{S,i}^* + q_{D,i}^*$ in Equation
857 3, is used to compute the structure-awareness loss \mathcal{L}_S .

Table 6: The optimal configuration of hyper-parameters in IDEA.

Figure 5: Explanation performance (ROC-AUC \uparrow) versus the weighted parameter λ_Q (y-axis) and λ_S (x-axis) in the SAD objective, on (a). Mutagenicity, (b). Benzene, (c).Alkane, and (d). Fluoride.

C HYPER-PARAMETER ANALYSIS

In Table 6, we summarize the optimal configuration of hyper-parameters in IDEA for each dataset.

C.1 STRUCTURE-AWARE DISENTANGLEMENT OBJECTIVE

Here, we investigate the impact of the weighted parameters λ_Q and λ_S in the strcuture-aware disentanglement objective defined as Eq.7,

$$\mathcal{L}_{\text{SAD}} = \mathcal{L}_D + \lambda_S \cdot \mathcal{L}_S + \lambda_Q \cdot \mathcal{L}_Q.$$

The evaluated result is presented in Figure 5. As the weighted hyper-parameters range from 0.1 to 5.0, we can notice that the optimal performance is more likely to be achieved when the objective weights are balanced, i.e., along the diagonal direction of the heatmap. For the Mutagenicity and Benzene datasets, the best performance is achieved by setting $\lambda_S = \lambda_Q = 1.0$. For the Alkane and Fluoride datasets, the best configurations of weighted parameters are $\lambda_S = 0.5, \lambda_Q = 0.1$ and $\lambda_S = 0.1, \lambda_Q = 0.5$, without severe unbalance.

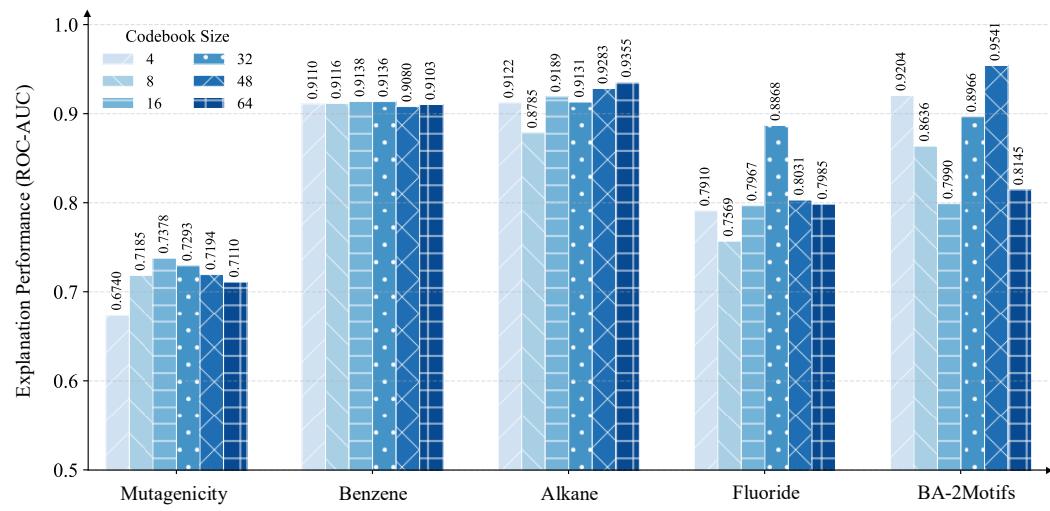


Figure 6: Explanation performance (ROC-AUC \uparrow) versus the codebook size in IDEA framework, on Mutagenicity, Benzene, Alkane, Fluoride, and BA-2Motifs datasets.

Table 7: Runtime (Second \downarrow) of four native explainers with different architectures and the corresponding IDEA variants. *Times* is defined as IDEA/Native.

Model	Mutagenicity	Benzene	Alkane	Fluoride	Average
PGExplainer +IDEA <i>Times</i>	4.92	3.80	2.24	6.67	4.41
	14.53	10.34	5.43	19.13	12.36
	2.95	2.72	2.42	2.87	2.80
ReFine +IDEA <i>Times</i>	13.14	39.44	13.21	28.10	23.47
	21.04	61.90	20.29	50.45	38.42
	1.60	1.57	1.54	1.80	1.64
V-InFoR +IDEA <i>Times</i>	5.31	11.70	7.17	18.69	10.72
	13.66	29.19	19.25	45.48	26.90
	2.57	2.49	2.68	2.43	2.51
ProxyExplainer +IDEA <i>Times</i>	20.90	15.23	7.33	14.82	14.57
	21.52	16.52	7.90	15.85	15.45
	1.03	1.08	1.08	1.07	1.06

C.2 CODEBOOK SIZE

In this section, we investigate the impact of the codebook size, i.e., the number of the codewords within the graph quantizer. As shown in Figure 6, the codebook size ranges among $\{4, 8, 16, 32, 48, 64\}$. In general, a codebook with appropriate size can improve the explanation performance, since it serves as the foundation during structural information disentanglement and explanatory prototype modeling. For the Fluoride dataset, a codebook consisting of 8 codewords causes a performance degradation by 0.1299.

D EXPLANATION VISUALIZATION

From Figure 7 to Figure 10, we present the explanation visualization of the ground truth, IDEA, and four SOTA GNN explainers based on the label preserving framework.

As shown in Figure 7, only IDAE assigns the highest importance score to NH_2 . PGExplainer and ProxyExplainer assign medium scores to NH_2 , V-InFoR identifies part of the NH_2 group, and GNNExplainer fails to detect NH_2 . In Figure 8, IDEA, PGExplainer, and ProxyExplainer successfully identify the benzene ring. In particular, IDEA detects the two rings within the molecule, while

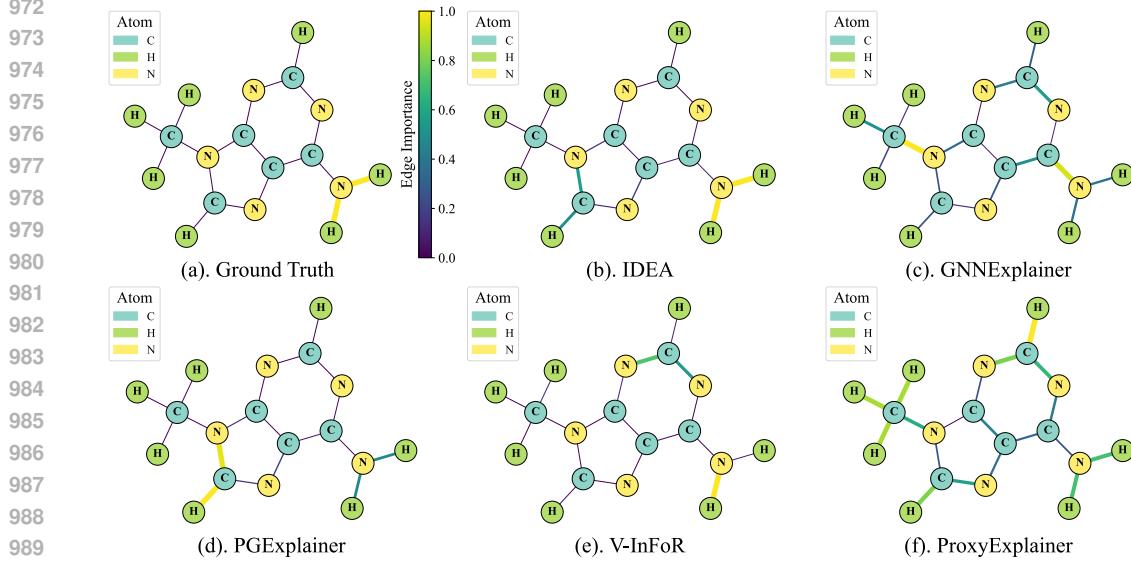


Figure 7: Explanation visualization of ground truth, IDAE, and four baselines on Mutagenicity.

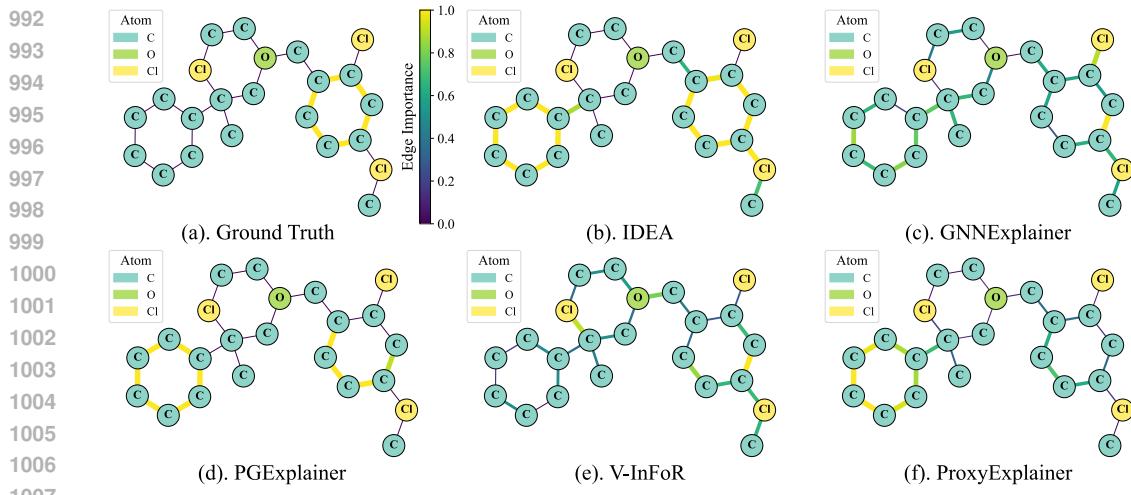


Figure 8: Explanation visualization of ground truth, IDAE, and four baselines on Benzene.

1010 PGExplainer and ProxyExplainer notice only part of the second benzene ring. GNNExplainer and
1011 V-InFoR fail to assign high scores to the benzene rings. For the Alkane dataset, IDEA and GNNExplainer
1012 identify the chlorine atom Cl as the explanation, yet the other three explainers completely
1013 ignore the influential substructures. In Figure 10, only IDEA and V-InFoR can discriminate the
1014 explanatory structure from the confounding structures to some extent. The other three explainers
1015 assign nearly identical scores to all edges.

E TIME COMPLEXITY

1019 In this section, we first provide a theoretical analysis of the time complexity of the IDEA framework.
1020 Then, we report the runtime of diverse explainer architectures, incorporating with both the IDEA
1021 framework and the label preserving framework. Given the node presentation matrix $H_N \in \mathbb{R}^{N \times d}$,
1022 HGTokenizer approximates it by two graph quantizers, including two matrix multiplication operations
1023 and two argmin operations. The codebook within the graph quantizer belongs to a matrix in
1024 $\mathbb{R}^{K \times d}$. Hence, the time complexity of quantization distance \mathcal{D} is
1025

$$\vartheta_{\mathcal{D}} = NKd. \quad (18)$$

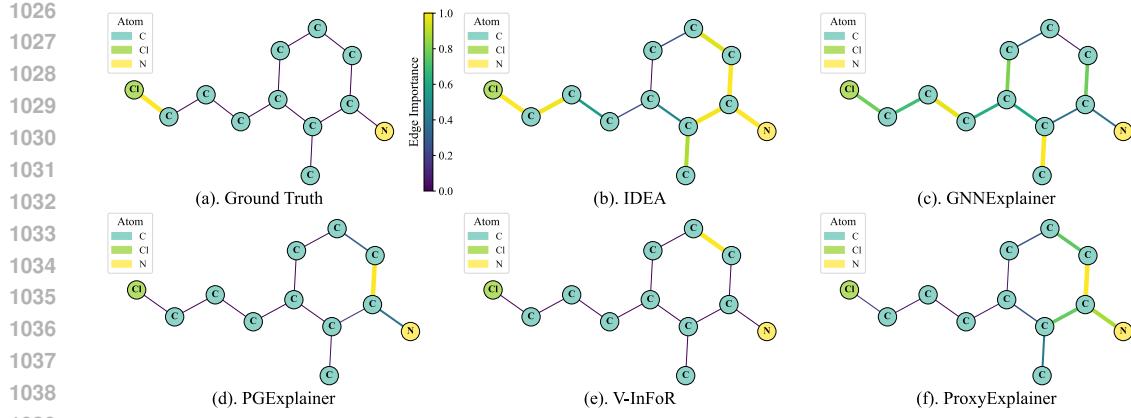


Figure 9: Explanation visualization of ground truth, IDEAE, and four baselines on Alkane.

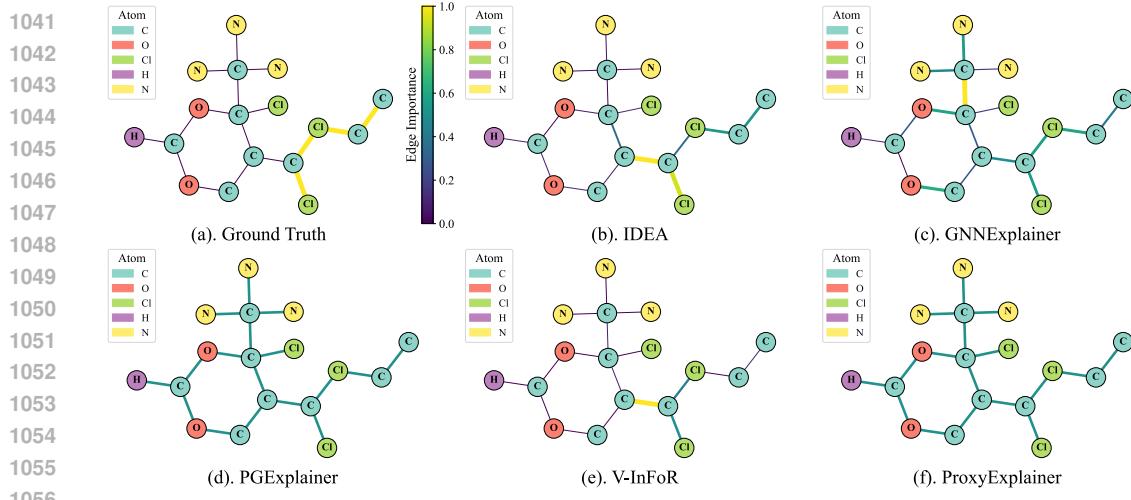


Figure 10: Explanation visualization of ground truth, IDEAE, and four baselines on Fluoride.

Since the time complexity of argmin is NK , the total complexity of HGTokenizer is

$$\vartheta_{\text{HGT}} = 2NK(d+1). \quad (19)$$

Therefore, the complexity of IDEAE, including the structural information disentanglement and the explanatory prototype alignment, is derived as,

$$\vartheta_{\text{IDEAE}} = 2NK(d+1) + 3K(d+1) = O(NKd). \quad (20)$$

According to Eq.20, the time complexity is linear to the node number of input graph, the codebook size, and the hidden dimension of target GNN.

In Table 7, we report the runtime of four different GNN explainers and their counterparts shifted to the IDEAE framework. One can note that the runtime of IDEAE variants is of the same magnitude, compared with the native explainer adopting the label preserving framework.

F SUPPLEMENTARY EXPERIMENT

F.1 WEIGHTED COMBINATION

As a natural expansion, we integrate IDEAE with the label preserving framework and the mixed optimization objective is defined as the convex combination as follows,

$$\mathcal{L}_{\text{Mix}} = \alpha \cdot \mathcal{L}_{\text{IDEAE}} + (1 - \alpha) \cdot \mathcal{L}_{\psi}, \quad 0 \leq \alpha \leq 1, \quad (21)$$

where \mathcal{L}_{ψ} denotes the label preserving loss. Typically, \mathcal{L}_{ψ} is defined as the mutual information between the predictions of the input graph and the explanation subgraph, i.e., $\text{MI}(\hat{y}, \hat{y}_g)$. The evaluate

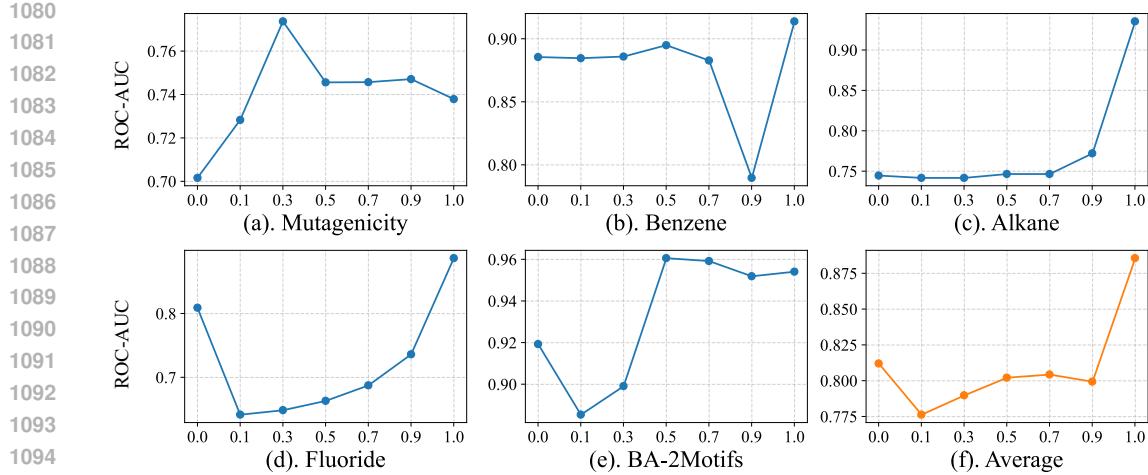


Figure 11: Explanation performance (ROC-AUC \uparrow) of the combination of the IDEA objective and the label preserving objective, on Mutagenicity, Benzene, Alkane, Fluoride, and BA-2Motifs.

Table 8: Explanation performance (ROC-AUC \uparrow) of IDEA and the conjoint variant.

Model	Mutagenicity	Benzene	Alkane	Fluoride	Average
IDEA	0.7379	0.9138	0.9319	0.8868	0.8676
IDEA-Joint	0.4805	0.5447	0.8725	0.8349	0.6832

results reveal that the effectiveness of the integration depends on the specific dataset. For the Mutagenicity dataset, the integration with α equals 0.3 achieves a significant improvement over both IDEA and the label preserving framework. However, for the Benzene, Alkane, and Fluoride datasets, the weighted integration is inferior to both IDEA and the label preserving framework, which might be caused by the counteract effect between the two optimization objectives.

F.2 CONJOINT OPTIMIZATION OF IDEA

In our main experiment, IDEA is a dual-stage framework, where the Structural Information Disentanglement and the Explanatory Prototype Alignment are conducted separately. The dual stage implementation not only reduces the difficulty of IDEA optimization, but also avoids the counteraction effect between the optimization objectives. To empirically validate the rationality of dual-stage IDEA, we further implement an IDAE variant *IDEA-Joint* where the two stages are conducted jointly. The optimization objective of *IDEA-Joint* is defined as follows,

$$\mathcal{L}_{\text{Joint}} = \mathcal{L}_{\text{IDAE}} + \lambda_{\text{SAD}} \cdot \mathcal{L}_{\text{SAD}}, \quad (22)$$

with $\mathcal{L}_{\text{IDEA}}$ and \mathcal{L}_{SAD} defined by Eq.11 and Eq.7, respectively. In Table 8, we present the performance comparison between IDEA and the conjoint variant, within the same hyper-parameter search range. We can notice the evident gap between *IDEA-Joint* and IDEA, which implies the difficulty of *IDEA-Joint* optimization, despite a possible performance upper bound better than IDEA.

F.3 ROBUSTNESS TO LABEL NOISE

To investigate the robustness of the IDEA explainer to label noise (Zhong et al., 2023), we perturb the information disentanglement stage by flipping the GNN prediction \hat{y} in Eq.5 and present the result in Table 9. For comparision, we evaluate the explanation performance of two typical explainers, i.e., GNNExplainer (Ying et al., 2019) and PGEExplainer (Luo et al., 2020), with the same setting of label noise. Specifically, the intensity of the label noise ranges from 0.00% to 50.00%, with an interval of 5.00%. As shown by the result, the IDEA explainer stably maintains the high quality of the generated explanation, with the maximum performance degradation of 0.0076 and 0.0070 in the Mutagenicity and Benzene datasets, respectively. In contrast, two typical GNN explainers based on

1134
 1135 Table 9: Explanation performance (ROC-AUC \uparrow) versus label noise intensity on Mutag and Benzene
 1136 datasets. Δ_{\max} presents the maximum performance degradation with noise intensity increasing.

Noise Intensity	Mutagenicity			Benzene		
	GNNEExplainer	PGExplainer	IDEA	GNNEExplainer	PGExplainer	IDEA
0.00%	0.6155	<u>0.7016</u>	0.7379	0.6886	<u>0.8855</u>	0.9138
5.00%	0.6140	<u>0.6989</u>	0.7358	0.6662	<u>0.8856</u>	0.9128
10.00%	0.6063	<u>0.6824</u>	0.7359	0.6505	<u>0.8856</u>	0.9135
15.00%	0.5937	<u>0.6819</u>	0.7363	0.6326	<u>0.8860</u>	0.9139
20.00%	0.5954	<u>0.6810</u>	0.7320	0.6149	<u>0.5784</u>	0.9132
25.00%	0.5965	<u>0.6805</u>	0.7366	0.5966	<u>0.5931</u>	0.9128
30.00%	0.6050	<u>0.6802</u>	0.7319	0.5788	<u>0.5932</u>	0.9128
35.00%	0.6048	<u>0.6801</u>	0.7303	0.5636	<u>0.6302</u>	0.9132
40.00%	0.6065	<u>0.6798</u>	0.7366	0.5431	<u>0.6591</u>	0.9131
45.00%	0.6048	<u>0.6795</u>	0.7327	0.5282	<u>0.7033</u>	0.9068
50.00%	0.6058	<u>0.6791</u>	0.7328	0.5056	<u>0.7340</u>	0.9130
$\Delta_{\max} \downarrow$	<u>0.0218</u>	0.0225	0.0076	<u>0.1830</u>	0.3071	0.0070

1151 the label preserving framework, GNNEExplainer and PGExplainer, suffer from severe performance
 1152 degradation, which is $14.03 \times$ times and $22.58 \times$ times greater than that of IDEA.

G THEORETICAL JUSTIFICATION

1156 During the explanatory prototype alignment stage, we adopt the assignment probability of the input
 1157 representation (H'_G or H_g) over the explanatory codebook \mathcal{C}_D to reflect its location within the pro-
 1158 tototypical representation space. In this section, we elaborate the justification of this practice. Within
 1159 the explanatory codebook \mathcal{C}_D , we have K prototype codewords $\{q_1, q_2, \dots, q_K\} \subset \mathbb{R}^d$, which ex-
 1160 pand the prototypical representation space. Taking the prototype codewords $\{q_1, q_2, \dots, q_K\}$ as the
 1161 anchors, the L_2 distance between the input representation h and the anchor q_k is

$$\varphi_k = \|h - q_k\|^2 = h^T h + q_k^T q_k - 2q_k^T h. \quad (23)$$

1164 For $k \geq 2$, by subtracting $\varphi_1 = \|h - q_1\|^2$, we can derive the following equation

$$\varphi_k - \varphi_1 = (q_k^T q_k - q_1^T q_1) - 2(q_k - q_1)^T h, \quad (24)$$

1166 which is equivalent to the equation below,

$$(q_k - q_1)^T h = \frac{1}{2} (q_k^T q_k - q_1^T q_1 + \varphi_1 - \varphi_k). \quad (25)$$

1170 For $k = 2, 3, \dots, K$, stacking $(q_k - q_1)^T h$ induces the following equation in matrix formulation,

$$\begin{bmatrix} (q_2 - q_1)^T \\ (q_3 - q_1)^T \\ \vdots \\ (q_K - q_1)^T \end{bmatrix} h = \frac{1}{2} \begin{bmatrix} q_2^T q_2 - q_1^T q_1 + \varphi_1 - \varphi_2 \\ q_3^T q_3 - q_1^T q_1 + \varphi_1 - \varphi_3 \\ \vdots \\ q_K^T q_K - q_1^T q_1 + \varphi_1 - \varphi_K \end{bmatrix}, \quad (26)$$

1176 which can be briefly noted as

$$Ah = b, \quad A \in \mathbb{R}^{(K-1) \times d}, \quad b \in \mathbb{R}^{(K-1)}. \quad (27)$$

1180 Theoretically, the prototype codewords and the induced prototypical representation space are gen-
 1181 erated by a collection of latent variables $\{z_1, z_2, \dots, z_t\} \subset \mathbb{R}^{d'}$ with $d' < d$, which objectively
 1182 determine the explanatory substructures while being unobservable. Therefore, Eq.27 implies a coun-
 1183 terpart in the latent space $\mathbb{R}^{d'}$ as follows,

$$A'h' = b', \quad A' \in \mathbb{R}^{(K-1) \times d'}, \quad b' \in \mathbb{R}^{(K-1)}. \quad (28)$$

1186 In this equation, when $K \geq d' + 1$, h' has a unique solution. Therefore, we adopt the assignment
 1187 probability based on the quantization distance to indicate the location of the input representation,
 instead of training an additional projector.

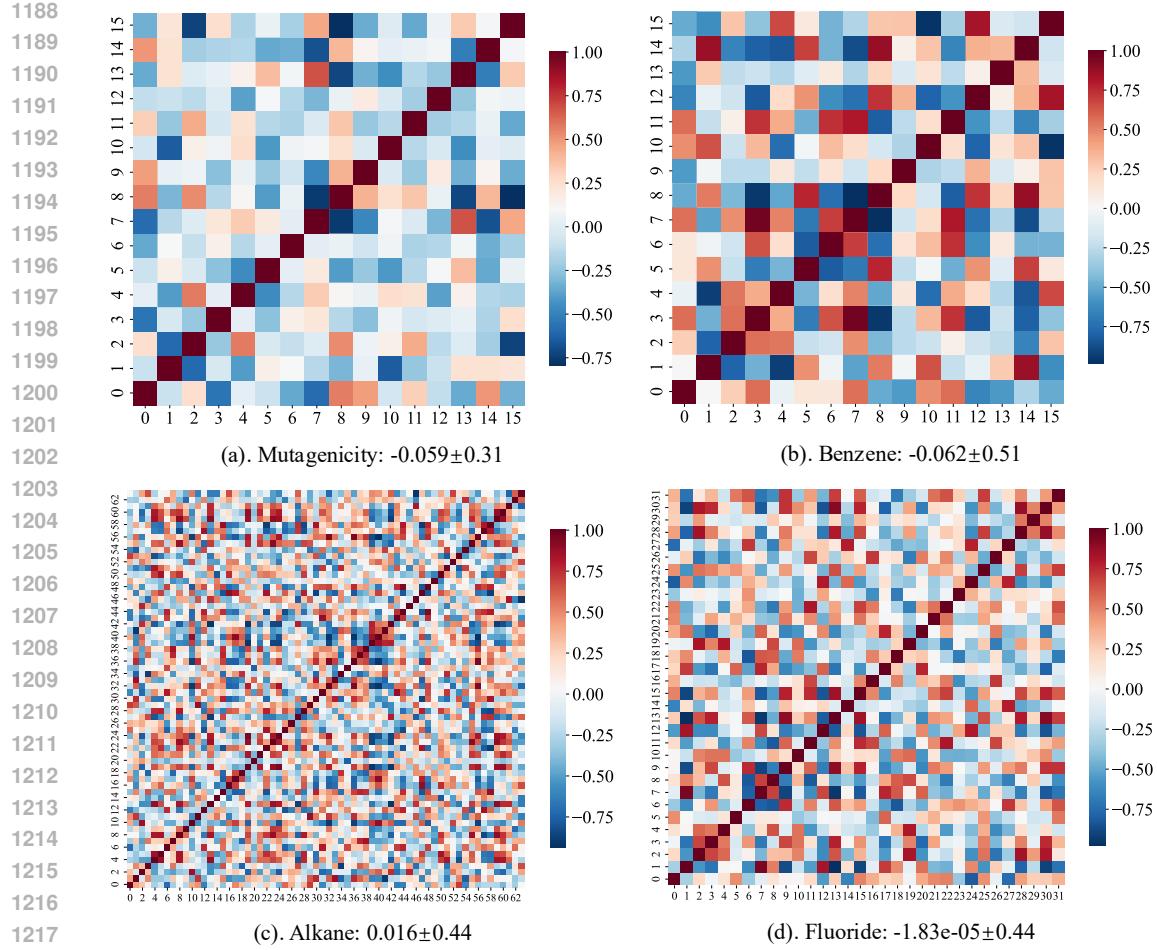


Figure 12: Pair-wised cosine similarity of codewords. The number behind the dataset name represents Mean \pm Std.

We denote the unknown mapping function from the latent space $\mathbb{R}^{d'}$ to the prototypical space \mathbb{R}^d as $\mathcal{H} : \mathbb{R}^{d'} \rightarrow \mathbb{R}^d$. For two representations $x, y \in \mathbb{R}^d$, the corresponding representations in $\mathbb{R}^{d'}$ are denoted as $x' = \mathcal{H}^{-1}(x)$ and $y' = \mathcal{H}^{-1}(y)$. In our method, we minimize the difference between the assignment probabilities of x and y over the prototypes $\{q_1, q_2, \dots, q_K\}$, in order to minimize the distance between x' and y' in the latent space. Theoretically, the strict validity of this measurement lies in three conditions. First, $K \geq d'$, which holds with large probability. Second, the prototype representations $\{q_1, q_2, \dots, q_K\}$ are linearly independent. As illustrated in Figure 12, we present the cosine similarity of the codewords, demonstrating that the codewords approximately satisfy the linearly independent requirement. Third, the hypothetical mapping function \mathcal{H} is linear or can be approximated by linear functions.

H PROTOTYPE CASE STUDY

Assignment Probability. First, to explore the implicit relationship between the prototypical embeddings (i.e., codebooks) and human-intelligible substructures, we present the assignment probabilities distribution in Figure 13. Specifically, for real-world dataset Benzene and synthetic dataset BA-2Motifs, we visualize the average probabilistic distributions of class 0 and class 1 over the shallow and deep codebooks. For the real-world dataset Benzene, the distributions of class 0 and class 1 over the shallow codebook are similar, and the codeword 5 with the largest probability may correspond to the most frequent non-explanatory substructure (carbon-chlorine bond). On the deep codebook, the distribution patterns obviously differ. For the deep codebook, the codeword 0 may correspond to

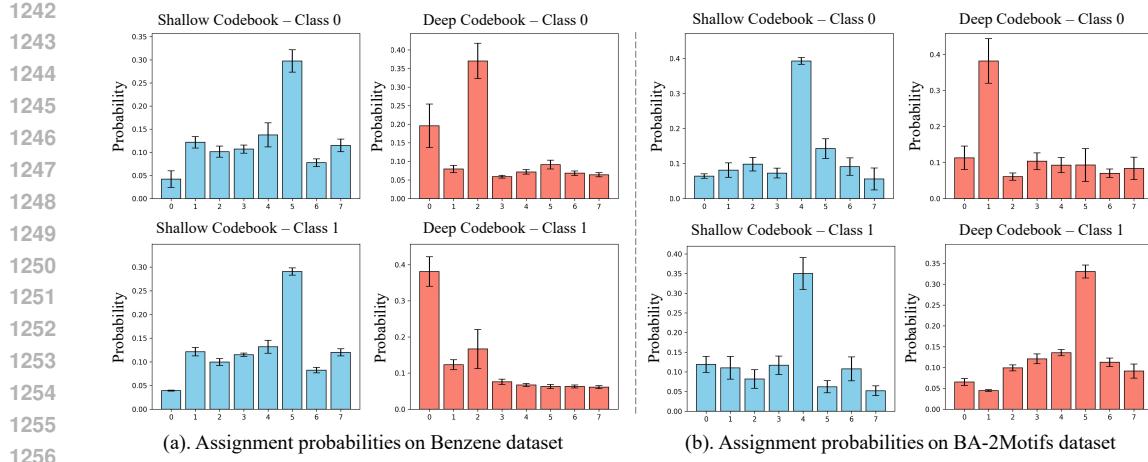


Figure 13: Average probabilistic distributions over the shallow and deep codebooks on (a). Benzene dataset and (b). BA-2Motifs dataset.

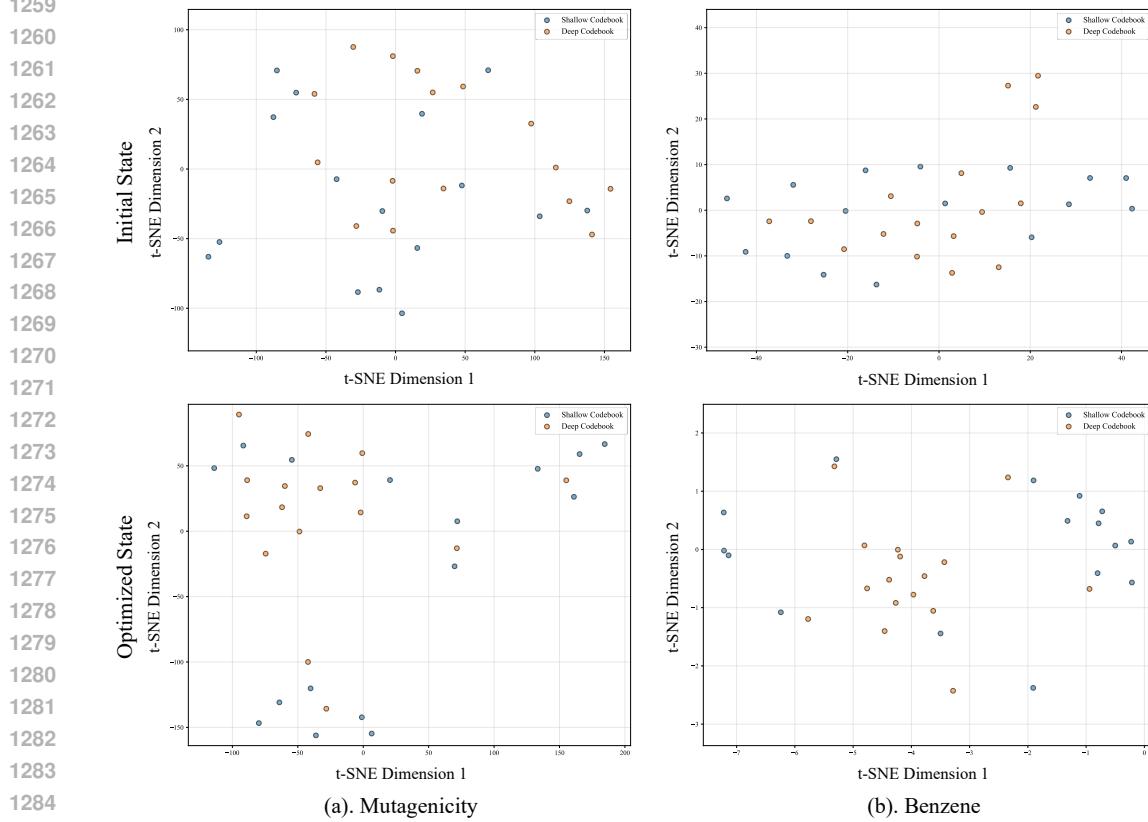


Figure 14: t-SNE visualization of codewords on (a). Mutagenicity dataset and (b) Benzene dataset.

the benzene rings which directly decides the labels of class 1, and the codeword 2 may correspond to the carbon-oxygen bond which is common in class 0. For the synthetic dataset BA-2Motifs, the shallow distribution patterns of class 0 and class 1 are also similar. The deep shallow distribution has two peaks, i.e., codeword 1 and codeword 5, which may correspond to the two kinds of motifs in BA-2Motifs. To sum up, the similar distribution pattern on shallow codebook and significantly different patterns on deep codebook can indicate that the learned prototypes in codebooks are implicitly related to substructures.

t-SNE Visualization. Furthermore, we visualize the learned codewords in shallow and deep codebooks based on t-SNE algorithm (van der Maaten & Hinton, 2008). As shown by Figure 14 and

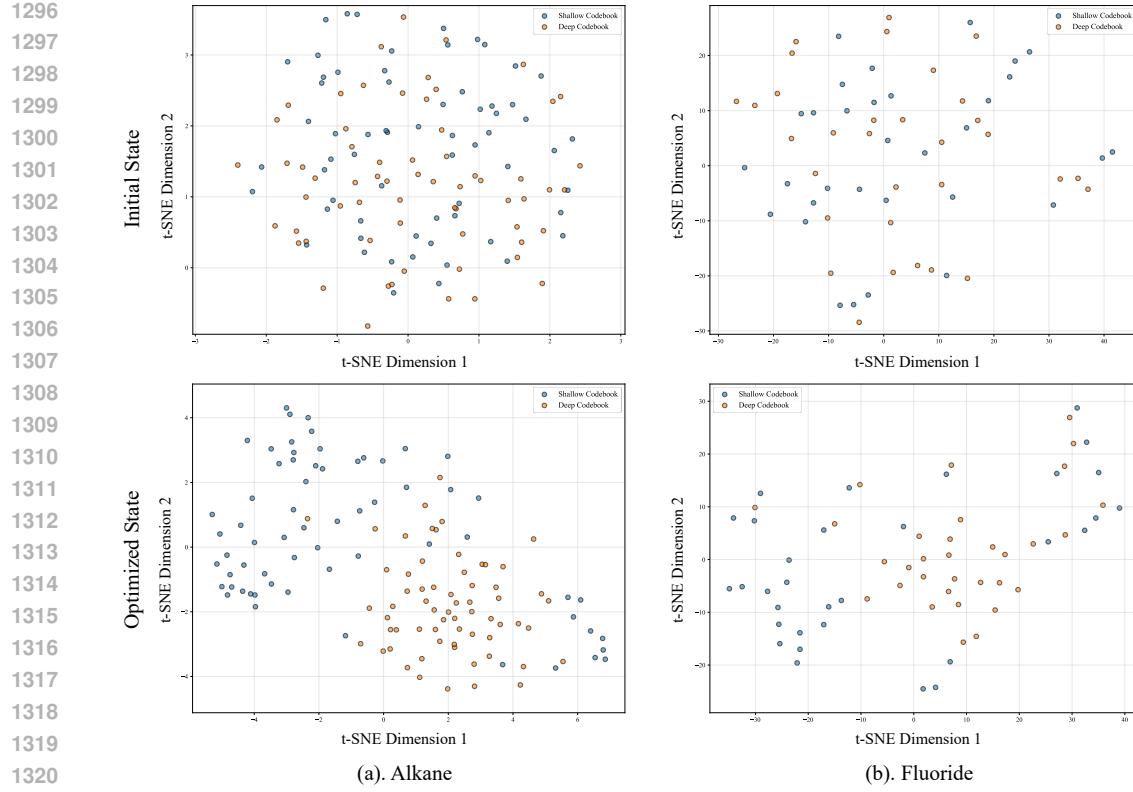


Figure 15: t-SNE visualization of codewords on (a). Alkane dataset and (b) Fluoride dataset.

Table 10: Explanation performance (Fidelity₊ \uparrow) of IDEA and SOTA baselines across five datasets.

Fidelity ₊	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs
GNNEExplainer	0.2136 \pm 0.0005	0.5614 \pm 0.0005	0.5435 \pm 0.0130	0.1242 \pm 0.0026	0.4067 \pm 0.0033
PGExplainer	0.2012 \pm 0.0097	0.7250 \pm 0.0028	0.7826 \pm 0.0063	0.4097 \pm 0.0118	0.4375 \pm 0.0030
GraphMask	0.0982 \pm 0.0080	0.4450 \pm 0.0169	0.5659 \pm 0.0180	0.2070 \pm 0.0029	0.3750 \pm 0.0043
ReFine	0.2161 \pm 0.0041	0.5690 \pm 0.0048	0.6224 \pm 0.0033	0.6132 \pm 0.0077	0.2068 \pm 0.0024
V-InFoR	0.1954 \pm 0.0004	0.5265 \pm 0.0031	0.6883 \pm 0.0013	0.6298 \pm 0.0005	0.3793 \pm 0.0058
D4Explainer	0.0698 \pm 0.0181	0.5248 \pm 0.0080	0.6093 \pm 0.0058	0.6047 \pm 0.0026	0.2127 \pm 0.0014
MixupExplainer	0.1277 \pm 0.0074	0.4910 \pm 0.0047	0.4579 \pm 0.0053	0.3672 \pm 0.0009	0.2131 \pm 0.0082
ProxyExplainer	0.1841 \pm 0.0132	0.7473 \pm 0.0118	0.6904 \pm 0.0052	0.6607 \pm 0.0351	0.3064 \pm 0.0027
IDEA	0.2207 \pm 0.0093	0.8292* \pm 0.0081	0.8043* \pm 0.0160	0.6988* \pm 0.0042	0.4450* \pm 0.0004
Improvement	2.13%	10.96%	2.77%	5.77%	1.71%

Figure 15, the first row presents the t-SNE visualization of the initial codewords, and the second row presents that of the codewords after optimization, i.e., prototypes. We can notice that in the initial state, the shallow and deep codewords mix together without clear boundary. After optimization, the deep codewords are approximately separable from the shallow ones. The deep codewords prefer to cluster into a mass, while the shallow codewords still distribute dispersedly.

I FAITHFULNESS EVALUATION

To comprehensively evaluate the effectiveness of IDEA, we present faithfulness metrics based on fidelity in this section (Amara et al., 2022). Specifically, Fidelity₊ measures the change degree of the GNN prediction after removing the explanation subgraph, Fidelity₋ measures the change degree

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Table 11: Explanation performance (1-Fidelity \uparrow) of IDEA and SOTA baselines.

1-Fidelity \downarrow	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs
GNNEExplainer	0.5975 \pm 0.0053	0.4370 \pm 0.0051	0.1658 \pm 0.0070	0.2679 \pm 0.0114	0.7366 \pm 0.0031
PGExplainer	0.7714 \pm 0.0165	0.5222 \pm 0.0037	0.3787 \pm 0.0048	0.2232 \pm 0.0167	0.9055 \pm 0.0033
GraphMask	0.6174 \pm 0.0032	0.4365 \pm 0.0065	0.2683 \pm 0.0058	0.1487 \pm 0.0013	0.5005 \pm 0.0051
ReFine	0.6604 \pm 0.0044	0.5056 \pm 0.0082	0.3237 \pm 0.0022	0.2863 \pm 0.0104	0.8330 \pm 0.0140
V-InFoR	0.6375 \pm 0.0020	0.4524 \pm 0.0039	0.3886 \pm 0.0070	0.2871 \pm 0.0004	0.7872 \pm 0.0093
D4Explainer	0.6451 \pm 0.0240	0.4497 \pm 0.0019	0.3691 \pm 0.0086	0.2577 \pm 0.0151	0.9710 \pm 0.0038
MixupExplainer	0.6745 \pm 0.0115	0.4962 \pm 0.0063	0.3750 \pm 0.0014	0.2665 \pm 0.0051	0.9513 \pm 0.0077
ProxyExplainer	0.7912 \pm 0.0058	0.6483 \pm 0.0156	0.4191 \pm 0.0028	0.3594 \pm 0.0177	0.9697 \pm 0.0062
IDEA	0.8018 * \pm 0.0086	0.6964 * \pm 0.0148	0.4190 \pm 0.0158	0.3612 * \pm 0.0010	0.9981 * \pm 0.0003
Improvement	1.34%	7.42%	-0.02%	5.00%	2.93%

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Table 12: Explanation performance (Harmonic mean \uparrow) of IDEA and SOTA baselines.

Harmonic Mean	Mutagenicity	Benzene	Alkane	Fluoride	BA-2Motifs
GNNEExplainer	0.3146 \pm 0.0013	0.4914 \pm 0.0031	0.2541 \pm 0.0096	0.1696 \pm 0.0019	0.5240 \pm 0.0035
PGExplainer	0.3191 \pm 0.0136	0.6071 \pm 0.0035	0.5104 \pm 0.0056	0.2888 \pm 0.0169	0.5899 \pm 0.0034
GraphMask	0.1693 \pm 0.0119	0.4404 \pm 0.0069	0.3640 \pm 0.0089	0.1731 \pm 0.0019	0.4287 \pm 0.0031
ReFine	0.3256 \pm 0.0051	0.5354 \pm 0.0066	0.4259 \pm 0.0027	0.3903 \pm 0.0110	0.3313 \pm 0.0036
V-InFoR	0.2991 \pm 0.0006	0.4866 \pm 0.0035	0.4967 \pm 0.0060	0.3944 \pm 0.0005	0.5119 \pm 0.0063
D4Explainer	0.1254 \pm 0.0301	0.4843 \pm 0.0042	0.4597 \pm 0.0080	0.3612 \pm 0.0152	0.3490 \pm 0.0021
MixupExplainer	0.2146 \pm 0.0106	0.4935 \pm 0.0034	0.4123 \pm 0.0030	0.3088 \pm 0.0037	0.3481 \pm 0.0106
ProxyExplainer	0.2985 \pm 0.0178	0.6943 \pm 0.0140	0.5216 \pm 0.0036	0.4655 \pm 0.0232	0.4657 \pm 0.0036
IDEA	0.3460 * \pm 0.0114	0.7569 * \pm 0.0119	0.5509 * \pm 0.0171	0.4762 \pm 0.0018	0.6156 * \pm 0.0004
Improvement	6.26%	9.02%	5.62%	2.30%	4.36%

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of the GNN prediction when only retain the explanation subgraph, formally defined as follows,

$$\text{Fidelity}_+ = 1 - \frac{1}{|\mathcal{G}_{\text{test}}|} \sum_i \mathbb{I}(f(G_i \setminus g_i) = f(G_i)), \quad (29)$$

$$\text{Fidelity}_- = 1 - \frac{1}{|\mathcal{G}_{\text{test}}|} \sum_i \mathbb{I}(f(g_i) = f(G_i)), \quad (30)$$

where $\mathcal{G}_{\text{test}}$ is the test set, f is the target GNN model, G_i is the i -th test graph sample, and g_i is the corresponding explanation subgraph identified by GNN explainer.For readability, we report Fidelity_+ , 1-Fidelity_- , and their harmonic mean in Tables 10, 11, and 12 respectively, which are better when they are higher and belong to $[0, 1]$. The results also demonstrate the superiority of IDEA when compared with the SOTA baselines.

J LIMITATION

Accessibility to target GNN. According to the taxonomy of GNN explanation methods, the accessibility of the GNN explainer to the target GNN to be explained can be categorized into black-box, gray-box, and white-box. The black-box accessibility takes the GNN model as an oracle and only requires the GNN predictions. On the contrary, the white-box accessibility demands the permission to the model internal parameters or the model gradients (Pope et al., 2019). Actually, IDEA requires the gray-box accessibility to utilize the GNN encoded representations, which limits the application of IDEA to completely black-box GNN models.

Approximately linear assumption on unknown mapping function \mathcal{H} . In Appendix G, we introduce a unobserved function \mathcal{H} that maps the latent space $\mathbb{R}^{d'}$ to our prototypical space \mathbb{R}^d . The strict

1404 validity of $\mathcal{L}_{\text{IDEA}}$ in the explanatory prototype alignment stage necessitates that \mathcal{H} is approximately
1405 linear at least. Hence, a highly non-linear function \mathcal{H} might become a potential limitation of IDEA.
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1409 K FUTURE WORK

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1411 A promising direction for future work is to extend the proposed quantization-based explanation
1412 framework from instance-level to model-level interpretability. One possibility is to construct a
1413 global dictionary of reference quantization prototypes that summarizes the model’s decision
1414 behavior across the entire dataset. By analyzing how deep quantization patterns cluster in latent space,
1415 such a dictionary could reveal class-level structural regularities or decision boundaries, analogous
1416 to prototype-based global explanations in prior work. Furthermore, integrating hierarchical or dy-
1417 namic prototype discovery may help capture more nuanced variations in quantized representations,
1418 enabling a more comprehensive characterization of the model’s reasoning process.

1419 L USE OF LARGE LANGUAGE MODELS

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1421 Large language models (LLMs) are used in this work solely for auxiliary purposes. Specifically, they
1422 assisted in improving the accuracy of writing by identifying and correcting grammatical issues and
1423 refining terminology choice, as well as in suggesting appropriate color schemes for figure design.
1424 All research ideas, methodological developments, experiments, and the main body of the manuscript
1425 are independently conceived, conducted, and written by the authors.
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