

# A Disorder-Aware Multi-fidelity Framework for Robust Prediction of Superconducting Critical Temperature

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## 1. Introduction

Superconductivity enables lossless current transport and high-field electromagnetic devices [1, 2], but discovering high- $T_c$  materials remains challenging [3]. While machine learning offers a promising shortcut by learning structure–property relations from large databases, two practical bottlenecks limit predictive accuracy for  $T_c$ . First, experimental crystal structures frequently exhibit disorder, where a crystallographic site may contain multiple chemical species (substitutional disorder) or multiple displaced instances (positional disorder). Second, high-fidelity 3D crystal structures with experimentally measured  $T_c$  are scarce; meanwhile, low-fidelity structure proxies can be obtained cheaply (e.g., composition-matched approximations) but are noisier.

Prior disordered-crystal models (e.g., SODNet) handle substitutional disorder by linearly combining elemental embeddings according to occupancies, effectively collapsing a multi-instance site into a single averaged representation [4]. This can obscure disorder effects and reduce robustness, especially on the disorder-only subset where correct modeling of local environments is crucial [4]. In parallel, multi-fidelity learning has improved materials property prediction by combining small high-fidelity datasets with larger low-fidelity ones, but the approach must carefully account for reliability gaps between fidelities [5, 6, 7].

We propose FiDeTGraph, combining (i) explicit disorder modeling via virtual nodes and (ii) fidelity-aware training via a graph-level fidelity embedding, yielding improved and robust  $T_c$  prediction under disorder and data scarcity.

## 2. Methods

### 2.1 Virtual-node representation for disordered sites

We convert a periodic crystal into a graph whose nodes are atomic sites and edges connect near neighbors within a cutoff. For CIFs containing disordered sites, we parse each raw disordered cluster and split it into single-atom instances  $\{S_{c,k}\}$  (one per distinct species instance or displaced position). We then add one auxiliary virtual node  $v_c$  located at the cluster centroid and connect  $v_c$  bidirectionally to all  $S_{c,k}$ . This avoids occupancy-weighted collapse and allows  $v_c$  to summarize higher-order disorder context through message passing.

**Two modalities.** *Substitutional disorder (SD)*: multiple species share the same coordinate with fractional occupancies; we create one instance per species and connect them to  $v_c$ . *Positional disorder (PD)*: the same species appears at multiple displaced coordinates

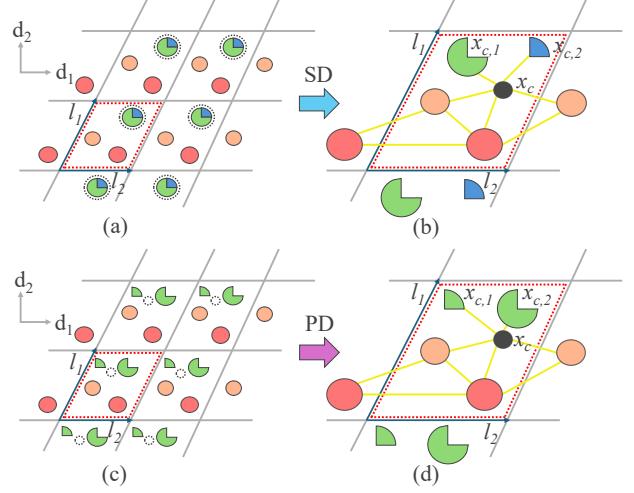


Fig. 1: Illustration of the periodic pattern of disordered crystals. Dotted red lines mark the minimum repeat cells, while grey lines indicate one possible unit cell tiled to form the infinite crystal. Dotted black circles denote virtual node placements, and yellow lines represent atomic connections in the crystal graph. (a)→(b): Transformation of a substitutionally disordered 2D crystal. Each multi-atom substitutional site is split into single-atom sites at the same fractional coordinate, with a virtual node bidirectionally connected to all atoms in the cluster ( $x_c = x_{c,k}$ ,  $k \in K_c$ , where  $K_c$  is the set of atoms at that site). (c)→(d): Transformation of a positionally disordered 2D crystal. Positional disorder introduces shifts breaking atomic symmetry. In the graph, a virtual node is placed at the centroid of each positional cluster and linked bidirectionally to its atoms ( $x_c = \frac{1}{K_c} \sum_{k=1}^{K_c} x_{c,k}$ , where  $K_c$  is the set of atoms in the cluster).

with partial occupancies; we keep all displaced instances and connect them to  $v_c$  at the centroid. Illustration is provided in Fig. 1.

### 2.2 Multi-fidelity data and supercell-permuted augmentation

We use SuperCon3D as high-fidelity data (experimentally curated 3D structures with measured  $T_c$ ) [4]. As low-fidelity data, we use 3DSCMP, a composition-matched dataset built from Materials Project structures with approximations when exact matches are not available, and include non-superconductors [8, 9]. To increase structural diversity aligned with disorder, we generate  $2 \times 2 \times 2$  supercells and sample multiple supercell-permuted variants by converting fractional

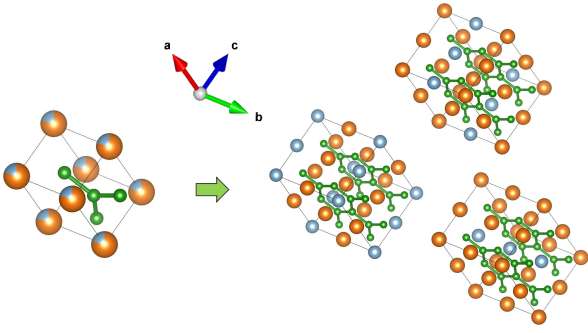


Fig. 2: Illustration of generating three distinct supercell-permuted variants of a crystal structure.

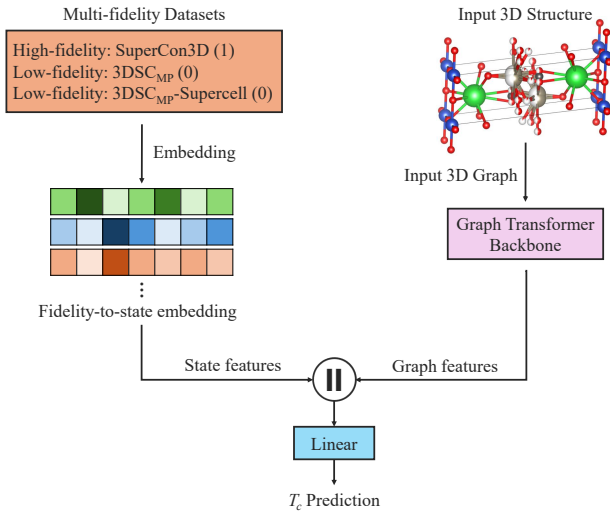


Fig. 3: FiDeTGraph architecture. Each crystal is converted to a 3D graph and encoded by an SE(3)-equivariant graph transformer to obtain graph features. A fidelity label indexes a learnable fidelity embedding, which is concatenated ( $\parallel$ ) with graph features and fed to a linear head to predict  $T_c$ .

occupancies into discrete assignments while preserving global stoichiometry, as illustrated in Fig. 2. These variants provide implicit augmentation and controlled structural uncertainty.

### 2.3 FiDeTGraph: SE(3) graph transformer with fidelity embedding

As illustrated in Fig. 3, FiDeTGraph processes the virtual-node crystal graph using an SE(3)-equivariant graph transformer backbone [10], producing node embeddings that are pooled into a graph representation  $h_g$ . Each sample also carries a discrete fidelity label  $f_g$  (e.g., SuperCon3D vs. 3DSCMP vs. 3DSCMP-supercell), mapped by a trainable embedding lookup  $W_F(f_g)$ . We concatenate  $h_g$  with  $W_F(f_g)$  and predict  $T_c$ :

$$\hat{y}_g = \phi(h_g \parallel W_F(f_g)).$$

The fidelity embedding lets the model adapt its prediction to data reliability, exploiting low-fidelity coverage while anchoring to high-fidelity supervision.

Table 1: Comparison of model performance on the SuperCon3D dataset, evaluated using mean absolute error (MAE) and coefficient of determination ( $R^2$ ) in log K. Results are reported for both the full dataset (order + disorder) and the disorder-only subset.

Method	MAE (logK)	$R^2$ (logK)
SuperCon3D: disorder subset		
XGB-Magpie	$0.586 \pm 0.066$	$0.673 \pm 0.087$
XGB-Magpie+DSOAP	$0.577 \pm 0.066$	$0.688 \pm 0.083$
iComformer	$0.683 \pm 0.080$	$0.544 \pm 0.194$
SODNet	$0.551 \pm 0.081$	$0.608 \pm 0.224$
SODNetV	$0.513 \pm 0.077$	$0.695 \pm 0.135$
FiDeTGraph	<b><math>0.414 \pm 0.043</math></b>	<b><math>0.795 \pm 0.086</math></b>
SuperCon3D: full dataset		
XGB-Magpie	$0.706 \pm 0.040$	$0.688 \pm 0.050$
XGB-Magpie+DSOAP	$0.707 \pm 0.041$	<b><math>0.692 \pm 0.048</math></b>
iComformer	$0.750 \pm 0.052$	$0.572 \pm 0.061$
SODNet	$0.709 \pm 0.064$	$0.614 \pm 0.067$
SODNetV	$0.674 \pm 0.066$	$0.637 \pm 0.072$
FiDeTGraph	<b><math>0.598 \pm 0.049</math></b>	$0.685 \pm 0.062$

## 3. Result

Table 1 compares FiDeTGraph with baselines on SuperCon3D [4] for both the full dataset and the disorder subset. We also report SODNetV, which integrates our virtual-node representation into SODNet [4], to isolate the benefit over occupancy-weighted averaging. Results are shown as mean $\pm$ std for MAE and  $R^2$ .

**Crystal representation improvement with SODNetV.** On the disorder subset, SODNetV reduces MAE from 0.551 to 0.513 and increases  $R^2$  from 0.608 to 0.695, showing that explicit disorder clusters preserve information lost by occupancy-weighted collapse.

**Feature representation improvement with FiDeTGraph.** FiDeTGraph improves MAE to 0.414 and  $R^2$  to 0.795 on the disorder subset, and also improves on the full dataset. This suggests fidelity-aware training can leverage broad low-fidelity coverage while learning to discount its noise [5, 6, 7].

## 4. Conclusion

We introduce FiDeTGraph, a disorder-aware multi-fidelity framework for robust  $T_c$  prediction from 3D crystal structures. FiDeTGraph (i) models disordered sites via virtual nodes and (ii) integrates heterogeneous data using a graph-level fidelity embedding within an SE(3)-equivariant graph transformer. On SuperCon3D, it consistently outperforms strong baselines on both the disorder-only subset and the full dataset. Future work will study uncertainty calibration across fidelities, finer-grained fidelity modeling, and scaling to broader materials families for large-scale screening, with principled high-throughput evaluation and ablations under varying disorder levels.

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