Density functional theory (DFT) is the most successful and widely used approach for computing the electronic structure of matter. However, for tasks involving large sets of candidate molecules, running DFT separately for every possible compound of interest is forbiddingly expensive. In this paper, we propose a neural network based machine learning algorithm which, assuming a sufficiently large training sample of actual DFT results, can instead learn to predict certain properties of molecules purely from their molecular graphs. Our algorithm is based on the recently proposed covariant compositional networks (CCN) framework, and involves tensor reduction operations that are covariant with respect to permutations of the atoms. This new approach avoids some of the representational limitations of other neural networks that are popular in learning from molecular graphs, and yields promising results in numerical experiments on the Harvard Clean Energy Project and QM9 molecular datasets.

I. INTRODUCTION

Density functional theory (DFT) is the workhorse of modern quantum chemistry, due to its ability to calculate many properties of molecular systems with high accuracy. However, this accuracy comes at a significant computational cost, generally making DFT too costly for applications such as chemical search and drug screening, which may involve hundreds of thousands of compounds. Methods that help overcome this limitation could lead to rapid developments in biology, medicine, and materials engineering.

Recent advances in machine learning, specifically, deep learning, combined with the appearance of large datasets of molecular properties obtained both experimentally and theoretically, present an opportunity to learn to predict the properties of compounds from their chemical structure rather than computing them explicitly with DFT. A machine learning model could allow for rapid and accurate exploration of huge molecular spaces to find suitable candidates for a desired molecule.

Central to any machine learning technique is the choice of a suitable set of descriptors, or features used to parametrize and describe the input data. A poor choice of features will limit the expressiveness of the learning architecture and make accurate predictions impossible. On the other hand, providing too many features may make training difficult, especially when training data is limited. Hence, there has been a significant amount of work on designing good features for molecular systems. Predictions of energetics based on molecular geometry have been explored extensively, using a variety of parametrizations. This includes bond types and/or angles, radial distance distribution, the Coulomb matrix and related structures, the Smooth Overlap of Atomic Positions (SOAP), permutation-invariant distances, symmetry functions for atomic positions, Moment Tensor Potentials, and Scattering Networks.

Recently, the problem of learning from the structure of chemical bonds alone, i.e., the molecular graph, has attracted a lot of interest, especially in light of the appearance of a series of neural network architectures designed specifically for learning from graphs. Much of the success of these architectures stems from their ability to pick up on structure in the graph at multiple different scales, while satisfying the crucial requirement that the output be invariant to permutations of the vertices (which, in molecular learning, correspond to atoms). However, as will explain, the specific way that most of these architectures ensure permutation invariance still limits their representational power.

In this paper, we propose a new type of neural network for learning from molecular graphs, based on the idea of covariant compositional networks (CCNs), recently introduced in Ref. Importantly, CCNs are based on explicitly decomposing compound objects (in our case, molecular graphs) into a hierarchy of subparts (subgraphs), offering a versatile framework that is ideally suited to capturing the multiscale nature of molecular structures from functional groups through local structure to overall shape. In a certain sense, the resulting models are the neural networks analog of coarse graining. In addition, CCNs offer a more nuanced take on permutation invariance than other graph learning algorithms: while the overall output of a CCN is still invariant to the permutation of identical atoms, internally, the activations of the network are covariant rather than invariant, allowing us to better preserve information about the relationships between atoms. We demonstrate the success of this architecture through experiments on benchmark datasets, including QM9 and the Harvard Clean Energy Project.
II. LEARNING FROM MOLECULAR GRAPHS

This paper addresses the problem of predicting chemical properties directly from each compound’s molecular graph, which we will denote \( \mathcal{G} \) (Figure 1, left). As such, it is related to the sizable literature on learning from graphs. In the kernel machines domain this includes algorithms based on random walk, counting subgraphs, spectral ideas, label propagation schemes with hashing, and even algebraic ideas.

Recently, a sequence of neural network based approaches have also appeared, starting with Ref. 24. Some of the proposed graph learning architectures directly seek inspiration from the type of classical convolutional neural networks (CNNs) that are used for image recognition. These methods involve moving a filter across vertices to create feature representations of each vertex based on its local neighborhoods. Other notable works on graph neural networks include Refs. 25, 40–42. Very recently, Ref. 25 showed that many of these approaches can be seen as message passing schemes, and coined the term message passing neural networks (MPNNs) to refer to them collectively.

Regardless of the specifics, the two major issues that graph learning methods need to grapple with are invariance to permutations and capturing structure at multiple different scales. Let \( A \) denote the adjacency matrix of \( \mathcal{G} \), and suppose that we change the numbering of the vertices by applying a permutation \( \sigma \). The adjacency matrix will then change to \( A' \), with

\[
A'_{i,j} = A_{\sigma^{-1}(i),\sigma^{-1}(j)}.
\]

However, topologically, \( A \) and \( A' \) still represent the same graph. Permutation invariance means that the represen-

tation \( \phi(\mathcal{G}) \) learned or implied by our graph learning algorithm must be invariant to these transformations. Naturally, in the case of molecules, invariance is restricted to permutations that map each atom to another atom of the same type.

The multiscale property is equally crucial for learning molecular properties. For example, in the case of a protein, an ideal graph learning algorithm would represent \( \mathcal{G} \) in a manner that simultaneously captures structure at the level of individual atoms, functional groups, interactions between functional groups, subunits of the protein, and the protein’s overall shape.

A. Compositional networks

The idea of representing complex objects in terms of a hierarchy of parts has a long history in machine learning. We have recently introduced a general framework for encoding such part-based models in a special type of neural network, called covariant compositional networks (CCNs). In this paper we show how the CCN formalism can be specialized to learning from graphs, specifically, the graphs of molecules. Our starting point is the following definition.

**Definition 1** Let \( \mathcal{G} \) be the graph of a molecule made up of \( n \) atoms \( \{e_1, \ldots, e_n\} \). The compositional neural network (comp-net) corresponding to \( \mathcal{G} \) is a directed acyclic graph (DAG) \( \mathcal{N} \) in which each node (neuron) \( n_i \) is associated with a subgraph \( \mathcal{P}_i \) of \( \mathcal{G} \) and carries an activation \( f_i \). Moreover,

1. If \( n_i \) is a leaf node, then \( \mathcal{P}_i \) is just a single vertex of \( \mathcal{G} \), i.e., an atom \( e_{\ell(i)} \), and the activation \( f_i \) is some initial label \( l_i \). In the simplest case, \( f_i \) is a “one-hot”
analogy, in the following we will sometimes refer to $P_i$. In this sense, CNNs are a specific kind of compositional model of neural networks in computer vision. In particular, convolutional neural networks (CNNs), which are the mainstay of deep learning algorithms, can be interpreted as a neural network, in which each node is a “neuron” that receives inputs $f_i$, $f_2$, ..., $f_k$, and outputs the activation $f_i = \Phi_i(f_1, f_2, ..., f_k)$, where $f_1, f_2, ..., f_k$ denote the activations of the children of $n_i$. Here, $\Phi_i$ is called the aggregation function of node $i$.

Algorithm 1 
High level schematic of message passing in the notations of the present paper.

```
for each vertex $i$
  for $\ell = 1$ to $L$
    for each vertex $i$
      $f_i^{\ell} \leftarrow \Phi_i(f_1^{\ell-1}, f_2^{\ell-1}, ..., f_k^{\ell-1})$
      $\phi(G) \equiv f_i \rightarrow \phi_i(f_1^{\ell}, f_2^{\ell}, ..., f_k^{\ell})$
```

vector that identifies what type of atom resides at the given vertex.

2. $\mathcal{N}$ has a unique root node $n_i$, for which $\mathcal{P}_r = \mathcal{G}$, and the corresponding $f_i$ represents the entire molecule.

3. For any two nodes $n_i$ and $n_j$, if $n_i$ is a descendant of $n_j$, then $\mathcal{P}_i$ is a subgraph of $\mathcal{P}_j$, and

$$f_i = \Phi_i(f_c, f_{c2}, ..., f_{ck}),$$

where $f_{c1}, ..., f_{ck}$ denote the activations of the children of $n_i$. Here, $\Phi_i$ is called the aggregation function of node $i$.

Note that we now have two separate graphs: the original graph $\mathcal{G}$, and the network $\mathcal{N}$ that represents the “is a subgraph of” relationships between different subgraphs of $\mathcal{G}$. One of the fundamental ideas of this paper is that $\mathcal{N}$ can be interpreted as a neural network, in which each node $n_i$ is a “neuron” that receives inputs $f_{c1}, f_{c2}, ..., f_{ck}$, and outputs the activation $f_i = \Phi_i(f_{c1}, f_{c2}, ..., f_{ck})$. For now we treat the activations as vectors, but will soon generalize them to be tensors.

There is some freedom in how the system $\{\mathcal{P}_i\}$ of subgraphs is defined, but the default choice is $\{\mathcal{P}_i\}$, where $\mathcal{P}_i$ is the subgraph of vertices within a radius of $\ell$ of vertex $i$. In this case, $\mathcal{P}_i = \{i\}$, $\mathcal{P}_i \ell$ consists of the immediate neighbors of $i$, plus itself and so on. The aggregation function is discussed in detail in Section IV.

Conceptually, comp-nets are closely related to convolutional neural networks (CNNs), which are the mainstay of neural networks in computer vision. In particular,

1. Each neuron in a CNN only aggregates information from a small set of neurons from the previous layer, similarly to how each node of a comp-net only aggregates information from its children.

2. The so-called effective receptive fields of the neurons in a CNN, i.e., the image patches for which each neuron is responsible for, form a hierarchy of nested sets similar to the hierarchy of $\{\mathcal{P}_i\}$ subgraphs.

In this sense, CNNs are a specific kind of compositional network, where the atoms are pixels. Because of this analogy, in the following we will sometimes refer to $\mathcal{P}_i$ as the receptive field of neuron $i$, dropping the “effective” qualifier for brevity.

As mentioned above, an alternative popular framework for learning from graphs is message passing neural networks (MPNNs). An MPNN operates in rounds: in each round $\ell = 1, ..., L$, every vertex collects the labels of its immediate neighbors, applies a nonlinear function $\Psi$, and updates its own label accordingly. From the neural networks point of view, the rounds correspond to layers and the labels correspond to the $f_i^\ell$ activations (Algorithm 1). More broadly, the classic Weisfeiler-Lehman test of isomorphism follows the same logic, and so does the related Weisfeiler-Lehman kernel, arguably the most successful kernel-based approach to graph learning.

In the above mentioned base case when $\{\mathcal{P}_i\}$ is the collection of all subgraphs of $\mathcal{G}$ of radius $\ell = 0, 1, 2, ..., $, a comp-net can also be thought of as a message passing algorithm: the messages received by vertex $i$ in round $\ell$ are the activations $\{f_{u_j}^{\ell-1} | u_j \in B(i, 1)\}$, where $B(i, 1)$ is the ball of radius one centered at $i$ (note that this contains not just the neighbors of $i$, but also $i$ itself). Conversely, MPNNs can be seen as comp-nets, where $\mathcal{P}_i^\ell$ is the subgraph defined by the receptive field of vertex $i$ in round $\ell$. A common feature of MPNNs, however, is that the $\Psi$ aggregation functions that they employ are invariant to permuting their arguments. Most often, $\Psi$ just sums all incoming messages and then applies a nonlinearity. This certainly guarantees that the final output of the network, $\phi(G) = f_i$, will be permutation invariant. However, in the next section we argue that it comes at the price of a significant loss of representational power.

III. COVARIANT COMPOSITIONAL NETWORKS

One of the messages of the present paper is that invariant aggregation functions, of the type popularized by message passing neural networks, are not the most general way to build compositional models for compound objects, such as graphs. To understand why this is the case, once again, an analogy with image recognition is helpful. Classical CNNs face two types of basic image transformations: translations and rotations. With respect to translations (barring pooling, edge effects and other complications), CNNs behave in a quasi-invariant way, in the sense that if the input image is translated by an integer amount $(t_x, t_y)$, the activations in each layer $\ell = 1, 2, ..., L$ translate the same way: the activation of neuron $n_{t,j}^\ell$ is simply transferred to neuron $n_{t+1, j+1}^\ell$, i.e., $f_{t+1,j+1}^\ell = f_{t,j}^\ell$. This is the simplest manifestation of a well studied property of CNNs called equivariance.

With respect to rotations, however, the situation is more complicated: if we rotate the input image by, e.g., 90 degrees, not only will the part of the image that fell in the receptive field of neuron $n_{t,j}^\ell$ move to the receptive field of a different neuron $n_{t', j'}^\ell$, but the orientation of the receptive field will also change. For example, features which were previously picked up by horizontal filters will now be picked up by vertical filters. Therefore, in general, $f_{t,j}^\ell \neq f_{t,j}^\ell$ (Figure C).

It can be shown that one cannot construct a CNN for images that behaves in a quasi-invariant way with respect...
to both translations and rotations, unless every filter is directionless. It is, however, possible to construct a CNN in which the activations transform in a predictable and reversible way, \( f'_{i,j} = R(f_{i,j}) \), for some fixed function \( R \). This phenomenon is called steerability, and has a significant literature in both classical signal processing and the neural networks field.

The situation in compositional networks is similar. We have examined so far, by virtue of the aggregation function being symmetric in its arguments, are all quasi-invariant (with respect to permutations) in the sense that if \( N \) and \( N' \) are two comp-nets for the same graph differing only in a reordering \( \sigma \) of the vertices of the underlying graph \( G \), and \( n_i \) is a neuron in \( N \) while \( n'_i \) is the corresponding neuron in \( N' \), then \( f_i = f'_i \) for any permutation \( \sigma \in S_n \).

Quasi-invariance amounts to asserting that the activation \( f_i \) at any given node must only depend on \( \mathcal{P}_i = \{e_{j_1}, \ldots, e_{j_k}\} \) as a set, and not on the internal ordering of the atoms \( e_{j_1}, \ldots, e_{j_k} \) making up the receptive field. At first sight this seems desirable, since it is exactly what we expect from the overall representation \( \phi(G) \). On closer examination, however, we realize that this property is potentially problematic, since it means that \( n_i \) loses all information about which vertex in its receptive field has contributed what to the aggregate information \( f_i \). In the CNN analogy, we can say that we have lost information about the orientation of the receptive field. In particular, if higher up in the network \( f_i \) is combined with some other feature vector \( f_j \) from a node with an overlapping receptive field, the aggregation process has no way of taking into account which parts of the information in \( f_i \) and \( f_j \) come from shared vertices and which parts do not (Figure 3).

The solution is to regard the \( \mathcal{P}_i \) receptive fields as ordered sets, and explicitly establish how \( f_i \) co-varies with the internal ordering of the receptive fields. To emphasize that henceforth the \( \mathcal{P}_i \) sets are ordered, we will use parentheses rather than braces to denote them.

**Definition 2** Assume that \( N \) is the comp-net of a graph \( G \), and \( N' \) is the comp-net of the same graph but after its vertices have been permuted by some permutation \( \sigma \). Given any \( n_i \in N \) with receptive field \( \mathcal{P}_i = \{e_{p_1}, \ldots, e_{p_m}\} \), let \( n'_i \) be the corresponding node in \( N' \) with receptive field \( \mathcal{P}'_i = \{e_{q_1}, \ldots, e_{q_m}\} \). Assume that \( \pi \in S_m \) is the permutation that aligns the orderings of the two receptive fields, i.e., for which \( e_{q_{\pi(p)}} = e_{p_\pi} \). We say that the comp-nets are **covariant to permutations** if for any \( \pi \), there is a corresponding function \( R_\pi \) such that \( f'_i = R_\pi(f_i) \).

To make the form of covariance prescribed by this definition more specific, we make the assumption that the \( \{f \mapsto R_\pi(f)\}_{\pi \in S_m} \) maps are linear. This allows us to treat them as matrices, \( \{R_\pi\}_{\pi \in S_m} \). Furthermore, linearity also implies that \( \{R_\pi\}_{\pi \in S_m} \) form a representation of \( S_m \) in the group theoretic sense of the word.
of representation should not be confused with the neural networks sense of representations of objects, as in “\(f_i\) is a representation of \(P_i\”\).

The representation theory of symmetric groups is a rich subject that goes beyond the scope of the present paper. However, there is one particular representation of \(S_m\) that is likely familiar even to non-algebraists, the so-called defining representation, given by the \(P_r \in \mathbb{R}^{n \times n}\) permutation matrices

\[
[P_r]_{i,j} = \begin{cases} 
1 & \text{if } \pi(j) = i \\
0 & \text{otherwise.}
\end{cases}
\]

It is easy to verify that \(P_{\pi_2\pi_1} = P_{\pi_2}P_{\pi_1}\), for any \(\pi_1,\pi_2 \in S_m\), so \(\{P_r\}_{r \in S_m}\) is indeed a representation of \(S_m\). If the transformation rules of the \(f_i\) activations in a given comp-net are dictated by this representation, then each \(f_i\) must necessarily be a \(|P_r|\) dimensional vector, and intuitively each component of \(f_i\) carries information related to one specific atom in the receptive field, or the interaction of that specific atom with all the others collectively. We call this case first order permutation covariance.

**Definition 3** We say that \(n_i\) is a **first order covariant node** in a comp-net if under the permutation of its receptive field \(P_r\), by any \(\pi \in S(|P_r|)\), its activation transforms as \(f_i \mapsto P_{\pi} f_i\).

If \((R_{\rho})_{\rho \in \Phi}\) is a representation of a group \(\Phi\), the matrices \((R_{\rho} \otimes R_{\kappa})_{\kappa \in \Phi}\) also form a representation. Thus, one step up in the hierarchy from \(P_r\)-covariant comp-nets are \(P_r \otimes P_r\)-covariant comp-nets, where the \(f_i\) feature vectors are now \(|P_r|^2\) dimensional vectors that transform under permutations of the internal ordering by \(\pi\) as \(f_i \mapsto (P_{\pi} \otimes P_{\pi}) f_i\). If we reshape \(f_i\) into a matrix \(F_i \in \mathbb{R}^{(|P_r|)^2 \times |P_r|}\), then the action

\[
F_i \mapsto P_{\pi} F_i P_{\pi}^T
\]

is equivalent to \(P_r \otimes P_r\) acting on \(f_i\). In the following, we will prefer this more intuitive matrix view, since it makes it clear that feature vectors that transform this way express relationships between the different constituents of the receptive field. Note, in particular, that if we define \(A_{\pi_{\rho}}\) as the restriction of the adjacency matrix to \(P_{\rho}\) (i.e., if \(P_{\rho} = (e_{\rho,1}, \ldots, e_{\rho,n})\) then \([A_{\pi_{\rho}}]_{a,b} = A_{\pi_{\rho}} e_{\rho,a} e_{\rho,b}\), then \(A_{\pi_{\rho}}\) transforms exactly as \(F_i\) does in the equation above.

**Definition 4** We say that \(n_i\) is a **second order covariant node** in a comp-net if under the permutation of its receptive field \(P_r\), by any \(\pi \in S(|P_r|)\), its activation transforms as \(f_i \mapsto P_{\pi} F_i P_{\pi}^T\).

Taking the pattern further lets us define third, fourth, and general, \(k\)th order nodes, in which the activations are \(k\)th order tensors, transforming under permutations as \(f_i \mapsto F_i'\), where

\[
[F_i']_{j_1,j_2, \ldots, j_k} = [P_{\pi}]_{j_1,j_1'} [P_{\pi}]_{j_2,j_2'} \cdots [P_{\pi}]_{j_k,j_k'} [F_i]_{j_1',j_2', \ldots, j_k'}.
\]

Here and in the following, for brevity, we use the Einstein summation convention, whereby any dummy index that appears twice on the right hand side of an equation is automatically summed over.

In general, we will call any quantity which transforms under permutations according to \((1)\) a \(k\)th order \(P\)-tensor. Saying that a given quantity is a \(P\)-tensor then not only means that it is representable by an \(m \times n \times \cdots \times m\) array, but also that this array transforms in a specific way under permutations.

Since scalars, vectors and matrices can be considered \(0^{\text{th}}, 1^{\text{st}}\) and \(2^{\text{nd}}\) order tensors, the following definition covers both quasi-invariance and first and second order covariance as special cases. To unify notation and terminology, in the following we will always talk about feature tensors rather than feature vectors, and denote the activations as \(F_i\) rather than \(f_i\).

**Definition 5** We say that \(n_i\) is a **\(k\)th order covariant node** in a comp-net if the corresponding activation

\[
F_i \mapsto P_{\pi} F_i P_{\pi}^T
\]
A covariant compositional network (CCN) is a comp-net in which each node’s activation is covariant to permutations in the above sense. Hence we can talk about first, second, third, etc. order CCNs (CCN 1D, 2D, . . .). In the first few layers of the network, however, the order of the nodes might be lower (Figure 1).

The real significance of covariance, both here and in classical CNNs, is that while it allows for a richer internal representation of the data than fully invariant architectures, the final output of the network can still easily be made invariant. In covariant comp-nets this is achieved by collapsing the input tensors of the root node n0 at the top of the network into invariant scalars, for example by computing their sums and traces (reducing them to zeroth order tensors), and outputting permutation invariant combinations of these scalars, such as their sum.

IV. COVARIANT AGGREGATION FUNCTIONS

It remains to explain how to define the Φ aggregation functions so as to guarantee covariance. Specifically, we show how to construct Φ such that if the Fc1,...,Fcℓ inputs of a given node nℓ at level ℓ are covariant k-th order P-tensors, then Fa = Φ(Fc1,...,Fcℓ) will also be a k-th order P-tensor. The aggregation function that we define consists of five operations executed in sequence: promotion, stacking, reduction, mixing, and an elementwise nonlinear transform. Practically relevant CCNs tend to have multiple channels, so each Fa is actually a sequence of d separate P-tensors Fc1,...,Fcℓ. However, except for the mixing step, each channel behaves independently, so for simplicity, for now we drop the channel index.

1. Promotion

Each child tensor Fc is captured information about a different receptive field Pc, so before combining them we must “promote” each Fc, to a |Pc| × . . . × |Pc| tensor Fa, whose dimensions are indexed by the vertices of P; rather than the vertices in each Pc. Assuming that Pc = (e1,...,epc) and Pb = (e1,...,epb), this is done by defining a |Pc| × |Pc| indicator matrix

\[ μ_{i,j}^{c} \rightarrow a = \begin{cases} 1 & \text{if } q_i = p_i \\ 0 & \text{otherwise,} \end{cases} \]

and setting

\[ [F_c]_{j_1,...,j_k} = \sum [F_c]_{e_1} [μ_{e_1}^{c} → b]_{j_1,...,j_k} , \]

where, once again, Einstein summation is in use, so summation over j1,...,jk is implied. Effectively, the promotion step aligns all the child tensors by permuting the indices of Fc to conform to the ordering of the atoms in Pc, and padding with zeros where necessary.

2. Stacking

Now that the promoted tensors Fc1,...,Fcℓ all have the same shape, they can be stacked to form a |Pc1| × . . . × |Pcℓ| dimensional k + 1-th order tensor T, with

\[ T_{j_0,...,j_k} = \begin{cases} [F_c]_{j_0,...,j_k} & \text{if } P_c_i \text{ is the subgraph} \\ 0 & \text{otherwise.} \end{cases} \]

It is easy to see that T itself transforms as a P-tensor of order (k + 1).

We may also add additional information to T by taking its tensor product with another P-tensor. In particular, to explicitly add information about the local topology, we may tensor multiply T by AiχPc, the restriction of the adjacency matrix to Pc. This will give us an order (k + 3) tensor S = T ⊗ AiχPc. Otherwise, we
For example, one way to drop the rank of \( S \) to \( k \) is to sum out three of its indices, \( Q_{i_1 \ldots i_k} = \sum_{i_{a_1}, i_{a_2}, i_{a_3}} S_{i_1 \ldots i_k}. \) Note that while this notation does not make it explicit, \( i_{a_1}, i_{a_2} \) and \( i_{a_3} \) must be removed from amongst the indices of \( Q \). Another way to drop the rank is to contract over three indices, \( Q_{i_1 \ldots i_k} = \sum_{i_{a_1}, i_{a_2}, i_{a_3}} S_{i_1 \ldots i_k} \delta_{i_{a_1}, i_{a_2}, i_{a_3}}, \) where \( \delta_{i_{a_1}, i_{a_2}, i_{a_3}} \) is the generalized Kronecker symbol. A third way is to contract over two indices and sum over one index, and so on. The crucial fact is that each of these tensor operations is still a covariant \( P \)-tensor.

In general, the number of different ways that an order \( k+q \) tensor \( S \) can be reduced to order \( k \) depends on both \( q \) and \( k \). For example, when \( k = 2 \) and \( q = 3 \), there are 50 different possible tensor reductions (excluding diagonals). In contrast, when \( q = 1 \) (i.e., we are not multiplying by the adjacency matrix), we only have \( k+1 \) possibilities, corresponding to summing \( S \) over each of its dimensions. No matter which case we are in, however, and how many contractions \( Q_1, \ldots, Q_r \) our network actually computes (in our experiments using second order nodes, we compute 18 different ones), what is important is that the resulting order \( k \) tensors satisfy the \( P \)-tensor property.

### 4. Mixing with learnable weights

The reduction step can potentially produce quite a large number of order \( k \) tensors, \( Q_1, \ldots, Q_r \). We reduce this number by linearly mixing \( Q_1, \ldots, Q_r \), i.e., taking \( d' < r \) linear combinations of the form

\[ \tilde{Q}^{(i)} = \sum_{j=1}^{r} w_{i,j}^{(i)} Q_j. \]

This is again a covariant operation, and the mixing weights are the actual learnable parameters of our neural network.

### 5. Nonlinearity

Finally, to get the actual activation of our neuron \( a \), we add an additive bias \( b_{t,c} \), and an elementwise nonlinearity \( \sigma \) (specifically, the ReLU operator \( \sigma(x) = \max(0, x) \)), as is standard in neural networks. Thus, ultimately, the output of the aggregation function is the collection of \( P \)-covariant tensors

\[ F_a^{(c)} = \sigma \left[ \sum_{c=1}^{d} \sum_{j=1}^{r} w_{c,c}^{(j)} Q_j^{(c')} + b_{t,c} \mathbf{1} \right], \]

with \( c \in \{1, 2, \ldots, d'\}. \) As usual in neural networks, the \( W_t \) weight tensors are learned by backpropagation and some form of stochastic gradient descent.

### V. EXPERIMENTS

We tested our CCN framework on three different types of datasets that involve learning the properties of molecules from their structure: (a) four relatively small datasets of small molecules that are standard benchmarks in the kernels literature (MUTAG, PTC, NCI1 and NCI109), (b) the Harvard Clean Energy Project (QM9) and (c) QM9. The first two types of datasets are pure graph classification/regression tasks. QM9 also has physical (spatial) features, which go somewhat beyond the scope of the present paper. Therefore, on QM9 we conducted separate experiments with and without these physical features (QM9(b) vs. QM9(a)).

In each case, we used second order CCNs (CCN2D) and included the tensor product with the restricted adjacency matrix, as described in Section 4. However, for computational reasons, we only used 18 of the 50 possible contractions. The base features of each vertex were initialized with computed histogram alignment kernel features of depth up to 10: each vertex receives a base label \( l_i = \text{concat}_{j=1}^{10} H_j(i) \) where \( H_j(i) \in \mathbb{R}^d \) (with \( d \) being the total number of distinct discrete node labels) is
the vector of relative frequencies of each label for the set of vertices at distance equal to \( j \) from vertex \( i \). The network was chosen to be three levels deep, with the number of output channels at each level fixed to 10.

To run our experiments, we used our own custom-built neural network library called GraphFlow. Writing our own deep learning software became necessary because at the time we started work on the experiments, none of the standard frameworks such as TensorFlow, PyTorch or MXNet had efficient support for the type of tensor operations required by CCN. GraphFlow is a fast, general purpose deep learning library that offers automatic differentiation, dynamic computation graphs, multithreading, and GPU support for tensor contractions. In addition to CCN, it also implements other graph neural networks, including Neural Graph Fingerprints, PSCN and Gated Graph Neural Network. We also provide a reference implementation of CCN1D and CCN2D in PyTorch.

In each experiment we used 80% of the dataset for training, 10% for validation, and 10% for testing. For the kernel datasets we performed the experiments on 10 separate training/validation/test stratified splits and averaged the resulting classification accuracies. Our training technique used mini-batch stochastic gradient descent with the Adam optimization method and a batch size of 64. The initial learning rate was set to 0.001, and decayed linearly after each step towards a minimum of \( 10^{-6} \).

A. Graph kernel datasets

Our first set of experiments involved three standard “graph kernels” datasets: (1) MUTAG, which is a dataset of 188 mutagenic aromatic and heteroaromatic compounds, (2) PTC, which consists of 344 chemical compounds that have been tested for positive or negative toxicity in lab rats, (3) NCI1 and NCI109, which have 4110 and 4127 compounds respectively, each screened for activity against small cell lung cancer and ovarian cancer lines. In each of these datasets, each molecule has a discrete label (i.e., toxic/non-toxic, aromatic/heteroaromatic) and the goal is to predict this label. We compare CCN 2D against the graph kernel results reported in Ref. 92 (C-SVM algorithm with the Weisfeiler–Lehman kernel), Weisfeiler–Lehman edge kernel, Shortest Paths Graph Kernel, Graphlets Kernel and the Multiscale Laplacian Graph Kernel, Neural Graph Fingerprint (with up to 3 levels and a hidden size of 10) and the “patchy-SAN” convolutional algorithm (PSCN). The results are presented in Table I.

B. Harvard Clean Energy Project

The Harvard Clean Energy Project (HCEP) dataset consists of 2.3 million organic compounds that are candidates for use in solar cells. The inputs are molecular graphs (derived from their SMILES strings), and the regression target is power conversion efficiency (PCE). The experiments were run on a random sample of 50,000 molecules.

On this dataset we compared CCN to the following algorithms: Lasso, ridge regression, random forests, Gradient Boosted Trees (GBT), the Optimal Assignment Weisfeiler–Lehman Graph Kernel, Neural Graph Fingerprints and PSCN. For the first four of these baseline methods, we created simple feature vectors from each molecule: the number of bonds of each type (i.e., number of H–H bonds, number of C–O bonds, etc.) and the number of atoms of each type. Molecular graph fingerprints uses atom labels of each vertex as base features. For ridge regression and Lasso, we cross-validated over \( \lambda \). For random forests and GBT, we used 400 trees, and cross validated over maximum depth, minimum samples for a leaf, minimum samples to split a node, and learning rate (for GBT). For Neural Graph Fingerprints, we used up to 3 layers and a hidden layer size of 10. In PSCN, we used a patch size of 10 with two convolutional layers and a dense layer on top as described in their paper.

C. QM9 Dataset

QM9 has recently emerged as a molecular dataset of significant interest. QM9 contains ~134k organic molecules with up to nine atoms (C, H, O, N and F)
NGF and PSCN are as described for HCEP. CCN architecture is as described above, and settings for considering only heavy atoms and exclude hydrogen. The neural graph fingerprints, and PSCN. For this test we architecture against the Weisfeiler–Lehman graph kernel, Gradient boosted trees, Random forest, Ridge regression, Lasso, and report the MAE for each.

<table>
<thead>
<tr>
<th>Method</th>
<th>CCN 2D</th>
<th>WLGK</th>
<th>NGF</th>
<th>PSCN</th>
<th>Test MAE</th>
<th>Test RMSE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lasso</td>
<td>0.340</td>
<td>0.449</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ridge regression</td>
<td>0.867</td>
<td>1.437</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Random forest</td>
<td>0.854</td>
<td>1.376</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gradient boosted trees</td>
<td>1.004</td>
<td>1.799</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Weisfeiler–Lehman kernel</td>
<td>0.805</td>
<td>1.096</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Neural graph fingerprints</td>
<td>0.851</td>
<td>1.177</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PSCN ($k = 10$)</td>
<td>0.718</td>
<td>0.973</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Second order CCN (our method)</td>
<td>0.340</td>
<td>0.449</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

TABLE II. HCEP regression results. Error of predicting power conversion efficiency in units of percent.

We performed two experiments on the QM9 dataset, with the goal of providing a benchmark of CCN as a graph learning framework, and demonstrating that our framework can predict molecular properties to the same level as DFT. In both cases, we trained our system on each of the thirteen target properties of QM9 independently, and report the MAE for each.

1. QM9(a)

We use the QM9 dataset to benchmark the CCN architecture against the Weisfeiler–Lehman graph kernel, Neural Graph Fingerprints, and PSCN. For this test we consider only heavy atoms and exclude hydrogen. The CCN architecture is as described above, and settings for NGF and PSCN are as described for HCEP.

<table>
<thead>
<tr>
<th></th>
<th>CCN</th>
<th>DFT error</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha$ (Bohr$^3$)</td>
<td>0.22</td>
<td>0.4</td>
</tr>
<tr>
<td>$C_\alpha$ (cal/(mol K))</td>
<td>0.07</td>
<td>0.34</td>
</tr>
<tr>
<td>$G$ (eV)</td>
<td>0.06</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP (eV)</td>
<td>0.12</td>
<td>1.2</td>
</tr>
<tr>
<td>$H$ (eV)</td>
<td>0.06</td>
<td>0.1</td>
</tr>
<tr>
<td>HOMO (eV)</td>
<td>0.09</td>
<td>2.0</td>
</tr>
<tr>
<td>LUMO (eV)</td>
<td>0.09</td>
<td>2.6</td>
</tr>
<tr>
<td>$\mu$ (Debye)</td>
<td>0.48</td>
<td>0.1</td>
</tr>
<tr>
<td>$\omega_1$ (cm$^{-1}$)</td>
<td>2.81</td>
<td>28</td>
</tr>
<tr>
<td>$R_2$ (Bohr$^2$)</td>
<td>4.00</td>
<td>-</td>
</tr>
<tr>
<td>$U$ (eV)</td>
<td>0.06</td>
<td>0.1</td>
</tr>
<tr>
<td>$U_0$ (eV)</td>
<td>0.05</td>
<td>0.1</td>
</tr>
<tr>
<td>ZPVE (eV)</td>
<td>0.0039</td>
<td>0.0097</td>
</tr>
</tbody>
</table>

TABLE III. QM9(a) regression results (mean absolute error). Here we have only used the graph as the learning input without any physical features.

We used both physical atomic information (vertex features) and bond information (edge features) including: atom type, atomic number, acceptor, donor, aromatic, hybridization, number of hydrogens, Euclidean distance and Coulomb distance between pairs of atoms. All the information is encoded in a vectorized format. Our physical features were taken directly from the dataset used in Ref. 25 in addition to the graph of each molecule.

2. QM9(b)

To compare to DFT error, we performed a test of the QM9 dataset with each molecule including hydrogen atoms. We used both physical atomic information (vertex features) and bond information (edge features) including: atom type, atomic number, acceptor, donor, aromatic, hybridization, number of hydrogens, Euclidean distance and Coulomb distance between pairs of atoms. All the information is encoded in a vectorized format. Our physical features were taken directly from the dataset used in Ref. 25 without any special feature engineering.

To include the edge features into our model along with the vertex features, we used the concept of line graphs from graph theory. We constructed the line graph for each molecular graph in such a way that an edge of the molecular graph corresponds to a vertex in its line graph, and if two edges in the molecular graph share a common vertex then there is an edge between the two correspond-
FIG. 6. Molecular graph of C$_2$H$_4$ (left) and its corresponding line graph (right). The vertices of the line graph correspond to edges of the molecular graph; two vertices of the line graph are connected by an edge if their corresponding edges on the molecular graph share a vertex.

We present results for both the CCN 1D and CCN 2D architectures. For CCN 1D, our network is seven layers with 64 input channels; at the first and second layer the number of channels is halved, and beyond that each layer has 16 channels. For the CCN 2D architecture, we used three layers, with 32 channels at the input and 16 and the remaining layers. We report the mean average error for each learning target in its corresponding physical unit and compare it against the DFT error given in Ref. 25.

D. Discussion

Overall, our CCN outperforms the other algorithms on a significant fraction of the experiments we implemented. On the subsampled HCEP dataset, CCN outperforms all other methods by a very large margin. For the graph kernels datasets, the SVM with the Weisfeiler–Lehman kernels achieve the highest accuracy on NCI1 and NCI109; while CCN wins on MUTAG and PTC. Perhaps this poor performance is to be expected, since the datasets are small and neural networks usually require tens of thousands of training examples to be effective. Indeed, neural graph fingerprints and PSCN also perform poorly compared to the Weisfeiler–Lehman kernels. In the QM9(a) experiment, CCN obtains better results than the three other graph learning algorithms on all 13 learning targets.

In the QM9(b) experiment, the error of CCN is smaller than that of DFT itself on 11 of 12 learning targets (Ref. 25 does not have DFT error for R2). However, other recent works have obtained even stronger results. Looking at our results, we find that values depending strongly on position information, such as the dipole moment and average electronic spatial extent, are predicted poorly when we include physical features. In contrast, properties that are not expected to strongly depend on spatial extent are predicted significantly better. This suggests that our spatial input features were not fully exploited, and that feature engineering position information could significantly enhance the power of our CCN.

Our custom deep learning library enabled all the above results to be obtained reasonably efficiently. The prediction time for CCN 1D and CCN 2D on QM9(b) comes out to 6.0 ms/molecule and 7.2 ms/molecule, respectively, making it possible to search through a million candidate molecules in under two hours.

VI. CONCLUSIONS

In this paper we presented a general framework called covariant compositional networks (CCNs) for learning the properties of molecules from their graphs. Central to this framework are two key ideas: (1) a compositional structure that generalizes message passing neural networks (MPNNs) and (2) the concept of covariant aggregation functions based on tensor algebra.

We argue that CCNs can extract multiscale structure from molecular graphs and keep track of the local topology in a manner the MPNNs are not able to. We also introduced the GraphFlow software library that provides an efficient implementation of CCNs. Using GraphFlow, we were able to show that CCNs often outperform existing state-of-the-art algorithms in learning molecular properties.

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\[ \ell = 0 \]
\[ \ell = 1 \]
$\ell = 2$
\[ T = \]

\[ [Q_1]_{i,j} = \sum_k T_{i,j,k} \]

\[ [Q_2]_{i,j} = \sum_k T_{i,k,j} \]

\[ [Q_1]_{i,j} = \sum_k T_{i,i,j} \]

\[ F^{(c)} = \sigma \left( \sum_j w_{c,j} Q_j + b_c 1 \right) \]