

<b>Title</b>	Z-Matrix template-based substitution approach for enumeration of 3D molecular structures
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## ABSTRACT

The exhaustive enumeration of 3D chemical structures based on Z-matrix templates has recently been used in the quantum chemical investigation of constitutional isomers, diastereomers and rotamers. This simple yet powerful initial structure generation approach can apply beyond the investigation of compounds of identical formula by quantum chemical methods. This paper aims to provide a short description of the overall concept followed by a practical tutorial to the approach.

- The four steps required for Z-matrix template-based substitution are template construction, generation of tuples for substitution sites, removal of duplicate tuples and substitution on the template.
- The generated tuples can be used to create chemical identifiers to query compound properties from chemical databases.
- All of these steps are demonstrated in this paper by common model compounds and are very straightforward for an undergraduate audience to reproduce. A comparison of the approach in this tutorial and other options is also discussed.

## SPECIFICATIONS TABLE

<b>Subject Area</b>	Chemistry
<b>More specific subject area</b>	Cheminformatics
<b>Method name</b>	Z-matrix template-based substitution
<b>Name and reference of original method</b>	N/A
<b>Resource availability</b>	Source codes are available as supplementary information in this paper.

## Method details

### 20 1. Introduction

Initial structures (Z-matrix or Cartesian coordinate) are important starting points for the *in silico* investigation of chemical species. Robust and exhaustive processes to generate chemical structures have been described previously in different contexts [1-9]. However, there are still no consistent one-size-fits-all standard for structural enumeration. Most of the existing methods are based on  
25 molecular graphs for representation of molecular structures and intrinsically lack crucial spatial information in terms of configuration and conformation of generated structures. Molecular graph-based methods may also suffer from resonance, unusual bond types or infeasible structures. There are ad hoc solutions to overcome these limitations [10] but, alternatively, a new method may be used instead or in combination with the existing methods.

30 Chemists, by their manual intuition and labour, have been able to identify template structures and substitution points for the combinatorial investigation of compounds. Inspired by the use of this approach in DDT analogues [5], we successfully applied it to 26 classes of compounds to exhaustively generate over ten thousand 3D structures for further investigation by quantum chemical methods [11-15]. Based on these previous reports, this is our first paper devoted to the  
35 methodology of generic structure generation using Z-matrix template-based substitution. The concept and tutorial (template construction, generation of tuples for substitution sites, removal of duplicate tuples and substitution on the template) are described in the next section. Comparison of this approach to other existing methods and future work are discussed in the last section.

### 2. Z-matrix template-based substitution approach

40 Three dimensional molecular structures are often represented by a Z-matrix or Cartesian coordinates. The two representations can easily be interconverted by freely available software. We use Z-matrix for convenience as bond lengths, bond angles and torsional angles, which are natural quantities for chemists, can be explicitly laid out. (Cartesian coordinates would be very difficult to  
45 manipulate using this template-based substitution method.) As mentioned earlier, templates and substitution sites must be identified manually by human. For simplicity, in this article, we use hydrogen and halogen atoms (F, Cl, Br and I) as substitutions. The substitution approach can help us explore structures of different chemical compositions and structures of identical chemical formula (constitutional, configurational and conformational isomers) at the same time.

In our tutorial, we demonstrate step-by-step how to generate an exhaustive collection of halo-  
50 substituted benzenes. Preferred toolkits on Windows platform are Notepad++ [16] for plain-text editing, Wolfram's Mathematica [17] for generation of tuples and duplicate elimination, GNU's sed [18] on Cygwin [19] for substitution into the template file, and IQmol [20] for visualization. These may be replaced by other generic software available on the user's platform.

#### 2.1. Template construction

55 The first step of the procedure, construction of the template, can be achieved on any text editor. In this example, Notepad++ was used. The template molecule is defined as a Z-matrix with the substituting atoms in lowercase strings. (The use of lowercase letters is helpful for a case-sensitive replacement in later steps.) The example shown in Figure 1 is a template for the generation of halo-  
60 substituted benzenes. The six halogen atom substitution sites are labelled as a, b, c, d, e and f. This template can be manually constructed by hand from scratch or by editing a Z-matrix from a molecular graphic software such as IQmol. For complicated molecules, it would be easier to draw or import the structure in such a program before manual manipulation. IQmol can help us visually identify the atom numbers corresponding to desired substitution sites by using Display > Atom Labels > Index. In this example, we see from IQmol that six hydrogen atoms are numbered 7 to 12 and therefore  
65 change the letter H (for H atom) on the corresponding lines to lowercase letters a to f accordingly. Bond length are defined as variables below the Z-matrix. (Bond and torsional angles are manually

defined as variables.) Therefore, a universal replacement of the letter a to a substituent atom (e.g. F) in step 4 will have two effects on the file: the type of atom (F) and bond length (CF) will be defined at the same time for the 7<sup>th</sup> atom in the Z-matrix.

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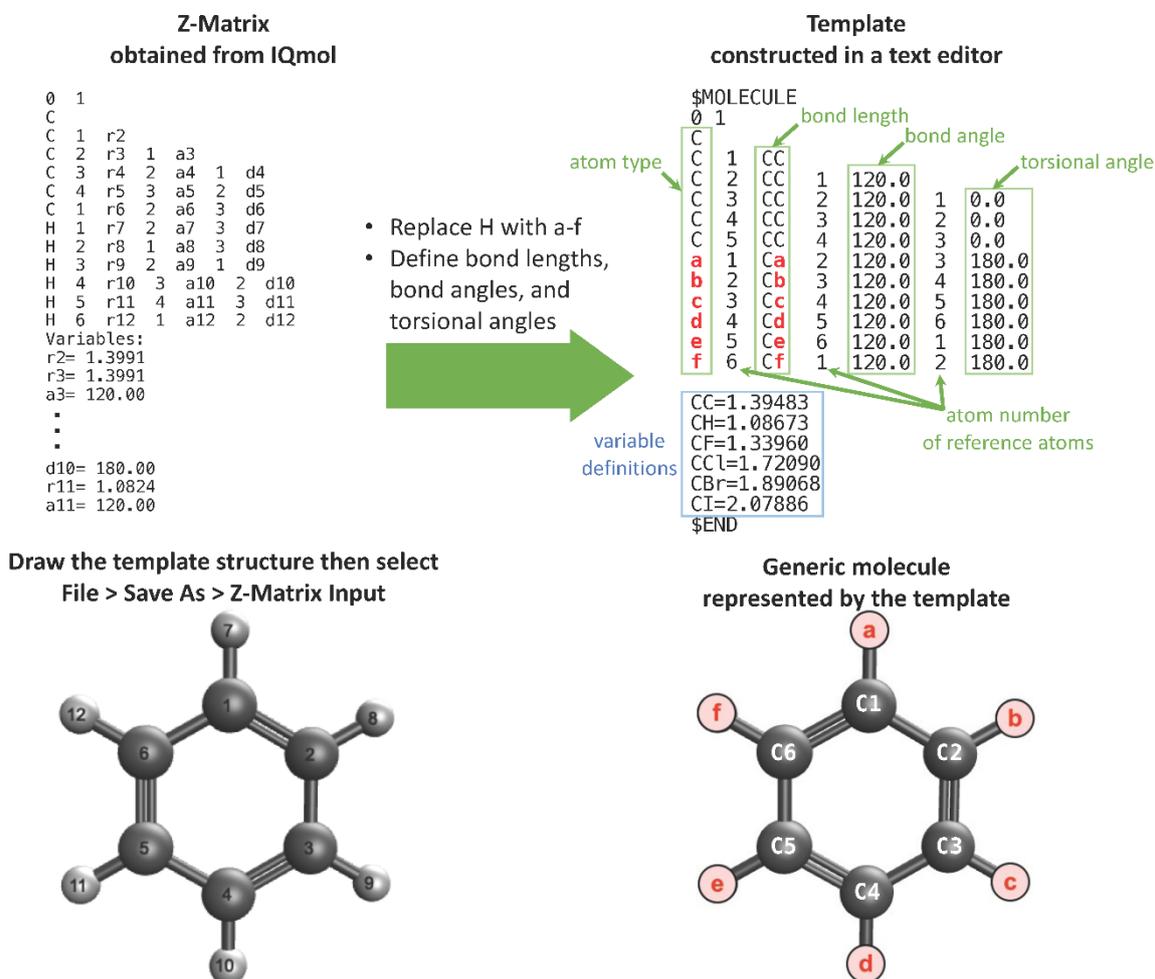


Figure 1 Example of template for benzene in Q-Chem [21] input file format. Substitution positions (shown in red text) are labeled as a, b, c, d, e and f. H, F, Cl, Br, or I will take the place of each label after the process is complete. In the first line, 0 1 are charge and multiplicity of the structure which is irrelevant to the discussion here but required by the file format. Each successive line provides the atom type and its relative position to three other atoms in the previous lines specified by bond length, bond angle and torsional angle.

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## 2.2. Generation of tuples for substitution sites

The provided Wolfram Mathematica notebook (Figure 2 and the Supplementary information) has a list named **elements** that contains the possible substituents. When generating halo-substituted benzenes, the possible substituents are H, F, Cl, Br and I atoms. Hence, **elements** = {"H", "F", "Cl", "Br", "I"}. **elements** can be modified when other substituting atoms or functional groups are studied. Tuples[**elements**, *k*] generates a list **all** containing all possible *k*-tuples from the elements in **elements**. The number of tuples generated in this step is equivalent to  $l^k$  where *l* is the length of **elements** and *k* is the size of each tuple. For benzene, possible substitutions for the slots a, b, c, d, e and f can be represented as a 6-tuple (*k* = 6). Therefore, the number of tuples generated from this step is  $5^6 = 15625$ .

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```

In[1]:= elements = {"H", "F", "Cl", "Br", "I"};
all = Tuples[elements, 6]

Out[1]=
{{(H, H, H, H, H, H), (H, H, H, H, H, F), (H, H, H, H, H, Cl),
(H, H, H, H, H, Br), (H, H, H, H, H, I), (H, H, H, H, F, H), (H, H, H, H, F, F),
(H, H, H, H, F, Cl), (H, H, H, H, F, Br), (H, H, H, H, F, I), (H, H, H, H, Cl, H),
(H, H, H, H, Cl, F), (H, H, H, H, Cl, Cl), ... 15 600 ..., (I, I, I, I, Cl, Br),
(I, I, I, I, Cl, I), (I, I, I, I, Br, H), (I, I, I, I, Br, F),
(I, I, I, I, Br, Cl), (I, I, I, I, Br, Br), (I, I, I, I, Br, I), (I, I, I, I, I, H),
(I, I, I, I, I, F), (I, I, I, I, I, Cl), (I, I, I, I, I, Br), (I, I, I, I, I, I)}}

```

Figure 2 Mathematica code used to generate tuples for substitution of benzene. A total of  $5^6$  or 15625 tuples were generated for halo-substituted benzenes. Duplicate entries are underlined using the same color.

### 2.3. Removal of duplicate tuples

90 The Mathematica notebook also contains operations to identify and remove duplicates and enantiomeric structures (Figure 3). Each structure in the list of tuples **all** is rotated and flipped. If any of the resulting rotations or flips has been previously encountered, the corresponding tuple is discarded. Otherwise, the tuple is added to **finalist**. For example, the tuple {H, H, H, H, H, F} and {H, F, H, H, H, H} both refer to the same structure: fluorobenzene. Assuming the former comes earlier in **all**, it will be appended to **finalist**; the latter tuple will be discarded. For any number of substituents  $n$ , this method has a complexity of  $O(n^2)$ . The number of tuples in **finalist** can be verified mathematically [11-14].

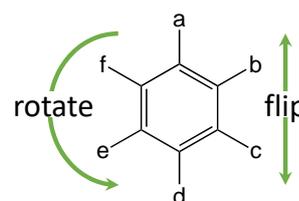
```

equiv[a_, i_, j_] :=
Module[{f, s, k}, (*Rotate/flip compounds to filter out repetitions*)
f = Reverse[a[[i]]]; (*Flip compounds*)
For[k = 0, k ≤ 5, k++,
s = RotateLeft[a[[j]], k]; (*Rotate compounds*)
If[a[[i]] == s || f == s, Break[]]];
If[k ≤ 5, True, False]];

count = Table[0, {i, 1, n}];
For[i = 1, i < n, i++,
If[count[[i]] ≠ 0, Continue[]];
For[j = i + 1, j ≤ n, j++,
If[equiv[all, i, j], count[[j]] = i]
]]; // AbsoluteTiming

(*Final list of structures*)
finalist = {};
Count[count, 0];
For[i = 1, i ≤ n, i++,
If[count[[i]] == 0, AppendTo[finalist, all[[i]]]];
Length[finalist]

```



Number of tuples  
Out[ ] = 15 625 **before**  
Out[ ] = 1505 **after**  
duplicate removal  
Out[ ] = {751.659 wall time

100 Figure 3 Mathematica code used to eliminate identical and enantiomeric structures. The code used about 752 seconds of wall time and yielded 1505 unique structures. These results are consistent with combinatorial analysis of the halogenated benzene isomers [13].

### 2.4. Substitution on the template

105 Once the collection of tuples has been modified from the previous steps, GNU sed is used to replace the labels a, b, c, d, e and f in the template with appropriate atoms from the tuples in **finalist** (Figure 4). The list of sed commands corresponding to all tuples are generated automatically from

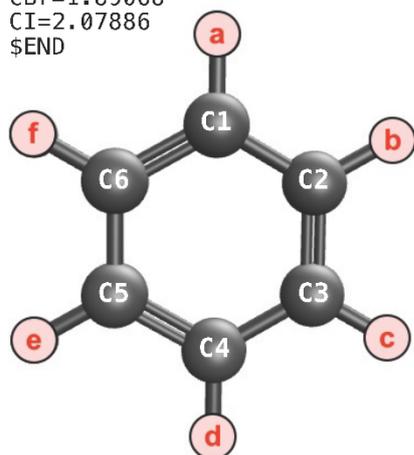
Mathematica. For each tuple, the substitution would result in a 3D chemical structure that can be visualized with any molecular graphic software and used as input files for further calculation.

#### GNU sed

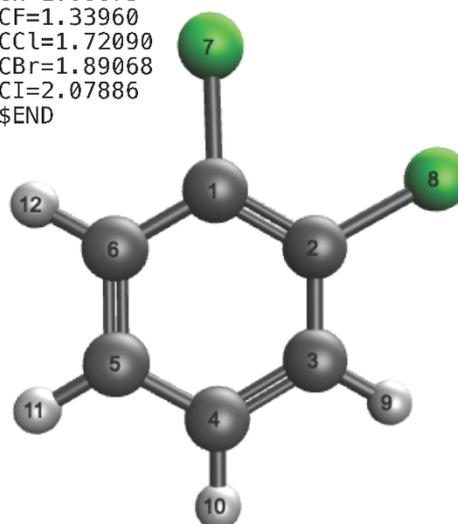
```
cat templateB-MP2.inp | sed 's/a/Cl/g;s/b/Cl/g;s/c/H/g;s/d/H/g;s/e/H/g;s/f/H/g;' > MP2/ClClHHHH.inp
```

<pre>\$MOLECULE 0 1 C C 1 CC C 2 CC 1 120.0 C 3 CC 2 120.0 1 0.0 C 4 CC 3 120.0 2 0.0 C 5 CC 4 120.0 3 0.0 a 1 Ca 2 120.0 3 180.0 b 2 Cb 3 120.0 4 180.0 c 3 Cc 4 120.0 5 180.0 d 4 Cd 5 120.0 6 180.0 e 5 Ce 6 120.0 1 180.0 f 6 Cf 1 120.0 2 180.0</pre>	<p>Apply the substitutions</p> <p>GNU sed →</p>	<pre>\$MOLECULE 0 1 C C 1 CC C 2 CC 1 120.0 C 3 CC 2 120.0 1 0.0 C 4 CC 3 120.0 2 0.0 C 5 CC 4 120.0 3 0.0 Cl 1 CCl 2 120.0 3 180.0 Cl 2 CCl 3 120.0 4 180.0 H 3 CH 4 120.0 5 180.0 H 4 CH 5 120.0 6 180.0 H 5 CH 6 120.0 1 180.0 H 6 CH 1 120.0 2 180.0</pre>
--	---	--

```
CC=1.39483
CH=1.08673
CF=1.33960
CCL=1.72090
CBr=1.89068
CI=2.07886
$END
```



```
CC=1.39483
CH=1.08673
CF=1.33960
CCL=1.72090
CBr=1.89068
CI=2.07886
$END
```



110 *Figure 4 Example of creating an input file from a template file by applying substitutions using GNU sed. A 3D chemical structure of the file above is visualised in IQmol [20].*

#### 2.5. Extension to chemical identifiers and database queries

115 Linear notations are simple descriptions 3D structures and, more importantly, can be used as computer inputs. Many types of linear notations exist, namely the IUPAC international chemical identifier (InChI) and the simplified molecular-input line-entry (SMILES) system. In this article, each tuple in **finalist** was converted into a SMILES string (Figure 5). As with the Z-matrix, a string template is constructed first. In the case of benzene, the template is

$$[a]C1=C([b])C([c])=C([d])C([e])=C1[f]$$

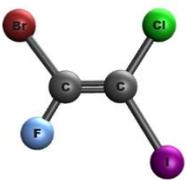
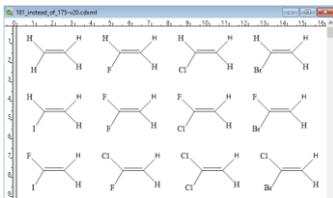
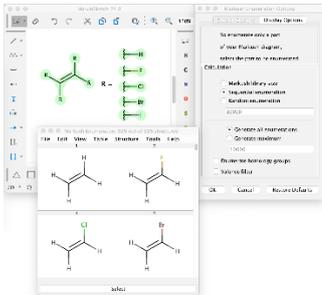
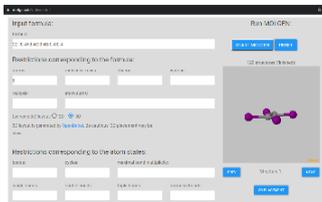
120 where the letters a to f can be substituted by each element in the tuple. SMILES strings for each compound can be used to reference various properties of known compounds from databases.

125 Database queries provide quick look up of the compound properties and can verify the uniqueness of the generated structures. The National Institutes of Health maintains an open-access chemistry database called PubChem (<https://pubchem.ncbi.nlm.nih.gov>) [22, 23] that contains information such as chemical structures, identifiers, and properties of various small molecules and macromolecules. Each SMILES string can be submitted into the PubChem database to obtain a unique PubChem CID (Figure 5). Duplicate structures can be identified if any two SMILES strings return the



### 3. Discussion, Conclusion and Future work

**Table 1.** Comparison of the discussed approach and available software in the market.

	Screen Shot	Description
<b>Z-matrix template-based substitution approach (This paper)</b>		A total of 175 unique structures were correctly generated [11].
<b>ChemDraw 20.1 [27]</b>		ChemDraw initially generated 625 structures, followed by removal of duplicates and finally displayed (generally only up to 200 structures) 181 structures. There are still duplicate entries in the generated structures.
<b>KNIME [28]</b>	N/A	See the text.
<b>MarvinSketch 21.8 [29]</b>		MarvinSketch generated 625 structures and did not remove any duplicates.
<b>MOLGEN 5.0 [30]</b>		MOLGEN quickly returned 120 structures for 2D option and took a few minutes for the 3D option.

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This paper describes the concept of the Z-matrix template-based substitution approach and provides a simple practical tutorial to demonstrate the concept on Windows. This tutorial can be adapted to work on Mac, Linux and even Raspberry Pi by which Mathematica is free. There are also other alternative programs to implement the concept. For example, the code may be rewritten in other languages/platforms/frameworks such as Jupyter [31] and the results can be visualized in Avogadro [32] or GaussView [33].

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The approach has been used to study many classes of compounds from a simple and small class of molecules such as ethane and ethene to larger and more complex structures such as dioxin-like compounds [11-15]. The substitution scheme in the template can lead to different compounds of the same class, constitutional isomers, configurational isomers and conformational isomers. However, given limitation of other existing off-the-shelf software, a relatively simple class of halogenated ethenes is selected as a model example for comparison as shown in Table 1. Surprisingly, without warning, the three programs yielded 6 extra, 450 extra or 55 missing entries. (See Supplementary information for more details. We also attempted on some codes/workflows on popular KNIME [28] but did not manage to produce any results for this example case.) Therefore, this example of halogenated ethenes raises a very important concern that are typical of molecular databases and libraries. The integrity of data can be improved if initial structures from upstream are generated correctly.

Our approach presented here for educational purposes is straightforward and may be used in classrooms for training. The codes are available in the Supplementary information and expected to be modified for specialized uses beyond tutorial purposes. Computer coding/scripting is inevitably an integral part of this tutorial. Fortunately, by expressing our ideas in Mathematica, the number of lines of code can be fairly at minimum. The natural next step after this tutorial is filtering for molecular structures in which desired conditions are fulfilled. For example, in our previous work, we labelled structures as *E* or *trans*, *Z* or *cis*, geminal, *gauche*, *anti*, *ortho*, *meta*, *para*. Custom-made codes/scripts are freely available in the references [11-14] and may be modified to fit the needs of users.

Two limitations that can be addressed in future are the use of non-single atom substituents and the efficiency of the duplicate removal step. The first limitation will generally require a consideration of the torsional angles of the substituent groups with respect to the template. The second limitation may be overcome by using a different computer language, sacrificing the simplicity and brevity of Mathematica codes. An alternative approach is to represent each structure as a SMILES string and filter duplicates using the PubChem database. For example, searching C1C1=CC=CC(F)=C1 and FC1=CC(C1)=CC=C1 returns the same compound: 1-chloro-3-fluorobenzene. Hence, one of the structures is a duplicate and can be removed. Although this approach may only work for compounds that are identified, PubChem also allows quick access the properties of the compounds which is particularly useful when enumerating structures for drug discovery and smart materials.

### Supplementary materials

A zip file containing Mathematica code and results

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### Author Contributions

Conceptualization, W.L. and T.L.; data curation, W.L. and T.L.; formal analysis, W.L.; funding acquisition, T.L.; investigation, T.L.; methodology, W.L. and T.L.; project administration, T.L.; resources, T.L.; software, T.L.; supervision, T.L.; validation, W.L. and T.L.; visualization, W.L.; writing—original draft preparation, W.L. and T.L.; writing—review and editing, W.L. and T.L. All authors have read and agreed to the published version of the manuscript.

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### Availability of data and materials

Data and materials for the examples are available as additional materials.

### Declaration of interests:

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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