

# Hands-On Tutorial: Data-Mining the QM9 Dataset

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 (Dated: July 9, 2024)

This tutorial introduces the application of the QM9 dataset using Python. We explore basic aspects of data retrieval, statistics, and analysis using the `qm9pack` Python module.

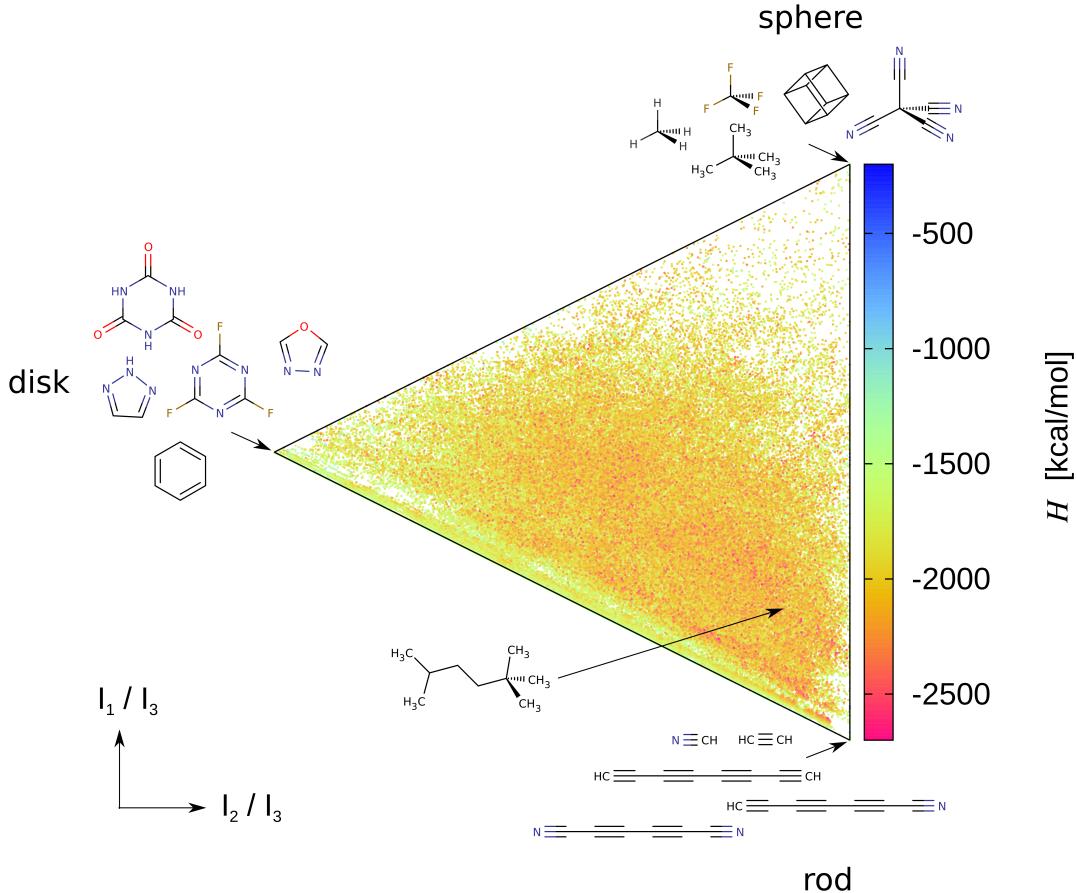


FIG. 1. Distribution of QM9 molecules as a function of their shape and stability. The  $x$  and  $y$  axes are normalized moments of inertia ( $I_1/I_3$  and  $I_2/I_3$ ), and the atomization enthalpy ( $H$  in kcal/mol) from density functional theory calculations is color-coded. Also shown are the representative 1D (rod-shaped), 2D (disc-shaped), and 3D (near-spherical) molecules at the corners. Each single dot corresponds to one or many QM9 molecules.

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## I. INTRODUCTION

The QM9 dataset [1] contains minimum energy geometries and various properties of 133,885 molecules, calculated using the density functional theory method B3LYP and the 6-31G(2df,*p*) basis set. Among these, 3,054 molecules faced convergence issues during structure optimization and were excluded, resulting in a final dataset of 130,831 molecules. The 3,054 ‘uncharacterized’ molecules have been analyzed separately, highlighting the critical role of quantum chemistry approximations in establishing the correspondence between a molecular graph and its three-dimensional structure [2]. For each of the 130,831 molecules, the dataset contains the SMILES representation[3] collected from the GDB17 database[4] containing 166.4 billion molecular graphs. In this tutorial, we will use the Python modules Pandas[5, 6], Matplotlib[7], NumPy[8], and SciPy[9]. The QM9 dataset is shared through the module `qmlpack`, which uses Pandas and Numpy.

### 1. Energies in the QM9 dataset

The QM9 dataset reports four thermochemistry energies defined according to Ref. 10: internal energy at zero kelvin (0 K), denoted customarily as  $U_0$ ; internal energy at 298.15 K (room temperature), denoted customarily as  $U_T$ ; enthalpy at 298.15 K, denoted customarily as  $H_T$ ; Gibbs free energy at 298.15 K, denoted customarily as  $G_T$ . These four energies can be queried using the keys (or column names): `InternalEnergy_0K_au`, `InternalEnergy_298K_au`, `Enthalpy_298K_au`, and `GibbsFreeEnergy_298K_au`. Here are the formal definitions of these energies:

1.  $U_0$  is the energy of the molecule at 0 K, which is the sum of its electronic energy (including the classical electron-electron repulsion term),  $E_{\text{electronic}}$ , and the zero-point vibrational energy (ZPVE)

$$U_0 = E_{\text{electronic}} + \text{ZPVE}. \quad (1)$$

2.  $U_T$  is the room temperature internal energy, which is the sum of the  $E_{\text{electronic}}$  and the total thermal corrections to energy along all degrees of freedom (translational, rotational, vibrational, and electronic),  $E_{\text{tot}}$

$$U_T = E_{\text{electronic}} + E_{\text{tot}}. \quad (2)$$

Note that  $E_{\text{tot}}$  includes ZPVE.

3.  $H_T$  is the room temperature enthalpy, which is the sum of  $E_{\text{electronic}}$ ,  $E_{\text{tot}}$ , and the energy due to the volume of the system, which under the ideal gas assumption is  $k_B T$ .

$$H_T = E_{\text{electronic}} + E_{\text{tot}} + k_B T. \quad (3)$$

The enthalpy correction  $E_{\text{tot}} + k_B T$  is often denoted as  $H_{\text{corr}}$ .

4.  $G_T$  is the room temperature Gibbs free energy, which is the sum of  $E_{\text{electronic}}$ , free energy correction defined as  $G_{\text{corr}} = H_{\text{corr}} - TS_{\text{tot}}$ , where  $S_{\text{tot}}$  is the total entropy along all degrees of freedom (translational, rotational, vibrational, and electronic).

$$G_T = E_{\text{electronic}} + G_{\text{corr}}. \quad (4)$$

The absolute values of  $U_0$ ,  $U_T$ ,  $H_T$ , and  $G_T$  of molecules can be used to calculate the change in the corresponding property during a reaction. For example, for a reaction  $A \rightarrow B$ , one can calculate the change in the free energy as  $\Delta G = G_B - G_A$ .

For most applications, one might prefer energies that quantify the stability of the molecule. Hence, one has to consider the relative values of the energies compared to a reference, such as free atoms. The molecular atomization energy is the sum of all bond energies, defined as

$$E_{\text{atomization}} = U_0^{\text{molecule}} - \sum_{A \in \text{atoms}} U_0^A \quad (5)$$

As stated above,  $U_0^{\text{molecule}}$  includes the ZPVE. For the free atoms, there are no vibrational degrees of freedom; hence,

$U_0^A$  is the same  $E_{\text{electronic}}$ . TABLE I contains the energies of the CHONF atoms calculated using the DFT method, B3LYP, using the basis set, 6-31G(2df, p), as reported in [1] and can be accessed from the original data repository[11].

TABLE I. Reference thermochemical energies of H, C, N, O, F atoms in hartree, collected from Ref. 11.

Element	$U_0$	$U_T$	$H_T$	$G_T$
H	-0.500273	-0.498857	-0.497912	-0.510927
C	-37.846772	-37.845355	-37.844411	-37.861317
N	-54.583861	-54.582445	-54.581501	-54.598897
O	-75.064579	-75.063163	-75.062219	-75.079532
F	-99.718730	-99.717314	-99.716370	-99.733544

## II. BASIC EXERCISES

### A. Loading the QM9 Dataset

*Exercise A.1: Load the dataset*

In the first exercise, we will load the `qm9pack` module, fetch the QM9 dataset (`qm9`), and perform initial exploratory analysis.

---

```
import qm9pack # Import the qm9pack module

# Fetch the QM9 dataset and store it in a DataFrame
df = qm9pack.get_data('qm9')

# Print the summary statistics of the dataset
print(df.describe())

# Print the first 5 rows of the dataset
print(df.head())

# Print the last 5 rows of the dataset
print(df.tail())
```

---

<OUTPUT>  
Long output, not shown.

---

### B. Exploring the Content of QM9 Dataset

*Exercise B.1: Overview of columns*

Let us find the names of all columns (properties) in `qm9`.

---

```
import qm9pack # Import the qm9pack module

# Fetch the QM9 dataset and store it in a DataFrame
df = qm9pack.get_data('qm9')

# Iterate over each column in the DataFrame and print the column name
for key in df.columns:
    print(key)
```

---

```
<OUTPUT>
XYZ_file
Index
SMILES
InChi
N_atoms
Stoichiometry
Elements
XYZ_Ang
Mulliken_pop
Harmonic_Freq_cmi
RotA_GHz
RotB_GHz
RotC_GHz
Dipole_debye
Polarizability_bohr3
HOMO_au
LUMO_au
HOMO_LUMO_gap_au
R2_bohr2
ZPVE_au
InternalEnergy_0K_au
InternalEnergy_298K_au
Enthalphy_298K_au
GibbsFreeEnergy_298K_au
Heatcapacity_Cv_cal_mol_K
```

---

*Exercise B.2: helper*

Get more details about one of the columns in `qm9`.

---

```
import qm9pack # Import the qm9pack module

# Fetch the QM9 dataset and store it in a DataFrame
df = qm9pack.get_data('qm9')

# Define a specific column name for which to print more details
key = 'RotC_GHz'

# Use the helper function from qm9pack to print more details for the
# specified column
qm9pack.helper(key)
```

---

```
<OUTPUT>
'RotC_GHz': Rotational constant C in GHz.
```

---

*Exercise B.3: helper for all columns*

Get more details about all the columns in `qm9`.

---

```

import qm9pack # Import the qm9pack module

# Fetch the QM9 dataset and store it in a DataFrame
df = qm9pack.get_data('qm9')

# Iterate over each column in the DataFrame and print more details for
# each column
for key in df.columns:
    qm9pack.helper(key)

```

---

<OUTPUT>

'XYZ\_file': The file containing the XYZ coordinates of the molecule as submitted in the original QM9 article (<https://doi.org/10.1038/sdata.2014.22>). The name 'dsgdb9nsd\_000001.xyz' contain data for molecule-1 and so on. Overall, qm9 contains 130831 molecules

'Index': A unique identifier for each molecule in the dataset which ranges from 1 to 133885 of which 3054 will be missing as the corresponding molecular structures failed to converge with the DFT method, B3LYP, and the basis set, 6-31G(2df,p)

'SMILES': Simplified Molecular Input Line Entry System representation of the molecule.

'InChi': IUPAC International Chemical Identifier for the molecule.

'N\_atoms': The number of atoms in the molecule.

'Stoichiometry': The stoichiometric formula of the molecule encoded as the array containing numbers of H, C, N, O, and F atoms. For CH4, the list corresponds to [4,1,0,0,0]

'Elements': List of elements present in the molecule. For CH4, the list is ['C','H','H','H','H']

'XYZ\_Ang': The XYZ coordinates of the molecule in Angstroms calculated using the DFT method, B3LYP, and the basis set, 6-31G(2df,p).

'Mulliken\_pop': Mulliken population analysis data for the molecule in units of charge of an electron, e.

'Harmonic\_Freq\_cmi': Harmonic vibrational frequencies of the molecule in cm<sup>-1</sup>.

'RotA\_GHz': Rotational constant A in GHz.

'RotB\_GHz': Rotational constant B in GHz.

'RotC\_GHz': Rotational constant C in GHz.

'Dipole\_debye': Dipole moment of the molecule in debye.

'Polarizability\_bohr3': Polarizability of the molecule in bohr<sup>3</sup>.

'HOMO\_au': Highest Occupied Molecular Orbital energy in atomic units, hartree.

'LUMO\_au': Lowest Unoccupied Molecular Orbital energy in atomic units, hartree.

'HOMO\_LUMO\_gap\_au': Energy gap between HOMO and LUMO in atomic units, hartree.

'R2\_bohr2': Spread of the electron density calculated as the expectation value of the operator, R<sup>2</sup>, in bohr<sup>2</sup>

'ZPVE\_au': No help content available for this key.

'InternalEnergy\_0K\_au': Internal energy of the molecule at 0 kelvin.

'InternalEnergy\_298K\_au': Internal energy of the molecule at 298.15 kelvin.

'Enthalphy\_298K\_au': Enthalpy of the molecule at 298.15 kelvin.

'GibbsFreeEnergy\_298K\_au': Gibbs free energy of the molecule at 298.15 kelvin.

'Heatcapacity\_Cv\_cal\_mol\_K': Heat capacity at constant volume in cal/(mol K).

---

*Exercise B.4: Cartesian coordinates using makexyz*

Store the Cartesian coordinates of a molecule in qm9 corresponding to an index.

---

```

import qm9pack # Import the qm9pack module

# Fetch the QM9 dataset and store it in a DataFrame
df = qm9pack.get_data('qm9')

# Save XYZ for a molecule using its index
index = 0
filename = 'Mol_0.xyz'
qm9pack.makexyz(index, df, filename)

index = 1
filename = 'Mol_1.xyz'
qm9pack.makexyz(index, df, filename)

```

---

```

<OUTPUT>
5
Mol_0.xyz
C   -0.01269814    1.08580416    0.00800100
H    0.00215042   -0.00603132    0.00197612
H    1.01173084    1.46375116    0.00027657
H   -0.54081507    1.44752661   -0.87664372
H   -0.52381363    1.43793264    0.90639729
4
Mol_1.xyz
N   -0.04042605    1.02410775    0.06256380
H    0.01725746    0.01254521   -0.02737716
H    0.91578937    1.35874519   -0.02875776
H   -0.52027774    1.34353213   -0.77554261

```

---

#### *Exercise B.5: Collect coordinates of all molecules*

Store the Cartesian coordinates of all molecules in qm9 in the file qm9\_130831\_molecules.xyz. WARNING: The code will run for a while and will create an approximately 500 MB file.

---

```

import qm9pack                      # Import the qm9pack module
import os                           # Import the os module

df = qm9pack.get_data('qm9')         # Fetch the QM9 dataset

filename = 'qm9_130831_molecules.xyz' # Output filename

# Create the output file
with open(filename, 'w') as f:
    pass

# Loop through each molecule in the dataset
for index in range(len(df)):
    tmpfile = 'mol_' + str(index) + '.xyz' # Temporary filename

    qm9pack.makexyz(index, df, tmpfile)     # Create the XYZ file

    # Append contents to the main output file
    with open(tmpfile, 'r') as temp_file:
        contents = temp_file.read()

```

```

with open(filename, 'a') as final_file:
    final_file.write(contents)

os.remove(tmpfile)                                # Remove temporary file

```

---

<OUTPUT>  
Long output, not shown.

---

#### *Exercise B.6:Filter molecules using Stoichiometry*

Let us find all molecules in `qm9` matching a stoichiometry. Let us use C2H6O corresponding to two constitutional isomers, ethanol (CH3CH2OH) and dimethylether (CH3OCH3). We will filter the dataset to make a filtered DataFrame. Then, we will go over each molecule in this subset and print SMILES and InChi strings.

NOTE: You can modify this exercise and retrieve any other properties for a set of constitutional isomers. You can use the names of the columns from II B Exercise B.1. For example, if you want to print SMILES and dipole moment, you can modify the last line of the code as

```
print(mol['SMILES'], mol['Dipole_debye'])
```

---

```

import qm9pack

df = qm9pack.get_data('qm9')

# stoichiometry is a string of list with number of H, C, N, O, and F atoms
stoi = "[6,2,0,1,0]" # Six H, two C, zero N, one O, and zero F

# Filter the DataFrame to match the stoichiometry
filtered_df = df[df['Stoichiometry'].apply(lambda x: x == stoi)]

# Iterate over each row in the filtered DataFrame
for _, mol in filtered_df.iterrows():
    # Print SMILES and InChi for each molecule
    print(mol['SMILES'], mol['InChi'])

```

---

<OUTPUT>  
CCO InChI=1S/C2H6O/c1-2-3/h3H,2H2,1H3  
COC InChI=1S/C2H6O/c1-3-2/h1-2H3

---

### III. ADVANCED EXERCISES

#### *Exercise C.1:All stoichiometries in QM9*

Let us find all the unique stoichiometries in `qm9` and find their counts. We will find that the most populated stoichiometry corresponds to C7H10O2, containing 6095 molecules, which has been extensively studied in Ref. 12. NOTE: Remember, Python counts from zero.

---

```

import qm9pack

df = qm9pack.get_data('qm9')

# Get counts of unique values in the 'Stoichiometry' column, in descending order
value_counts = df['Stoichiometry'].value_counts(ascending=False)

```

```
# Iterating over each unique value and its count
for index, count in value_counts.items():
    print(f"{index}: {count}") # Printing each unique value and its count

<OUTPUT>
[10,7,0,2,0]: 6094
[11,7,1,1,0]: 5858
[9,6,1,2,0]: 5630
[9,7,1,1,0]: 5215
[12,8,0,1,0]: 4918
[12,7,0,2,0]: 4612
[7,6,1,2,0]: 3872
[8,6,2,1,0]: 3556
[10,8,0,1,0]: 3171
[14,8,0,1,0]: 3154
[8,7,0,2,0]: 3009
...
...
```

## ACKNOWLEDGMENTS

I am grateful to everyone who has reached out with inquiries regarding the QM9 data, which served as the primary inspiration for developing this package. Big thanks to OAvL for letting me dive into the QM9 project and for treating me to an unforgettable dinner on the evening we completed the QM9 article. I acknowledge the support of the Department of Atomic Energy, Government of India, under Project Identification No. RTI 4007.

## IV. DATA AVAILABILITY

The qm9pack is maintained here: <https://github.com/raghurama123/qm9pack>

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