Molecular Point Group prediction of coordination compounds using ML

Outline

7th School of Computational Chemistry, AI & ML

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Outline

Outline



- Introduction
- 2 Methodology
- Results and discussion
- 4 Conclusions
- 6 Acknowledgements

Metals in biological systems



- Our interest in the prediction of groups of points is based on the study of iron-siderophores stereoisomerism, therefore, we focus on metals in biological systems.
- In biological systems, metal ions are always coordinated by water, biomolecules, or others called ligands.
- The metal-ligand interaction depends on the chemical nature of both.
- Pearson explained this association in terms of "Hard and Soft Acids and Bases".

$$(n-1)d^x ns^2 \rightarrow (n-1)d^{x-i}$$



¹J. Am. Chem. Soc. 1963, 85, 22, 3533–3539

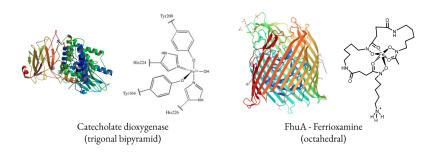
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Coordinated Number

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- The coordination number of a central atom in a molecule or crystal is the number of atoms, molecules or ions bonded to it.
- Some examples of geometry in proteins with iron: tetrahedron (rubredoxin), trigonal bipyramide (catecholate dioxygenase), pyramid (tyrosine hydroxylase), octahedron (lipo-oxygenase)²:



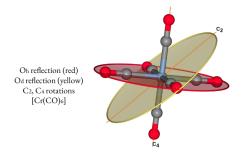
²Toma HE. 2015. Química bioinorgánica e ambiental. Blucher Ltda, São Paulo, p. 268.

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Group of Point



- The structural organization around the metal can be classified according to the Theory of Groups, by a "Group of point".
- These can be determined by symmetry operations: identity, proper reflection, improper reflection, rotation, and inversion³.
- Applications: chirality, hybridization, analysis of molecular vibrations, activity in infrared and Raman spectroscopy, etc.



³https://symotter.org/gallery

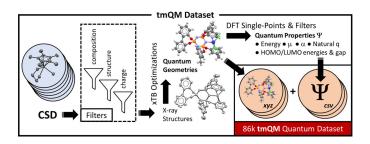
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Introduction

Datasets

Outline





tmQM: 7 filters

- All structures contain a single TM^a
- Minimum of one C and one H atoms. Allowed: B, Si, N, P, etc.
- Excluded: counterions, polymeric structures, all structures without three-dimensional coordinates, disordered atoms, charge higher than 1 and lower than 1.

^aJ. Chem. Inf. Model. 2020, 60, 12, 6135-6146

Introduction

Datasets

Outline



SMILES	CSD_code	Point_Group
[Sc]123(ON(O1)[O])(ON([O])O2)ON([O])O3.n1ccccc1C1=[N]=C([N]C(=N1)N)c1ncccc1	DUCVIG	C(s)
[La]123(O[C](C=C(O1)C(F)(F)F)C(F)(F)F)(OC(=C[C](O2)C(F)(F)F)C(F)(F)F)O[C](C=C(O3)C(F)	KINJOG	C(1)
[La]12345(I)(I)[N@@](C[C]6N2C=CN=C6)(C[C]2N3C=CN=C2)[C@@H]2[C@@H]([N@@]1(C[C]1	OBIQAS	C(1)
[Y]12345Oc6c([CH][N@]3CC[N@](CC[N@@]4[CH]c3c(O1)c(ccc3)C(C)(C)C)CC[N@@]5[CH]c1c(C		C(1)
[Sc]12([P](c3cc(ccc3N1c1ccc(cc1[P]2(C(C)C)C(C)C)C)(C(C)C)C(C)C)(Nc1c(cccc1C(C)C)C(C)C)	EGEKIL	C(1)
[Sc](C[Si](C)(C)C)(C[Si](C)(C)C)C[Si](C)(C)C.[Si](N(CCOC)CCOC)(C)(C)C	TEQTAL	C(1)
[Sc]1(Cl)(Cl)N(C(=C[C](N1c1c(cccc1C(C)C)C(C)C)C(C)(C)C)C(C)(C)C)C(C)C)C(C)C)C(C)CCCC1C(C)CCCCCCCC	XIQJEM	C(1)
[Y](C) C .C1CCC01.C1CCC01.C1CCC01.C1CCC01	TATTIS	C(1)

CSDSymmetry

- Provides an extremely flexible source of symmetry related information: molecular point group, space group, Z, Z' and the symmetry of the occupied Wyckoff position for molecules in the CSD.
- Intersected with chemical or substructural searches performed in ConQuest.
- CSDSymmetry is a relational database built using Microsoft Access (2007) and is available as a free download (terms and conditions apply)^a.

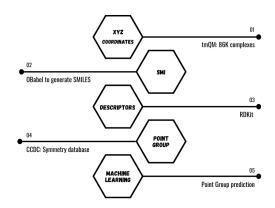
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ahttps://www.ccdc.cam.ac.uk/community/csd-community/csdsymmetry/

Summary



Available from Google Colab⁴.



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⁴https://github.com/inefable12/OhTd_PointGroup_qmTM_CCDC

Libraries and Data



Acknowledgements

1. Libraries

```
!pip install pycaret
         from pycaret.utils import version
         version()
Out[2]: '2.3.10'
         import pandas as pd
         import numpy as np
         from pycaret.classification import *
        data2.info()
       RangeIndex: 628 entries, 0 to 627
       Columns: 201 entries. Point Group to fr urea
       dtypes: float64(201)
       memory usage: 986.3 KB
```

Pre-processing

Outline



Delete columns with entropy 0

```
for column in df:
  min = df[column].min()
  max = df[column].max()
  if max == min:
    del(df[column])
    continue
```

Normalization

```
for column in df:
    if column != "Value":
        min = df[column].min()
        max = df[column].max()
    for i in range(len(df[column])):
        df[column][i] = (df[column][i]-min)/(max-min)
```

PyCaret



- Setup(df, target = 'Point_Group', session_id=123)
- Compare models()

	Model	Accuracy	AUC	Recall	Prec.	F1	Карра	MCC	TT (Sec)
et	Extra Trees Classifier	0.7449	0.8271	0.812	0.7594	0.7812	0.4744	0.4840	0.592
rf	Random Forest Classifier	0.7266	0.8230	0.800	0.7395	0.7664	0.4365	0.4447	0.565
gbc	Gradient Boosting Classifier	0.7224	0.8000	0.784	0.7435	0.7615	0.4292	0.4333	0.642
lightgbm	Light Gradient Boosting Machine	0.7199	0.8188	0.780	0.7408	0.7579	0.4249	0.4300	0.242
ridge	Ridge Classifier	0.7041	0.0000	0.792	0.7175	0.7512	0.3871	0.3939	0.019
Ir	Logistic Regression	0.6995	0.7689	0.808	0.7079	0.7521	0.3730	0.3846	0.408
ada	Ada Boost Classifier	0.6995	0.7470	0.752	0.7347	0.7384	0.3837	0.3894	0.237
dt	Decision Tree Classifier	0.6857	0.6841	0.700	0.7361	0.7150	0.3646	0.3675	0.034
svm	SVM - Linear Kernel	0.6720	0.0000	0.880	0.6672	0.7520	0.2891	0.3406	0.026
knn	K Neighbors Classifier	0.6513	0.6928	0.756	0.6717	0.7088	0.2751	0.2834	0.122
lda	Linear Discriminant Analysis	0.6449	0.6798	0.720	0.6749	0.6947	0.2697	0.2736	0.037
qda	Quadratic Discriminant Analysis	0.5715	0.5716	0.580	0.6815	0.5474	0.1425	0.1553	0.036
dummy	Dummy Classifier	0.5695	0.5000	1.000	0.5695	0.7257	0.0000	0.0000	0.014
nb	Naive Bayes	0.5195	0.6184	0.344	0.6626	0.4341	0.0877	0.1085	0.020

Model



• et = create_model('et')

		Accuracy	AUC	Recall	Prec.	Prec. F1		
	Fold							
	0	0.7500	0.8905	0.8800	0.7333	0.8000	0.4739	
	1	0.7045	0.8084	0.8000	0.7143	0.7547	0.3863	
	2	0.7273	0.7832	0.8400	0.7241	0.7778	0.4298	
	3	0.7045	0.7716	0.6800	0.7727	0.7234	0.4091	
	4	0.8182	0.8674	0.9200	0.7931	0.8519	0.6199	
	5	0.7955	0.8874	0.9600	0.7500	0.8421	0.5639	
	6	0.7273	0.7968	0.7600	0.7600	0.7600	0.4442	
	7	0.6818	0.7937	0.6400	0.7619	0.6957	0.3676	
	8	0.7727	0.8505	0.7600	0.8261	0.7917	0.5426	
	9	0.7674	0.8211	0.8800	0.7586	0.8148	0.5069	
	Mean	0.7449	0.8271	0.8120	0.7594	0.7812	0.4744	
	Std	0.0413	0.0415	0.0981	0.0313	0.0470	0.0782	

Tuned model



Acknowledgements

• tuned et = tune model(et, optimize = 'AUC')

class sklearn.ensemble.ExtraTreesClassifier(n_estimators=100, *, criterion='gini', max_depth=None, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='sqrt', max_leaf_nodes=None, min_impurity_decrease=0.0, boostrap=False, oob_score=False, n_jobs=None, random_state=None, verbose=0, warm_start=False, class_weight=None, ccp_alpha=0.0, max_samples=None) [source]

		Accuracy	AUC	UC Recall Prec.		F1	Kappa	
	Fold							
	0	0.7727	0.8695	0.760	0.8261	0.7917	0.5426	
	1	0.6818	0.8000	0.760	0.7037	0.7308	0.3433	
	2	0.6818	0.7747	0.760	0.7037	0.7308	0.3433	
	3	0.7273	0.7779	0.760	0.7600	0.7600	0.4442	
	4	0.7500	0.7789	0.800	0.7692	0.7843	0.4873	
	5	0.7727	0.8505	0.960	0.7273	0.8276	0.5122	
	6	0.6364	0.7811	0.680	0.6800	0.6800	0.2589	
	7	0.6364	0.7200	0.600	0.7143	0.6522	0.2772	
	8	0.7045	0.8042	0.640	0.8000	0.7111	0.4163	
	9	0.7674	0.8200	0.760	0.8261	0.7917	0.5295	
	Mean	0.7131	0.7977	0.748	0.7510	0.7460	0.4155	
	Std	0.0504	0.0401	0.093	0.0505	0.0523	0.0993	

Receiver Operating Characteristic (ROC)



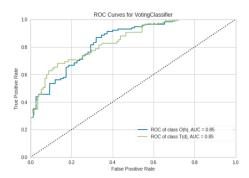
Acknowledgements

sensitivity, recall, hit rate, or true positive rate (TPR)
$$TPR = \frac{TP}{P} = \frac{TP}{TP + FN} = 1 - FNR$$

specificity, selectivity or true negative rate (TNR)

$$TNR = \frac{TN}{N} = \frac{TN}{TN + FP} = 1 - FPR$$

Area Under Curve (AUC)



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et + rf + gbc ?



PyCaret: Blend_models(estimator_list=[et,rf,gbc])

Model	Accuracy	AUC	Recall	Prec.	F1	Карра
Extra Trees Classifier	0.74	0.83	0.81	0.76	0.781	0.47
Random Forest Classifier	0.73	0.82	0.80	0.74	0.766	0.44
Gradient Boosting Classifier	0.72	0.80	0.78	0.74	0.762	0.43
Ensemble et + rf + gbc	0.74	0.83	0.81	0.75	0.779	0.47

Alvarado-Huayhuaz et al. 7aEQC2022 14

Conclusions

Outline



Acknowledgements

- The ensemble et, rf and gbc models fit best to predict the Oh and Td point groups of the coordination compounds
- Perspectives: Using quantum descriptors (global and local reactivity) using PRIMoRDiA (Macromolecular Reactivity Descriptors Access) for a generalized point group classification model.

Acknowledgements







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