OpenEnsembles: A Python Resource for Ensemble Clustering

Tom Ronan TOM_RONAN@HOTMAIL.COM Shawn Anastasio Zhijie Qi Roman Sloutsky Kristen M. Naegle Department of Biomedical Engineering and the Center for Biological Systems Engineering Washington University in St. Louis St. Louis, MO 63122, USA

SHAWN.ANASTASIO@WUSTL.EDU QIZHIJIE@WUSTL.EDU SLOUTSKY@WUSTL.EDU KNAEGLE@WUSTL.EDU

Pedro Henrique S. Vieira Tavares

PEDROHSVT@GMAIL.COM

Department of Computer Science University of Arizona Tucson, AZ 85721, USA

Editor: Antti Honkela

Abstract

In this paper we introduce OpenEnsembles, a Python toolkit for performing and analyzing ensemble clustering. Ensemble clustering is the process of creating many clustering solutions for a given dataset and utilizing the relationships observed across the ensemble to identify final solutions, which are more robust, stable or better than the individual solutions within the ensemble. The OpenEnsembles library provides a unified interface for applying transformations to data, clustering data, visualizing individual clustering solutions, visualizing and finishing the ensemble, and calculating validation metrics for a clustering solution for any given partitioning of the data. We have documented examples of using OpenEnsembles to create, analyze, and visualize a number of different types of ensemble approaches on toy and example datasets. OpenEnsembles is released under the GNU General Public License version 3, can be installed via Conda or the Python Package Index (pip), and is available at https://github.com/NaegleLab/OpenEnsembles.

Keywords: Unsupervised Learning, Ensembles, Clustering, Ensemble Clustering, Finishing Techniques

1. Introduction

Clustering, a type of unsupervised learning, has been instrumental in a large number of fields for reducing data dimensionality, identifying important features, and uncovering the underlying structure of relationships that give rise to the sampled data under consideration. However, a single clustering result may represent a spurious solution (such as when an algorithm is stuck in a local minima) or instead represent just one of many possible structures within of complex data (such as when partitioning of an image identifies underlying shapes but fails to find differences in lighting). Ensemble clustering can be used to overcome the limitations of a single clustering solution by clustering repeatedly, each time making some

License: CC-BY 4.0, see https://creativecommons.org/licenses/by/4.0/. Attribution requirements are provided at http://jmlr.org/papers/v18/18-100.html.

^{©2018} Tom Ronan, Shawn Anastasio, Zhijie Qi, Pedro Henrique S. Vieira Tavares, Roman Sloutsky, and Kristen M. Naegle.

perturbation to either the data or the approach to clustering. The ensemble of clustering results provides more information about the structure of the underlying data, and how likely any particular grouping of objects is across the ensemble. There are several aspects to performing ensemble clustering, which include: (i) determining and implementing the appropriate perturbations, (ii) deriving a single clustering result that is representative of all the clustering solutions in the ensemble (finishing), and (iii) assessing the results of the finished ensemble, in comparison to the results of an individual solution, to understand the structure and quality of solutions (validation metrics). Our previous review on clustering in biological data covers the types of ensemble clustering and its applications (Ronan et al., 2016) in detail, where Figure 1 contains a table of example ensemble approaches and their motivations. Here, we describe the open source Python toolkit for easily implementing, visualizing, and analyzing ensemble clustering.

2. Architecture

There are three main OpenEnsembles classes that pair with the main aspects of ensemble clustering: data (storing and manipulating data), cluster (clustering data), and validation (assessing the degree of success of a clustering solution according to an objective such as compactness or connectedness). A common feature across these classes is that they are container objects for housing data, either data matrices (data class), clustering solutions (cluster class), or validation metric results of a clustering solution (validation class). Additionally, each class has a primary function (to transform, cluster, or calculate), where the classes create a common interface for interacting with a variety of transformations, clustering algorithms, and validation metrics. Interacting with any specific transformation of data, retrieving a specific clustering solution or validation metric is done by using the user-defined dictionary key that describes the specific instance. Here we will demonstrate many of the OpenEnsembles features by recreating the first publication of the use of ensemble clustering – Ana Fred's use of ensembles to form a final solution through the majority vote across many non-deterministic k-means solutions (Fred, 2001). OpenEnsembles is built using many open source Python projects, including: scikit-learn (Pedregosa et al., 2012), Pandas (McKinney, 2010), Matplotlib (Hunter, 2007), NetworkX (Hagberg et al., 2008), and NumPy (Walt et al., 2011).

Data

Data is instantiated using a pandas DataFrame object, therefore all the flexibility of loading data from different file formats can be used to coerce the data of interest into an OpenEnsembles data object and metadata can be retained for future analysis. Once instantiated, data can be transformed or used as the basis for clustering or plotting. The *data* container class keeps track of new transformations of the 'parent' data with user-defined keys. Figure 1 shows the instantiation of an OpenEnsembles data object with 200 samples making two half-moon structures. Available transformations currently include: log, principal component analysis (PCA), range scaling, z-score, and internal normalization (such as normalizing to a specific data feature).



Figure 1: Code and outputs of OpenEnsembles. An ensemble approach (Fred, 2001) to find stable and optimal solutions from the combination of many solutions of the non-deterministic k-means algorithm with majority vote. Code for plotting figure panels is not included (for brevity). Kmeans can only find clusters that are spheroidally shaped, but as an ensemble, it can identify alternate structures. DRI stands for determinant ratio index – a measure of connectedness in clusters

Cluster

The cluster class is instantiated based on an OpenEnsembles data object, on which all clustering will be performed. OpenEnsembles provides a common interface to clustering, currently providing an interface to all available scikit-learn clustering algorithms. For example, code line 16 (Figure 1) shows how OpenEnsembles is used to call k-means clustering, with K=16 clusters, on the 'parent' data source. Any algorithmic parameters desired are then passed as a dictionary of variable parameters. For example, here, in order to reproduce Ana Fred's original study, we have to overwrite the default arguments of scikit-learn's k-means algorithm, which has ensemble clustering baked into it to lend increased determinism. By looping around OpenEnsembles clustering with random initializations, we are producing

a new clustering solution each time, which is added to the clustering object container and is accessed using the unique key (here it is k-means_(number)).

Often, one wants to produce a final partition derived from consensus across the ensemble of solutions – i.e. 'finish' the ensemble by building a final, single partitioning of the data. In the current version of OpenEnsembles, we have implemented majority vote as proposed by Ana Fred (Fred, 2001) and mixture models as proposed by Topchy et al. (Topchy et al., 2005). Additionally, there are two finishing techniques that operate on the co-occurrence matrix, as we have proposed previously (Schaberg et al., 2017) (Naegle et al., 2012). An entry in the co-occurrence matrix is the number of times a pair of objects cluster across the ensemble. One method treats the co-occurrence matrix as a similarity matrix and uses linkage clustering to identify clusters (Figure 1). The second method treats the cooccurrence matrix as an adjacency matrix and then finds complete subgraphs within the thresholded co-occurrence matrix via k-cliques and percolation Palla et al. (2005). Final partitions are returned as clustering objects and can be plotted and evaluated like any other clustering solution (Figure 1).

Validation

Quantitative evaluation of how well data is clustered, according to a particular objective function, is called a validation metric. Different validation metrics prioritize different aspects of clustering outcomes such as connectivity, compactness, or separation. We have written a Python package of 28 validation metrics, covering the breadth of the clValid R package of validation metrics (Brock et al., 2008). These validation metrics are available for direct use, or through the OpenEnsembles validation class, which wraps calls to validation metrics for a unified interface with other OpenEnsembles classes. As one can see from the determinant ratio index plot in Figure 1, as the number of clustering solutions in the ensemble increases, the solution both (a) stabilizes and (b) correctly identifies the number of inherent, connected clusters within the data.

Conclusion

Implementation and analysis of ensemble clustering may now be done within in succinct and readable Python code (here, roughly 20 lines of code to reproduce an entire paper of results, Figure 1). Beyond the main functionality of OpenEnsembles, to perform, finish, and validate clustering solutions on data, OpenEnsembles also contains features for calculating co-occurrence, mutual information (overlap/similarity between clustering solutions), and plotting of data and matrices generated. Future work will ideally incorporate expanded selections of algorithms and fuzzy partitioning of data, which is especially amenable to ensemble clustering.

Acknowledgments

We wish to thank the developers of the open source Python scientific and machine learning community. Pedro Henrique S. Vieira Tavares was supported by the Coordination for the Improvement of Higher Education Personnel (CAPES) and the Brazil Scientific Mobility Program.

References

- Guy Brock, Vasyl Pihur, Susmita Datta, and Somnath Datta. clValid : An R Package for Cluster Validation. J. Stat. Softw., 25(4):1–22, 2008.
- Ana Fred. Finding consistent clusters in data partitions. In Josef Kittler and Fabio Roli, editors, Mult. Classif. Syst., pages 309–318. Springer, lncs 2096 edition, 2001.
- Aric A Hagberg, Los Alamos National, and Los Alamos. Exploring Network Structure, Dynamics, and Function using NetworkX. In Proc. 7th Python Sci. Conf. (SciPy 2008), number SciPy 2008, pages 11–15, 2008.
- John D. Hunter. Matplotlib: A 2D Graphics Environment. Comput. Sci. Eng., (9):90–95, 2007.
- Wes McKinney. Data Structures for Statistical Computing in Python. In Stéfan van der Walt and Jarrod Millman, editors, Proc. 9th Python Sci. Conf., pages 51–56, 2010.
- Kristen M Naegle, Forest M White, Douglas A Lauffenburger, and Michael B Yaffe. Robust co-regulation of tyrosine phosphorylation sites on proteins reveals novel protein interactions. *Mol. Biosyst.*, 8(10):2771–2782, Aug 2012.
- Gergely Palla, Imre Derényi, Illés Farkas, and Tamás Vicsek. Uncovering the overlapping community structure of complex networks in nature and society. *Nature*, 435(7043): 814–8, 2005.
- Fabian Pedregosa, Gaël Varoquaux, Alexandre Gramfort, Vincent Michel, Bertrand Thirion, Olivier Grisel, Mathieu Blondel, Peter Prettenhofer, Ron Weiss, Vincent Dubourg, Jake Vanderplas, Alexandre Passos, David Cournapeau, Matthieu Brucher, Matthieu Perrot, and Édouard Duchesnay. Scikit-learn: Machine Learning in Python. J. Mach. Learn. Res., 12:2825–2830, 2012.
- Tom Ronan, Zhijie Qi, and Kristen M. Naegle. Avoiding common pitfalls when clustering biological data. Sci. Signal, 9(432):re6, 2016.
- Katherine E. Schaberg, Venktesh S Shirure, Elizabeth A Worley, Steven C George, and Kristen M Naegle. Ensemble clustering of phosphoproteomic data identifies differences in protein interactions and cell-cell junction integrity of HER2-overexpressing cells. *Integr. Biol.*, 9:539–547, 2017.
- Alexander Topchy, Anil K Jain, and William Punch. Clustering ensembles: models of consensus and weak partitions. *IEEE Trans. Pattern Anal. Mach. Intell.*, 27(12):1866– 81, Dec 2005.
- S. V. D. Walt, S. C. Colbert, and G. Varoquaux. The NumPy Array: A structure for efficient numerical computation. *Comput. Sci. Eng.*, 13(2):22–30, 2011.