

PMLB v1.0: an open source dataset collection for benchmarking machine learning methods

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Summary

PMLB (Penn Machine Learning Benchmark) is an open source data repository containing a curated collection of datasets for evaluating and comparing machine learning (ML) algorithms. Compiled from a broad range of existing ML benchmark collections, PMLB unifies over 150 publicly available datasets from diverse sources such as Kaggle and OpenML, enabling systematic assessment of different ML methods. These datasets cover a range of applications, from binary/multi-class classification to regression problems with combinations of categorical and continuous features. PMLB has both a Python interface (`pmlb`) and an R interface (`pmlbr`), both with detailed documentation that allow the user to access datasets using a simple `fetch_data` function.

Statement of need

Benchmarking is a standard practice to illustrate the strengths and weaknesses of algorithms with regards to different problem characteristics. In machine learning, benchmarking often involves assessing the performance of specific ML models — namely, how well they predict labels for new samples (supervised learning) or detect patterns among samples with no pre-existing labels (unsupervised learning) over a group of benchmark datasets [1,2]. PMLB was designed to provide a suite of such datasets, as well as the framework for conducting automatic evaluation of the different algorithms.

The first release of PMLB [3] received overwhelmingly positive feedback from the ML community, reflecting the pressing need for a collection of standardized datasets to evaluate models. As the repository becomes more widely used, community members have requested new features such as additional information about the datasets, as well as new functions to select datasets given specific criteria. In this paper, we review existing functionality and present new enhancements that help facilitate frictionless interaction with the repository, both from the perspective of database contributors and end-users.

Differentiating attributes

New datasets with rich metadata

Since its initial release, we have made substantial improvements in the collection of new datasets as well as other helpful supporting features. Furthermore we have redesigned the repository structure, and PMLB now includes benchmark datasets for regression problems (Fig. 1). To fulfill [requests made by several users](#), each dataset also includes a `metadata.yaml` file that contains general descriptive information about the dataset itself (an example can be viewed [here](#)). Specifically, for each dataset, the metadata file includes a web address to the original source of the dataset, a text description of the dataset's purpose, the publication associated with the dataset generation, the type of learning problem it was designed for (i.e., classification or regression), keywords (e.g., "simulation", "ecological", "bioinformatics"), and a description of individual features and their coding schema (e.g., 'non-promoter'= 0, 'promoter'= 1).

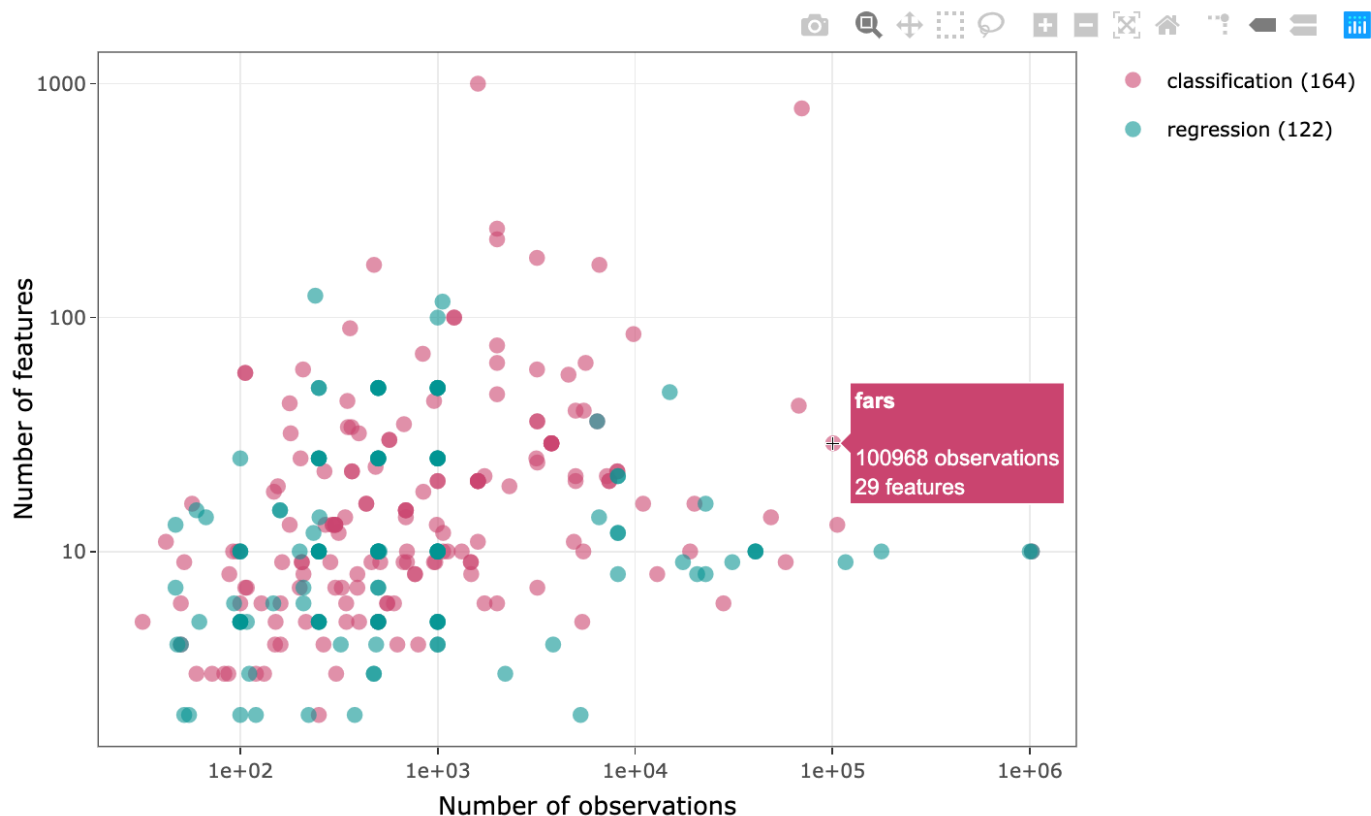


Figure 1: Characteristics of datasets in the PMLB collection

We are grateful for the open source contributors who have gradually increased the number of datasets with metadata. By carefully examining the data source and gathering important information about the dataset, contributors have flagged serious issues with some datasets such as the [incorrect column](#) assigned as ‘target’ in the [bupa](#) dataset.

User-friendly interfaces

On the project PMLB [home page](#), the user can now browse, sort, filter and search from a lookup table of datasets with summary statistics (Fig. 2). To select datasets with specific parameters, one can type in the box at the bottom of each numeric column in the format `low ... high`. For example, if the user wants to view all *classification* datasets with *80 to 100 observations*, they would select *classification* at the bottom of `Task` and type `80 ... 100` at the bottom of the `n_observations` column. The `CSV` button enables the download of the table with selected criteria.

CSV

Show 10 entries

Search:

Dataset	n_observations	n_features	n_classes	Endpoint	Imbalance	Task	Metadata
adult	48842	14	2	binary	0.27	classification	
agaricus_lepiota	8145	22	2	binary	0	classification	
allbp	3772	29	3	categorical	0.88	classification	
allhyper	3771	29	4	categorical	0.93	classification	
allhypo	3770	29	3	categorical	0.78	classification	
allrep	3772	29	4	categorical	0.91	classification	
analcataids	50	4	2	binary	0	classification	
analcataasbestos	83	3	2	binary	0.01	classification	
analcataauthorship	841	70	4	categorical	0.08	classification	
analcatabankruptcy	50	6	2	binary	0	classification	

All

All

All

All

All

All

All

All

Showing 1 to 10 of 286 entries

Previous

1

2

3

4

5

...

29

Next

Figure 2: The user can browse, sort, filter and search the summary statistics table

On this main website, we also published a detailed contribution guide with step-by-step instruction on how to get started. Our goal was to simplify the steps newcomers need to take to contribute. Specifically, we have automated many of these steps with continuous integration using the GitHub Actions service. When a new dataset is added, its summary statistics (e.g., number of observations, number of classes, etc.) is automatically computed, its profiling report is generated (see below), a corresponding metadata template is added to the dataset folder, and the list of dataset names is updated. Other checks included in the continuous integration workflow also help reduce both the reviewer and contributor’s workload.

In addition to the Python library, we have integrated an [R library](#) – both can be simply installed with `pip install pmlb` or `install.packages('pmlbr')`, respectively. This R library has been adapted from a [separate repository](#) that seemed to be unmaintained. However, because the original source code was released under a [GPL-2 license](#), we were able to adapt the code to make it compatible with the new repository structure in this release and offer additional functionality. Its detailed vignettes also make PMLB a helpful resource for new users to begin testing their methods with benchmark datasets. These vignettes contain straightforward examples of how to automate the tedious task of comparing different ML methods on all the benchmark datasets based on specified metrics.

PMLB now includes original data rows with missing data (i.e., NA). The core function of PMLB, `fetch_data()`, retains previous behavior (`dropna=True`) by default, which excludes all rows with missing data. However, if the user chooses to treat the missing values differently, they can use `fetch_data()` with the option `dropna=False` to obtain the original dataset and apply their own removal or imputation method. Defining the neighborhood to be the datasets’ metadata/characteristics space, we also enabled the option to select the nearest PMLB datasets given a data frame. This functionality would be helpful for users who would like to find PMLB datasets with similar characteristics to their own to make inference on their dataset, e.g., where to start the hyperparameter search. An API reference that details the user-facing functions and variables within the PMLB Python and R library is included in the PMLB page.

Pandas profiling reports

For each dataset, we use [pandas profiling](#) to provide a report for exploratory analysis. In addition to descriptive statistics of the features as provided by `pandas.describe` (Python) or `skimr::skim` (R), pandas profiling gives a more extensive exploration of the dataset such as correlation structure among the features and flaggings of duplicate rows. Browsing a report allows a user or contributor to easily assess the dataset quality and make necessary changes. For example, if a feature is flagged as having a unique value for each row in the report, it is likely that this feature is an observation identifier and should be removed from the dataset.

The profiling reports can be accessed by clicking on the dataset name in the data table or the data point in the interactive chart on the home page. Alternatively, all the reports can be viewed on the repository's [gh-pages](#) branch.

Efficiency

We have significantly reduced the repository size and started to track all data files with [Git Large File Storage](#) for efficient cloning of the repository. With the Large File Storage service, we now store large files on the GitHub.com remote server (with no limits on data storage) and include text pointers to these files in our repository. Users who want to interact with the entire repository on their local machine only need git LFS [installed and set up for their user account](#) or download the zip file from GitHub.

References

1. **Man vs. computer: Benchmarking machine learning algorithms for traffic sign recognition**

J. Stallkamp, M. Schlipsing, J. Salmen, C. Igel

Neural Networks (2012-08) <https://doi.org/f3z6dz>

DOI: [10.1016/j.neunet.2012.02.016](https://doi.org/10.1016/j.neunet.2012.02.016) · PMID: [22394690](https://pubmed.ncbi.nlm.nih.gov/22394690/)

2. **An empirical comparison of supervised learning algorithms**

Rich Caruana, Alexandru Niculescu-Mizil

Association for Computing Machinery (ACM) (2006) <https://doi.org/bmstc2>

DOI: [10.1145/1143844.1143865](https://doi.org/10.1145/1143844.1143865)

3. **PMLB: a large benchmark suite for machine learning evaluation and comparison**

Randal S. Olson, William La Cava, Patryk Orzechowski, Ryan J. Urbanowicz, Jason H. Moore

BioData Mining (2017-12-11) <https://doi.org/gfrbw5>

DOI: [10.1186/s13040-017-0154-4](https://doi.org/10.1186/s13040-017-0154-4) · PMID: [29238404](https://pubmed.ncbi.nlm.nih.gov/29238404/) · PMCID: [PMC5725843](https://pubmed.ncbi.nlm.nih.gov/PMC5725843/)