

Machine Learning in R

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Why a Machine Learning Framework?



- New algorithms are mostly implemented in C(++) with bindings to R/python/julia
- Frameworks unify the API, crucial for comparison of many algorithms
- Popular Frameworks:
 - Python: sk-learn
 - Julia: mlj
 - R: caret (no longer maintained), tidymodels, <u>mlr</u>
 - Rapidminer
 - Weka
 - ο...

mlr



- Abstraction for machine learning in R:
 - > 100 Learners, > 30 performance measures, > 30 variable selection filters
 - classification, regression, clustering, survival, multiclass, anomaly detection, functional data analysis
 - tuning, visualization, pipelines, parallelization
 - Addons for Bayesian Optimization, AutoML, XAI,
- Popular and stable, recommended by <u>NIST</u>
- > 20 Contributors, 8 GSOC projects

	🖄 stack overflow	Products Customers	Use cases	Q [mlr]	
[PDF] mlr: Machine Learning in R <u>B Bischl, M Lang, L Kotthoff, J Schiffner of Machine Learning</u> , 2016 - jmlr.org The mlr package provides a generic, object-oriented, and extensible framework for classification regression, survival analysis and clustering for the R language. It provides a unified interface to more than 160 basic learners and includes meta-algorithms and model ☆ 10 Zitiert von: 242 Ähnliche Artikel Alle 16 Versionen ※	Home PUBLIC Stack Overflow Tags Users Jobs	Questions ta mir is a machine learning other packages. Learn more Top users	package for R that pr	rovides an interfa	Cuestion ace to many
IPDFJ To Tune or Not to Tune the Number of Trees in Random Forest. Probst, AL Boulesteix - Journal of Machine Learning Research, 2017 - jmlr.org Automated Neuron Detection in High-Content Fluorescence Microscopy Images G Mata, <u>M Radojević, C Fernandez-Lozano, I Smal</u> - Neuroinformatics, 2019 - Springer medicines to positively impact this relation to function, and the deuted diseases inconstituting the relation to function, and the deuted disease inconstituting the relation to function in the deuted disease inconstituting the relation to function in the deuted disease inconstituting the relation to function in	ation of SUDGIOUP anführer - Bioinformatics york for model-bar congrehensive R tool ptimization, which addr hating the given object Artikel Alle 6 Version Orecasting bird mig nee, 2018 - science.scie e each year during seas e unpredictability of the intinental scale by leve e Artikel Alle 12 Vers	s, 2019 - academic.out ased optimization v preprint arXiv, 20 bibox for model-based resses the problem of tive function through inen gration encemag.org sonal migrations, but eff	of expension of expension optimization f expensive a surrogate	ve black-	361



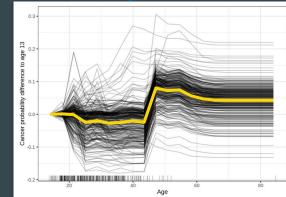
- Reboot started by <u>MCML</u> (mlr3) and <u>ATI</u> (mlj)
- Object orientation

mlr3

- Modularization into multiple packages
- Native support for big data
- Full parallelization support (from threading to distributed computing on HPCs)
- First released version includes:
 - o objects for all building blocks: tasks, learners, measures, resamplings, ...
 - parallel resampling and benchmarking
 - hyperparameter tuning in <u>mlr3tuning</u>
 - nested resampling
 - data flow programming as DAGs in <u>mlr3pipelines</u>

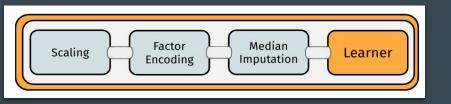
mlr3 is for scientists

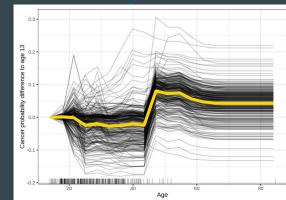
- Completely reproducible results
- Compare many algorithms with only a few lines of code
- Interpretable machine learning (XAI)
- Publication-ready yet customizable plots
- Construct custom pipelines
- Extend objects for your domain as needed



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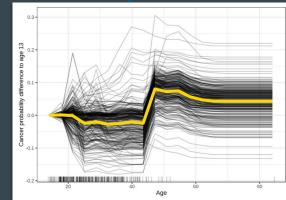
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```
graph_stack = gunion(list(
        po("learner_cv", learner = lrn("regr.lm")),
        po("learner_cv", learner = lrn("regr.svm")),
        po("nop"))) %>>%
        po("featureunion") %>>%
        lrn("regr.ranger")
```

