Optimizer's dilemma: optimization strongly influences model selection in transcriptomic prediction

This manuscript (<u>permalink</u>) was automatically generated from <u>greenelab/optimizer-manuscript@877e056</u> on June 8, 2023.

Authors

• Jake Crawford

Genomics and Computational Biology Graduate Group, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

Casey S. Greene [™]

Department of Biochemistry and Molecular Genetics, University of Colorado School of Medicine, Aurora, CO, USA; Center for Health AI, University of Colorado School of Medicine, Aurora, CO, USA

■ — Correspondence possible via <u>GitHub Issues</u> or email to Casey S. Greene <casey.s.greene@cuanschutz.edu>.

Abstract

Motivation

Most models can be fit to data using various optimization approaches. While model choice is frequently reported in machine-learning-based research, optimizers are not often noted. We applied two different implementations of LASSO logistic regression implemented in Python's scikit-learn package, using two different optimization approaches (coordinate descent and stochastic gradient descent), to predict driver mutation presence or absence from gene expression across 84 pan-cancer driver genes. Across varying levels of regularization, we compared performance and model sparsity between optimizers.

Results

In general, we found that coordinate descent (implemented in the liblinear library) and SGD tended to perform comparably after model selection and tuning. However, SGD models generally resisted overfitting as regularization strength decreased and model complexity increased, and liblinear models tended to be less robust to overfitting. We also found that learning rate tuning on a held-out dataset was critical for SGD to achieve competitive performance with liblinear. We believe that the choice of optimizers should be clearly reported as a part of the model selection and validation process, to allow readers and reviewers to better understand the context in which results have been generated.

Availability and implementation

The code used to carry out the analyses in this study is available at https://github.com/greenelab/pancancer-evaluation/tree/master/01_stratified_classification. Performance/regularization strength curves for all genes in the Vogelstein et al. 2013 dataset are available at https://doi.org/10.6084/m9.figshare.22728644.

Introduction

Gene expression profiles are widely used to classify samples or patients into relevant groups or categories, both preclinically [1,2] and clinically [3,4]. To extract informative gene features and to perform classification, a diverse array of algorithms exist, and different algorithms perform well across varying datasets and tasks [1]. Even within a given model class, multiple optimization methods can often be applied to find well-performing model parameters or to optimize a model's loss function. One commonly used example is logistic regression. The widely used scikit-learn Python package for machine learning [5] provides two modules for fitting logistic regression classifiers:

LogisticRegression, which uses the liblinear coordinate descent method [6] to find parameters that optimize the logistic loss function, and SGDClassifier, which uses stochastic gradient descent [7] to optimize the same loss function.

Using scikit-learn, we compared the liblinear (coordinate descent) and SGD optimization techniques for prediction of driver mutation status in tumor samples, across a wide variety of genes implicated in cancer initiation and development [8]. We applied LASSO (L1-regularized) logistic regression, and tuned the strength of the regularization to compare model selection between optimizers. We found that across a variety of models (i.e. varying regularization strengths), the training dynamics of the optimizers were considerably different: models fit using liblinear tended to perform best at fairly high regularization strengths (100-1000 nonzero features in the model) and overfit easily with low regularization strengths. On the other hand, after tuning the learning rate, models fit using SGD tended to perform well across both higher and lower regularization strengths, and overfitting was less common.

Our results caution against viewing optimizer choice as a "black box" component of machine learning modeling. The observation that LASSO logistic regression models fit using SGD tended to perform well for low levels of regularization, across diverse driver genes, runs counter to conventional wisdom in machine learning for high-dimensional data which generally states that explicit regularization and/or feature selection is necessary. Comparing optimizers or model implementations directly is rare in applications of machine learning for genomics, and our work shows that this choice can affect generalization and interpretation properties of the model significantly. Based on our results, we recommend considering the appropriate optimization approach carefully based on the goals of each individual analysis.

Methods

Data download and preprocessing

To generate binary mutated/non-mutated gene labels for our machine learning model, we used mutation calls for TCGA Pan-Cancer Atlas samples from MC3 [9] and copy number threshold calls from GISTIC2.0 [10]. MC3 mutation calls were downloaded from the Genomic Data Commons (GDC) of the National Cancer Institute, at https://gdc.cancer.gov/about-data/publications/pancanatlas. Thresholded copy number calls are from an older version of the GDC data and are available here: https://figshare.com/articles/dataset/TCGA PanCanAtlas Copy Number Data/6144122. We removed hypermutated samples, defined as two or more standard deviations above the mean non-silent somatic mutation count, from our dataset to reduce the number of false positives (i.e., non-driver mutations). Any sample with either a non-silent somatic variant or a copy number variation (copy number gain in the target gene for oncogenes and copy number loss in the target gene for tumor suppressor genes) was included in the positive set; all remaining samples were considered negative for mutation in the target gene.

RNA sequencing data for TCGA was downloaded from GDC at the same link provided above for the Pan-Cancer Atlas. We discarded non-protein-coding genes and genes that failed to map, and removed tumors that were measured from multiple sites. After filtering to remove hypermutated samples and taking the intersection of samples with both mutation and gene expression data, 9074 total TCGA samples remained.

Cancer gene set construction

In order to study mutation status classification for a diverse set of cancer driver genes, we started with the set of 125 frequently altered genes from Vogelstein et al. [8] (all genes from Table S2A). For each target gene, in order to ensure that the training dataset was reasonably balanced (i.e., that there would be enough mutated samples to train an effective classifier), we included only cancer types with at least 15 mutated samples and at least 5% mutated samples, which we refer to here as "valid" cancer types. In some cases, this resulted in genes with no valid cancer types, which we dropped from the analysis. Out of the 125 genes originally listed in the Vogelstein et al. cancer gene set, we retained 84 target genes after filtering for valid cancer types.

Classifier setup and optimizer comparison details

We trained logistic regression classifiers to predict whether or not a given sample had a mutational event in a given target gene using gene expression features as explanatory variables. Based on our previous work, gene expression is generally effective for this problem across many target genes, although other -omics types can be equally effective in many cases [11]. Our model was trained on gene expression data (X) to predict mutation presence or absence (y) in a target gene. To control for varying mutation burden per sample and to adjust for potential cancer type-specific expression patterns, we included one-hot encoded cancer type and \log_{10} (sample mutation count) in the model as covariates. Since gene expression datasets tend to have many dimensions and comparatively few samples, we used a LASSO penalty to perform feature selection [12]. LASSO logistic regression has the advantage of generating sparse models (some or most coefficients are 0), as well as having a single tunable hyperparameter which can be easily interpreted as an indicator of regularization strength, or model complexity.

To compare model selection across optimizers, we first split the "valid" cancer types into train (75%) and test (25%) sets. We then split the training data into "subtrain" (66% of the training set) data to

train the model on, and "holdout" (33% of the training set) data to perform model selection, i.e. to use to select the best-performing regularization parameter, and the best-performing learning rate for SGD in the cases where multiple learning rates were considered. In each case, these splits were stratified by cancer type, i.e. each split had as close as possible to equal proportions of each cancer type included in the dataset for the given driver gene.

LASSO parameter range selection and comparison between optimizers

The scikit-learn implementations of coordinate descent (in liblinear / LogisticRegression) and stochastic gradient descent (in SGDClassifier) use slightly different parameterizations of the LASSO regularization strength parameter. liblinear 's logistic regression solver optimizes the following loss function:

$$\hat{w} = \operatorname{argmin}_{w} \left(C \cdot \ell(X, y; w) \right) + ||w||_{1}$$

where $\ell(X,y;w)$ denotes the negative log-likelihood of the observed data (X,y) given a particular choice of feature weights w. SGDClassifier optimizes the following loss function:

$$\hat{w} = \operatorname{argmin}_{w} \ell(X, y; w) + \alpha ||w||_{1}$$

which is equivalent with the exception of the LASSO parameter which is formulated slightly differently, as $\alpha = \frac{1}{C}$. The result of this slight difference in parameterization is that <code>liblinear</code> C values vary inversely with regularization strength (higher values = less regularization, or greater model complexity) and <code>SGDClassifier</code> α values vary directly with regularization strength (lower values = less regularization, or greater model complexity).

For the liblinear optimizer, we trained models using C values evenly spaced on a logarithmic scale between (10^{-3} , 10^{7}); i.e. the output of numpy logspace (-3, 7, 21). For the SGD optimizer, we trained models using the inverse range of α values between (10^{-7} , 10^{3}), or numpy logspace (-7, 3, 21). These hyperparameter ranges were intended to give evenly distributed coverage across genes that included "underfit" models (predicting only the mean or using very few features, poor performance on all datasets), "overfit" models (performing perfectly on training data but comparatively poorly on cross-validation and test data), and a wide variety of models in between that typically included the best fits to the cross-validation and test data.

For ease of visual comparison in our figures, we plot the SGD α parameter directly, and the liblinear C parameter inversely (i.e. $\frac{1}{C}$). This orients the x-axes of the relevant plots in the same direction: lower values represent lower regularization strength or higher model complexity, and higher values represent higher regularization strength or lower model complexity, for both optimizers.

SGD learning rate selection

scikit-learn's SGDClassifier provides four built-in approaches to learning rate scheduling: constant (a single, constant learning rate), optimal (a learning rate with an initial value selected using a heuristic based on the regularization parameter and the data loss, that decreases across epochs), invscaling (a learning rate that decreases exponentially by epoch), and adaptive (a learning rate that starts at a constant value, which is divided by 5 each time the training loss fails to decrease for 5 straight epochs). The optimal learning rate schedule is used by default.

When we compared these four approaches, we used a constant learning rate of 0.0005, and an initial learning rate of 0.1 for the adaptive and invscaling schedules. We also tested a fifth approach that we called "constant_search", in which we tested a range of constant learning rates in a grid search on a validation dataset, then evaluated the model on the test data using the best-performing constant learning rate by validation AUPR. For the grid search, we used the following range of constant learning rates: {0.000005, 0.00001, 0.00005, 0.0001, 0.0005, 0.001, 0.01}. Unless otherwise specified, results for SGD in the main paper figures used the constant_search approach, which performed the best in our comparison between schedulers.

Results

liblinear and SGD LASSO models perform comparably, but liblinear is prone to overfitting

For each of the 125 driver genes from the Vogelstein et al. 2013 paper, we trained models to predict mutation status (presence or absence) from RNA-seq data, derived from the TCGA Pan-Cancer Atlas. For each optimizer, we trained LASSO logistic regression models across a variety of regularization parameters (see Methods for parameter range details), for 4 cross-validation splits x 2 replicates (random seeds) for a total of 8 different models per parameter. Cross-validation splits were stratified by cancer type.

Previous work has shown that pan-cancer classifiers of Ras mutation status are accurate and biologically informative [13]. We first evaluated models for KRAS mutation prediction. As model complexity increases (more nonzero coefficients) for the liblinear optimizer, we observe that performance increases then decreases, corresponding to overfitting for high model complexities/numbers of nonzero coefficients (Figure 1A). On the other hand, for the SGD optimizer, we observe consistent performance as model complexity increases, with models having no nonzero coefficients performing comparably to the best (Figure 1B). In this case, top performance for SGD (a regularization parameter of 10^{-1}) is slightly better than top performance for liblinear (a regularization parameter of $1/3.16 \times 10^2$): we observed a mean test AUPR of 0.722 for SGD vs. mean AUPR of 0.692 for liblinear.

To determine how relative performance trends with liblinear tend to compare across the genes in the Vogelstein dataset at large, we looked at the difference in performance between optimizers for the best-performing models for each gene (Figure 1C). The distribution is centered around 0 and more or less symmetrical, suggesting that across the gene set, liblinear and SGD tend to perform comparably to one another. We saw that for 52/84 genes, performance for the best-performing model was better using SGD than liblinear, and for the other 32 genes performance was better using liblinear. In order to quantify whether the overfitting tendencies (or lack thereof) also hold across the gene set, we plotted the difference in performance between the best-performing model and the largest (least regularized) model; classifiers with a large difference in performance exhibit strong overfitting, and classifiers with a small difference in performance do not overfit (Figure 1D). For SGD, the least regularized models tend to perform comparably to the best-performing models, whereas for liblinear the distribution is wider suggesting that overfitting is more common.

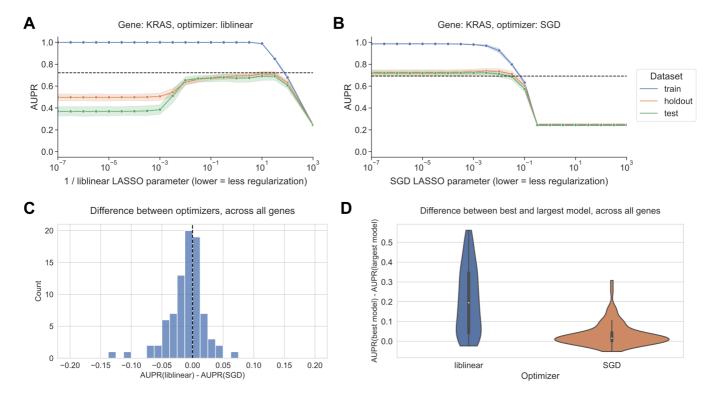


Figure 1: A. Performance vs. inverse regularization parameter for KRAS mutation status prediction, using the liblinear coordinate descent optimizer. Dotted lines indicate top performance value of the opposite optimizer. **B.** Performance vs. regularization parameter for KRAS mutation status prediction, using the SGD optimizer. "Holdout" dataset is used for SGD learning rate selection, "test" data is completely held out from model selection and used for evaluation. **C.** Distribution of performance difference between best-performing model for liblinear and SGD optimizers, across all 84 genes in Vogelstein driver gene set. Positive numbers on the x-axis indicate better performance using liblinear, and negative numbers indicate better performance using SGD. **D.** Distribution of performance difference between best-performing model and largest (least regularized) model, for liblinear and SGD, across all 84 genes. Smaller numbers on the y-axis indicate less overfitting, and larger numbers indicate more overfitting.

SGD is sensitive to learning rate selection

The SGD results shown in Figure 1 select the best-performing learning rate using a grid search on the holdout dataset, independently for each regularization parameter. We also compared against other learning rate scheduling approaches implemented in scikit-learn (see Methods for implementation details and grid search specifications). For KRAS mutation prediction, we observed that the choice of initial learning rate and scheduling approach affects performance significantly, and other approaches to selecting the learning rate performed poorly relative to liblinear (black dotted lines in Figure 2) and to the grid search. We did not observe an improvement in performance over liblinear or the grid search for learning rate schedulers that decrease across epochs (Figure 2A, C, and D), nor did we see comparable performance when we selected a single constant learning rate for all levels of regularization without the preceding grid search (Figure 2B). Notably, scikit-learn's default "optimal" learning rate schedule performed relatively poorly for this problem, suggesting that tuning the learning rate and selecting a well-performing scheduler is a critical component of applying SGD successfully for this problem (Figure 2D). We observed similar trends across all genes in the Vogelstein gene set, with other learning rate scheduling approaches performing poorly in aggregate relative to both liblinear and SGD with the learning rate grid search (Supplementary Figure TODO).

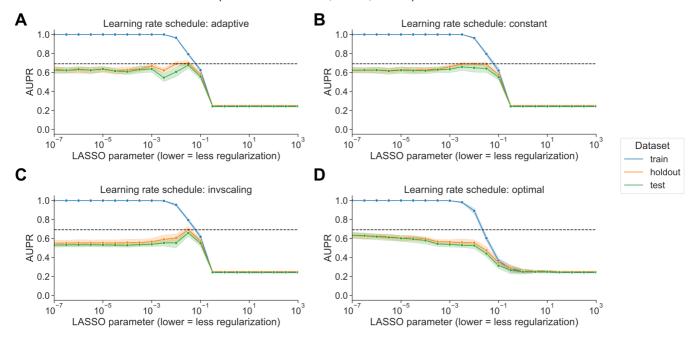


Figure 2: A. Performance vs. regularization parameter for KRAS mutation prediction, using SGD optimizer with adaptive learning rate scheduler. Dotted line indicates top performance value using liblinear, from Figure 1A. **B.** Performance vs. regularization parameter, using SGD optimizer with constant learning rate scheduler and a learning rate of 0.0005. **C.** Performance vs. regularization parameter, using SGD optimizer with inverse scaling learning rate scheduler. **D.** Performance vs. regularization parameter, using SGD optimizer with "optimal" learning rate scheduler.

We next sought to determine whether there was a difference in the magnitudes of coefficients in the models resulting from the different optimization schemes. Following up on the trend in Figure 1, where we saw that the best-performing SGD model had many nonzero coefficients, we also see that in general across all genes, the best-performing SGD models tend to be bimodal, sometimes having few nonzero coefficients but often having many/all nonzero coefficients (Figure 3A). By contrast, the liblinear models are almost always much sparser with fewer than 2500 nonzero coefficients, out of ~16100 total input features.

Despite the SGD models performing best with many nonzero coefficients, it could be the case that many of the coefficients could be "effectively" 0, or uninformative to the final model. However, Figure 3B provides evidence that this is not the case, with most coefficients in the best-performing KRAS mutation prediction model using SGD being considerably larger than the coefficients in the best-performing model using liblinear, and very few close to 0. This emphasizes that the different optimization methods result in fundamentally different models, relying on different numbers of features with nonzero coefficients in different magnitudes, rather than converging to similar models.

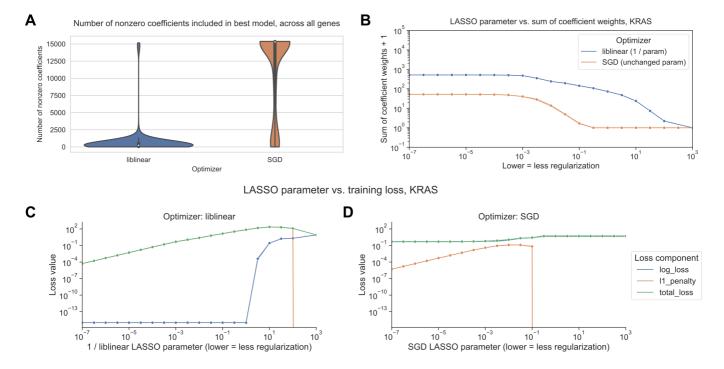


Figure 3: A. Distribution across genes of the number of nonzero coefficients included in best-performing LASSO logistic regression models. Violin plot density estimations are clipped at the ends of the observed data range, and boxes show the median/IQR. **B.** Distribution of coefficient magnitudes for a single KRAS mutation prediction model (random seed 42, first cross-validation split), colored by optimizer. The x-axis shows the base-10 logarithm of the absolute value of each coefficient + 1 (since some coefficients are exactly 0), and the y-axis shows the base-10 log of the count of coefficients in each bin. Other random seeds and cross-validation splits are similar.

Discussion

Our results suggest that even for the same model, LASSO logistic regression, optimizer choice can affect model selection and performance. Existing gene expression prediction benchmarks and pipelines typically use a single model implementation (and thus a single optimizer). To our knowledge, the phenomenon we observed with SGD has not been documented in other applications of ML to genomic or transcriptomic data. In the broader machine learning research community, however, similar patterns have been observed for both linear models and deep neural networks (e.g. [14,15]). This is often termed "benign overfitting": the idea that "overfit" models, in the sense that they fit the training data perfectly and perform worse on the test data, can still outperform models that do not fit the training data as well or that have stronger explicit regularization. Benign overfitting has been observed with, and attributed to, optimization using SGD, which is thought to provide a form of implicit regularization [16,17].

We recommend thinking critically about optimizer choice, but this can be challenging for users that are inexperienced with machine learning or unfamiliar with how certain models are fit under the hood. For example, R's glmnet package uses a cyclical coordinate descent algorithm to fit logistic regression models [18], which would presumably behave similarly to liblinear, but this is somewhat opaque in the glmnet documentation itself. LASSO logistic regression is a convex optimization problem, meaning there is a single unique optimum of the loss function in contrast to more complex models such as neural networks, but this optimum can be computationally intensive to find in practice and there is no closed-form solution [19]. Increased transparency and documentation in popular machine learning packages with respect to optimization, especially for models that are challenging to fit, would benefit new and unfamiliar users.

Similar to what we see in our SGD-optimized models, there exist other problems in gene expression analysis where using all available features is better than using a subset. For example, using the full gene set improves correlations between preclinical cancer models and their tissue of origin, as compared to selecting genes based on variability or tissue-specificity [20]. On the other hand, when predicting cell line viability from gene expression profiles, selecting features by Pearson correlation improves performance over using all features, similar to our liblinear classifiers [21]. An avenue of future work for our SGD classifiers would be to interpret the coefficients and compare them systematically to the coefficients found using liblinear. It could be useful to understand if the two optimization methods emphasize the same pathways or functional gene sets, or if there are patterns to which driver mutations perform better with more/fewer nonzero coefficients.

Data and code availability

The data analyzed during this study were previously published as part of the TCGA Pan-Cancer Atlas project [22], and are available from the NIH NCI Genomic Data Commons (GDC). The scripts used to download and preprocess the datasets for this study are available at https://github.com/greenelab/pancancer-evaluation/tree/master/00 process data, and the code used to carry out the analyses in this study is available at https://github.com/greenelab/pancancer-evaluation/tree/master/01 stratified classification, both under the open-source BSD 3-clause license. Equivalent versions of Figure 1A and 1B for all 84 genes in the Vogelstein et al. 2013 gene set are available on Figshare at https://doi.org/10.6084/m9.figshare.22728644, under a CCO license. This manuscript was written using Manubot [23] and is available on GitHub at https://github.com/greenelab/optimizer-manuscript under the CCO-1.0 license.

References

1. The ability to classify patients based on gene-expression data varies by algorithm and performance metric

Stephen R Piccolo, Avery Mecham, Nathan P Golightly, Jérémie L Johnson, Dustin B Miller *PLOS Computational Biology* (2022-03-11) https://doi.org/gr43qd

DOI: 10.1371/journal.pcbi.1009926 · PMID: 35275931 · PMCID: PMC8942277

2. Supervised learning is an accurate method for network-based gene classification

Renming Liu, Christopher A Mancuso, Anna Yannakopoulos, Kayla A Johnson, Arjun Krishnan *Bioinformatics* (2020-04-14) https://doi.org/gmvnfc

DOI: 10.1093/bioinformatics/btaa150 · PMID: 32129827 · PMCID: PMC7267831

3. Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes

Joel S Parker, Michael Mullins, Maggie CU Cheang, Samuel Leung, David Voduc, Tammi Vickery, Sherri Davies, Christiane Fauron, Xiaping He, Zhiyuan Hu, ... Philip S Bernard *Journal of Clinical Oncology* (2009-03-10) https://doi.org/c2688w

DOI: <u>10.1200/jco.2008.18.1370</u> · PMID: <u>19204204</u> · PMCID: <u>PMC2667820</u>

4. Prediction of adjuvant chemotherapy benefit in endocrine responsive, early breast cancer using multigene assays

Kathy S Albain, Soonmyung Paik, Laura van't Veer

The Breast (2009-10) https://doi.org/bp4rtw

DOI: <u>10.1016/s0960-9776(09)70290-5</u> · PMID: <u>19914534</u>

5. Scikit-learn: Machine Learning in Python

Fabian Pedregosa, Gaël Varoquaux, Alexandre Gramfort, Vincent Michel, Bertrand Thirion, Olivier Grisel, Mathieu Blondel, Peter Prettenhofer, Ron Weiss, Vincent Dubourg, ... Édouard Duchesnay

Journal of Machine Learning Research (2011) http://jmlr.org/papers/v12/pedregosa11a.html

6. LIBLINEAR: A Library for Large Linear Classification

Rong-En Fan, Kai-Wei Chang, Cho-Jui Hsieh, Xiang-Rui Wang, Chih-Jen Lin *Journal of Machine Learning Research* (2008) http://jmlr.org/papers/v9/fan08a.html

7. Online Learning and Stochastic Approximations

Leon Bottou

(1998) https://wiki.eecs.yorku.ca/course archive/2012-13/F/6328/ media/bottou-onlinelearning-98.pdf

8. Cancer Genome Landscapes

B Vogelstein, N Papadopoulos, VE Velculescu, S Zhou, LA Diaz, KW Kinzler *Science* (2013-03-28) https://doi.org/6rg

DOI: 10.1126/science.1235122 · PMID: 23539594 · PMCID: PMC3749880

9. Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines

Kyle Ellrott, Matthew H Bailey, Gordon Saksena, Kyle R Covington, Cyriac Kandoth, Chip Stewart, Julian Hess, Singer Ma, Kami E Chiotti, Michael McLellan, ... Armaz Mariamidze Cell Systems (2018-03) https://doi.org/gf9twn

DOI: 10.1016/j.cels.2018.03.002 · PMID: 29596782 · PMCID: PMC6075717

10. GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers

Craig H Mermel, Steven E Schumacher, Barbara Hill, Matthew L Meyerson, Rameen Beroukhim, Gad Getz

Genome Biology (2011-04) https://doi.org/dzhjqh

DOI: 10.1186/gb-2011-12-4-r41 · PMID: 21527027 · PMCID: PMC3218867

11. Widespread redundancy in -omics profiles of cancer mutation states

Jake Crawford, Brock C Christensen, Maria Chikina, Casey S Greene Genome Biology (2022-06-27) https://doi.org/ggfqnm

DOI: 10.1186/s13059-022-02705-y · PMID: 35761387 · PMCID: PMC9238138

12. **Regression Shrinkage and Selection Via the Lasso**

Robert Tibshirani

Journal of the Royal Statistical Society: Series B (Methodological) (1996-01)

https://doi.org/gfn45m

DOI: 10.1111/j.2517-6161.1996.tb02080.x

13. Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome **Atlas**

Gregory P Way, Francisco Sanchez-Vega, Konnor La, Joshua Armenia, Walid K Chatila, Augustin Luna, Chris Sander, Andrew D Cherniack, Marco Mina, Giovanni Ciriello, ... Armaz Mariamidze Cell Reports (2018-04) https://doi.org/gfspsb

DOI: 10.1016/j.celrep.2018.03.046 · PMID: 29617658 · PMCID: PMC5918694

Benign overfitting in linear regression 14.

Peter L Bartlett, Philip M Long, Gábor Lugosi, Alexander Tsigler Proceedings of the National Academy of Sciences (2020-04-24) https://doi.org/gigsxq DOI: 10.1073/pnas.1907378117 · PMID: 32332161 · PMCID: PMC7720150

15. Understanding deep learning requires rethinking generalization

Chiyuan Zhang, Samy Bengio, Moritz Hardt, Benjamin Recht, Oriol Vinyals arXiv(2017-02-28) https://arxiv.org/abs/1611.03530

16. Understanding deep learning (still) requires rethinking generalization

Chiyuan Zhang, Samy Bengio, Moritz Hardt, Benjamin Recht, Oriol Vinyals Communications of the ACM (2021-02-22) https://doi.org/gh57fd

DOI: 10.1145/3446776

Benign Overfitting of Constant-Stepsize SGD for Linear Regression 17.

Difan Zou, Jingfeng Wu, Vladimir Braverman, Quanquan Gu, Sham Kakade Proceedings of Thirty Fourth Conference on Learning Theory (2021-07-21) https://proceedings.mlr.press/v134/zou21a.html

18. **Regularization Paths for Generalized Linear Models via Coordinate Descent**

Jerome Friedman, Trevor Hastie, Robert Tibshirani Journal of Statistical Software (2010) https://doi.org/bb3d

DOI: 10.18637/jss.v033.i01

Efficient L1 Regularized Logistic Regression 19.

Su-In Lee, Honglak Lee, Pieter Abbeel, Andrew Y Ng AAAI 2006 (2006) https://ai.stanford.edu/~pabbeel//pubs/LeeLeeAbbeelNg_el1rlr_AAAI2006.pdf

20. Evaluating cancer cell line and patient-derived xenograft recapitulation of tumor and non-diseased tissue gene expression profiles

Avery S Williams, Elizabeth J Wilk, Jennifer L Fisher, Brittany N Lasseigne Cold Spring Harbor Laboratory (2023-04-13) https://doi.org/gr6jr4

DOI: <u>10.1101/2023.04.11.536431</u> · PMID: <u>37090499</u> · PMCID: <u>PMC10120639</u>

21. Gene expression has more power for predicting <i>in vitro</i> cancer cell vulnerabilities than genomics

Joshua M Dempster, John M Krill-Burger, James M McFarland, Allison Warren, Jesse S Boehm, Francisca Vazquez, William C Hahn, Todd R Golub, Aviad Tsherniak *Cold Spring Harbor Laboratory* (2020-02-24) https://doi.org/ghczbr
DOI: 10.1101/2020.02.21.959627

22. The Cancer Genome Atlas Pan-Cancer analysis project

John N Weinstein, Eric A Collisson, Gordon B Mills, Kenna RMills Shaw, Brad A Ozenberger, Kyle Ellrott, Ilya Shmulevich, Chris Sander, Joshua M Stuart

Nature Genetics (2013-09-26) https://doi.org/f3nt5c

DOI: <u>10.1038/ng.2764</u> · PMID: <u>24071849</u> · PMCID: <u>PMC3919969</u>

23. Open collaborative writing with Manubot

Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter

PLOS Computational Biology (2019-06-24) https://doi.org/c7np

DOI: <u>10.1371/journal.pcbi.1007128</u> · PMID: <u>31233491</u> · PMCID: <u>PMC6611653</u>

Supplementary Material

In the main text (Results and Methods), we described why and how we binned models to allow a comparison of model complexity across optimizers with parameters that vary in opposite directions. We also visualized the mapping of parameters to deciles, for <code>liblinear</code> and SGD separately, to quantify how well and how uniformly the model size deciles cover the range of parameters we used in the study. Figure $\underline{S1}$ shows this mapping for KRAS mutation status classification. The scikit-learn SGD implementation uses a regularization parameter α in which higher values mean more regularization (and thus models with fewer nonzero parameters), which is why lower SGD parameters map to higher deciles and vice-versa. <code>liblinear</code>, on the other hand, uses an inverse regularization parameter C in which higher values mean less regularization, so lower parameters map to lower deciles. We can see that most deciles contain anywhere from 1-3 different parameters (i.e. different models).

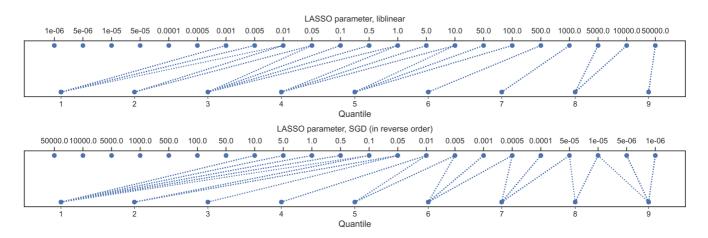


Figure S1: Mapping of parameter to decile, KRAS mutation status classification, for liblinear and SGD optimizers separately. Note that for the SGD plot, the parameter axis is inverted, since lower regularization parameters map to higher deciles in the nonzero coefficient distribution.

To motivate the choice of deciles of the nonzero coefficient distribution over a linear binning scheme, we also visualized the distribution of nonzero coefficients for KRAS mutation prediction models, showing the boundaries of deciles and linear bins. We see that the distribution is skewed toward very simple models (using no nonzero parameters, or only a few) and toward complex models (with most parameters set to be nonzero), so many of the linear bins covering intermediate values contain no models or very few models (Figure S2). Based on this, and the observation that the distributions look similar for most genes, we decided to bin models based on deciles to ensure more uniform coverage of models with different complexities. We also plotted the performance results for linear bins, similar to figures 1A and 1B in the main text, and general trends were mostly the same, although variation was mostly compressed to the smallest and largest bins.

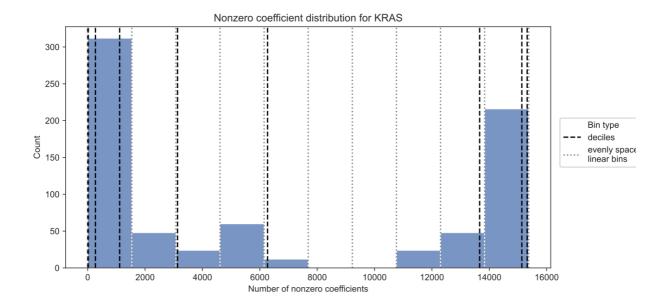


Figure S2: Distribution of nonzero coefficients across parameters, KRAS mutation status classification. Grey dotted lines show boundaries for 10 linear bins, and black dotted lines show boundaries for deciles of nonzero coefficient distribution.

We can also visualize performance directly against the regularization parameters used for both liblinear and SGD. We can see that the trends are generally the same for KRAS, with liblinear overfitting for more complex models to the right of the plot, and SGD performing best for more complex models to the left of the plot (Figure S3). Although it ultimately preserves the same message, we think this is visually more challenging to interpret than the plots in Figure 1 that use decile bins: since the parameters vary in different directions it makes it harder to assess which model is performing better, and for which level of regularization/complexity on the x-axis the best performance is reached, etc.

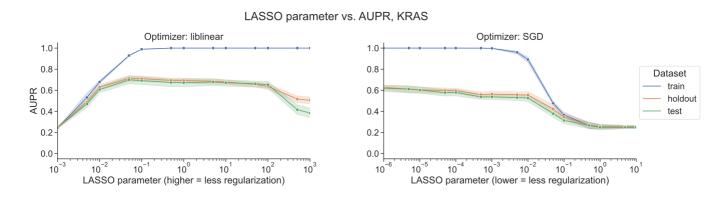


Figure S3: Performance vs. regularization parameter for KRAS mutation status classification, for liblinear and SGD optimizers separately.