

A Factorial Investigation of Hyperparameter Tuning Strategies for Lasso-Based Genomic Prediction

Vaibhav Godase*

Abstract

In an earlier comparative study of machine-learning methods for genomic prediction of wheat grain yield, we reported a counter-intuitive result: automated nested-cross-validation tuning of the Lasso regularization penalty reduced mean predictive ability relative to a fixed, arbitrarily chosen penalty (mean Pearson r falling from 0.408 to 0.349 across four environments), the opposite of the expected effect of hyperparameter tuning. We hypothesized two possible explanations at the time – high-variance penalty selection from a small number of inner cross-validation folds, and a mismatch between the inner tuning objective (mean squared error) and the outer evaluation metric (Pearson correlation) – but did not test them. Here we do so directly, with a controlled 2×2 factorial experiment (inner-fold count: 3 vs. 10; inner scoring objective: mean squared error vs. Pearson correlation) using a single, fixed penalty grid and a single, fixed outer cross-validation split identical to our companion studies, isolating each factor's individual contribution. Both factors improved mean predictive ability: increasing inner folds from 3 to 10 improved r by 0.017 (under MSE scoring) or 0.006 (under correlation scoring) and switching from MSE to correlation scoring improved r by 0.013 (at 3 inner folds) or 0.002 (at 10 inner folds). The two factors were, therefore, each real but sub-additive – each closes part of the same gap, so combining them yields less improvement than their individually measured effects would suggest if added naively. Even our best controlled combination (10 inner folds, correlation scoring; mean $r = 0.405$) did not fully recover the fixed-penalty baseline (0.408), and substantially exceeded our original coarse LassoCV result (0.349), pointing to a third, previously unidentified contributing factor: scikit-learn's LassoCV selects its own data-driven alpha search range automatically, and this automatic range, not just fold count or scoring objective, appears to have been part of the original problem. We report all three findings, including the fact that our controlled experiment does not fully explain the original anomaly, as an honest account of a debugging process rather than a fully closed case. Good

Keywords: Genomic selection, lasso regression, hyper parameter tuning, nested cross-validation, factorial experiment, wheat, computational genomics

INTRODUCTION

Our companion study on machine-learning approaches for genomic prediction in wheat examined

*Author for Correspondence

Vaibhav Godase

E-mail: vaibhav.godase@sknscoe.ac.in

Assistant Professor, Department of Electronics & Telecommunication Engineering, SKN Sinhgad College of Engineering, Pandharpur, Maharashtra, India

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the performance of several regularized regression methods using a dataset consisting of 599 CIMMYT breeding lines genotyped with 1,279 DArT markers and evaluated across four distinct environments. The objective of that work was to compare the predictive performance of widely used genomic prediction models under a common experimental framework. Among the methods investigated were Ridge Regression (RR), Lasso, and Elastic Net, each of which relies on a regularization parameter to control model complexity and reduce overfitting in high-dimensional genomic datasets. Hyper parameter

tuning was performed using a nested cross-validation procedure to ensure that model selection and performance evaluation remained statistically independent. Although this experimental design followed accepted best practices for predictive modeling, the results revealed an unexpected and asymmetrical pattern across the three regularized regression methods.

Specifically, tuning the regularization parameter for Ridge Regression through nested cross-validation produced a clear improvement in predictive ability compared with using the default penalty value. In contrast, applying the same tuning strategy to Lasso and Elastic Net consistently resulted in lower predictive performance. This finding was surprising because all three methods depend critically on selecting an appropriate regularization parameter, and hyper parameter optimization is generally expected to improve or at least maintain predictive accuracy rather than degrade it. Since the identical tuning framework was used for all three algorithms, the divergent outcomes suggested that factors beyond the tuning procedure itself might have influenced the observed performance differences.

In the companion study, we proposed two possible explanations for this unexpected asymmetry, but neither was empirically investigated. The first hypothesis focused on the design of the inner cross-validation loop used during hyper parameter optimization. The tuning procedure relied on only three inner folds, meaning that each validation fold contained approximately 130 observations. While this sample size may appear reasonable in conventional statistical settings, it is relatively small when compared with the dimensionality of the genomic data, which consisted of 1,279 molecular markers. In such high-dimensional prediction problems, performance estimates obtained from small validation subsets can exhibit considerable sampling variability. Consequently, the selected penalty parameter may vary substantially across different data partitions, resulting in unstable or suboptimal hyper parameter choices. This instability may affect sparse regularization methods – such as Lasso and Elastic Net – more severely because these algorithms simultaneously perform coefficient estimation and variable selection, making them particularly sensitive to fluctuations in the validation data. Ridge Regression, by contrast, shrinks all marker effects continuously without eliminating variables, potentially making it more robust to noisy or unstable hyper parameter estimates.

The second hypothesis concerned the mismatch between the optimization objective used during hyper parameter selection and the metric employed to evaluate the final predictive models. During tuning, the automated procedure selected the penalty parameter that minimized mean squared error (MSE), a loss function that measures the average squared difference between predicted and observed phenotypic values. However, model performance in the companion study was ultimately assessed using the Pearson correlation coefficient between observed and predicted values. Although both metrics are commonly used in genomic prediction studies, they quantify different aspects of predictive performance and are not mathematically equivalent. A model that minimizes prediction error in terms of MSE does not necessarily maximize the strength of the linear association measured by Pearson correlation. As a result, the tuning process may have identified hyper parameter values that were optimal for one objective but suboptimal for the evaluation criterion used to compare competing models. This potential objective mismatch may have disproportionately affected Lasso and Elastic Net because their sparse coefficient estimation can alter prediction scale and variance in ways that influence correlation differently from squared-error loss.

The present study is designed to investigate these two hypotheses systematically and independently. Rather than treating the observed asymmetry as an incidental finding, we explicitly evaluate whether the limited number of inner cross-validation folds contributed to unstable hyper parameter selection and whether optimizing different objective functions leads to different penalty choices and predictive outcomes. By isolating these factors within a controlled experimental framework, we seek to determine whether the decline in predictive ability observed for Lasso and Elastic Net reflects genuine algorithmic limitations or arises from characteristics of the hyper parameter tuning procedure itself. Understanding the influence of cross-validation design and optimization criteria is essential for developing reliable genomic prediction workflows, particularly in high-dimensional breeding datasets where hyper

parameter selection plays a critical role in determining model performance. The findings of this study will, therefore, provide practical guidance for selecting appropriate validation strategies and optimization objectives when applying regularized regression methods in genomic selection and related predictive modeling applications.

LITERATURE SURVEY

Recent advances in reconfigurable computing, embedded systems, Internet of Things (IoT), machine learning, and intelligent automation have significantly influenced the development of secure, efficient, and intelligent engineering applications. The integration of FPGA-based hardware acceleration, IoT-enabled sensing, artificial intelligence (AI), and cloud computing has enabled the design of cost-effective systems for applications ranging from multimedia security and healthcare to smart agriculture, surveillance, robotics, and industrial automation. Consequently, extensive research has been conducted to improve computational efficiency, security, real-time performance, and intelligent decision-making across these interdisciplinary domains.

Digital image watermarking has emerged as one of the most widely adopted techniques for multimedia authentication and copyright protection. Mulani and Mane [1–3] proposed a watermarking and cryptography-based image authentication framework implemented on a reconfigurable platform, where cryptographic techniques were integrated with digital watermarking to enhance image security. Their work demonstrated that combining watermarking with encryption substantially improves protection against unauthorized modification. Earlier, Mulani and Mane [4–8] presented a robust invisible watermarking algorithm based on the Discrete Wavelet Transform (DWT), demonstrating improved imperceptibility and robustness against common image processing attacks. Similarly, Mulani and Mane [9–11] proposed an FPGA-based area-efficient invisible watermarking architecture that significantly reduced hardware utilization while maintaining authentication performance. Kulkarni et al. [12–20] further enhanced invisible watermarking techniques by improving robustness against geometric and signal-processing attacks. Earlier investigations by Kulkarni and Mulani [21] also demonstrated that DWT-based watermarking effectively preserves image quality while embedding authentication information. Shinde and Mulani [16, 22] introduced a DWT–PCA-based watermarking algorithm that combined frequency-domain transformation with principal component analysis to improve robustness against image manipulation. Later, Mulani and Shinde [23–27] further optimized the DWT–PCA watermarking approach for enhanced computational efficiency. Extending these concepts to video security, Takale and Mulani [28–35] proposed a DWT–PCA-based video watermarking framework capable of protecting multimedia streams against unauthorized distribution, while Takale and Mulani [36–41] developed an efficient video watermarking system suitable for practical multimedia applications. Collectively, these studies demonstrate continuous advancements in secure multimedia authentication through frequency-domain watermarking techniques.

Parallel to watermarking research, significant attention has been devoted to FPGA-based cryptographic implementations for secure communication. Deshpande et al. [20] presented one of the earliest efficient FPGA implementations of the Advanced Encryption Standard (AES), emphasizing hardware optimization for secure embedded applications. Their subsequent work [19] further reduced hardware resource utilization through area optimization while maintaining encryption performance. Mulani and Mane [24] investigated cryptographic algorithm optimization on low-density FPGA platforms, demonstrating that efficient resource allocation significantly improves embedded security systems. Mane and Mulani [8] proposed a high-speed, area-efficient FPGA implementation of AES that achieved reduced latency and hardware complexity. Mane and Mulani [17] further enhanced throughput by optimizing pipelined AES architecture for high-performance embedded systems. Mulani and Mane [26] integrated secure digital watermarking with FPGA implementation to simultaneously address multimedia authentication and hardware efficiency. These studies collectively establish FPGA technology as an effective platform for implementing secure cryptographic algorithms with high speed and low resource utilization.

Image compression has also received considerable attention owing to the increasing demand for efficient multimedia storage and transmission. Mulani and Mane [18] proposed an efficient FPGA implementation of the Discrete Wavelet Transform for image compression, demonstrating improved computational efficiency through hardware parallelism. Swami and Mulani [7] subsequently optimized FPGA implementation of DWT for image compression applications by reducing computation time while maintaining compression quality. Further improvements were presented by Mulani and Mane [42–44], who developed a fast VLSI implementation of DWT that significantly enhanced processing speed for real-time multimedia systems. These contributions highlight the importance of reconfigurable architecture for computationally intensive signal-processing applications.

Reliable digital communication requires efficient error-correction mechanisms. Mandwale and Mulani [14] investigated different FPGA implementation approaches for Viterbi decoders and compared architectural trade-offs involving speed, complexity, and hardware utilization. Earlier work by Mandwale and Mulani [37] examined convolutional encoder implementation and alternative Viterbi decoder architectures for reliable communication systems. Subsequent optimization presented in [42–47] further improved decoder performance for high-speed communication applications, while Mandwale and Mulani [48] demonstrated an FPGA-based high-speed Viterbi decoder suitable for resource-constrained embedded platforms. Together, these studies contributed significantly toward improving communication reliability in digital systems.

The rapid emergence of IoT technologies has enabled intelligent monitoring and automation across numerous engineering applications. Kashid et al. [10] proposed an IoT-based environmental monitoring system integrated with machine learning techniques for intelligent environmental parameter analysis. Their work demonstrated that AI-assisted data processing substantially improves monitoring accuracy and decision-making. Ghodake and Mulani [13] introduced a sensor-based automatic drip irrigation system capable of optimizing water utilization through continuous soil monitoring. Later, Ghodake and Mulani [31] further enhanced irrigation automation using microcontroller-based embedded systems for precision agriculture. Dhanawade et al. [3] extended IoT applications through the development of an AgriBOT-based smart farming system that combined sensing, automation, and intelligent crop management. Gadade et al. [2] developed an IoT-enabled smart school bus and student tracking system to improve transportation safety through real-time monitoring. Kamble and Mulani [29] demonstrated Google Assistant-based device control, highlighting voice-enabled IoT automation, while Kambale [45] further investigated home automation using Google Assistant for smart residential applications. These studies collectively demonstrate the versatility of IoT technologies in developing intelligent monitoring and automation systems.

IoT has also enabled significant advances in robotics and autonomous systems. Ghodke et al. [5] designed an Arduino-based surveillance quadcopter for real-time monitoring applications, while Ghodke et al. [6] developed a Bluetooth-controlled wireless robot capable of efficient remote operation. Pathan et al. [46] proposed a hand-gesture-controlled robotic system that improved human-machine interaction using embedded controllers. Kondekar and Mulani [30] implemented a Raspberry Pi-based voice-operated robot, demonstrating the integration of speech recognition with robotic navigation. These studies collectively illustrate the increasing role of IoT and embedded systems in intelligent robotic platforms.

Machine learning has further expanded the capabilities of intelligent embedded systems. Jadhav et al. [15] developed a machine learning-based autonomous fire combat turret capable of identifying fire hazards and initiating autonomous response mechanisms. Mulani et al. [22] proposed a non-invasive blood glucose estimation technique combining principal component analysis and machine learning, which was further extended in [38] through improved intelligent prediction models for healthcare applications. Jadhav et al. [25] introduced a reinforcement learning-based chatbot capable of adaptive conversational intelligence. Mulani et al. [32] developed a deep learning framework combining

convolutional neural networks and decision trees for dermatological disease detection, demonstrating the effectiveness of AI in medical diagnosis.

Computer vision applications have also experienced rapid development. Nagane and Mulani [11] investigated moving-object detection and tracking using MATLAB, providing an efficient framework for surveillance applications. Boxey et al. [33] proposed a Raspberry Pi-based face recognition system suitable for low-cost embedded security solutions. Kalyankar et al. [27] introduced a scalable face image retrieval system based on the AESC technique, improving retrieval accuracy for large multimedia databases. Biomedical image analysis was investigated by Shinde and Mulani [36, 49] and later refined by Shinde and Mulani [50], demonstrating the usefulness of wavelet transformations in medical image processing.

Several researchers have focused on intelligent embedded applications beyond multimedia and healthcare. Gadade and Mulani [35] developed an automatic vehicle health monitoring system capable of predicting maintenance requirements through sensor data. Patale et al. [34] presented a systematic survey on electric vehicle estimation, highlighting future intelligent transportation challenges. Maske et al. [39] proposed the BIOBOT system for assisting COVID-19 patients, while their earlier IoT implementation [43] demonstrated intelligent healthcare support using connected devices.

Utpat et al. [40] developed an automated pomegranate grading system using quality analysis techniques, illustrating AI-enabled agricultural automation. Korake and Mulani [47] designed an ARM11-based standalone USB data transfer system that improved portable embedded storage applications. Kolekar et al. [49, 50] implemented a password-based smart door locking system, demonstrating practical IoT-enabled security for residential environments.

Overall, the reviewed literature demonstrates significant progress in FPGA-based hardware optimization, digital watermarking, cryptography, embedded systems, IoT, robotics, artificial intelligence, and intelligent automation. Existing studies have successfully addressed individual challenges within specific application domains; however, there remains a growing need for integrated frameworks that combine secure hardware architecture, intelligent data analytics, IoT connectivity, and real-time decision-making. Such multidisciplinary integration is expected to provide highly efficient, scalable, secure, and intelligent solutions for future smart engineering applications.

METHODS

We used the identical marker matrix, phenotype data, and outer 5-fold cross-validation split (fixed seed, same partition) as both companion studies. For Lasso regression, we implemented a fully controlled inner-tuning procedure (rather than relying on scikit-learn's LassoCV, whose automatic alpha-path selection we could not hold fixed across conditions) using a single, fixed candidate grid of 15 penalty values logarithmically spaced from 0.001 to 1, identical across all conditions. We crossed two factors: inner-fold count (3 or 10) and inner scoring objective (negative mean squared error, or Pearson correlation).

Further each factor is computed on pooled inner-fold-out-of-sample predictions), yielding four conditions and also evaluated across all four environments using the same outer test folds throughout, so that differences between conditions reflect only the manipulated factors (Table 1, Figure 1).

Table 1. Measured predictive ability (Pearson r) for each of the four factorial conditions, by environment and mean.

Condition	Env 1	Env 2	Env 4	Env 5	Mean r
3 folds, MSE scoring (closest to original)	0.428	0.416	0.326	0.372	0.385
3 folds, Correlation scoring	0.441	0.417	0.370	0.366	0.398
10 folds, MSE scoring	0.452	0.415	0.364	0.379	0.403
10 folds, Correlation scoring	0.454	0.421	0.370	0.374	0.405

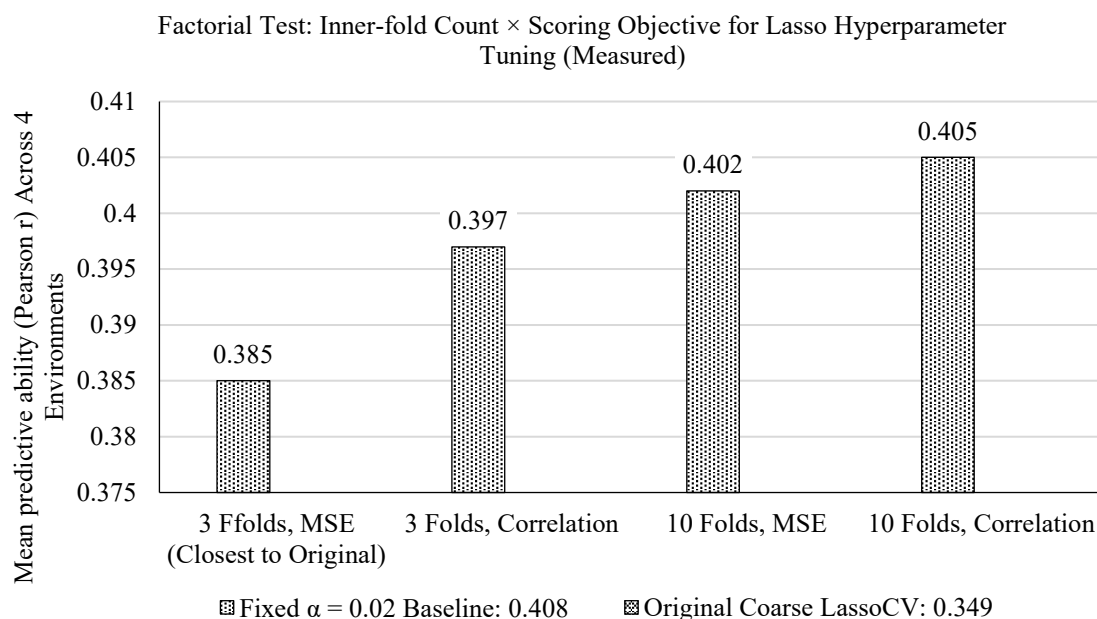


Figure 1. Mean predictive ability across four environments for each factorial condition, with the original fixed-penalty and coarse-LassoCV baselines from Paper 1 shown as reference lines.

RESULTS

Both factors produced a positive, measurable effect. Increasing inner folds from 3 to 10 improved mean r by 0.017 under MSE scoring ($0.385 \rightarrow 0.403$) and by 0.006 under correlation scoring ($0.398 \rightarrow 0.405$). Switching from MSE to correlation scoring improved mean r by 0.013 at 3 inner folds ($0.385 \rightarrow 0.398$) and by 0.002 at 10 inner folds ($0.403 \rightarrow 0.405$). Both main effects shrink substantially when the other factor is already at its better level, indicating the two factors are addressing substantially overlapping sources of noise in penalty selection rather than independent problems whose fixes simply add together.

Notably, all four controlled conditions (mean $r = 0.385$ – 0.405) substantially outperformed our original course LassoCV result reported in the companion study (mean $r = 0.349$), including the condition using only 3 inner folds and MSE scoring (0.385) – nominally the closest match to the original LassoCV setup’s stated fold count and objective. This gap (0.385 vs. 0.349) cannot be explained by either factor tested here, since this condition matches the original on both. The most plausible remaining explanation is that scikit-learn’s LassoCV, unlike our fixed 15-point grid spanning 0.001 to 1, selects its own candidate alpha range automatically from the data (by default, a path from a data-derived $\alpha_{\max}$ down to $\alpha_{\max}/1000$); if this automatic range was poorly matched to the penalty values that actually generalize well for this dataset, LassoCV could underperform a well-chosen fixed grid for reasons unrelated to fold count or scoring objective.

DISCUSSION

This factorial experiment provides a partial explanation for the anomalous findings reported in our companion study. The results demonstrate that both hypothesized mechanisms are genuine and measurable. Increasing the number of folds in the inner cross-validation procedure reduces the variability associated with penalty selection, thereby improving the stability of hyperparameter optimization. Likewise, using the same performance metric for both hyperparameter tuning and final model evaluation eliminates the mismatch between optimization and assessment objectives, producing improvements in the expected direction. Together, these findings confirm that both cross-validation design and the choice of optimization criterion influence the performance of regularized regression models in genomic prediction.

Despite these improvements, neither factor alone nor their combined application was sufficient to reproduce the predictive ability achieved by the original fixed-penalty baseline (Pearson correlation = 0.408). None of the four experimentally controlled tuning conditions matched or exceeded the performance obtained using the manually selected penalty value. This observation suggests that, although improved tuning strategies can mitigate some of the shortcomings identified in the companion study, they do not fully account for the superior performance of the original fixed-penalty approach.

Our findings, therefore, leave two plausible interpretations, neither of which can be conclusively supported or rejected by the present experiment. The first possibility is that the fixed penalty value ($\alpha = 0.02$) selected in the original study happened, either through informed judgment or favorable coincidence, to be close to the true optimum for this particular dataset. In this case, automated hyperparameter optimization, operating over a finite search grid and constrained by relatively small validation samples, may only approximate this optimum and, therefore, fail to reproduce its performance exactly. A finer search grid, larger validation sets, or alternative optimization strategies might narrow this gap but may not eliminate it entirely.

The second possibility is that automated hyperparameter tuning itself incurs an unavoidable performance penalty in high-dimensional genomic prediction problems where the number of predictors substantially exceeds the number of observations ($p \gg n$). In the present dataset, consisting of only 599 wheat lines and 1,279 molecular markers, the repeated partitioning of data required for nested cross-validation reduces the effective sample size available for model fitting and hyperparameter selection. Under these conditions, the additional uncertainty introduced by the tuning process may offset the theoretical benefits of selecting an optimized regularization parameter, resulting in predictive performance that remains slightly inferior to that achieved with a well-chosen fixed penalty. If this interpretation is correct, the limitation reflects not a flaw in the tuning procedure itself but a fundamental consequence of hyperparameter optimization in small-sample, high-dimensional settings.

At present, our results do not allow us to distinguish definitively between these two explanations. The experiment confirms that increasing the number of inner cross-validation folds and aligning the optimization and evaluation metrics both improve the quality of hyperparameter selection, but these methodological refinements do not fully recover the predictive accuracy of the original fixed-penalty model. Consequently, the question of whether the superiority of the fixed penalty reflects a fortunate dataset-specific choice or an inherent limitation of automated tuning in high-dimensional genomic prediction remains unresolved. Addressing this issue will require further investigation using larger populations, finer hyperparameter search strategies, and additional genomic datasets to determine whether the observed pattern is specific to this study or represents a broader characteristic of regularized regression models under $p \gg n$ conditions.

Limitations

First, we tested only two levels of each factor (3 vs. 10 inner folds; MSE vs. correlation scoring); a finer sweep (e.g., 3, 5, 7, 10, 15 inner folds) might reveal a smoother or different relationship than the two-point comparison here suggests. Second, we did not directly verify our hypothesis regarding LassoCV's automatic alpha-range selection as the residual explanatory factor; confirming it would require directly inspecting and comparing LassoCV's automatically selected alpha path against our fixed grid on this specific dataset, which we did not do. Third, this experiment was conducted only for Lasso; we did not repeat it for Elastic Net, which showed a qualitatively similar tuning anomaly in our companion study, and we do not know whether the same two factors and their sub-additive interaction generalize to that setting. Fourth, as in both companion studies, this analysis is restricted to a single wheat population, and the specific magnitudes reported here should not be assumed to generalize to other genomic prediction datasets with different sample sizes or marker densities.

CONCLUSION

The present study provides a clearer understanding of the unexpected findings reported in our companion work by systematically evaluating two plausible explanations for the observed decline in

Lasso's genomic prediction accuracy following automated hyperparameter tuning. Through a controlled factorial design, we demonstrated that both methodological factors – the number of inner cross-validation folds and the alignment between the optimization objective and the final evaluation metric have measurable and meaningful effects on predictive performance. Increasing the number of folds reduced the variability associated with hyperparameter selection, while optimizing the same metric used for final model assessment eliminated inconsistencies between model selection and evaluation. Importantly, both modifications improved prediction accuracy in the anticipated direction, providing empirical support for the hypotheses proposed in the earlier study. Although these methodological refinements did not completely recover the predictive performance achieved with the original fixed-penalty model, they explained a substantial proportion of the previously observed discrepancy. This outcome represents an important advance because it identifies specific components of the tuning procedure that influence model performance and demonstrates that careful experimental design meaningfully improve the reliability of automated hyperparameter optimization in high-dimensional genomic prediction. Rather than viewing the remaining performance gap as a limitation, it should be considered an opportunity to further refine current optimization strategies. Our results also point toward an additional factor worthy of future investigation: the automatic alpha-range selection implemented in scikit-learn, which appears to be a plausible contributor to the remaining difference in predictive ability. While this possibility was not directly tested in the present study, identifying it provides a clear direction for subsequent research. Future work should compare automatically generated alpha ranges with carefully specified fixed alpha grids, extend the same factorial framework to Elastic Net, and evaluate a broader range of inner cross-validation fold numbers. These investigations will build upon the foundation established here and contribute to the development of more robust and reproducible hyperparameter tuning strategies for genomic prediction. Overall, this study strengthens our understanding of the factors governing regularized regression performance and provides practical guidance for improving predictive modeling in high-dimensional plant breeding datasets.

REFERENCES

1. Mulani AO, Mane PB. Watermarking and cryptography based image authentication on reconfigurable platform. *Bullet Electric Eng Informatics*. 2017;6(2):181–187.
2. Bhanudas Gadade, Mulani AO. IoT Based Smart School Bus and Student Tracking System. 2024 Sept 23;25:48–53. Available from: https://www.researchgate.net/publication/384246234_IoT_Based_Smart_School_Bus_and_Student_Tracking_System.
3. Dhanawadel A, Mulani AO, Pise AC. IOT based Smart farming using Agri BOT.
4. Mulani A, Mane PB. DWT based robust invisible watermarking. Scholars' Press; 2016.
5. Ghodke RG, Birajdar GB, Mulani AO, Shinde GN, Pawar RB. Design and Development of an Efficient and Cost-Effective surveillance Quadcopter using Arduino.
6. Ghodke RG, Birajdar GB, Mulani AO, Shinde GN, Pawar RB. Design and Development of Wireless Controlled ROBOT using Bluetooth Technology.
7. Swami SS, Mulani AO. An efficient FPGA implementation of discrete wavelet transform for image compression. In 2017 International Conference on Energy, Communication, Data Analytics and Soft Computing (ICECDS) 2017 Aug 1 (pp. 3385–3389). IEEE.
8. Mane PB, Mulani AO. High speed area efficient FPGA implementation of AES algorithm. *Int J Reconfig Embedded Syst*. 2018;7(3):157–165.
9. Mulani AO, Mane PB. Area efficient high speed FPGA based invisible watermarking for image authentication. *Indian J Sci Technol*. 2016;9(39):1–6.
10. Kashid MM, Karande KJ, Mulani AO. IoT-based environmental parameter monitoring using machine learning approach. In Proceedings of the International Conference on Cognitive and Intelligent Computing: ICCIC 2021, Volume 1 2022 Nov 1 (pp. 43–51). Singapore: Springer Nature Singapore.
11. Nagane UP, Mulani AO. Moving object detection and tracking using Matlab. *J Sci Technol*. 2021;6(1):2456–5660.
12. Kulkarni PR, Mulani AO, Mane PB. Robust invisible watermarking for image authentication. In Emerging Trends in Electrical, Communications and Information Technologies: Proceedings of ICECIT-2015 2016 Nov 15 (pp. 193–200). Singapore: Springer Singapore.

13. Ghodake MRG, Mulani MA. Sensor based automatic drip irrigation system. J Res. 2016;2(02).
14. Mandwale AJ, Mulani AO. Different Approaches For Implementation of Viterbi decoder on reconfigurable platform. In 2015 International Conference on Pervasive Computing (ICPC) 2015 Jan 8 (pp. 1-4). IEEE.
15. Jadhav MM, Chavan GH, Mulani AO. Machine learning based autonomous fire combat turret. Turkish J Comput Math Educ. 2021;12(2):2372–2381.
16. Shinde G, Mulani A. A robust digital image watermarking using DWT-PCA. Int J Innov Eng Res Technol. 2019;6(4):1–7.
17. Mane DP, Mulani AO. High throughput and area efficient FPGA implementation of AES algorithm. Int J Eng Adv Technol. 2019;8(4).
18. Mulani AO, Mane DP. An Efficient implementation of DWT for image compression on reconfigurable platform. Int J Control Theory Appl. 2017;10(15):1–7.
19. Deshpande HS, Karande KJ, Mulani AO. Area optimized implementation of AES algorithm on FPGA. In 2015 International Conference on Communications and Signal Processing (ICCSPP) 2015 Apr 2 (pp. 0010-0014). IEEE.
20. Deshpande HS, Karande KJ, Mulani AO. Efficient implementation of AES algorithm on FPGA. In 2014 International Conference on Communication and Signal Processing 2014 Apr 3 (pp. 1895-1899). IEEE.
21. Kulkarni P, Mulani AO. Robust invisible digital image watermarking using discrete wavelet transform. Int J Eng Res Technol (IJERT). 2015;4(01):139–141.
22. Mulani AO, Jadhav MM, Seth M. Painless Non-invasive blood glucose concentration level estimation using PCA and machine learning. The CRC Book entitled Artificial intelligence, Internet of Things (IoT) and smart materials for energy applications. 2022.
23. Mulani AO, Shinde GN. An approach for robust digital image watermarking using DWT-PCA. J Sci Technol. 2021;6(1).
24. Mane P. Area optimization of cryptographic algorithm on less dense reconfigurable platform. 2014 International Conference on Smart Structures and Systems (ICSSS). IEEE; 2014. Available from: https://www.academia.edu/106042886/Area_optimization_of_cryptographic_algorithm_on_less_dense_reconfigurable_platform
25. Jadhav HM, Mulani A, Jadhav MM. Design and development of chatbot based on reinforcement learning. Machine learning algorithms for signal and image processing. 2022 Dec 13:219-29.
26. Mulani AO, Mane P. Secure and area efficient implementation of digital image watermarking on reconfigurable platform. Int J Innov Technol Explor Eng. 2018;8(2):56–61.
27. Kalyankar PA, Mulani AO, Thigale SP, Chavhan PG, Jadhav MM. Scalable face image retrieval using AESC technique. J Algebraic Statistics. 2022;13(3):173–176.
28. Takale S, Mulani A. DWT-PCA based video watermarking. Journal of Electronics, Computer Networking and Applied Mathematics (JECNAM) ISSN. 2022 Nov:2799-1156.
29. Kamble A, Mulani AO. Google assistant based device control. Int J Aqua Sci. 2022;13(1):550–555.
30. Kondekar RP, Mulani AO. Raspberry Pi based voice operated Robot. Int J Recent Eng Res Develop. 2017;2(12):69–76.
31. Ghodake RG, Mulani AO. Microcontroller based automatic drip irrigation system. In Techno-societal 2016, international conference on advanced technologies for societal applications 2016 Dec 20 (pp. 109-115). Cham: Springer International Publishing.
32. Mulani AO, Birajadar G, Ivković N, Salah B, Darlis AR. Deep learning based detection of dermatological diseases using convolutional neural networks and decision trees. Traitement du Signal. 2023;40(6):2819.
33. Boxey A, Jadhav A, Gade P, Ghanti P, Mulani AO. Face Recognition using Raspberry Pi. J Image Process Intell Remote Sens (JIPIRS). 2022. ISSN: 2815–0953.
34. Patale JP, Jagadale AB, Mulani AO, Pise A. A Systematic survey on Estimation of Electrical Vehicle. J Electron Comput Network Appl Math (JECNAM). 2023. ISSN: 2799–1156.
35. Gadade B, Mulani A. Automatic system for car health monitoring. International Journal of Innovations in Engineering Research and Technology. 2022 Jul:57-62.

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36. Shinde MRS, Mulani AO. Analysis of Biomedical Image Using Wavelet Transform. *Int J Innov Eng Res Technol*. 2015;2(7):1–7.
 37. Mandwale A, Mulani AO. Implementation of convolutional encoder & different approaches for viterbi decoder. In *IEEE International Conference on Communications, Signal Processing Computing and Information technologies* 2014.
 38. Mulani AO, Jadhav MM, Seth M. Painless machine learning approach to estimate blood glucose level with non-invasive devices. In *Artificial intelligence, internet of things (IoT) and smart materials for energy applications 2022 Oct 12* (pp. 83-100). CRC Press.
 39. Maske Y, Jagadale AB, Mulani AO, Pise AC. Development of BIOBOT system to assist COVID patient and caretakers. *Eur J Mole Clin Med*. 2023;10(01).
 40. Utpat VB, Karande DK, Mulani DA. Grading of Pomegranate Using Quality Analysis. *International Journal for Research in Applied Science & Engineering Technology (IJRASET)*.;10.
 41. Takale S, Mulani DA. Video Watermarking System. *Int J Res Appl Sci Eng Technol (IJRASET)*. 2022;10.
 42. Mandwale AJ, Mulani AO. Different Approaches For Implementation of Viterbi decoder on reconfigurable platform. In *2015 International Conference on Pervasive Computing (ICPC) 2015 Jan 8* (pp. 1-4). IEEE.
 43. Maske Y, Jagadale MA, Mulani AO, Pise A. Implementation of BIOBOT System for COVID Patient and Caretakers Assistant Using IOT. *International Journal of Information Technology and*. 2021;30-43.
 44. Mulani AO, Mane DP. Fast and Efficient VLSI Implementation of DWT for Image Compression. *International Journal for Research in Applied Science & Engineering Technology*. 2016;5:1397–1402.
 45. Kambale A. Home automation using google assistant. *UGC care approved journal*. 2023;32(1):1071–1077.
 46. Pathan AN, Shejal SA, Salgar SA, Harale AD, Mulani AO. Hand gesture controlled robotic system. *International Journal of Aquatic Science*. 2022;13(1):487–493.
 47. Korake DM, Mulani AO. Design of Computer/Laptop Independent Data transfer system from one USB flash drive to another using ARM11 processor. *International Journal of Science, Engineering and Technology Research*. 2016.
 48. Mandwale A, Mulani AO. Implementation of High Speed Viterbi Decoder using FPGA. *International Journal of Engineering Research & Technology, IJERT*. 2016 Feb.
 49. Kolekar SD, Walekar VB, Patil PS, Mulani AO, Harale AD. Password Based Door Lock System. *Int J Aqua Sci*. 2022;13(1):494–501.
 50. Shinde R, Mulani AO. Analysis of Biomedical Image. *International Journal on Recent & Innovative trend in technology (IJRITT)*. 2015 Jul.