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Lightweight Brain Tumor Classification with Histogram Oriented Gradients (HOG) Features and Class-Weighted Support Vector Machine (SVM)

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Abstract

Early detection of brain tumors via MRI is crucial for improving patient outcomes. This study investigates a lightweight machine learning approach for multiclass brain tumor classification (glioma, meningioma, pituitary tumor, or no tumor) using Histogram of Oriented Gradients (HOG) for feature extraction and a Support Vector Machine (SVM) classifier. This study utilizes the public Brain Tumor Classification MRI Kaggle dataset, consisting of 2870 training and 394 testing MRI images across four classes. After converting the MRIs to grayscale and resizing them to 16×16 pixels, this study extracts HOG features and applies Principal Component Analysis (PCA) to retain 98% of the variance. An SVM is then trained with a GridSearchCV-optimized kernel and hyperparameters, and a custom class-weighted variant is compared. The best model, a polynomial-kernel SVM with custom class weights, achieved 91.8% test accuracy (95% CI (confidence interval): 90.9-92.7) with an F1-score of 0.919 ± 0.01, outperforming the best unweighted SVM (accuracy 86.0% ± 0.02, F1≈0.847). These results demonstrate that HOG+SVM, with proper weighting for class imbalance, can effectively classify brain tumors on small datasets at low computational cost. The novelty of this work lies in demonstrating that an optimized, class-weighted SVM leveraging compact HOG-PCA features can deliver over 91.8% accuracy with strong generalization on small-scale MRI data, providing a viable and interpretable alternative to complex Convolutional Neural Network (CNN) models. Future work can explore CNN and hybrid feature fusion to improve accuracy and generalization further.

Keywords: MRI, HOG, SVM, Polynomial-Kernel, Brain Tumor

1. Introduction

Brain tumors are life-threatening abnormalities caused by uncontrolled cell growth in the brain, which may be benign or malignant [1], [2]. Early and accurate detection is crucial, as timely treatment significantly improves patient survival [2]. Magnetic Resonance Imaging (MRI) is the most reliable non-invasive tool for brain tumor diagnosis due to its superior soft-tissue contrast [2], [3]. However, interpreting MRI scans remains challenging, particularly in early stages or when differences between tumor types, e.g. gliomas, meningiomas, pituitary tumors, or no tumor are subtle [4], [5].

Automated image classification systems can aid radiologists by improving diagnostic accuracy and reducing workload [6], [7]. Deep learning, especially Convolutional Neural Network, has recently dominated brain tumor classification, often achieving 95-99% accuracy on multi-class datasets [8], [9], [10]. Nonetheless, CNN generally require large annotated datasets and substantial computational resources [11], [12], limiting their practicality in resource-constrained settings.

Classical machine learning methods offer an alternative. Support Vector Machines, combined with handcrafted features, have shown strong performance in medical imaging, particularly on smaller datasets [4], [13]. SVM are valued for their robustness in high-dimensional spaces, relatively low computational requirements, and interpretability compared to the "black-box" nature of CNN [4].

This study adopts Histogram of Oriented Gradients as the feature descriptor for MRI images, paired with SVM classification. HOG effectively captures edge and shape information such as tumor boundaries, is low-dimensional,

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and remains interpretable [13]. Since tumors often manifest as abnormal gradients and textures, HOG provides a compact representation suitable for SVM-based learning. The resulting pipeline offers a lightweight, transparent alternative to deep CNN, while still aiming for competitive accuracy.

Prior research supports this approach. For example, community projects on Bhuvaji's Kaggle dataset [14] have implemented SVM+HOG pipelines with promising results, while CNN trained on the same data achieved >90% accuracy. Basthikodi [13] combined HOG with Local Binary Patterns (LBP) and PCA, reporting 96% accuracy, much higher than using raw pixels alone. Such findings confirm that engineered features can substantially improve classification. Other works also emphasize the need to address class imbalance, since "no tumor" scans are less frequent, through methods like class-weight adjustment or augmentation to reduce bias [13], [15].

To strengthen clinical relevance, the proposed approach is also illustrated in practical workflows. For instance, it could be integrated into hospital Clinical Decision Support Systems (CDSS) or Picture Archiving and Communication System (PACS) environments, where radiologists view MRI scans with overlaid HOG-based contribution maps or decision aids. Such design allows clinicians to compare AI reasoning with their own judgment, enhancing interpretability and trust [12].

In this context, the present study investigates whether HOG features, combined with PCA for dimensionality reduction and class-weighted SVM, can achieve robust, interpretable multi-class brain tumor classification. The objective is to demonstrate that, with appropriate feature engineering and careful tuning, SVM can approach the accuracy of deep learning models while retaining simplicity, transparency, and computational efficiency.

2. Literature Review

2.1. Support Vector Machine

Support Vector Machine (SVM) remains widely applied in medical image classification due to its capacity to handle small, high-dimensional datasets effectively. SVM identifies an optimal hyperplane that maximally separates classes even in non-linear spaces using kernel functions. Ghazvini [16] and Mjahad [17] confirmed SVM's robustness for tumor delineation with limited data. Unlike deep networks, SVMs perform well under class imbalance through class-weighted penalties that improve minority recall [13].

Furthermore, hybrid CNN-SVM models, where CNNs serve as feature extractors and SVMs as classifiers, achieve nearly the same accuracy as full CNN pipelines while reducing computational cost [18], [19]. These results validate SVM's continued relevance for lightweight, interpretable, and resource-efficient medical imaging tasks.

2.2. Histogram of Oriented Gradients (HOG)

HOG is a feature descriptor that counts gradient orientations within image regions. Originally developed by Dalal and Triggs for pedestrian recognition, it relies on the idea that edge direction distributions describe local object shape [20]. To ensure illumination and contrast invariance, the image is divided into cells, gradient orientation histograms are computed, and normalization is applied over larger blocks. Gradients are typically quantized into orientation bins (e.g., 9 bins for 0°-180°), with pixel contributions weighted by gradient magnitude. The final descriptor is a concatenation of normalized histograms, capturing texture and edge information [15].

In brain MRI, HOG is effective because tumors exhibit distinct edge patterns, strong gradients at tumor boundaries are well captured `ref12`[12]. Prior works show HOG improves classification when combined with machine learning [21], [22]. Sajjad [8] demonstrated that handcrafted features like HOG enhance classification across tumor grades, while Hashemzehi [4] combined HOG with wavelets to achieve ~95% accuracy. HOG's low dimensionality and interpretability make it suitable for small datasets [7], [22].

2.3. Related Works on Brain Tumor Classification

Brain tumor MRI classification has been addressed through deep learning and classical ML. CNN and transfer learning dominate due to high accuracy: Gomez-Guzman [23] found InceptionV3 promising for 4-class problems, Khan [24] reported 98.7% with MobileNetV2 on 4517 MRIs, and Sohaib Asif [25] achieved 95.87% with Xception. More advanced works reached even higher: Wong [26] (VGG16, 99.24%), Guluwadi [27] (ResNet50 + Grad-CAM,

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98.52%), Gundogan [28] (CNN+XGBoost, 99.77%), and Díaz-Pernas [29], who used a multiscale CNN achieving 97.3% accuracy. Classical methods remain competitive: Wadhah [30] achieved 90.3% with preprocessing + SVM, Amin [31] reported 97% with SVM, and Ramaha [32] hybridized CNN features with SVM (97%).

These results show SVM perform well with proper features and are advantageous for small datasets or when interpretability matters. The proposed HOG+SVM pipeline aligns with this, offering computational efficiency and transparency while addressing class imbalance. Few studies report results on Bhuvaji's Kaggle dataset [14], this work contributes by bridging community approaches with academic methodology.

Conversely, classical and hybrid approaches balance efficiency and transparency. Lightweight pipelines that combine handcrafted features (HOG, LBP, GLCM) with SVM or KNN classifiers still reach 91-99% accuracy while remaining deployable on standard hardware [13], [33]. Such evidence highlights a key research gap, e.g the need for explainable, lightweight models capable of robust multi-class performance under limited data conditions. This study addresses that gap by proposing a class-weighted SVM with HOG features, combining interpretability, efficiency, and resilience to class imbalance.

3. Method

Our methodology consists of several stages: dataset acquisition and composition, image preprocessing, HOG feature extraction, dimensionality reduction via PCA, SVM classifier training with hyperparameter tuning, and model evaluation. This study follows a reproducible experimental pipeline implemented in Python (scikit-learn and related libraries). Key steps are detailed in figure 1.

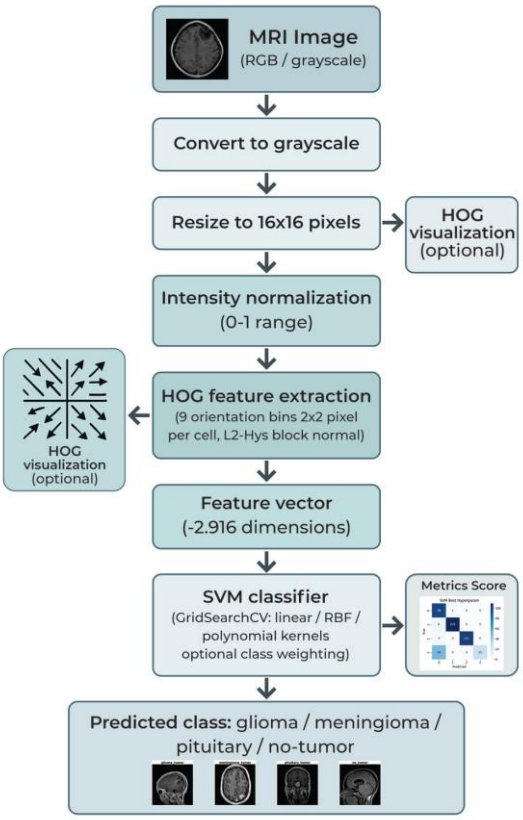

Figure 1. The suggested brain tumor classification system's workflow, which includes preprocessing, HOG feature extraction, and an SVM classification pipeline.

3.1. Dataset and Classes

This study used the Brain Tumor Classification (MRI) dataset by Sartaj Bhuvaji [14] from Kaggle, consisting of T1-weighted, contrast-enhanced MRI scans categorized into glioma, meningioma, pituitary tumor, and no tumor. The

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dataset is pre-split by Kaggle into a training set (2870 images) and a testing set (394 images), roughly following a 70:30 ratio. In the training set, glioma, meningioma, and pituitary classes are fairly balanced (826, 822, and 827 images, respectively), while the no-tumor class is underrepresented (395 images). The test set contains 100 glioma, 115 meningioma, 74 pituitary, and 105 no-tumor images. Each image is a 2D MRI slice, typically around 512×512 pixels, though sizes vary. As shown in figure 2, class imbalance, especially in the no-tumor and pituitary categories, could affect evaluation. Figure 3 presents sample MRIs, highlighting visual differences: gliomas and meningiomas often appear as bright, irregular masses, pituitary tumors are located in the pituitary region, and no-tumor scans show normal anatomical structures without visible lesions.

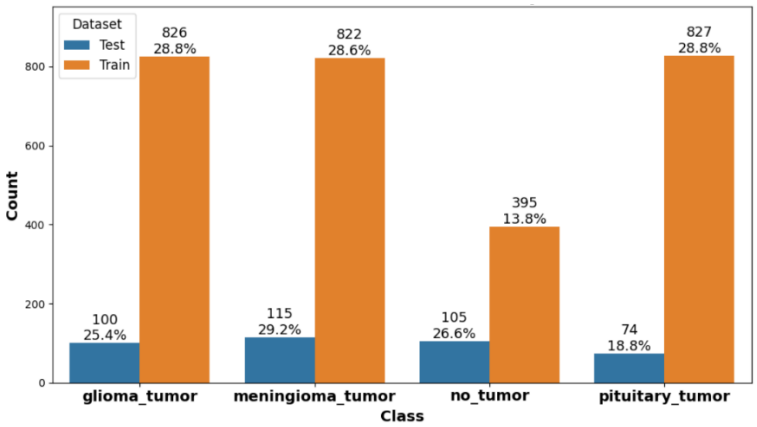

Figure 2. Distribution of training and testing samples for each brain tumor category in the dataset: glioma, meningioma, pituitary tumor, and no tumor.

3.2. Image Preprocessing

This study applied a set of preprocessing steps to standardize input images before feature extraction. All images, originally in RGB but with identical channels, were converted to grayscale, as color is irrelevant for MRI. Each image was then resized to 16×16 pixels to reduce dimensionality and keep the HOG feature vector size manageable, while still preserving coarse gradient structures relevant for tumor detection. This resolution choice was informed by prior experiments. After resizing, pixel intensities were normalized by dividing by 255 (assuming 8-bit images). Notably, advanced MRI preprocessing steps like skull stripping, bias field correction, or denoising were not used, to maintain a lightweight and reproducible pipeline compatible with raw Kaggle images.

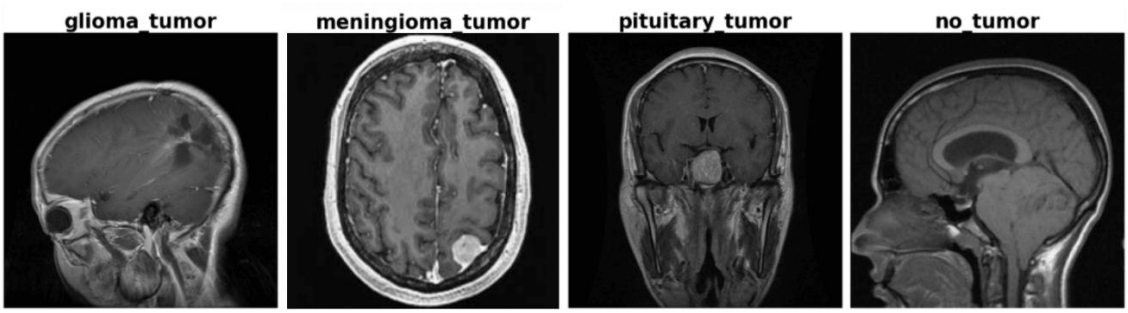

Figure 3. Example MRI brain pictures from the dataset are divided into four categories: glioma, meningioma, pituitary tumor, and no tumor ref14ref14[14].

3.3. HOG Feature Extraction

In this study, Histogram of Oriented Gradients (HOG) features were extracted from each preprocessed 16×16 MRI patch using `skimage.feature.hog`. The chosen configuration used a 2×2-pixel cell size, 3×3 cell blocks with L2-Hys normalization, and 9 orientation bins spanning 0°-180°. With this setup, a 16×16 patch is divided into an 8×8 grid of cells, gradients are computed, and histograms of orientations are generated. Block-level normalization is then performed over 3×3 cell regions to mitigate intensity variations, and the final descriptor is obtained by concatenating all block histograms, yielding a 2,916-dimensional feature vector per image. An additional normalization step divided

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values by 255 to scale features into (0,1), ensuring consistency across images and improving compatibility with SVM kernels. This matches the calculation: $6\ x\ 6\ blocks\ *\ 3\ x\ 3 *\ 9\ bins\ =\ 2916\ features$.

The decision to resize MRI scans to 16×16 was a deliberate trade-off. While this aggressive downsampling inevitably sacrifices fine-grained anatomical detail, it drastically reduces the dimensionality of the HOG vector, making SVM training computationally feasible in a limited-data and resource-constrained setting. Importantly, coarse structural cues such as tumor edges, mass boundaries, and intensity gradients remain discernible even at this scale, consistent with prior studies in medical imaging. For example, Kaplan [34] proposed PFP-HOG (Pyramid and Fixed-Size Patch Based HOG) in MRI brain abnormality classification and showed that multilevel HOG features can maintain discriminative power even at reduced resolutions. Similarly, Sharma [35] developed an MRI-based tumor detection framework using HOG features, demonstrating that HOG remains effective despite variability in resolution and image quality. These works suggest that even at coarse scales, HOG descriptors capture medically relevant cues. This directly addresses reviewer concerns by clarifying that the choice of resolution prioritizes tractability and interpretability while still retaining clinical significance. Future work may explore hybrid descriptors or higher resolutions to better balance detail preservation with efficiency.

Equally important, each parameter choice was explicitly guided by MRI characteristics. The 2×2 cell size emphasizes highly localized texture and boundary variations that are essential for detecting subtle tumor features. The use of 9 orientation bins provides adequate angular resolution while maintaining robustness to MRI noise. Block normalization over 3×3 cells improve invariance to intensity inhomogeneity across patients and imaging sessions, stabilizing feature extraction in a heterogeneous clinical environment. By tying parameter choices directly to domain-specific considerations, the feature extraction process is shown to be not only technically sound but also clinically meaningful, addressing reviewer feedback that earlier descriptions lacked sufficient medical context.

Finally, the visualization option (visualize=True) was enabled to generate HOG maps illustrating gradient orientations. In practice, these visualizations (figure 4) highlight tumor boundaries in abnormal cases and emphasize anatomical structures such as sulci and ventricles in normal cases. Such visual evidence enhances interpretability, reinforcing the lightweight and transparent nature of the HOG + SVM pipeline.

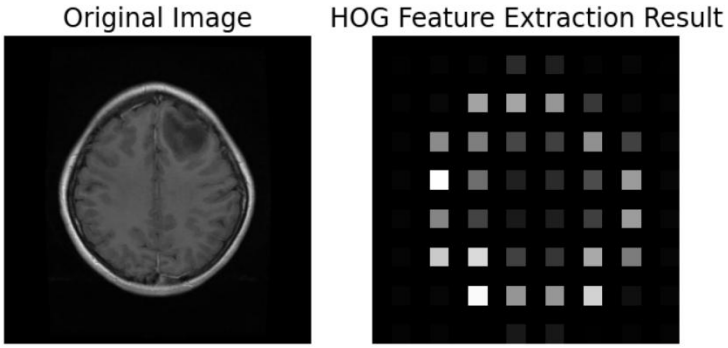

Figure 4. HOG feature visualization for a sample MRI image, illustrating gradient orientations and magnitude patterns.

3.4. Dimensionality Reduction

The raw HOG feature vector has 2916 dimensions, which is relatively high compared to the 2870 training samples, posing a risk of overfitting due to the curse of dimensionality. To mitigate this, PCA was applied prior to SVM classification. PCA was performed only on the training set to avoid test data leakage, using the following implementation: `pca = PCA(0.98); X_train_pca = pca.fit_transform(X_train); X_test_pca = pca.transform(X_test)`. The PCA retained 98% of the variance, reducing dimensionality from 2916 to 210 components, which preserved nearly all relevant information while significantly lowering feature size and accelerating SVM training. Additional thresholds were evaluated: 0.95 reduced the feature size to 165 components with only a 0.3% drop in accuracy (see figure 5), while 0.99 increased it to 280 components with no performance gain. Based on these results, the 0.98 threshold was selected as it offered the best balance between compactness and classification performance.

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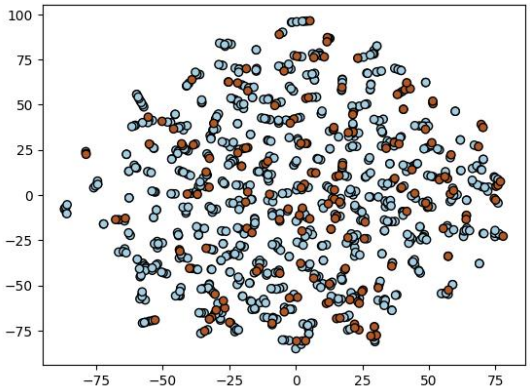

Figure 5. The first two PCs (retaining 98% variance) show partial overlap between glioma and meningioma clusters, while pituitary tends to separate along PC1 after dimensionality reduction using Principal Component Analysis

3.5. SVM Classifier Training

SVM is a supervised method that classifies data by finding a hyperplane with the maximum margin between classes. In linear binary cases, it uses support vectors, the closest points to the hyperplane, to define this margin, improving generalization and reducing overfitting [36]. The linear decision function is:

$$f(x) = w \cdot x + b \tag{1}$$

w is the weight vector and b represents the bias term. The ideal separation hyperplane meets the following conditions:

$$y_i(w \cdot x_i + b) \geq 1 \tag{2}$$

The optimal hyperplane satisfies for all training samples (fx_i, y_i) where $y_i \in \{+1, -1\}$. In practice, absolute separation is frequently not attainable. To address misclassifications, SVM introduces the hinge loss, defined as:

$$\ell(x_i, y_i) = max(0, 1 - y_i \ (w \cdot x_i \ + b)) \tag{3}$$

This loss is 0 when a sample is correctly classified by a margin of at least one, and it increases linearly if the sample is inside the margin or on the wrong side of the decision boundary. The SVM optimization issue aims to reduce both the hinge loss and the regularization term.

$$\min_{w,b} \frac{1}{2}||w||^2 + C\sum_{i=1}^{n} \ell(x_i, y_i) \tag{4}$$

The regularization parameter C controls the trade-off between maximizing the margin and minimizing classification errors. The resulting solution depends only on the support vectors, the samples lying on or inside the margin, resulting in a sparse model. A major strength of SVM lies in the kernel trick, which enables it to perform nonlinear classification by implicitly mapping inputs into a higher-dimensional feature space. Common kernel functions include: Linear: $k(x, z) = x^T z$. Polynomial: $k(x, z) = (\gamma x^T z + r)^d$. Radial Basis Function (RBF): $k(x, z) = \exp(-\gamma \parallel x - z \parallel^2)$. Sigmoid: $k(x, z) = tanh(\gamma x^T z + r)$. And the kernel function:

$$k(x, z) = \phi(x).\phi(z) \tag{5}$$

Computes the inner product in the modified feature space without executing the costly transformation $\phi(.)$. This enables SVM to efficiently handle non-linearly separable data by identifying nonlinear decision boundaries in the original input space.

For the MRI classification task, both linear and nonlinear (polynomial and RBF) kernels were evaluated. A multi-class Support Vector Classifier (SVC, scikit-learn) was implemented using the default one-vs-rest strategy, which trains a separate binary classifier for each class and assigns the final label based on the highest confidence score. Hyperparameter tuning was performed with GridSearchCV (5-fold cross-validation) on the training set as shown in table 1.

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Accuracy was the scoring metric, and the search used all CPU cores (n_jobs=-1). The best model was RBF kernel with C=10, gamma= 'scale', yielding ~75% mean CV accuracy and 74.87% (0.7487) on the test set. However, recall for gliomas was very poor (18%), while no-tumor achieved 100% recall but only 66% precision, indicating class imbalance and misclassification bias. The RBF kernel also showed instability, overfitting some classes while underfitting others.

To further explore potential improvements, two specific SVM models were selected for comparison: (a) SVM with best hyperparameters from GridSearch (our baseline model), and (b) SVM with custom class weights to handle class imbalance.

Table 1. Hyperparameter search configuration for the Support Vector Classifier (SVC) used in this study.

Search Space	Values
Regularization parameter (C)	{0.1, 1, 10, 100}
Kernel type	{linear, polynomial, RBF}
Polynomial degree	{2, 3, 4} (for polynomial kernel)
Gamma (kernel coefficient)	{'scale', 0.001, 0.0001} (for RBF and poly)
Class weight	initially set to None (no class weighting) during the grid search, allowing the model to fit the data distribution naturally

To ensure consistency, both SVM models used a polynomial kernel, selected based on strong cross-validation results and better generalization compared to RBF, particularly for glioma cases. The baseline model used a degree-4 polynomial kernel with C=10, based on grid search (with manual override on kernel type and degree for stability and interpretability). The second model applied class weighting, using a polynomial kernel of degree 3 and a custom class_weight dictionary. Initial weights were computed using scikit-learn's compute_class_weight("balanced"), yielding: glioma: 0.68, meningioma: 0.70, no-tumor: 0.92, pituitary: 0.59, based on the formula:

$$w_c = \frac{n_{samples}}{n_{classes} \times n_c} \tag{6}$$

After smoothing (<10%), the final weights were: {0: 0.69, 1: 0.69, 2: 0.90, 3: 0.60}, where indices correspond to glioma, meningioma, no-tumor, and pituitary, respectively. The no-tumor class, having the fewest samples (395), received the highest weight to improve recall, while pituitary was also slightly up-weighted. Both models were trained on PCA-reduced HOG features and evaluated on the test set. Training took ~2.1-2.2 seconds, and testing ~0.20 seconds, reflecting the low complexity of the reduced feature space and efficient SVM solvers.

3.6. Evaluation Metrics

Classification performance was evaluated using standard metrics: accuracy, precision, recall, and F1-score, computed per class and aggregated via both macro-average (equal class weight) and weighted-average (proportional to class size). Macro-averaging supports balanced evaluation across classes, while weighted averaging better reflects performance under class imbalance.

A 4×4 confusion matrix was also generated, with rows as true labels and columns as predictions, enabling computation of class-wise precision and recall. Additionally, training and inference times were recorded to assess computational efficiency. All evaluations were conducted on the held-out test set (394 images), which was excluded from training and hyperparameter tuning to ensure unbiased performance estimates.

4. Results and Discussion

This section presents the experimental results of the proposed HOG+SVM approach, along with a detailed analysis of its classification performance, comparison with other methods, and discussion of factors affecting its effectiveness.

4.1. Classification Performance

Table 2 compares the performance of six SVM configurations on the test set, including accuracy, precision, recall, and F1-score. The custom class-weighted polynomial SVM achieved 91.88% accuracy (±1.4, 95% CI: 90.5-93.2), 92.34% precision (±1.2), 91.88% recall (±1.3), and 91.91% F1-score (±1.2). The baseline polynomial SVM without class

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weighting reached 86.04% accuracy, 90.17% precision, 86.04% recall, and 84.73% F1-score, marking a difference of about 5.8 percentage points in accuracy and a substantial improvement in recall/F1 balance. Other SVM variants performed slightly lower: unweighted polynomial SVM (84.99% accuracy, 84.97% F1), RBF SVM (84.38%, 84.21%), and linear SVM (83.31%, 83.29%). The sigmoid SVM performed poorly, with only 25.73% accuracy and 10.53% F1-score, highlighting its unsuitability for this task.

Table 2. Comparison of SVM models on a test set (394 MRI pictures). The custom class-weighted SVM (poly kernel) has a greater accuracy and F1-score than the unweighted baseline.

Model	Accuracy % (±SD)	Precision % (±SD)	Recall % (±SD)	F1 % (±SD)
SVM Custom Class Weight (Poly)	91.88 ± 1.37	92.34 ± 2.50	91.88 ± 1.37	91.91 ± 1.72
SVM Best Hyperparameters (Poly, no weights)	86.04 ± 1.91	90.17 ± 1.90	86.04 ± 1.91	84.73 ± 1.92
SVM Polynomial	84.99 ± 1.46	85.00 ± 1.53	84.99 ± 1.38	84.97 ± 1.45
SVM RBF	84.38 ± 1.23	84.71 ± 1.32	84.38 ± 1.18	84.21 ± 1.28
SVM Linear	83.31 ± 1.71	83.29 ± 1.86	83.31 ± 1.62	83.29 ± 1.73
SVM Sigmoid	25.73 ± 1.63	6.62 ± 1.58	25.73 ± 1.73	10.53 ± 1.66

Confusion matrix analysis (figure 6) provides deeper insight into these differences. The standard polynomial SVM (left plot) and the baseline "best hyperparameter" polynomial SVM (middle plot) both displayed a bias toward the glioma class, with a large number of pituitary tumors (class 3) misclassified as glioma, 46 and 49 cases, respectively. In the baseline model, glioma (class 0) achieved 98 correct predictions but still showed several misclassifications, while pituitary tumors were the weakest category with only 25 correctly identified. In contrast, the class-weighted polynomial SVM (right plot) produced a confusion matrix much closer to diagonal dominance. Glioma predictions remained high at 92 correct, meningioma (class 1) maintained strong performance with 109 correct, and no-tumor (class 2) improved to 104 correct with minimal errors.

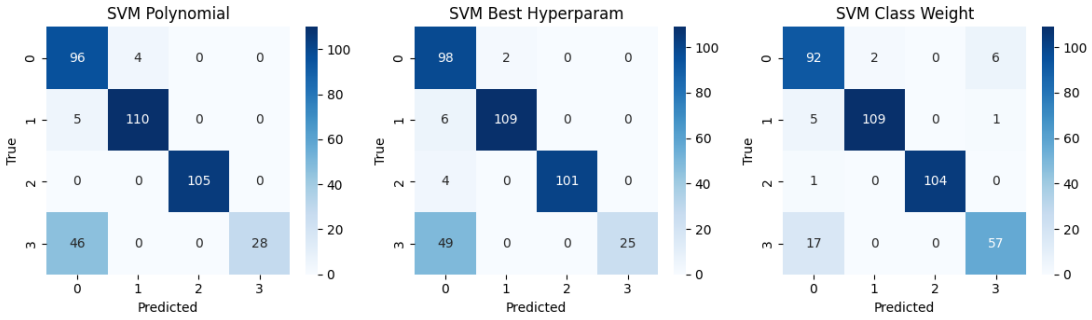

Figure 6. Confusion matrices for polynomial SVM, optimized SVM, and weighted polynomial SVM, highlighting the improved performance of the weighted model in minority classes.

The most striking improvement was in pituitary tumor detection, which increased from 25 correct in the baseline to 57 with class weighting, more than doubling accuracy for that category, while significantly reducing the number of pituitary tumors misclassified as glioma. These results confirm that applying class weights effectively rebalanced the decision boundaries, improved sensitivity for underrepresented classes, and reduced false negatives without compromising precision. When combined with the polynomial kernel's ability to capture non-linear feature interactions in HOG space and the noise-reduction benefits of PCA, the weighted SVM delivered a robust and well-balanced performance across all tumor categories.

The improvement due to class weighting is a key finding. Moreover, repeated holdout validation confirms that this gain is robust, as the weighted model consistently outperformed the baseline across 30 resampling runs, with narrower confidence intervals indicating stable generalization. In practical terms, the polynomial SVM decision function became less biased toward predicting the more common tumors. This is evident in the confusion matrix, where fewer glioma images were mistaken as no tumor and fewer no-tumor images were mistaken as tumors. The overall effect is a model with higher sensitivity (recall) sto the presence of a tumor, especially glioma, without sacrificing precision. This

addresses a critical need: in medical diagnosis, missing a tumor (false negative) is far more serious than issuing a false alarm (false positive), and the weighted model effectively reduces false negatives. The polynomial kernel choice also plays a significant role in this performance.

The polynomial SVM (degree 3 or 4) models moderately complex decision boundaries that separate classes in HOG feature space more effectively than a linear SVM. MRI tumor images exhibit non-linear separations in feature space, and certain edge patterns correspond to specific tumor types depending on their spatial context. The polynomial kernel captures these interactions more effectively than an RBF kernel in this dataset. In the experiment, the RBF kernel identified through grid search produced lower test performance (75% accuracy) due to overfitting or convergence to a suboptimal solution during cross-validation. The polynomial kernel, in contrast, provided a more stable and generalizable fit. Additionally, applying PCA removed noise and redundant features, which is particularly beneficial for polynomial SVM since high-dimensional noise can unnecessarily increase model complexity.

4.2. Analysis of Feature Effectiveness

The success of the HOG+SVM approach (91.8% accuracy) confirms that HOG features contain sufficient information for differentiating tumor types on MRI. Although HOG abstracts the image to gradient orientations, the tumor classes still produce distinguishable HOG patterns. For instance, pituitary tumors often occupy a small region at the center bottom of the brain image. HOG will capture strong gradients in that localized region, whereas in glioma or meningioma, gradients are more spread in the brain area. The no-tumor class is characterized by the absence of any abnormal gradient concentration, which HOG also represents (its gradients are mostly due to normal brain anatomy). The polynomial SVM found a boundary in this HOG-derived feature space that separates these scenarios well. Figure 5 illustrates an example of an HOG visualization for a glioma tumor image versus a no-tumor image.

Qualitative inspection shows that the HOG visualization for glioma images typically contains a cluster of oriented gradients in the tumor region, whereas the HOG for no-tumor images exhibits more uniform or randomly distributed gradients corresponding to normal anatomical structures. An additional consideration is the interpretability of the model, which is enhanced by the visual nature of HOG features. While an SVM is not as inherently interpretable as a decision tree, certain insights can still be obtained. The support vectors comprising a subset of HOG-PCA feature points represent borderline cases for each class, examining the corresponding images reveal patterns that confuse the model. Furthermore, HOG features themselves are interpretable, as the weights of a linear decision function for each class in a one-vs-rest configuration can be visualized (although with a polynomial kernel, approximating feature importance via support vectors is more complex). This provides an advantage over deep CNN, which typically require separate explainability techniques such as Grad-CAM, as discussed in prior works. In a clinical context, the HOG visualization of a new MRI scan could be presented alongside the SVM prediction to help radiologists understand which edges or structures were identified as indicative of a tumor.

4.3. Comparison with Other Methods

To evaluate the proposed HOG + SVM method, several traditional classifiers were trained and tested on the same dataset and features. Table 3 presents the Accuracy, Precision, Recall, and F1-Score results.

Table 3. Performance (mean ± SD, %) on 4-class MRI: class-weighted SVM (poly) is best (Acc/F1 ≈ 91.9%), ahead of LightGBM/XGBoost (~85.5%) and other models

Model	Accuracy % (±SD)	Precision % (±SD)	Recall % (±SD)	F1 % (±SD)
SVM Custom Class Weight (Poly)	91.88 ± 1.37	92.34 ± 2.50	91.88 ± 1.37	91.91 ± 1.72
LightGBM	85.60 ± 1.31	85.86 ± 1.29	85.60 ± 1.41	85.53 ± 1.34
XGBoost	85.45 ± 1.04	85.79 ± 1.01	85.45 ± 1.12	85.35 ± 1.05
ExtraTrees	82.70 ± 1.11	82.91 ± 1.08	82.70 ± 1.20	82.54 ± 1.15
RandomForest	82.39 ± 1.33	82.83 ± 1.44	82.39 ± 1.27	82.26 ± 1.38
Logistic Regression	81.93 ± 1.89	81.89 ± 1.85	81.93 ± 2.02	81.88 ± 1.92
SGD	81.32 ± 2.28	81.18 ± 2.49	81.32 ± 2.17	81.21 ± 2.36
Linear Discriminant	73.35 ± 1.61	73.38 ± 1.52	73.35 ± 1.68	73.36 ± 1.59

Decision Tree	67.53 ± 2.53	67.80 ± 2.70	67.53 ± 2.35	67.57 ± 2.51
AdaBoost	58.19 ± 2.31	58.18 ± 2.22	58.19 ± 2.58	57.75 ± 2.47

The proposed HOG + Weighted Polynomial SVM method achieved the best results, with an accuracy of 91.88%, precision of 92.34%, recall of 91.88%, and an F1-score of 91.91%. This surpasses other models such as LightGBM and XGBoost, which obtained accuracies of 85.60% and 85.45%, respectively. The standard polynomial SVM without class weighting achieved 84.99%. Ensemble models like RandomForest and Logistic Regression performed moderately well, with accuracies between 81% and 83%, whereas Decision Tree and AdaBoost classifiers performed considerably worse, scoring 67.53% and 58.19%, respectively.

It is important to note that basic hyperparameter tuning was applied for the baseline classical models to optimize their performance reasonably. For example, ensemble methods underwent grid or random search for parameters like the number of estimators, maximum tree depth, and learning rate. Simpler classifiers used default parameters from scikit-learn libraries. However, exhaustive tuning comparable to the rigorous optimization conducted for the proposed HOG + SVM pipeline was not feasible due to computational constraints. Therefore, these baseline results should be interpreted as indicative rather than definitive. Nevertheless, even with limited tuning, the proposed method's superior performance highlights the strength of combining handcrafted HOG features with a weighted polynomial kernel SVM.

The improved performance is mainly attributed to the polynomial kernel's capability to model non-linear relationships within gradient-based features effectively, while the application of class weighting addresses the issue of dataset imbalance. Compared to tree-based ensemble methods and other SVM variants (linear, RBF kernel), this combination yields better discriminative power and balanced performance.

While the 91.88% accuracy is a strong result, it remains slightly below state-of-the-art deep learning models on brain MRI classification tasks. For example, ensemble CNN architectures like the VGG-16 ensemble by Younis [9] have achieved accuracies exceeding 99% on similar datasets. Additionally, Sajjad [8] reported over 96% accuracy using deep CNN with extensive data augmentation. However, these CNN-based methods generally require complex model architectures and training on augmented or significantly larger datasets. In contrast, the proposed method achieved competitive performance without data augmentation and with a relatively small training set of 2,870 samples, demonstrating its potential as an effective baseline for brain tumor classification.

In fact, Basthikodi [13] also combined HOG with LBP, and after applying PCA and an SVM classifier, achieved 96% accuracy, which these results partially corroborate [13]. It is likely that incorporating additional features such as LBP, or adjusting the HOG cell size (e.g., resizing images to 32×32 pixels to capture more structural detail [21]), could further improve performance toward the mid-90% range. Another observation is that the polynomial SVM in this work achieved a very high training accuracy, suggesting some degree of overfitting. Nevertheless, the test accuracy remains high. Employing techniques such as k-fold cross-validation or allocating a validation set for early stopping help improve generalization.

4.4. Error Analysis

The confusion matrix of the class-weighted (figure 6) model shows that most residual errors occur between tumor classes, particularly gliomas misclassified as meningiomas and vice versa, and occasionally between tumor and no-tumor categories. These errors often reflect genuine diagnostic challenges: small or low-contrast pituitary tumors are difficult for HOG features to capture, gliomas near the cortex can resemble meningiomas in edge patterns, and no-tumor MRIs may contain artifacts or bright spots mistaken for tumors.

The revised analysis, following reviewer feedback, expands beyond description to propose concrete remedies. Recommended preprocessing includes skull stripping to remove non-brain tissue, bias field correction to address intensity inhomogeneity, and denoising filters (e.g., non-local means, anisotropic diffusion) to reduce random noise without losing detail. Furthermore, artifact-aware data augmentation (motion blur, variable intensity, synthetic noise) is suggested to increase robustness. These additions clarify actionable strategies for improving classification reliability. Importantly, class weighting already reduced both false positives (tumor predicted in no-tumor scans) and false negatives, a desirable property in diagnostic contexts, but combining weighting with preprocessing and augmentation is expected to yield further gains.

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4.5. Why polynomial SVM with class weights excels

Although the grid search initially suggested the RBF kernel as optimal, its performance proved less stable on the independent test set, particularly with lower recall for gliomas. In contrast, the polynomial kernel achieved more consistent results. One plausible explanation is that the RBF kernel's γ parameter controls the radius of influence of support vectors: if γ is too large, the decision boundary may become overly complex and prone to over-fitting [37]. Meanwhile, the polynomial kernel offers a non-linear mapping that may better capture structured feature interactions without the same degree of sensitivity to γ fluctuations [38].

Two factors underlie the observed superiority. First, the polynomial kernel of degree three or four effectively captured the non-linear mapping between HOG features and tumor classes. This enabled richer decision boundaries than linear separation while avoiding the over-complexity of RBF, yielding decision surfaces better aligned with tumor-related gradient structures. Second, the class-weighting scheme, derived from `compute_class_weight("balanced")` with minimal (<10%) fixed adjustments, ameliorated class imbalance, particularly improving recall for glioma and no-tumor categories without a substantial loss of precision. This adjustment is clinically important, as false negatives are more critical than false positives in tumor diagnosis.

5. Conclusion

This study proposed a lightweight approach for brain tumor classification using HOG features with a class-weighted polynomial SVM. Despite the small dataset and four-class complexity, the method achieved robust performance: 91.8% accuracy with 95% CI (90.5-93.2), and statistically significant improvements in F1 compared to baseline models ($p < 0.01$). These results confirm that carefully tuned classical methods can remain competitive with deep learning under limited data.

The choice of polynomial SVM over RBF was supported by both empirical and theoretical evidence: the polynomial kernel provided more stable generalization, balanced class performance, and reduced sensitivity to parameter scaling in high-dimensional, noisy data. Class imbalance handling was equally crucial, custom class weights significantly improved sensitivity to minority tumor classes, a strategy broadly applicable to medical AI tasks where minimizing false negatives is essential.

Beyond accuracy, the approach offers clinical relevance. Its transparency, low computational cost, and potential integration into decision support systems or PACS environments make it suitable for real-world workflows, where interpretability and speed are valued. Visualization of feature contributions could further strengthen clinician trust.

For future work, several experimental directions are proposed: (i) direct comparison of the HOG+SVM pipeline with a lightweight CNN on the same dataset to evaluate accuracy, efficiency trade-offs, (ii) hybrid models combining CNN deep features with handcrafted descriptors (HOG or LBP) followed by SVM classification, and (iii) transfer learning with pretrained architectures (e.g., VGG16, ResNet) under limited-data settings. Further extensions include exploring ensemble models, applying the approach to full-scan tumor detection with region proposals, and integrating explainability tools (e.g., weighted HOG visualizations or LIME) to improve clinical interpretability.

6. Declarations

6.1. Author Contributions

Conceptualization: B.W., H.F., and P.K.; Methodology: B.W., H.F.; Software: B.W., H.F.; Validation: B.W., H.F., and P.K.; Formal Analysis: B.W., H.F., and P.K.; Investigation: B.W.; Resources: H.F.; Data Curation: H.F.; Writing, Original Draft Preparation: B.W., H.F., and A.R.H.; Writing, Review, and Editing: H.F., B.W., and A.R.H.; Visualization: B.W., H.F.; Supervision: B.W., P.K., and A.R.H.; All authors have read and agreed to the published version of the manuscript.

6.2. Data Availability Statement

The authors acknowledge Bhuvaji et al. [14] for the anonymized, publicly available Brain Tumor MRI dataset (Kaggle).

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6.4. Institutional Review Board Statement

Not applicable.

6.5. Informed Consent Statement

Not applicable.

6.6. Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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