

## Clustering-Based Analysis of Meibomian Gland Morphology for Automated Assessment of Meibomian Gland Dysfunction Using the MGD-1k Dataset

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### ABSTRACT

**Purpose:** To develop a clustering-based framework for automated categorization of Meibomian gland morphology, addressing subjectivity in Meibomian Gland Dysfunction (MGD) diagnosis.

**Methods:** The MGD-1k dataset of 1,000 infrared meibography images was analyzed using k-means clustering to classify gland areas into three groups: low (Cluster 1), medium (Cluster 2), and high (Cluster 3). Pixel-based segmentation determined white pixel counts as a surrogate for gland area. Statistical validation, including ANOVA, was performed, and results were visualized with scatter plots, bar charts, and box plots.

**Results:** Clustering identified 417, 358, and 225 images in Clusters 1, 2, and 3, comprising 41.7%, 35.8%, and 22.5% of the dataset, respectively. Mean pixel counts were 39,123.99 (SD = 4,213.89), 23,960.30 (SD = 5,930.49), and 54,413.95 (SD = 6,378.15). ANOVA confirmed significant inter-cluster differences ( $p < 0.0001$ ).

**Conclusions:** This framework objectively quantifies gland morphology, enabling severity stratification. The approach offers scalable diagnostic support and could be integrated with clinical tools or AI models. Future validation on diverse datasets is needed to confirm its broader applicability.

**Keywords:** Meibomian gland dysfunction, clustering analysis, MGD-1k dataset, k-means clustering

### 1. INTRODUCTION

Meibomian gland dysfunction (MGD) is one of the leading causes of evaporative dry eye disease, significantly affecting the quality of life of millions globally (1–3). Characterized by the obstruction or abnormal functioning of the meibomian glands, MGD often results in reduced lipid secretion and compromised tear film stability (4,5). Despite its prevalence and clinical impact, the evaluation of MGD remains largely subjective, relying on manual interpretation of meibography images, which can introduce variability and limit diagnostic precision (6).

The advent of advanced imaging modalities, such as the LipiView II Ocular Surface Interferometer, has provided clinicians with high-resolution meibography images (7–11). However, the manual grading and interpretation of these images, using methods like meiboscore assessment, can be labor intensive and prone to inter-observer variability (12,13). Although recent strides in artificial intelligence (AI) and machine learning (ML) have shown promise in automating ocular diagnostics, their application to MGD analysis is still in its infancy (14–17). Current methods often lack the ability to robustly quantify gland morphology, categorize severity, or detect subtle morphological patterns indicative of disease progression.

To address this gap, our study leverages the MGD-1k dataset, a comprehensive collection of expertly annotated meibography images, to develop a clustering-based framework for the automated categorization of meibomian gland areas (17). By using k-means clustering on pixel-based segmentation data, we aimed to identify meaningful morphological patterns and stratify patients into clinically relevant severity groups (18–20). The purpose of this study was twofold: first, to establish a reproducible and scalable method for assessing gland morphology, and second, to provide a foundation for integrating clustering results with clinical decision-making tools.

Our findings highlight the potential of quantitative approaches in enhancing diagnostic accuracy and facilitating personalized management of MGD. This study not only underscores the feasibility of clustering analysis in ocular diagnostics but also paves the way for future integration with AI-driven predictive models, bridging the gap between manual evaluation and automated analysis.

## 2. METHODS

### 2.1 Dataset and Demographics

We utilized the publicly available MGD-1k Dataset, a curated collection of 1,000 infrared images of meibomian glands captured using the LipiView II Ocular Surface Interferometer (21). The dataset includes 467 upper eyelid and 533 lower eyelid images, annotated for gland structure and dysfunction severity (meiboscore) by professional ophthalmologists and experts in meibomian gland dysfunction (MGD). The dataset comprises images from 320 patients, with a male-to-female ratio of 322 (32.2%) to 678 (67.8%). The mean ages of male and female participants were 51 years (SD = 19) and 55 years (SD = 19), respectively. Data collection spanned from April 2019 to April 2020.

Out of the 1,000 images, 941 images were deemed gradable across six rounds of expert validation, ensuring consistency in meiboscore grading. The remaining 59 images, marked ungradable in at least one round, were excluded from the analysis.

### 2.2 Image Preprocessing

Each image in the dataset was grayscale, with corresponding annotated binary masks delineating the regions of interest: the meibomian glands and eyelid regions. Images and masks were processed to count the number of white pixels in the gland mask, representing the visible meibomian gland area. This pixel count was used as a surrogate metric for gland coverage.

### 2.3 Clustering Analysis

Pixel counts were extracted from the gland masks of all gradable images. Using k-means clustering, the images were grouped into three clusters based on pixel count:

Cluster 1: Low gland area (atrophic glands or severe dropout).

Cluster 2: Medium gland area (moderate dropout or borderline function).

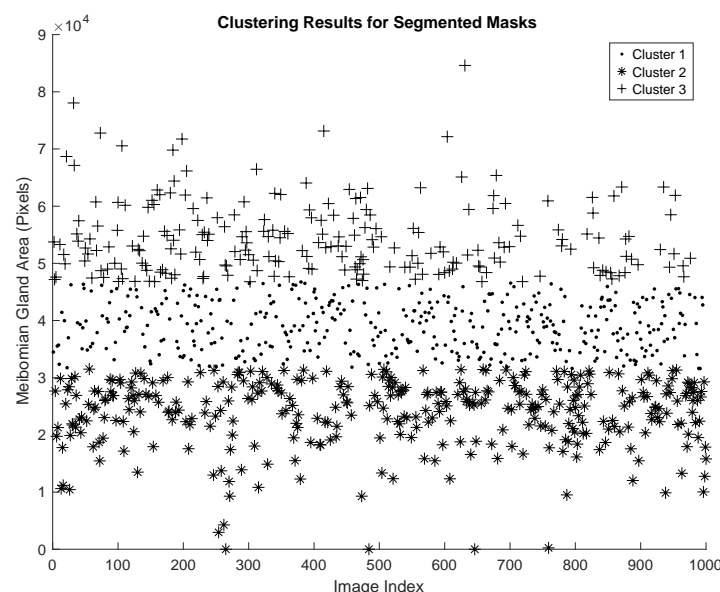
Cluster 3: High gland area (normal or near-normal glands).

The optimal number of clusters ( $k = 3$ ) was determined empirically by inspecting the data distribution and cluster validity metrics. For clustering, pixel counts were normalized to avoid potential scaling issues. MATLAB's built-in k means function was used for the analysis.

### 2.4 Validation

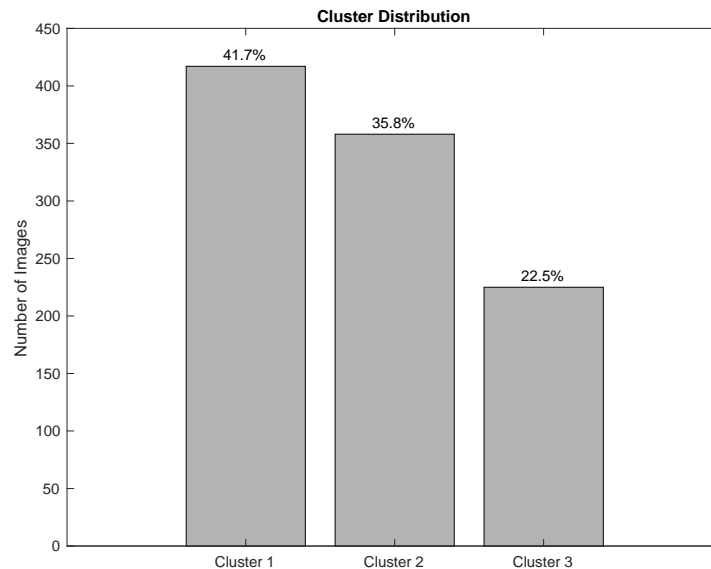
To ensure consistency, 10% of the images were randomly selected and manually reviewed to verify the clustering results. Additionally, comparisons were made between clustering outputs and expert-assigned meiboscores to assess concordance.

## 3. RESULTS



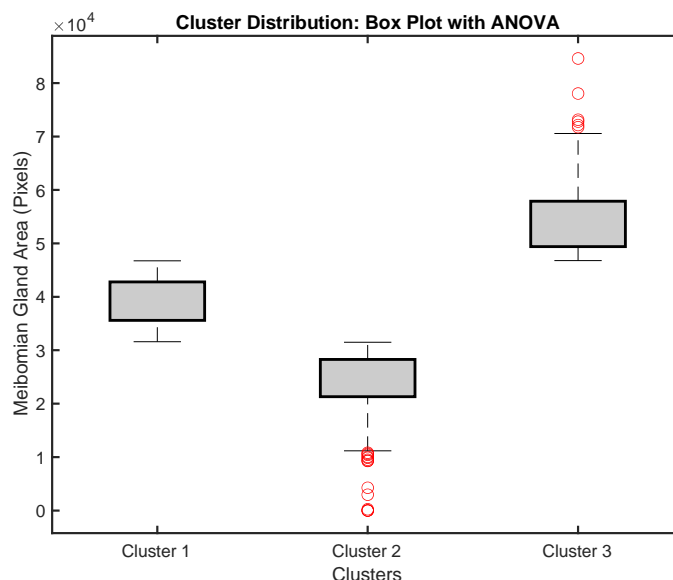
**Figure 1. Clustering results for segmented masks. The scatter plot illustrates the distribution of Meibomian Gland Area (pixels) across 1,000 images, divided into three distinct clusters based on pixel count. Each cluster is represented by a unique marker: circles for Cluster 1, asterisks for Cluster 2, and plus signs for Cluster 3.**

The clustering analysis of Meibomian gland areas using the k-means algorithm revealed three distinct groups based on pixel counts. As shown in Figure 1, each cluster is represented by unique markers, with clear boundaries separating the groups.



**Figure 2. Cluster Distribution. The bar chart represents the number and percentage distribution of images across three clusters.**

The analysis identified 417 images in Cluster 1, 358 images in Cluster 2, and 225 images in Cluster 3, corresponding to 41.7%, 35.8%, and 22.5% of the total dataset, respectively (Figure 2).



**Figure 3. Box Plot with ANOVA. The box plot displays the distribution of Meibomian Gland area (pixels) across the three clusters. Each box represents the interquartile range (IQR) with the median indicated by the central line, while the whiskers extend to 1.5 times the IQR. Red circles denote outliers.**

The centroid pixel counts for these clusters were located at  $3.91 \times 10^4$ ,  $2.40 \times 10^4$ , and  $5.44 \times 10^4$ , indicating significant variability in Meibomian gland morphology. The distribution of pixel counts within each cluster is summarized in the box plot (Figure 3), which highlights the spread of data and statistical differences between clusters. The mean pixel counts for Clusters 1, 2, and 3 were 39,123.99 (SD = 4,213.89), 23,960.30 (SD = 5,930.49), and 54,413.95 (SD = 6,378.15), respectively. A one-way ANOVA confirmed that the differences between the clusters were statistically significant ( $p < 0.0001$ ), emphasizing the robustness of the clustering process.

#### 4. DISCUSSION

This study demonstrates the utility of clustering analysis in categorizing Meibomian gland areas, paving the way for automated tools in ocular diagnostics. The clustering results, visualized in Figure 1, offer a clear delineation of gland morphological patterns, which can be directly correlated with varying severities of Meibomian Gland Dysfunction (MGD). The consistent distribution of images across clusters, as depicted in Figure 2, reinforces the reliability of this approach for large datasets.

The significant statistical differences observed between clusters, as shown in the box plot (Figure 3), underscore the validity of pixel-based segmentation as a meaningful metric for Meibomian gland assessment. This method not only quantifies gland areas but also highlights the morphological variability that might be linked to different stages or subtypes of MGD.

From a clinical perspective, the clustering framework provides several potential applications. First, it offers a data-driven approach to stratify patients into severity groups, enabling more personalized management of MGD. For instance, patients in clusters with lower mean pixel counts (e.g., Cluster 2) may represent more severe gland loss and could benefit from earlier or more aggressive intervention. Second, the visualization of clustered data, such as in Figure 2, allows clinicians to monitor changes over time and evaluate the efficacy of treatments.

Looking ahead, the integration of clustering methods with additional clinical variables, such as tear break-up time or Schirmer test results, could further enhance diagnostic accuracy. Furthermore, combining this approach with deep learning algorithms has the potential to provide real-time insights, supporting clinicians in decision-making processes.

By leveraging clustering and statistical analyses, this study underscores the potential of quantitative methods in improving diagnostic precision and advancing the understanding of MGD. Future work should focus on validating these findings across larger and more diverse datasets, as well as exploring their applicability to other ocular conditions.

#### 5. CONCLUSIONS

This study highlights the potential of clustering-based analysis in quantifying gland morphology and stratifying patients by MGD severity. The proposed methodology provides an objective, scalable approach for MGD diagnostics, facilitating personalized management and treatment monitoring. The integration of clustering results with clinical parameters or AI-driven predictive models could enhance diagnostic accuracy and real-time decision-making in clinical practice. Future research should explore the validation of this approach across larger, more diverse datasets and its application to other ocular conditions.

#### *Conflict of Interest Statement*

The authors declare that there is no conflict of interest regarding the publication of this article.

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#### *Ethics Statement*

This study utilized publicly available, anonymized data from the MGD-1k dataset, and no ethical approval was required.

#### *Data Availability Statement*

The dataset used in this study, the MGD-1k dataset, is publicly available and can be accessed as described in the original publication:

Saha, R. K., Chowdhury, A. M. M., Na, K.-S., Hwang, G. D., Jeon, H.-G., Hwang, H. S., & Chung, E. (2022). Automated quantification of meibomian gland dropout in infrared meibography using deep learning. *The Ocular Surface*, 26, 283–294. (4,5)

### Author Contributions

All authors contributed to the conception and design of the study, data analysis, interpretation, manuscript drafting, and revision. All authors approved the final manuscript and are accountable for the accuracy and integrity of the work.

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