

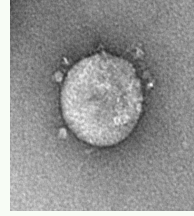
# Team BCE1: Computer Vision Techniques for the Segmentation and Morphological Analysis of Electron Microscopy Images of the Mouse Hepatitis Virus

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## Problem Definition

- Coronaviruses, like Mouse Hepatitis Virus (MHV) and SARS-CoV-2, appear roughly spherical in electron microscope (EM) images and are characterized by numerous spike proteins on their surfaces.
- Variant differences in shape, size, and spike protein density influence infectivity.
- Establish a ground truth mask for each image through manual segmentation.
- Design a pipeline for the automated segmentation of MHV particles.
- Develop a classification model to distinguish between mutant and wild type MHV particles.
- Obtain crucial morphological analysis of the two variant classes using the ground truth.



Wild Type MHV Particle

## Design Calculations and Analysis

Negative stain EM image mouse coronavirus

Initial automatic segmentation using SAM\*

Morphological Analysis and Comparison

Computer Vision System to Automatically Segment Virus Particles

Computer Vision System to Automatically Classify Virus Particles

Trained a ResNet18 CNN on segmentation masks to classify particles as wild type or mutant.

Developed a deep learning pipeline using U-Net to train on paired raw and masked images.

Less curves show strong model fit with stable validation loss, indicating good generalization without overfitting in classification and segmentation tasks.

U-Net shows stable training and strong validation, confirming the pipeline's ability to analyze viral morphology at scale with reduced manual input.

## Classification Results

| True Label \ Predicted Label | Wild Type | Mutant |
|------------------------------|-----------|--------|
| Wild Type                    | 77        | 19     |
| Mutant                       | 16        | 62     |

Confusion Matrix of ResNet18 Classifier Performance (n = 174)

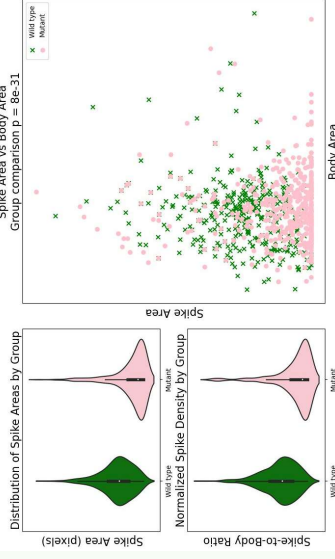
| ResNet18 Classifier Performance Summary |           |         |          |          |
|-----------------------------------------|-----------|---------|----------|----------|
| Class                                   | Precision | Recall  | F1 Score |          |
| Mutant                                  | 0.8260    | 0.8021  | 0.8148   |          |
| Wild type                               | 0.7564    | 0.7549  | 0.7759   |          |
| Accuracy                                |           |         |          | 0.7989   |
| Summary Metrics                         |           |         |          |          |
| Accuracy                                | 0.79851   | 0.79828 | 0.79851  | 0.798152 |

- The classification model achieved an overall accuracy of **79.9%** on the test set in distinguishing mutant vs. wild type particles.

- Misclassifications were slightly more frequent in the mutant  $\rightarrow$  wild type direction (19 cases) than wild type  $\rightarrow$  mutant (16 cases).

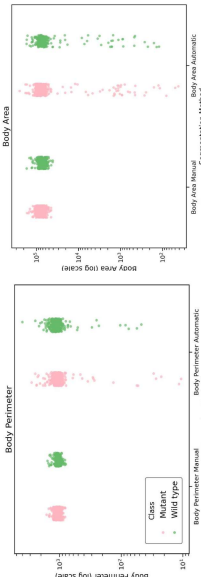
## Final Design

- Morphological analysis of spike and body areas by variant group showed statistically significant differences.



## Comparison of Manual and Automated Segmentation on Morphological Metrics

- Spike and body areas were calculated by counting the number of pixels in each segmented region.
- Grayscale masks were used, with spikes labeled as intensity 200 and bodies as 150.
- Each image was processed using Python's skimage.measure.regionprops to extract region properties.
- Total area was defined as the sum of pixels in each labeled region.
- These pixel counts correspond directly to the segmented morphological structures.



- Automated segmentation closely matched manual measurements of spike area, body area, and perimeter, with minor differences due to manual variability and contour smoothing.
- Clear morphological differences between mutant and wild type variants were preserved, supporting the use of automated methods for consistent, scalable analysis.

## Test Results

- The dataset of 869 labeled EM images was split into 521 training, 174 validation, and 174 testing images (60/20/20 split).
- The U-Net model achieved 85.1% accuracy on test images, confirming valid automatic segmentation.
- The ResNet18 classifier achieved 79.9% accuracy on segmented images, detecting meaningful morphological differences.
- Spike and body area metrics revealed consistent structural differences between wild type and mutant variants.
- Automated segmentation provides a scalable, objective alternative to manual annotation.
- These tools support future work in predicting infectivity and variant classification from viral morphology.

## Ethics



## Acknowledgements

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## References

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