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Characterization of Cough Mouth Opening for Accurate CFD Boundary Conditions

Zichen Fan*, Amin Hadizade, Christopher T. DeGroot, Eric Savory

Department of Mechanical and Materials Engineering, University of Western Ontario, London, Canada
*zfan68@uwo.ca

***Abstract*—**Airborne diseases have been a critical topic of study for decades, particularly following the COVID-19 global pandemic. Coughing plays an important role in the transmission of airborne diseases, serving both as a common respiratory activity and as a symptom of such diseases. Computational Fluid Dynamics (CFD) simulations have been widely employed to investigate the dynamics of cough airflow. Since the velocity of a single cough is time-dependent, accurately modeling its boundary conditions is essential. Previous experimental studies have primarily focused on volume flow rate data, often assuming a constant mouth opening area to calculate flow velocity, which can lead to unrealistic results. Given the variability of coughs, a representative model is necessary to define boundary conditions in CFD simulations of coughs. In this study, this model was developed by averaging data from individual cough events. To achieve this, a mathematical model was created to characterize the mouth opening of human cough. High-speed imaging and image processing techniques were utilized to capture the dynamics of mouth opening during coughing. Regression analysis employed an exponential distribution function, showing a time series relationship for the mouth opening area throughout a single cough. Preliminary results demonstrate that the characteristic velocity profile generated by the model aligns more closely with experimental cough velocity data compared to the velocity profile produced by a volume flow rate model with a constant mouth opening assumption.

***Keywords-component*—Computational Fluid Dynamics(CFD), Cough, Mouth opening area, Boundary condition**

I. INTRODUCTION

As of May 2, 2023, the global number of COVID-19 deaths reached 6,886,733 [1]. The emergence of COVID-19 in 2019 once again highlighted the critical importance of studying airborne diseases. Airborne diseases are defined as illnesses that can spread when individuals with certain infections cough, sneeze, or talk, releasing nasal and throat secretions into the air [2]. Pathogens can travel with these airflows and infect others. Among the several modes of transmission, coughing is common and significant for understanding and analysis. This is not only because coughing is a symptom of airborne diseases but also due to its effectiveness in spreading infectious agents [3].

The experimental study of cough airflow dynamics depends on methods such as schlieren and shadowgraph techniques, as well as particle image velocimetry (PIV). Although these experimental methods are highly accurate and precise, they have challenges, such as high cost, time-consuming procedures, a difficulty acquiring the subjects [4]. In contrast, computational methods, particularly Computational Fluid Dynamics (CFD) simulations, offer a cost-effective and accessible alternative to predict biological airflow dynamics [5].

For CFD simulations, the accuracy of boundary conditions is critical to achieving realistic results. Since the velocity of a single cough is inherently time-dependent, accurate transient boundary condition modelling is essential. Previous experimental studies have focused mainly on time-dependent volume flow rate data or experimental cough flow velocity data [6], [7]. However, these studies often assume a constant mouth opening area, which can negatively impact simulation accuracy.

To address this limitation, the present study develops a mathematical model to characterize the dynamics of human mouth opening area during a single cough. Using high-speed imaging and artificial-intelligence-assisted image processing techniques, the study captures time-dependent data on mouth opening during coughing. Preliminary results indicate that the characteristic velocity profile generated by the model aligns closely with experimental cough velocity data.

II. METHODOLOGY

A. Experimental Setup

An experimental study was conducted to capture the mouth opening dynamics during a single cough. The schematic of the experimental setup is shown in Fig. 1. A Basler acA1440-220 um camera was mounted on a tripod and positioned facing the volunteer to record a sequence of frames capturing mouth movements during coughing. The camera was connected to

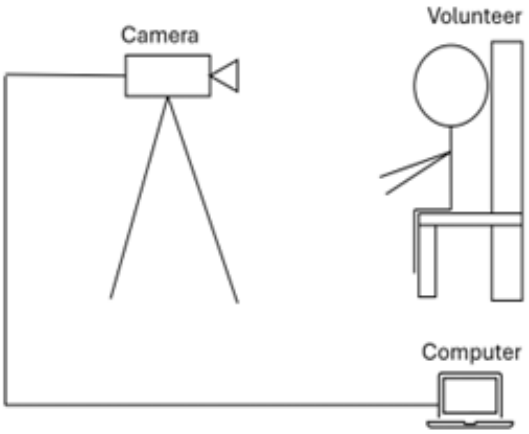

Figure. 1. Setup schematic

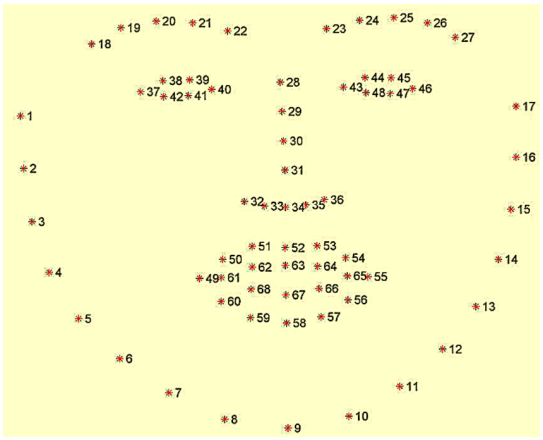

Figure. 2. 68 points facial landmarks adapted from [10]

Figure. 3. Output image before cough

a computer, which served as the data acquisition system and controlled the frame rate. The frame rate was managed using Pylon software, developed by the same manufacturer, and was set to 40 frames per second for this experiment. The camera was placed at an approximate distance of 1 m from the volunteer to ensure clear capture of all facial characteristics. A 24-year-old, healthy, male volunteer was selected to participate this experiment.

B. Experimental Procedures

The volunteer was first instructed to sit on a chair in the laboratory and face the camera. To ensure consistency in data collection, the volunteer was also asked to minimize head movement during the cough. Once the volunteer was ready, the researcher activated the camera to begin recording and signaled the volunteer to initiate the cough. The camera was programmed to capture 120 frames over a duration of 3 seconds, significantly longer than the average cough duration of 564 ms [8], to ensure that the entire cough event was recorded before the recording finished. The volunteer remained seated until all frames were successfully saved. Six coughs were captured in this study.

III. IMAGE PROCESSING AND DATA ANALYSIS

A. Image Processing

The raw data were captured by a 40fps camera and saved as TIFF files on the computer for analysis. The sequence of images was recorded in gray scale to enhance facial feature detection. In order to detect the face and extract the mouth opening from images, A Python program was developed using the `dlib` library, a C++ toolkit for machine learning algorithms, to calculate the pixel area of the mouth [9]. More specifically, `dlib` library used the Histogram of Oriented Gradients (HOG) to detect the face. After the face was detected, a pre-trained model was applied to extract the facial landmarks, which returned the coordinates of 68 points that maped the facial characteristics, as shown in Fig. 2 [10]. The model was based on an emsemble regression tree and pre-trained using the HELEN dataset [11], [12]. The mouth area was returned by calculating the area within 12 points from point 49 to point 60 in Fig. 2.

Examples of a processed frame before a cough and a processed frame during a cough can be found in Fig. 3 and Fig. 4. Since the program only detected the outer edges of the mouth, the mouth opening area was determined by calculating the increment in pixel area from the start of the cough event. The starting frame of the cough event was manually defined by inspecting the frame sequence to identify the key frame where mouth movement begins.

Since the analysis is based on two-dimensional images, only the pixel area could be directly measured. Therefore, a pixel-to-centimetre calibration was performed for each cough sequence to obtain a realistic mouth opening area. The first frame of each sequence was extracted for calibration, where two points were manually selected on the image, and the corresponding real-world distance in centimetres was assigned. This process established the pixel-to-centimetre ratio for conversion. The real mouth opening area was then calculated using:

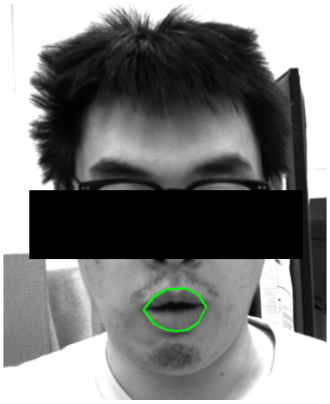

Figure. 4. Output image during cough

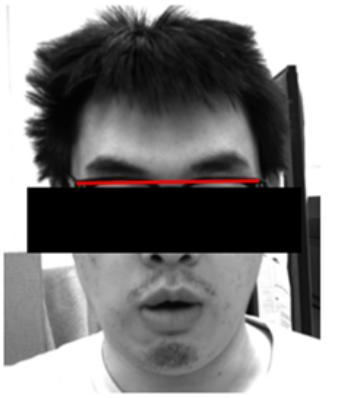

Figure. 5. Reference length(red line)

$$A_{\text{real}} = A_{\text{pixel}} \times \left(\frac{d_{\text{cm}}}{d_{\text{pixel}}} \right)^2 \tag{1}$$

where:

- A_{real} is the real mouth opening area in cm^2.
- A_{pixel} is the detected mouth opening area in pixels.
- d_{cm} is the real-world calibration distance in cm^2.
- d_{pixel} is the measured pixel distance.

In this study, the reference length was set to the length of the upper edge of the volunteer's glasses, which is represented by the red line in Fig. 5.

B. Data Analysis

To avoid random noise effects in the mouth area measurement and track the trend of the mouth opening during a cough, the simple moving average (SMA) technique was introduced to the data analysis. Equations (2) and (3) show the formula used for computing the moving average of the time-series data [13]:

$$\text{SMA} = \frac{P_M + P_{M-1} + \cdots + P_{M-(n-1)}}{n} \tag{2}$$

$$\text{SMA}_{\text{Next}} = \frac{P_M}{n} + \text{SMA}_{\text{Prev}} - \frac{P_{M-n}}{n} \tag{3}$$

where:

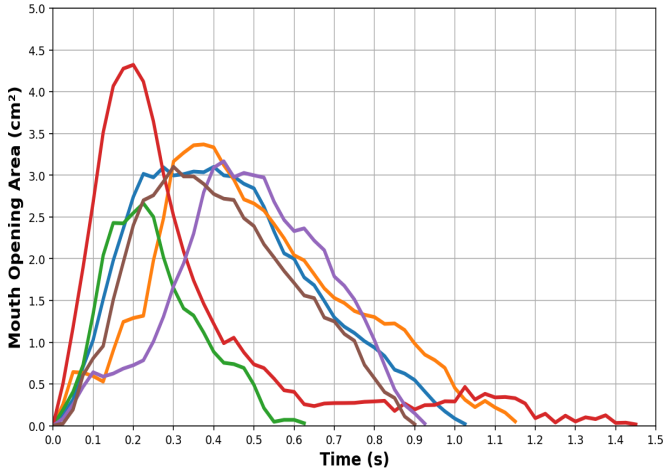

Figure. 6. Mouth opening area data form 6 cough events

- P_M is the data point value at time M.
- n is the window size.

In this study, the window size is chosen as $n = 7$ to smooth the raw output data and ensure that all characteristics of the mouth opening trend are properly analyzed after testing other values for n.

IV. RESULTS AND DISCUSSIONS

A. Results

TABLE. I
VARIATIONS OF COUGH MOUTH OPENING CHARACTERISTICS

Variations	Range	Average	Standard Deviation
CPMOA (cm^2)	2.66 – 4.32	3.29	0.51
PMOT (s)	0.20 – 0.42	0.32	0.09

Total six single cough event mouth opening data are analyzed in this study and will be discussed in this section. There are two important metrics: cough peak mouth opening area (CPMOA) and peak mouth opening time (PMOT), summarized in TABLE I. The cough peak mouth opening areas have a range from 2.66 cm^2 to 4.32 cm^2 with an average area of 3.29 cm^2 (0.51 SD). For the peak mouth opening time, the value varies from 0.2 s to 0.42 s, which have an average time at 0.32 s with 0.09 SD. Fig. 6 illustrates the transient mouth opening for all six single cough events recorded in this study.

B. Normalization of the Data

It shows that the variations among the individual cough can be highly diverse, with the maximum PMOT being twice as much as the minimum one. To better describe the characteristics of cough mouth opening, normalization analysis was performed. The mouth opening area was normalized by the CPMOA, and the time was normalized by the PMOT, as shown in Equations (4) and (5):

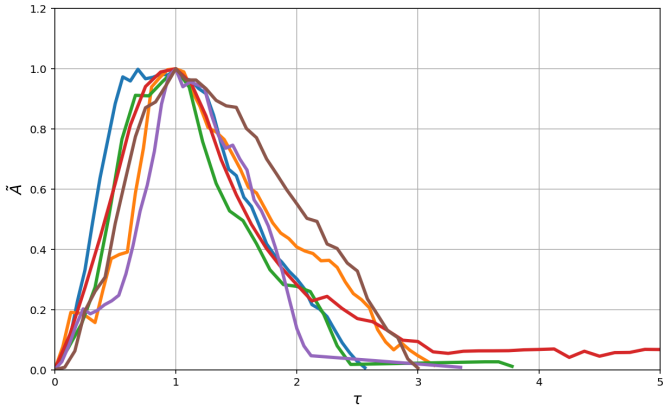

Figure. 7. Normalized mouth opening area from 6 cough events

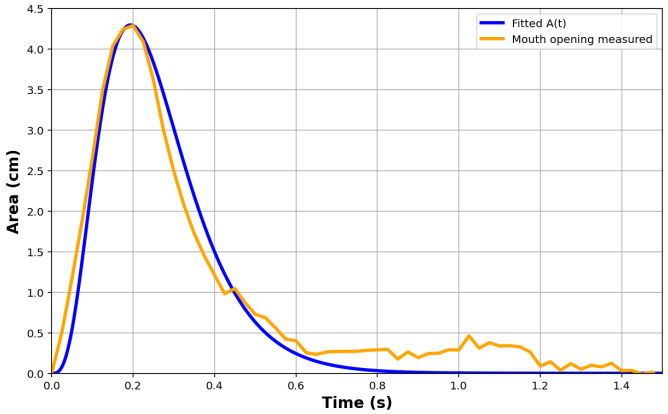

Figure. 8. Comparison between the mouth opening area calculated from (6) and a single cough mouth opening measurement

$$\tilde{A} = \frac{A}{\text{CPMOA}} \tag{4}$$

$$\tau = \frac{t}{\text{PMOT}} \tag{5}$$

where:

- A is mouth opening area in cm^2.
- t is time in second.

The data in Fig. 7 are the same as in Fig. 6, but in a normalized form. After normalization and re-arrangement, it can be observed that before the normalized time of 1, all curves are similar. After this point, there are some variations, but the overall trend remains consistent across all curves.

C. Curve Fitting Analysis

In Fig. 7, it can be seen that the overall normalized mouth opening area dynamic with time is close to the exponential distribution function. A modified exponential distribution was obtained to characterize the mouth opening area over time, as in Equation (6):

$$\tilde{A} = C \cdot e^{-a\tau} \cdot (1 - e^{-\tau})^{b-1} \tag{6}$$

where:

$$C = \frac{1}{e^{-a} \cdot (1 - e^{-1})^{b-1}}$$
$$a = 2.17$$
$$b = 4.57$$

To acquire the two parameters a and b, a non-linear curve fitting analysis was performed in Python using the `scipy` library to obtain the optimum parameter values, based on the normalized data of 6 cough events. Considering the normalization process discussed before, the fitting curve should pass through the point $(1, 1)$, which indicates that the maximum mouth opening area is associated with the peak mouth opening time. To represent this fact, the parameter C was introduced to constrain the fitting curve.

The black dash line in Fig. 7 illustrates the fitting curve. It shows that the fitting curve effectively captures the overall characteristics of all six recorded cough events and demonstrates a good fit.

Moreover, a comparison was made between the fitted mouth opening profile and the measurement data, which is shown in Fig. 8. The fitted profile presents a good fit alongside the mouth opening area measurement. However, it is evident that the fitted profile does not align well when the mouth is about to close, which occurs after approximately 0.6 seconds. This may be due to the difference in the subject's head position before and after the cough, which resulted in the mouth resting area being larger at the time of closure compared to the mouth area at the time of opening.

D. Application of the Mouth Opening Model

In this section, the new mouth opening model is integrated into the existing cough volume flow rate model, and comparisons are made between the new method and experimental cough velocity data.

The experimental cough velocity data were extracted from [8], which presented a cough velocity time-series profile averaged over 30 cough events from both male and female subjects using PIV experiments. After rearrangement based on the maximum velocity, the comparison of results from the integrated model, the cough volume flow rate model, and experimental data is shown in Fig. 9. The red curve is calculated based on the characterized cough volume flow rate model with consideration of a constant mouth opening area in [6]. The blue curve represents the results from an integrated model that combines the cough volume flow rate with the mouth opening dynamics model according to Equation (7):

$$v = \frac{V}{A} \tag{7}$$

where:

- v is velocity.
- V is volume flow rate reproduced from [6].
- A is mouth opening area based on present study.

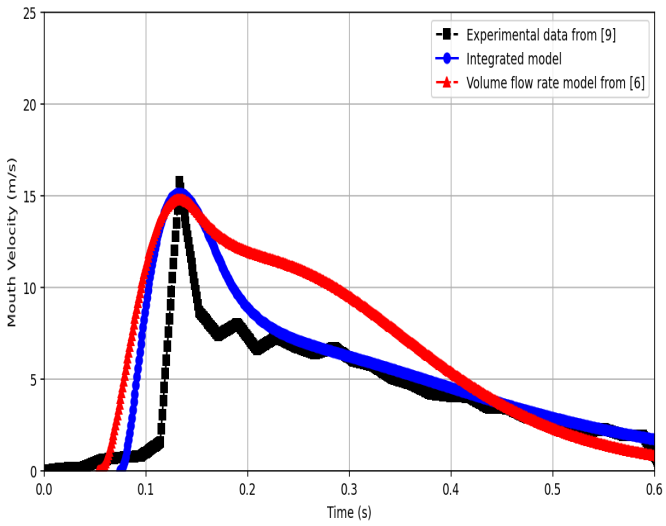

Figure. 9. Comparison among PIV results, volume flow rate model, and integrated model with present study

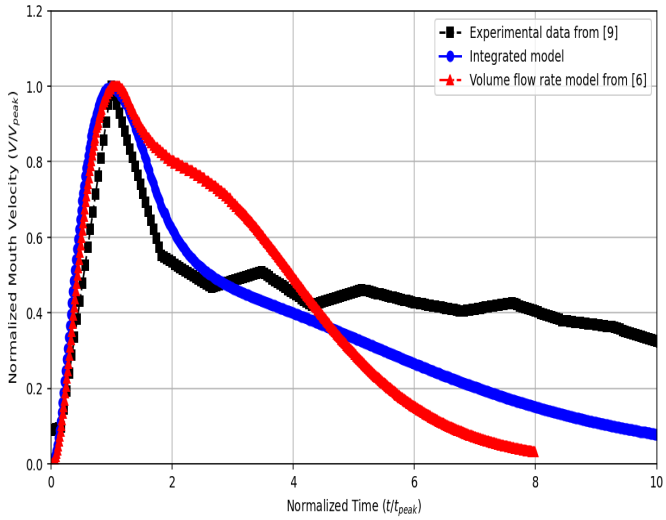

Figure. 10. Normalized cough velocity data from PIV results, volume flow rate model, and integrated model with present study

During the integration, it was assumed that the cough airflow begins 0.1 seconds after the mouth starts to open and lasts for 0.6 seconds. This assumption is based on observations reported in [6]. The black curve represents the results from PIV experiments [8]. It can be observed that the integrated model shows better agreement with the experimental data compared to the results obtained using a constant mouth opening, particularly after 0.2 seconds. This improvement is likely due to the dynamic mouth opening area in the model, which more accurately captures the mismatch between the peak cough flow rate time and the peak mouth opening time.

Fig. 10 indicates three cough velocity profiles in a dimensionless form. For the experimental data represented by the black curve, only the velocity data after 0.12 seconds were considered in Fig. 10, as the velocity remains nearly constant about 1 m/s before 0.12 seconds, as shown in Fig. 9, indicating that the cough had not started before this time. In the dimensionless form, the model with mouth opening dynamics performed even better in capturing a velocity jump before the dimensionless time of 2, compared to the model with a constant mouth opening that over-predicts the velocity between the dimensionless time of 2 and 4.

V. CONCLUSION AND FUTURE WORKS

This study utilized an exponentiated exponential distribution function to characterize human mouth opening area dynamics during a single cough event. An experiment was conducted using a high-speed camera and image processing to reveal the time-series mouth opening area data of six single coughs from a healthy male subject. Two inputs are required to calculate the mouth opening profile: cough peak mouth opening area and peak mouth opening time. By integrating the previous volume flow rate model, a new velocity profile was computed, providing a better representation of cough velocity, as validated by experimental cough velocity data.

Some potential improvements can be made to better characterize the cough velocity boundary condition:

1) A head-fixing device can be installed to hold the testing subject's head, limiting head movement during the cough to reduce measurement errors.
2) Additional volunteers can be included in the experiment to collect mouth opening area data from more diverse sources, such as different genders, ages, and heights.
3) A relationship between the two input variables (CPMOA and PMOT) and biological characteristics, such as mouth width and age, can be investigated to better estimate the cough boundary condition for individuals with unknown CPMOA and PMOT.

In the future, this new method for modelling the time-dependent velocity profile that could serve as a boundary condition for CFD simulations of a single cough event, giving more realistic results. Additionally, by combining it with passive particle dispersion—introduced through the Discrete Phase Model (DPM)—more realistic aerosol particle trajectories could be simulated.

REFERENCES

[1] J. Elflein, "Novel coronavirus (COVID-19) deaths by country worldwide 2023," Statista, Available: https://www-statista-com.translate.goog/statistics/1093256/novel-coronavirus-2019ncov-deaths-worldwide-by-country/(accessed Feb. 7, 2025).

[2] B. Ather, T. M. Mirza, and P. F. Edemekong, "Airborne precautions," StatPearls [Internet]. Available: https://www.ncbi.nlm.nih.gov/books/NBK531468/, (accessed Feb. 7, 2025).

[3] W. G. Lindsley et al., "Viable influenza A virus in airborne particles expelled during coughs versus exhalations," *Influenza and Other Respiratory Viruses*, vol. 10, no. 5, pp. 404–413, Apr. 2016. doi: 10.1111/irv.12390

[4] A. Hilgenstock and R. Ernst, "Analysis of installation effects by means of computational fluid dynamics—CFD vs experiments?," *Flow Measurement and Instrumentation*, vol. 7, no. 3–4, pp. 161–171, 1996. doi: 10.1016/s0955-5986(97)88066-1

[5] B. L. Smith, “The difference between traditional experiments and CFD Validation Benchmark Experiments,” *Nuclear Engineering and Design*, vol. 312, pp. 42–47, 2017. doi: 10.1016/j.nucengdes.2016.10.007

[6] J. K. Gupta, C.-H. Lin, and Q. Chen, “Flow dynamics and characterization of a cough,” *Indoor Air*, vol. 19, no. 6, pp. 517–525, 2009. doi: 10.1111/j.1600-0668.2009.00619.x

[7] W. Oh, R. Ooka, H. Kikumoto, and M. Han, “Numerical modeling of cough airflow: Establishment of spatial–temporal experimental dataset and CFD Simulation Method,” *Building and Environment*, vol. 207, 108531, 2022. doi: 10.1016/j.buildenv.2021.108531

[8] M. Han et al., “Measurements of exhaled airflow velocity through human coughs using particle image velocimetry,” *Building and Environment*, vol. 202, 108020, 2021. doi: 10.1016/j.buildenv.2021.108020

[9] “Dlib library,” http://dlib.net/, (accessed Feb. 7, 2025)

[10] G. Amato et al., ”A comparison of face verification with facial landmarks and deep Features,” in *Proc. 10th Int. Conf. Adv. Multimedia (MMEDIA)*, 2018.

[11] V. Kazemi and J. Sullivan, ”One millisecond face alignment with an ensemble of regression trees,” *2014 IEEE Conference on Computer Vision and Pattern Recognition*, Columbus, OH, USA, 2014, pp. 1867-1874, doi: 10.1109/CVPR.2014.241

[12] V. Le, J. Brandt, Z. Lin, L. Bourdev, and T. S. Huang, “Interactive facial feature localization,” *Lecture Notes in Computer Science*, pp. 679–692, 2012. doi:10.1007/978-3-642-33712-3_49

[13] S. Hansun, “A new approach of moving average method in time series analysis,” *2013 Conference on New Media Studies (CoNMedia)*, pp. 1–4, Nov. 2013, Universitas Multimedia Nusantara, Indonesia. doi: 10.1109/conmedia.2013.6708545