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Pulmonary response prediction through personalized basis functions in a virtual patient model

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ABSTRACT

Background and Objective: Recruitment maneuvers with subsequent positive-end-expiratory-pressure (PEEP) have proven effective in recruiting lung volume and preventing alveoli collapse. However, determining a safe, effective, and patient-specific PEEP is not standardized, and this more optimal PEEP level evolves with patient condition, requiring personalised monitoring and care approaches to maintain optimal ventilation settings.

Methods: This research examines 3 physiologically relevant basis function sets (exponential, parabolic, cumulative) to enable better prediction of elastance evolution for a virtual patient or digital twin model of MV lung mechanics, including novel elements to model and predict distension elastance. Prediction accuracy and robustness are validated against recruitment maneuver data from 18 volume-controlled ventilation (VCV) patients at 7 different baseline PEEP levels (0 to 12 cmH₂O) and 14 pressure-controlled ventilation (PCV) patients at 4 different baseline PEEP levels (6 to 12 cmH₂O), yielding 623 and 294 prediction cases, respectively. Predictions were made up to 12 cmH₂O of added PEEP ahead, covering 6 × 2 cmH₂O PEEP steps.

Results: The 3 basis function sets yield median absolute peak inspiratory pressure (PIP) prediction error of 1.63 cmH₂O for VCV patients, and median peak inspiratory volume (PIV) prediction error of 0.028 L for PCV patients. The exponential basis function set yields a better trade-off of overall performance across VCV and PCV prediction than parabolic and cumulative basis function sets from other studies. Comparing predicted and clinically measured distension prediction in VCV demonstrated consistent, robust high accuracy with $R^2 = 0.90-0.95$.

Conclusions: The results demonstrate recruitment mechanics are best captured by an exponential basis function across different mechanical ventilation modes, matching physiological expectations, and accurately capture, for the first time, distension mechanics to within 5–10 % accuracy. Enabling the risk of lung injury to be predicted before changing ventilator settings. The overall outcomes significantly extend and more fully validate this digital twin or virtual mechanical ventilation patient model.

1. Introduction

Protective mechanical ventilation (MV) strategies have improved intensive care unit (ICU) care by limiting tidal volumes and driving pressures [1–7]. Staircase recruitment maneuvers (RMs) followed with positive-end-expiratory-pressure (PEEP) is one common protective MV approach for acute respiratory distress syndrome (ARDS) and

respiratory failure patients to keep alveoli open and improve oxygenation [2,8–12]. However, insufficient, or excessive airway pressure or tidal volume can lead to ventilator induced lung injury (VILI), increasing morbidity and mortality [10,13–25]. Accurate, predictive, and patient-specific MV strategies could significantly advance care and minimise VILI [26–28].

Utilising an accurate predictive model of lung mechanics with a

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ventilated patient has significant potential in aiding clinical decisions. The predictive mechanics model would enable a safer setting of positive end expiratory pressure to minimise lung elastance and minimise the risk of over distention and ventilator induced lung injury [29]. More specifically, the elastance that is often referred to in lung mechanics is associated as that during inspiration. If the elastance is not at its optimal point, the alveolar are at risk of bursting or underinflating. In either case, oxygenation into the blood stream decreases. Optimal elastance correlates directly to the recruitable volume. If this value is set too low, the alveolar will not expand to their full potential, if set too high the alveolar are at risk of tissue damage due to overdistension. Another primary factor to be considered is selecting the optimal PEEP. This value changes the lung mechanics of a person under ventilation both by their value and shape of P-V loops. As this change is visibly different for each person, the use of prediction methods tailored to a person's lung mechanics has significant potential in aiding clinical decisions and preventing overdistension.

Currently, no effective standardised clinical method exists to determine optimal patient-specific PEEP, leading to uncertainty, variability, and increased risk [13,28,30–33]. Model-based methods are one way of personalising care [28]. While many models successfully capture lung dynamics [34–39], very few can accurately predict the pulmonary response over PEEP [26,40–42]. An accurate, predictive lung mechanics model, or virtual MV patient, would let clinicians test new MV settings without risk, enabling safer, more optimal, personalised care.

MV modes can be broadly classified as either volume-controlled ventilation (VCV) or pressure-controlled ventilation (PCV) [9,43,44]. VCV delivers a controlled flow to guarantee a targeted tidal volume but can lead to VILI if the resulting uncontrolled airway pressure is too high [45,46]. PCV sets a desired airway pressure profile and driving pressure, and the resulting tidal volume is an uncontrolled function of patient-specific lung mechanics [43,44,47]. To avoid overshoot in PCV an appropriate deceleration of input flow can be used [43,47,48]. Thus, the resulting tidal volume can be variable in PCV, increasing the risk of VILI [45,47–49].

Clinically, VCV sets peak inspiratory volume (PIV) to minimise risk of volutrauma. Similarly, PCV limits peak inspiratory pressure (PIP) to prevent barotrauma/overdistension [13,45,50]. However, no significant difference in clinical outcome between using a VCV approach or a PCV approach has been observed [43,47,49,51–53]. Hence, the choice of MV mode is primarily a function of patient synchrony and response to MV, and clinician preference [44,51].

Basis functions have been proposed as a method for targeted biomedical information simulation and prediction [26,41,42,54–64]. Well-defined, they offer additional, model-based insight into physiological mechanics and responses [26,41,59,65–69]. The ability of basis functions to model and predict lung elastance and resistance evolution was demonstrated using a linear single compartment lung model, but lacked accuracy in capturing some nonlinear lung mechanics, in both inspiration and expiration [26,55,56,66,70,71].

A nonlinear, physiologically-relevant hysteresis loop model (HLM) using basis functions accurately captured and predicted the evolution of lung mechanics as MV settings change for both VCV and PCV patients [42]. However, it did not assess if these basis functions were optimal compared to other choices. None of these approaches captured distension and its risk, which is critical to directly managing the risk of VILI.

This research extends this virtual MV patient model framework to include clinically critical, nonlinear lung distension mechanics, and assesses it across 3 basis function sets to compare performance in predicting lung mechanics in response to changes in PEEP. Performance trade-offs show which elements of these basis functions are necessary to guarantee accuracy and clinical relevance, and the inclusion of distension adds significant new clinical utility.

2. Methods

2.1. HLM lung mechanics model

The dynamic equation of motion for the HLM lung mechanics model is defined [42]:

$$M\dot{V}(t) + R\dot{V}(t) + K_e V(t) + K_{h1} V_{h1} + K_{h2} V_{h2} = f_V(t) + PEEP \quad (1)$$

Where M is the normalised mass, V is the volume of air delivered to the lungs, V_{h1} and V_{h2} are hysteretic volume response during inspiration and expiration, respectively, K_e represents the alveolar recruitment elastance (defined further in Section, Appendix A), named $k2$ in this approach to be predicted in the proposed basis functions, K_{h1} and K_{h2} , are determined by two nonlinear hysteretic springs for alveolar hysteresis elastance during inspiration and expiration, respectively. These are defined as:

$$K_{h1} = k1 - k2 \quad (2)$$

$$K_{h2} = k3 - k4 \quad (3)$$

where $k1$ - $k4$ can be identified from the constructed P-V loop using the HLA approach, as shown in the example of Fig. 1. For other parameters in Eq. (1), R is the airway resistance, PEEP is the positive end-expiratory pressure, and $f_V(t)$ is the steady-state input force. The detailed formulations for calculating each parameter can be found in Online Appendix A and Zhou et al. [42].

2.2. P-V loop identification

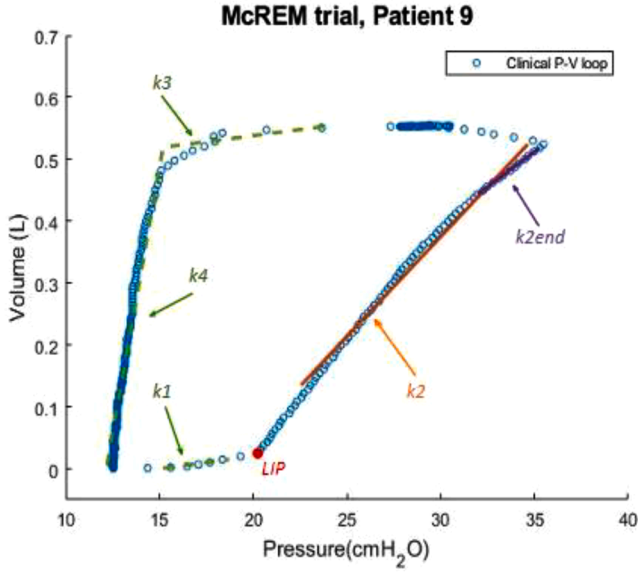
At any initial, baseline PEEP_{*i*} ($i = 1$) level, the hysteresis loop analysis method (HLA) is applied to identify elastance values for the whole breath. HLA separates the P-V loop for a breath into 5 segments, as shown in Fig. 1. For expiration, 2 segments are identified with two elastances, $k3$ and $k4$, respectively. For inspiration, the half cycle is first divided into 2 segments, with $k1$ and $k2$. Subsequently, the $k2$ segment is assessed using a statistical test to find any potentially, increased stiffness (reduced compliance) third segment, denoted $k2end$, arising from any distension. This last term, $k2end$, uses a separate basis function prediction procedure to capture possible over-distension as PEEP rises.

The lower inflection point is a critical piece defining where the analysis for $k2$ begins. It is also the point that is currently used to determine the minimal level of PEEP where alveolar recruitment begins. Examples are shown in Fig. 1 for VCV and PCV clinical PV loops constructed from McREM and Maastricht trial data, respectively.

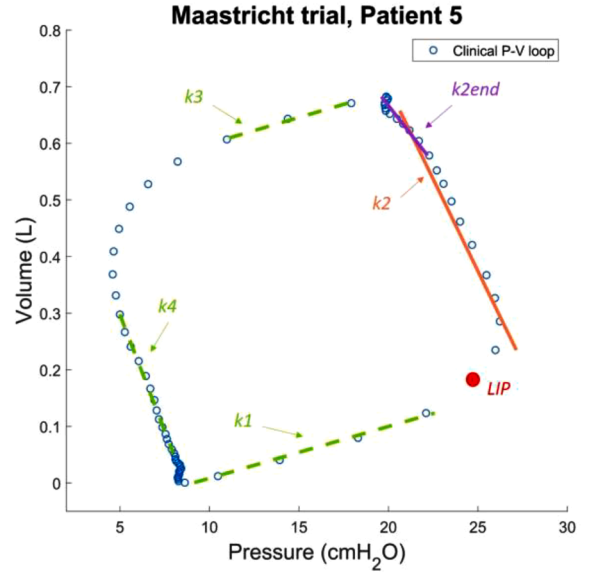
2.3. Basis function sets for elastance prediction

Using the same HLA identification procedure, three (3) physiologically relevant sets of basis function for predicting the evolution of recruitment elastance at higher PEEP levels ($k2_i, i > 1$) are examined as a function of the $k1$, $k2_1$, $k2end_1$, $k3$, $k4$ values identified using HLA from measured PV loop clinical data at a baseline PEEP ($i = 1$). Exponential (EXP) basis functions have been used in prior studies to estimate pulmonary elastance evolution [42,55,57], while basis parabolic (PARA) functions have also shown promise [26,41,63]. The third cumulative (CUMU) basis function set was developed and validated in prior work [64] and are also examined here with minor modification to suit the HLM model. The evolution and prediction of distension at higher PEEP levels ($k2end_i, i > 1$) is developed in prior work [72] and kept the same for all three basis function sets.

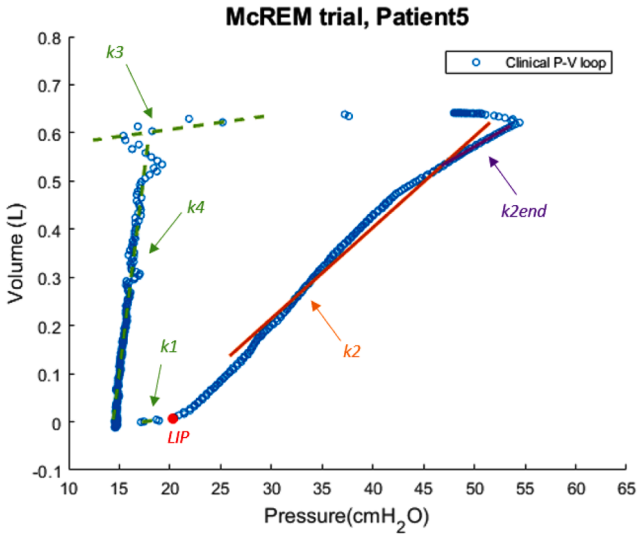
These three basis functions have been chosen as they include nonlinear recruitable response and linear distension response which are all physiologically relevant to the analysis of lung mechanics, specifically volume changes. There are a variety of other basis functions that are applicable for this analysis, however, these three represent some



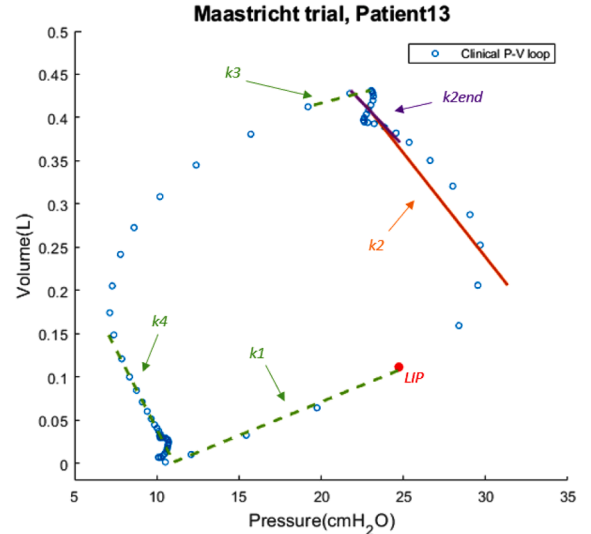
(a) the McREM trial (VCV mode) – typical distension



(b) the Maastricht trial (PCV mode) – typical distension



(c) the McREM trial (VCV mode) – extreme distension



(d) the Maastricht trial (PCV mode) – extreme distension

Fig. 1. Examples of HLA identification for measured clinical P-V loops, showing both typical distension and extreme distension cases. (a) the McREM VCV trial (typical distension), Patient 9 at PEEP = 12 cmH₂O and showing the lower inflection point (LIP); (b) the Maastricht PCV trial (typical distension), Patient 5 at PEEP = 8 cmH₂O, where k2end is negative sloped due to the adaptive tube compensation used in this PCV trial; (c) the McREM VCV trial (extreme distension), Patient 5 at PEEP = 14 cmH₂O and showing LIP; and (d) the Maastricht PCV trial (extreme distension), Patient 13 at PEEP = 10 cmH₂O.

clearly distinct and previously proven properties within this model framework.

2.3.1. Exponential basis function set – EXP

The exponential basis function set assumes elastance has a bowl shape across PEEP levels, and is the same as previously presented [42]:

$$k2_i = \left(\frac{PEEP_i}{k1} + \frac{k2_1}{k1} * e^{b \frac{PEEP_i}{k1}} \right) * k1 \quad (4)$$

$$b = \frac{k1}{PEEP_1} * \log \frac{k2_1 - PEEP_1}{k2_1} \quad (5)$$

Where b is the exponential rate of recruitment, all other terms are as

previously defined, and $PEEP_i$ is the predicted PEEP level.

2.3.2. Parabolic basis function set – PARA

The parabolic basis function set is derived from the proven functions in [26] with similar, but different overall shape as the EXP set, and re-derived in terms of $PEEP_i$ and the other baseline PEEP identified inputs for use in this analysis [63]:

$$k2_i = \left(\frac{PEEP_i}{k1 * \beta1} + \beta2 * \left(\beta1 - \frac{PEEP_i}{k1} \right)^2 \right) * k1 \quad (6)$$

$$\beta1 = 2 - \frac{\hat{k1}}{k1} \quad (7)$$

$$\beta 2 = \frac{\frac{k2_1}{k1} - \frac{PEEP_1}{k1 + \beta 1}}{\left(\beta 1 - \frac{PEEP_1}{k1}\right)^2} \quad (8)$$

Where all terms are previously defined or given here, and $PEEP_i$ is the prediction PEEP level. $\widehat{k1}$ is the average value of alveolar elastance for first inspiration segment, estimated with value 130 over both VCV and PCV datasets [42].

2.3.3. Cumulative basis function set – CUMU [64]

The cumulative basis function set models the evolution of elastance as continuously increasing at a combination of all the predicted PEEP levels, and is defined [63]:

$$k2_i = \left(\frac{\delta 1}{k1} * \sum_{j=2}^{j=i} \Phi_j + \delta 2 * PEEP_1 * \sum_{j=2}^{j=2} \Phi_j * \sum_{j=2}^{j=3} \Phi_j * \dots * \sum_{j=2}^{j=i} \Phi_j \right) * k1 \quad (9)$$

$$\delta 1 = \left(\frac{k2_1}{k1} - \frac{PEEP_1}{k1 - k2_1} \right) * k1 \quad (10)$$

$$\delta 2 = \frac{1}{k1 - k2_1} \quad (11)$$

$$\Phi_i = \begin{cases} (1 + PIP_{fiterror})^{-1} & , i = 2 \\ \vartheta_1 * (PEEP_i - PEEP_{i-1}) & , i > 2 \end{cases} \quad (12)$$

Where $\vartheta_1 = 0.0087$ and $PIP_{fiterror} = \frac{fitted\ PIP - clinical\ PIP}{clinical\ PIP}$ at baseline $PEEP_1$. The value assigned to ϑ_1 is derived using an optimization method by determining the local minima/maxima [73]. Since the highest PEEP level studied is lower than or equal to $PEEP_{max}=24$ cmH₂O, basing on prior work [64], the value of Φ_i when $PEEP_i > PEEP_{max}$ is not presented.

2.3.4. Basis function sets summary

Fig. 2 shows an example of the basis function terms changing over PEEP for all 3 basis function sets, where $k2_1 = 30$ cmH₂O/L, $k1 = 80$ cmH₂O/L, $PEEP_1 = 2$ cmH₂O and $PIP_{fiterror} = -1/35$. The goal is to delineate how each term in Eqs. (4), (6), and (9) for each basis function set, models elastance evolution. The EXP set captures exponentially falling elastance with increased recruitment combined with rising elastance due to possible distension or increasing lung filling as pressures rise. It is thus physiologically relevant and readily explicable. The PARA set is similar to EXP set in shape and assumptions, but showed

improvements in limited prior studies with a simpler single compartment lung mechanics model [26]. Finally, the CUMU set views net, overall, all-cause lung elastance as always rising as a function of PEEP, while the patient-specific rate of increase is related to patient-specific identified $k1$ and $k2$ values identified at baseline PEEP using HLA.

2.4. Distension prediction ($k2_{end}$)

In addition, for all three basis function sets, $k2_{end}$ captures the potential over-distention at the end of inspiration, which is clinically relevant as it indicates potential overdistension due to excessive pressure and VILI [13] and is proved to be effective in improving PIP predictions [72]. Then, in this approach, $k2_{end}$ prediction function remains the same as prior approach and for all 3 basis function sets:

$$k2_{end_i} = \left(\frac{PEEP_i}{k2_i} + \frac{k2_{end_1}}{k2_i} * (\theta 1 + (\Delta PEEP * \theta 2)^2) \right) * k2_i \quad (13)$$

$$\theta 1 = \frac{k2_{end_1} - PEEP_1}{k2_{end_1}} \quad (14)$$

$$\theta 2 = \frac{EELV_1}{PIV_1 - EELV_1} \quad (15)$$

Where $EELV_1$ is end expiratory volume and PIV_1 is peak inspiratory volume identified at baseline PEEP.

2.5. Overall identification and prediction procedure

The overall identification and prediction procedure flowchart is shown in Fig. 3. This method is outlined further in [42], including the extension of the original HLA method for both the LIP predictions in PCV and VCV modes. The method used for determining the value of distension, $k2_{end}$, differs depending on the mode of ventilation. For the PCV mode, $k2_{end}$ is held constant for the given breath under evaluation as determined from the identification stage. Contrarily, $k2_{end}$ is predicted at each evaluated breath for the VCV mode. This method is outlined further in [74].

Therefore, the ability to accurately predict any distension and the PIV or PIP is critical to avoiding unintended injury. The ability to also predict, with these values, the elastance level at each PEEP ($k2$) means we can minimise work of breathing and set PEEP to minimum elastance, while, as above, avoiding lung injury and over distension. These methods have been researched in prior work [7,75].

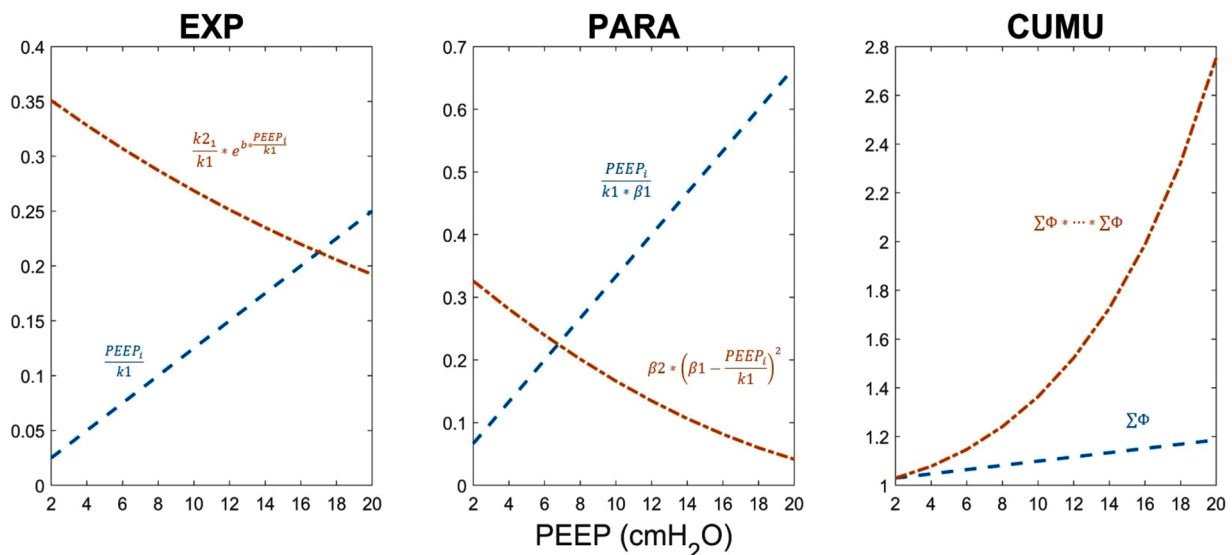


Fig. 2. Illustration of the contribution of each term and how they change over PEEP for all 3 basis function sets in Eqs. (4)–(12).

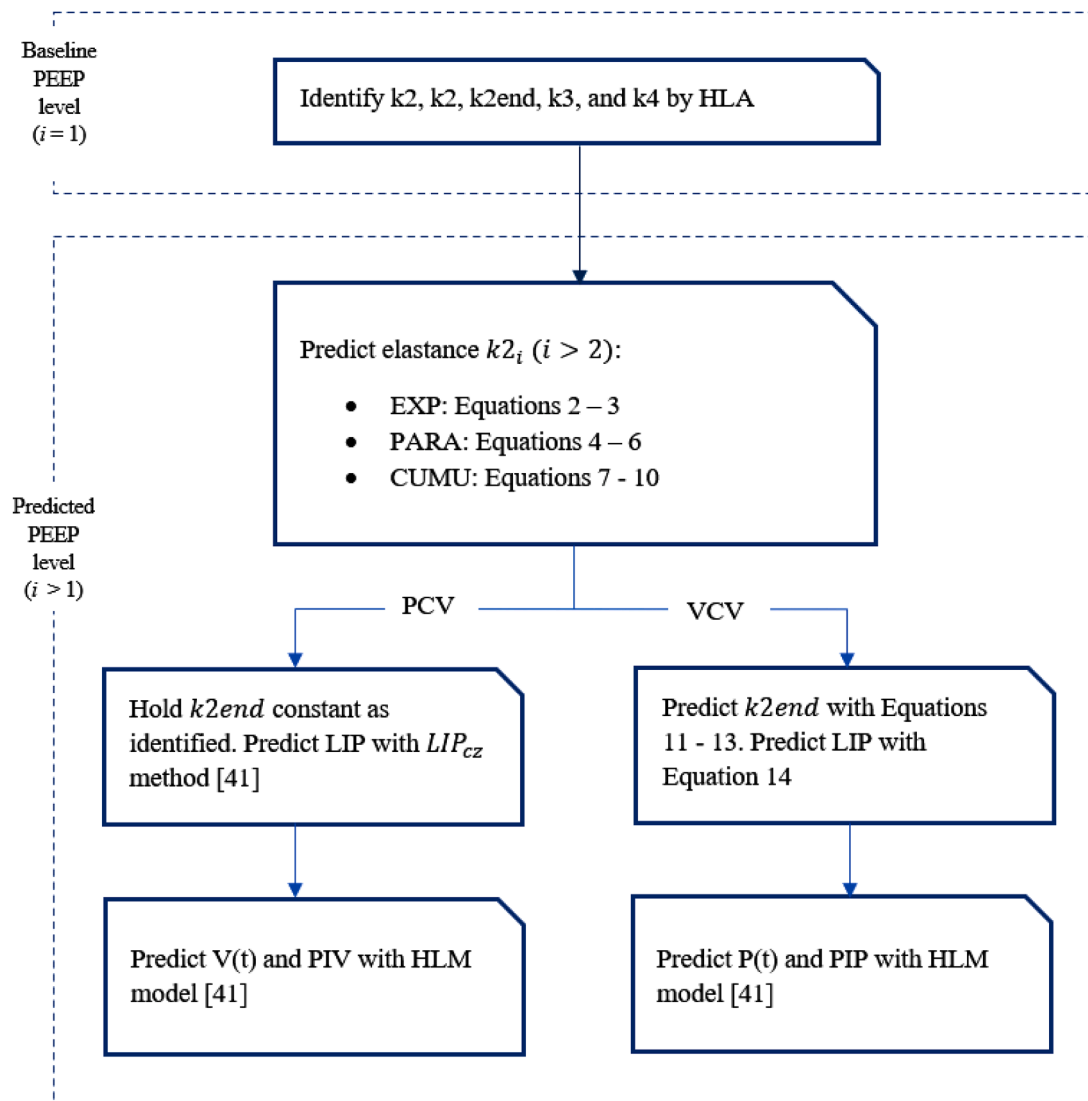


Fig. 3. Flowchart of the overall identification ($i = 1$) and prediction ($i > 1$) procedure.

In this research we are predicting the most likely value for each parameter. We use R-squared (R^2) as a metric to define these predictions in quantitative way for comparison. The most value R^2 are those for predictions 2 and 4 cmH_2O ahead. These are the clinically relevant scenarios and where this modelling could assist clinicians.

2.6. Patient data

Pressure and flow data from 32 ventilated patients in the ICU (18 from the McREM trial [76] and 14 from Maastricht trial) were used to validate the three (3) proposed basis function sets in this study.

2.6.1. VCV trial

In the McREM trial, all 18 patients were fully sedated and intubated under invasive volume-controlled ventilation, with tidal volume set to 8 ± 2 ml/kg based on ideal body weight [76]. The McREM trial was conducted across eight German university ICUs from September 2000 to February 2002. All 18 patients were ventilated with a Draeger Evita 4 ventilator. During ventilation, an end-inspiratory hold of 0.2 s is applied for each breath and data were sampled at 125 Hz. Patient demographics are in Table 1

One increasing staircase RM with 2 cmH_2O step was performed for each patient starting at 0 cmH_2O . The prediction procedure is applied

for further higher PEEP levels ($i = 2, \dots, 7$) after identification at baseline PEEP ($i = 1$). To test the robustness and generality of HLM model and basis function sets, prediction tests are applied across a range of baseline PEEP = 0, 2, 4, 6, 8, 10, and 12 cmH_2O with a further 6 prediction steps (2 cmH_2O interval) from each baseline level, yielding a maximum value for $\Delta PEEP = 2 \times 6$ steps = 12 cmH_2O . There are thus a total of 623 predictions across the 7 baseline PEEP test groups. The test group setting is shown schematically in Fig. 4.

2.6.2. PCV trial

The Maastricht trial comprised 14 patients recruited in Maastricht, Netherlands from November 2017 to February 2018 (METC 17–4–053). All patients were treated with Bi-level Positive Airway Pressure pressure-controlled ventilation with automatic tube compensation (ATC). Patient demographics are in Table 2.

One full staircase RM with increments and decrements of PEEP in 2 cmH_2O intervals was performed for each patient, where only the increasing RM arm is studied. Different from the McREM trial, RM baseline PEEP varies for all 14 patients (10 patients at 6 cmH_2O , 3 patients at 8 cmH_2O , and 1 patient at 10 cmH_2O). Thus, tests are applied at baseline PEEP = 6, 8, 10, and 12 cmH_2O , while prediction steps are also 6 further steps with 2 cmH_2O intervals, yielding maximum $\Delta PEEP = 2 \times 6$ steps = 12 cmH_2O . Thus, there are 294 predictions in

Table 1

VCV patients and clinical trial demographics in the McREM pilot trial [76]. TBI = Traumatic Brain Injury, SDH = Subarachnoid Hemorrhage, SAH = Subarachnoid and Subdural Hemorrhage.

Patient No	Gender	Age (years)	Length of MV (days)	PaO ₂ /FiO ₂ (mmHg)	Clinical Diagnostic
1	m	74	10	298	SAH, SDH
2	f	50	8	202	Pancreatitis, pneumonia
3	f	30	8	162	Peritonitis, sepsis
4	f	49	3	289	Pneumonia
5	m	34	10	192	open TBI
6	m	67	4	234	Post reanimation
7	m	39	10	188	Sigma perf., peritonitis
8	m	42	9	235	Pneumonia, pancreatitis
9	m	51	5	230	TBI, pneumonia
10	m	77	6	225	Pneumonia
11	m	37	10	163	Pneumonia
12	m	41	16	178	Peritonitis
13	m	62	2	288	SDH
14	m	39	7	143	TBI, pneumonia
15	m	74	9	271	S/P coronary artery bypass grafting, pneumonia
16	m	59	19	75	ARDS
17	m	45	8	173	Blunt abdominal trauma, pneumonia
18	m	42	11	260	Alcoholism, GI bleeding, sepsis

total across 4 baseline PEEP level test groups. The 4 test groups are analysed using the same procedure as for the McREM trial, where the first PEEP level is 6 cmH₂O in this case.

2.7. Validation and error analysis

In VCV, PIP is the critical indicator for VILI due to overdistension due to excessive pressure [13,45,50]. Similarly, in PCV, PIV reflects volutrauma risk [51,77]. Boxplots provide the PIP or PIV error distribution over all baseline PEEP levels with absolute median error noted. Correlations between clinical and model predicted PIP or PIV are plotted with R² values calculated for the 1:1 perfect match line to further show spread and error. In VCV patients, the value of *k2end* for PIP prediction is assessed by comparing PIP predictions with and without this term to show the error reduction achieved by accounting for distension.

2.8. Comparative variables

Elastance segment *k2* is used to determine *k2end*, where there is increased stiffness (reduced compliance) at the end of inspiration, associated with overdistension. Poor ventilator settings can lead to

overdistention, in turn leading to increased potential for barotrauma or volutrauma causing VILI. Thus, predicting *k2end* accurately is also critical to safely personalising MV care. Predicted and identified *k2* values were compared using absolute error. From this error, median errors were calculated to determine the relative performance of the basis functions.

For VCV patients, model predicted PIP values are compared to values from the McREM study. Equivalently, for PCV patients, PIV is compared to clinical values from the Maastricht study data. In both instances, signed and absolute errors were determined for each case, giving a median error at each respective baseline PEEP for the three basis function sets. These errors in combination with plotted trends assist in determining the most accurate and/or optimal basis functions for different MV modes.

3. Results

3.1. VCV patients and trial

3.1.1. Comparison of identified elastance and predicted elastance (*k2*) for VCV

The elastance prediction comparison for VCV was conducted across the same 7 different PEEP levels for each of the three basis functions (EXP, PARA and CUMU). As depicted in Fig. 5, the scatter plots observe a trend in which the identified elastance obtained from the measured data is typically higher than the predicted value. This is the case for all three basis functions. With the boxplots on the right-hand side, the PARA basis function shows the lowest errors and least bias (overall) of the three basis function sets, whereas the errors for the CUMU set are more than double that of the PARA set (median error comparison).

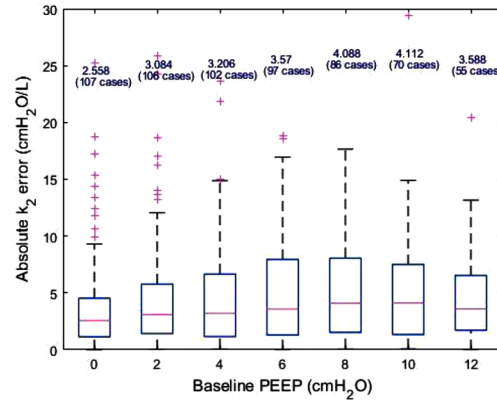
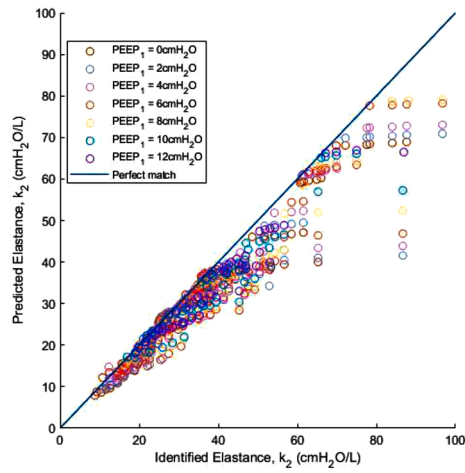
Table 2

PCV patients and clinical trial demographics in the Maastricht pilot trial. CABG = Coronary Artery Bypass Grafting, AVR = Aortic Valve Replacement.

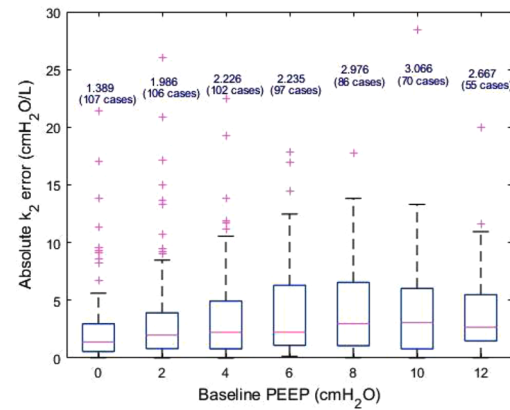
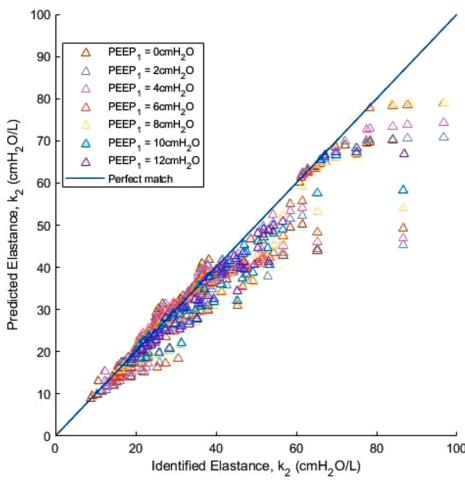
Patient No	Gender	Age (years)	PaO ₂ /FiO ₂ (mmHg)	Clinical Diagnostic
1	Male	77	255	CABG
2	Female	85	308	CABG
3	Male	57	323	CABG
4	Male	47	233	CABG
5	Male	73	150	AVR
6	Male	75	383	CABG
7	Female	71	443	AVR
8	Male	76	398	CABG
9	Female	64	255	Subarachnoid Haemorrhage
10	Female	68	428	Pneumonia
11	Female	78	143	Pneumonia
12	Female	18	83	Mitral and Tricuspid Valve Replacement
13	Female	71	443	Pneumonia
14	Male	36	158	CABG

Test group	No. PEEP level									
1 st	1	2	3	4	5	6	7	8	...	13
2 nd	1	2	3	4	5	6	7	8	...	13
...	...									
7 th	1	2	3	4	5	6	7	8	...	13

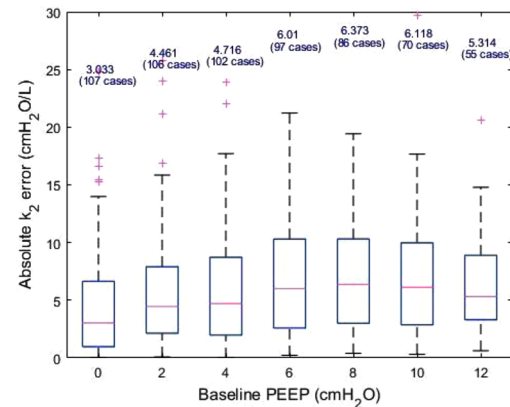
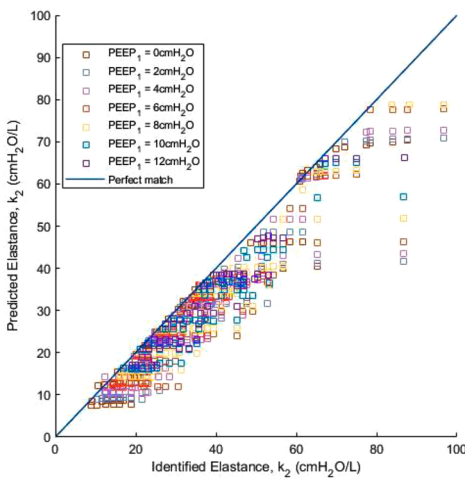
Fig. 4. Schematic test group setting for the McREM trial. Orange coloured levels present the identification baseline PEEP level, while blue coloured levels present the further 6 prediction levels used to test prediction. Intervals in 2 cmH₂O are set between each PEEP level, while first PEEP level is 0 cmH₂O by protocol. PEEP levels are numbered in these 2 cmH₂O steps [72].



a) EXP set



b) PARA set



c) CUMU set

Fig. 5. Correlation plots of Predicted k_2 vs Clinical k_2 (left) and boxplots for absolute k_2 prediction errors with noted median errors (cmH₂O/L) over 7 baseline PEEPs (right) for (a) EXP, (b) PARA, and (c) CUMU basis function sets with VCV data.

3.1.2. Peak inspiratory pressure (PIP) prediction for VCV

Boxplots of absolute PIP prediction errors across all 7 test groups (baseline PEEP = 0, 2, 4, 6, 8, 10, and 12 cmH₂O) with 6 prediction steps are shown in the right-hand side of Fig. 6, while the relationships

between clinical PIP and predicted PIP are presented separately in the left-hand side of Fig. 6 for all 3 sets (623 predictions) with overall R² values of 0.90, 0.85, and 0.88 for the EXP, PARA, and CUMU basis function sets, respectively. Table 3 shows the R² values over shorter

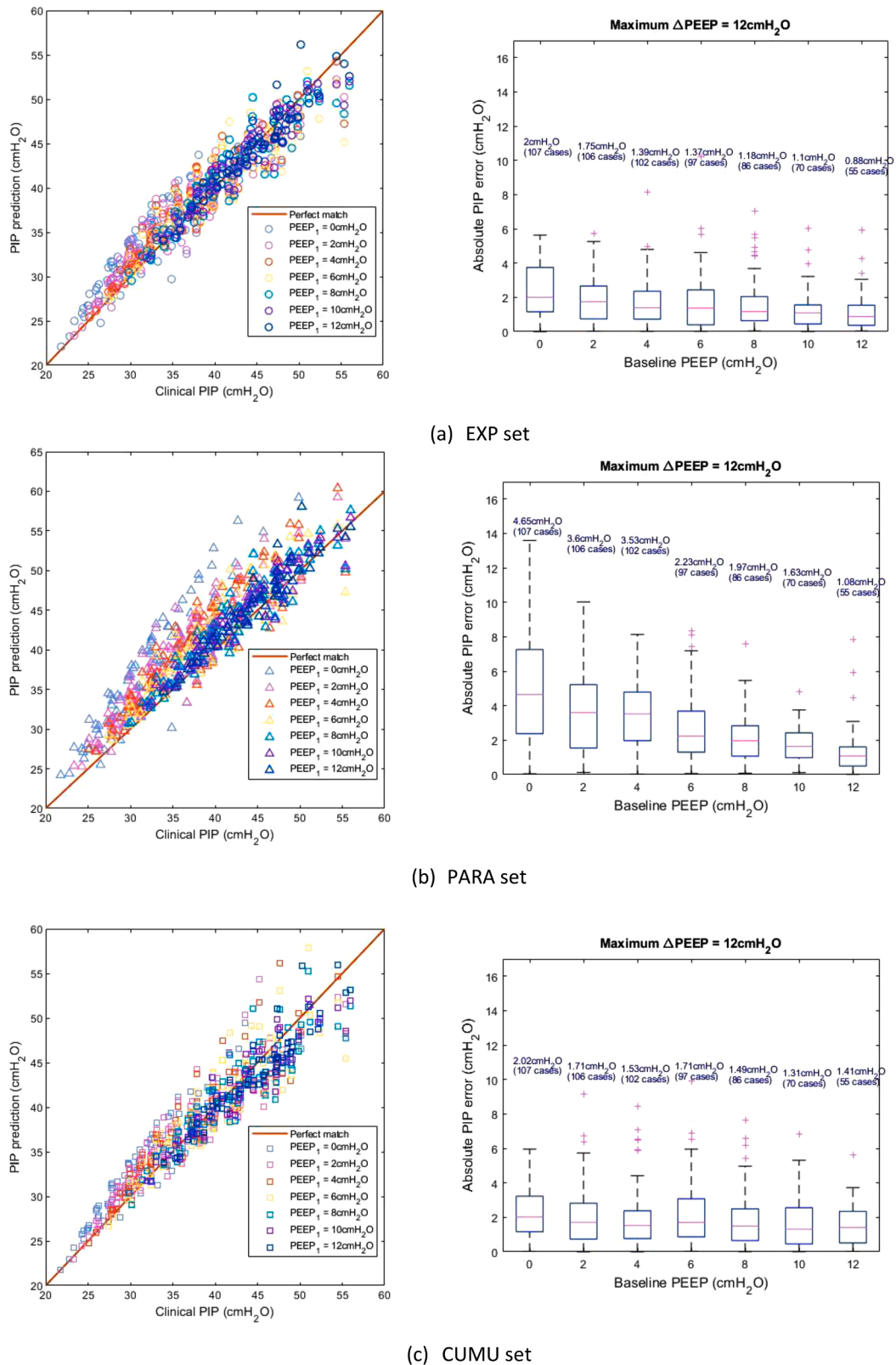


Fig. 6. Correlation plots of Predicted PIP vs Clinical PIP (left) and boxplots for PIP prediction errors with noted median errors (cmH₂O) over 7 baseline PEEPs (right) for (a) EXP, (b) PARA, and (c) CUMU basis function sets, yielding overall R² = 0.90 in EXP, R² = 0.85 in PARA, and R² = 0.88 in CUMU among 623 prediction cases in VCV.

prediction intervals are higher, ranging from $R^2 = 0.91-0.96$ in the first three rows of the table.

Comparing basis functions, the PARA set in VCV prediction yields the ‘worst’ performance with higher median errors and an overall lowest R^2 value = 0.85. However, the higher median error is partly a result of bias, with 70.6 % predictions of overshooting the clinical value, which has potential clinical utility in guiding MV as it can lead to more conservative clinical decisions. Bias for the other sets are 60.8 % for EXP and 53.0 % for CUMU. EXP and CUMU yield similar overall performance in all 7 predictions, while overall 90 % of PIP prediction errors are within 3.95 cmH₂O. However, EXP tends to have a better performance than CUMU at baseline PEEP ≥ 6 cmH₂O, and thus is better at clinically relevant PEEP levels.

3.2. PCV patients and trial

3.2.1. Comparison of identified elastance and predicted elastance (k_2) for PCV

Fig. 7 depicts the comparison of identified elastance and predicted elastance for PCV alongside their respective error boxplots. Comparisons were conducted for each of the three basis functions across four different baseline PEEP levels (PEEP = 6, 8, 10, 12 cmH₂O). The elastance values are all negative, due to the specific geometric shape of the P-V loops for PCV, as shown in Fig. 1(b). PCV typically shows a less accurate correlation between predicted and identified elastance than the VCV trial. When comparing basis functions, the CUMU basis function set provided the smallest errors overall (median error comparison).

For further comparison, Fig. 7 also shows the 10 % of outliers that were removed displayed in grey. Removal of these points has increased the accuracy of this prediction. In addition, the removal points coincide as 7 %, 20 %, 33 %, and 40 % of outlier points for baseline PEEP = 6, 8, 10 and 12, respectively. This result indicates the outliers leading to less accurate correlation in Fig. 7 are likely due to data quality rather than prediction efficacy of any of the three basis functions.

3.2.2. Peak inspiratory volume (PIV) prediction for PCV

Boxplots of PIV prediction errors (L) across all 4 baseline PEEP prediction groups (baseline PEEP from 6 to 12 cmH₂O) are shown in Fig. 8, while correlations between model predicted PIV and clinical PIV (294 predictions total) are also provided with R^2 values of 0.85, 0.81, and 0.80 for EXP, PARA, and CUMU, respectively. Finally, assessing only clinically relevant Δ PEEP = 2–6 cmH₂O prediction ranges (1 - 3 prediction steps further), Table 4 shows the R^2 values over shorter prediction intervals is higher than the overall values considering all Δ PEEP levels, ranging from $R^2 = 0.87-0.96$ in the first three rows of the table.

Comparing basis function performance for PCV prediction, the EXP set still yields the overall best performance. Even though EXP and PARA have a similar median error across all 4 prediction groups, CUMU tends to have more outliers and larger IQR, which explains the lower R^2 value.

Table 3

Decreasing R^2 value across different cumulative collections of prediction steps and intervals for all three basis functions for PIP prediction from any baseline PEEP₁ level for VCV in the MCREM cohort. The statistics by row are cumulative for 1 step forward, 1 step and 2 steps forward together, up to all 6 steps.

The MCREM trial	R^2 value of PIP prediction			Prediction cases
	EXP	PARA	CUMU	
1 step ahead	0.95	0.94	0.96	122
1 and 2 steps ahead	0.95	0.93	0.95	241
1–3 steps ahead	0.93	0.91	0.94	356
1–4 steps ahead	0.92	0.89	0.92	460
1–5 steps ahead	0.91	0.87	0.90	550
1–6 steps ahead	0.90	0.85	0.88	623

3.3. k_2 end prediction bias: overshoot and undershoot errors

Predictions of PIP and PIV (VCV and PCV respectively) are dependent on the prediction of k_2 end. Prediction of k_2 end is done using the same basis function as applied to the prediction of PIP or PIV. The distension prediction of k_2 end is incorporated to capture any overdistension occurring at the end of inspiration. Thus, this term is directly related to either PIP or PIV, depending on ventilation mode. With overshoot errors, k_2 end was overpredicted, whereas undershoot errors are a result of underpredicted k_2 end. It is important k_2 end is correctly predicted as overdistension results in the over inflation of alveoli and tissue damage, whereas under distension results in lower oxygenation rates and repeated opening and closing of alveoli, or atelectasis.

3.3.1. VCV patients and trial

The boxplots in Fig. 9, show the errors across each of the basis function sets for VCV collated to represent an overall spread and the respective median errors. Fig. 9 shows the boxplots for absolute errors and the signed errors. Overall, the PARA function sets observed the highest absolute median error with a median error of 2.455 cmH₂O, while EXP yields the lowest value of 1.399 cmH₂O. However, as shown in Fig. 9(b), EXP and PARA tend to underestimate and overestimate the PIP predictions, respectively, while the tendency of predictions in CUMU is not obvious.

3.3.2. PCV patients and trial

Boxplots in Fig. 10 depict the signed and absolute errors across each of the basis function sets for PCV, all collated to depict the overall spread and resultant median errors. Unlike the prediction error results for VCV, as shown in Fig. 9, there is no function set that significantly outweighs the performance of the other function sets in PCV. However, the absolute and signed boxplot errors for PIV prediction both agree that the CUMU set observes the highest median prediction error with 0.03 L (absolute) and -0.013 L (signed). Though the signed error is primarily used to show whether a basis function set is overshooting or undershooting, it also shows the true error range where the absolute error range is less functional. The median absolute errors for EXP and PARA are similar, with the PARA set having slightly larger outliers. However, the signed errors show that the PARA set has a larger error range than that of the EXP set. A more obvious representation of this analysis is in Section VCV patients and trial.

4. Discussion

Basis functions have long been proposed to simulate lung mechanics, among other physiological [59–62] and non-physiological system models, as well as in simple to complex lung mechanics models [40,55, 56,58,78]. In this approach, three (3) physiologically relevant basis function sets [42,57,63,64] are studied for elastance evolution prediction within the HLM lung mechanics model [42,63] with a goal of assessing overall best performance relative to potential clinical utility. With information identified only from one baseline PEEP level, further prediction of patient-specific lung mechanics response to help optimise MV settings can be accomplished for a targeted higher PEEP level (up to 6 further steps yielding maximum Δ PEEP = 12 cmH₂O assessed here), without requiring further information.

For PCV, the coupling of tidal volume and flow is the vital problem to conquer for mathematical approaches, where convergence needs to ensure a good balance between model complexity and prediction accuracy. In this approach, the mechanics simulation model is based on [42]. With 3 basis function sets tested, the stability of this nonlinear hysteresis model is further demonstrated in the results presented for both VCV and PCV trials. Further, the ability to accurately predict PIV and PIP provides the ability to safely minimise risk and optimise MV as patient condition evolves.

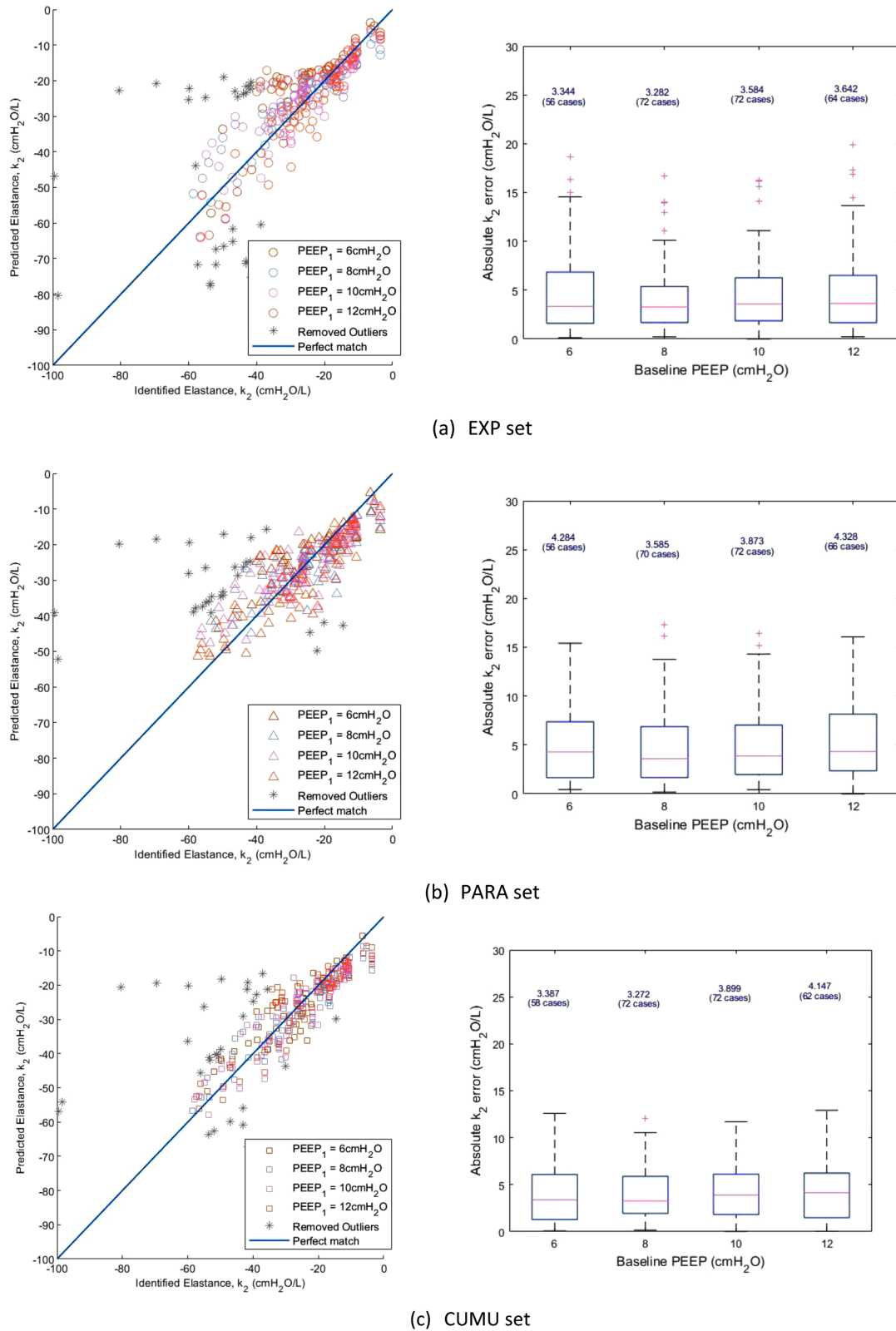


Fig. 7. Correlation plots of Predicted k_2 vs Clinical k_2 (left) and boxplots for k_2 prediction errors with noted median errors (L) over 4 baseline PEEPs (right) for (a) EXP, (b) PARA, and (c) CUMU basis function sets using the PCV MV method.

Correct identification of k_2 provides a solid base for accurate predictions for PIP/PIV. For the VCV trial, as shown in Fig. 5, there is a clear trend across all three basis functions where the identified k_2 value is typically higher than predicted. This bias result matches Fig. 9(b) where

overshoots are observed across all three basis functions for VCV. Amongst these three basis functions, the CUMU set observed the highest average median error of 5.622 cmH_2O . These averages are derived from the seven median absolute errors at each baseline PEEP level. In

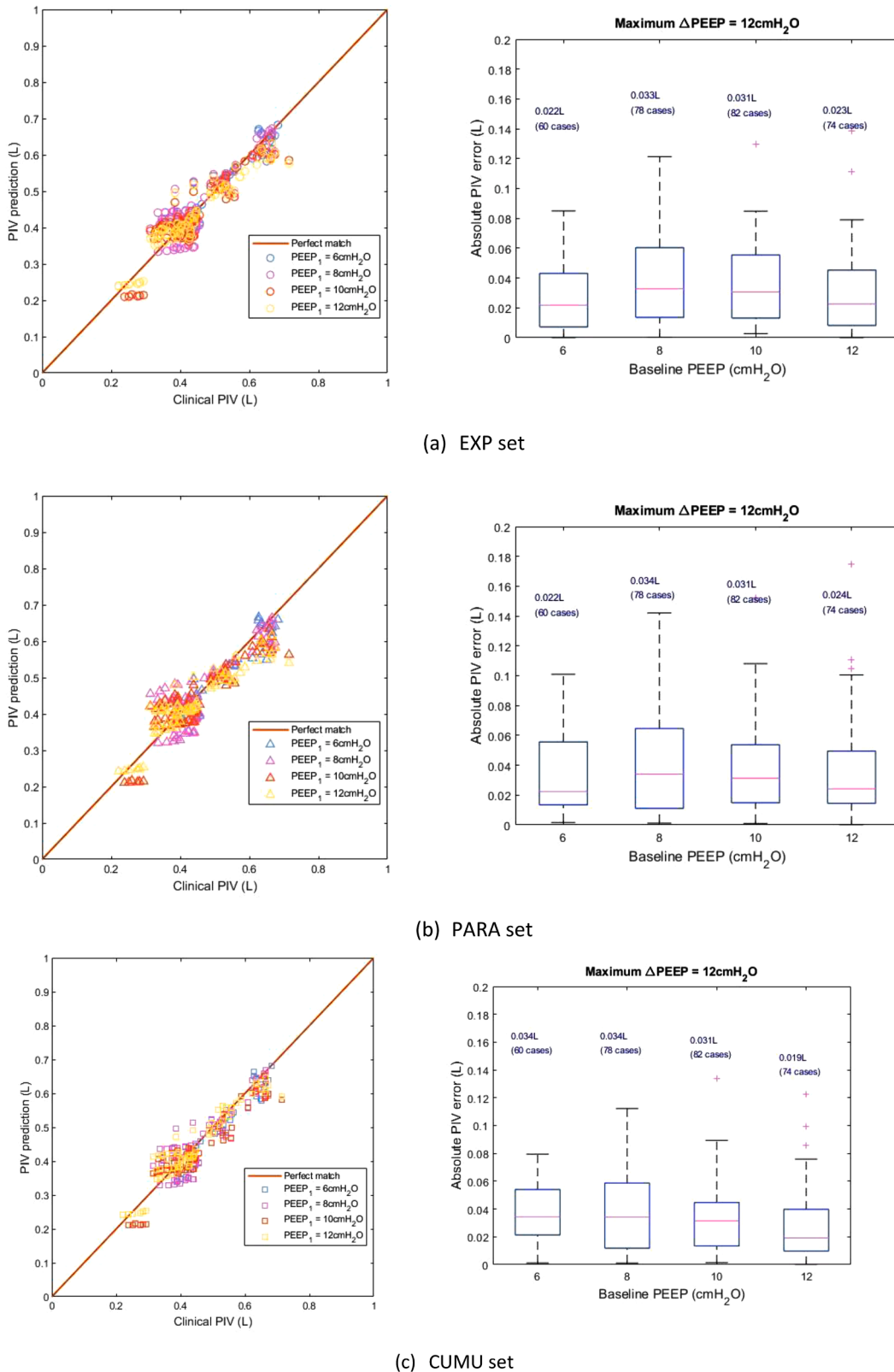


Fig. 8. Correlation plots of Predicted PIV vs Clinical PIV (left) and boxplots for PIV prediction errors with noted median errors (L) over 4 baseline PEEPs (right) for (a) EXP, (b) PARA, and (c) CUMU basis function sets, yielding overall $R^2 = 0.85$ in EXP, $R^2 = 0.81$ in PARA, and $R^2 = 0.80$ in CUMU among 294 prediction cases in PCV.

predicted PIP, which is 50.2 % greater than the lowest average median error of 2.798 cmH₂O associated with the PARA set. The EXP set yielded an average median error of 3.744 cmH₂O. For the PCV trial, as shown in

Fig. 7, the data is spread more evenly around the ‘perfect match’ 1:1 line indicating that both overshoot and undershoot are observed more evenly compared to the VCV trial. However, identified k_2 is still

Table 4

Decreasing R^2 value across different cumulative collections of prediction steps intervals for all three basis function shapes for PIV prediction from any baseline $PEEP_1$ level for PCV in the Maastricht cohort. The statistics by row are cumulative for 1 step forward, 1 step and 2 steps forward together, up to all 4 steps forward for the whole cohort. Thus, the last row presents the total cohort values.

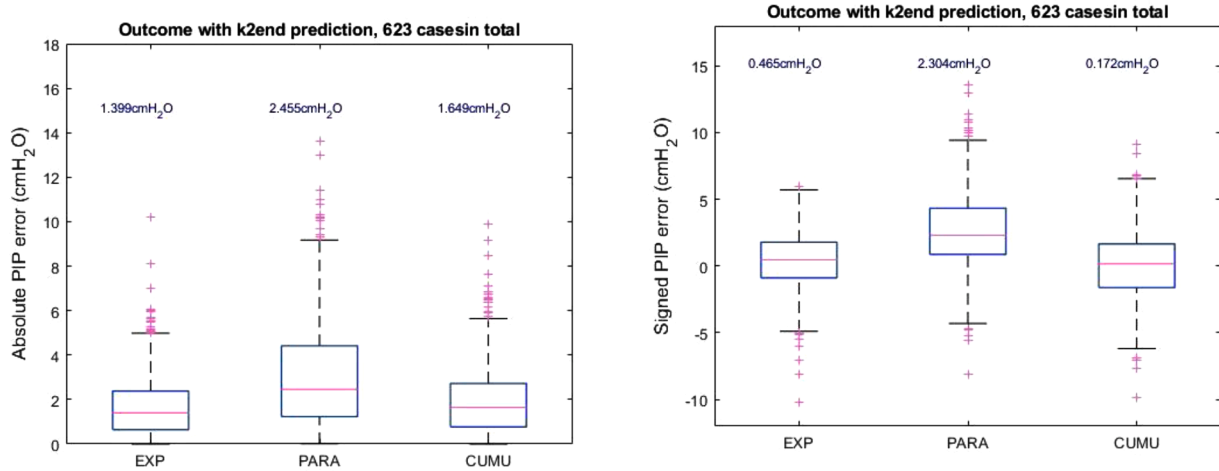
Maastricht	R^2 value of PIV prediction			Prediction cases
	EXP	PARA	CUMU	
1 step further	0.96	0.95	0.96	51
2 step further	0.94	0.90	0.92	102
3 step further	0.91	0.87	0.88	153
4 step further	0.88	0.84	0.84	204
5 step further	0.87	0.82	0.82	253
6 step further	0.85	0.81	0.80	294

typically higher than the predicted. Across the three basis functions, the PARA set had the highest average median error across all baseline PEEP levels of 4.328 cmH₂O (derived from each median absolute error individually) which was 24.4 % higher than the lowest average median error of 3.272 cmH₂O associated with the CUMU set. The EXP set yielded an

average median k_2 prediction error in PCV of 3.463 cmH₂O.

For the VCV trial, as shown in Table 3 the PARA set yields the lowest overall R^2 value, $R^2 = 0.85$, among 623 prediction cases totally. This result occurs due to 70.6 % of predictions overshooting the data for 440 out of 623 cases, compared with 60.8 % and 50.3 % for EXP and CUMU, while some positive bias can lead to a more conservative clinical decision. As shown in Figure 6 EXP has a more robust and accurate prediction than CUMU, with lower IQR upper limit PIP prediction error and fewer outliers. Note at lower baseline PEEP values (0 - 4 cmH₂O), although CUMU has a relatively lower median error, it has more outliers and larger IQR compared with the EXP results.

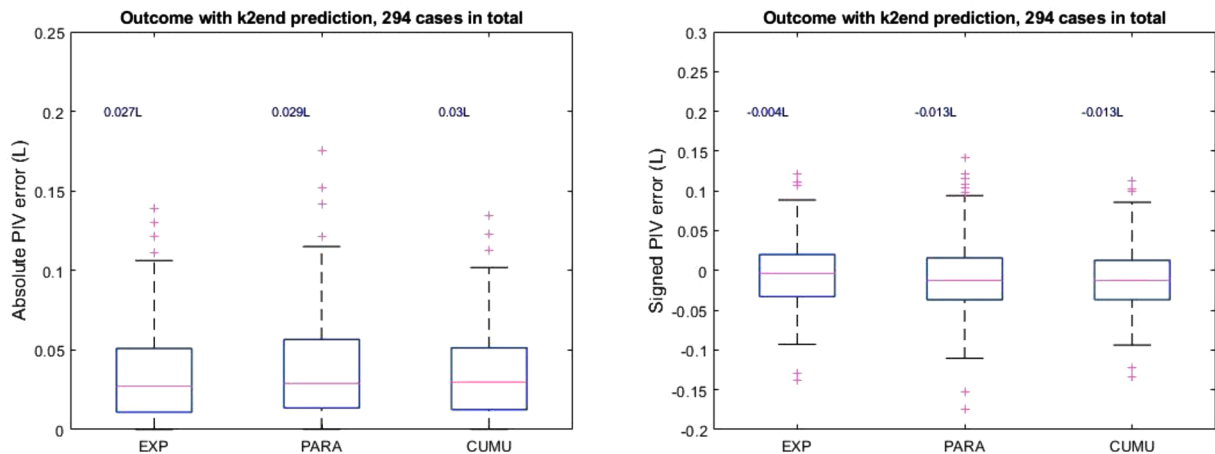
The overall absolute median error for PIP prediction in Fig. 6 tends to decrease as baseline PEEP increases. This outcome is possibly a result of slightly fewer prediction cases as baseline PEEP increases. However, given the relatively large number of predictions, the lower error at clinically relevant PEEP levels and clinically relevant smaller changes in PEEP is important. Equally, the higher prediction errors at lower baseline PEEP, from 0 to 4 cmH₂O, are relatively less critical and harmful for patients compared with higher baseline PEEP, where higher PIP and higher PIP prediction errors increases risk of VILI [13,79]. Similarly,



(a) Absolute errors with k_2end prediction

(b) Signed errors with k_2end prediction

Fig. 9. Comparison of absolute PIP prediction errors across 3 basis function sets (a) and (b) with signed prediction errors for the VCV data set (McREM).



(a) Absolute errors with k_2end prediction

(b) Signed errors with k_2end prediction

Fig. 10. Comparison of absolute PIV prediction errors across 3 basis function sets (a) and (b) with signed prediction errors for the PCV data set (Maastricht).

such low baseline PEEP levels are rarely encountered in adult ICU patients, as such low levels of MV support are supplied by less invasive or controlled ventilation modes [13,80], for which similar virtual patients are being derived [81,82].

For the VCV trial, the overall absolute and signed errors were analysed for PIP in Fig. 9. The signed median errors show that all three function sets observe an overall overshoot in the predicted PIP, the maximum signed median error being the PARA set at 2.304 cmH₂O and lowest signed median error being the CUMU set at 0.172 cmH₂O. The CUMU set also has the largest error spread with outliers at both overshoot and undershoot ends. The outliers for the PARA set are primarily within the overshoot region, whereas EXP set errors are primarily within the undershoot region. Considering the boxplots in Fig. 10 and the disparities between each function set, signed and absolute, the EXP function set yields the most consistent and accurate data for the predictions of PIP. Though it didn't yield the lowest signed median PIP error, the spread of this data and median results from the other analyses all coincide to agree with the verdict that EXP is best function set for these predictions.

Prediction of PIP is also largely based off elastance predictions. Section 3.1.1 highlights an overall undershoot in the prediction of elastance across all three basis functions. However, an overall overshoot was observed in the prediction of PIP. Conversely, Section 3.2.1 shows an overall overshoot in the elastance prediction in PCV where the PIV prediction undershoots oppositely. The way the models have adjusted to overshoot or undershoot correspondingly hints at the possibility of model compensation, such that where the elastance undershoots, the PIP will overshoot to provide a more balanced overall model.

The overall absolute and signed errors were also analysed for the PCV trial in Fig. 10. Signed errors for PIV analysis across the three basis function sets all show an undershoot in their predictions. The maximum signed median PIV error being -0.013 L from both the CUMU and PARA function sets. This is consistent with the two higher absolute median PIV errors corresponding to the CUMU and PARA sets. The highest absolute median PIV error being 0.03 L from the CUMU function set. The lowest signed median PIV error being 0.04 L and the lowest absolute median PIV error being 0.027 L, both from the EXP function set. In both sets, the PARA set observed the largest spread, highlighting a larger inconsistency in the results in comparison to the other two function sets. From looking at both the signed and absolute error boxplots in Fig. 10, and considering the differentials between these errors, the EXP set yields the most accurate and stable prediction data for both the PIV predicted data overall.

As for the PARA and CUMU sets, the highest errors occur somewhat randomly. Thus, the EXP set yields the most stable and accurate prediction across different baseline PEEP levels for VCV. All these results are consistent with reduced errors when considering only the first, clinically relevant 2–3 PEEP steps. This choice reflects balancing trade-offs between accuracy and robustness.

Similarly, higher median PIV prediction errors in PCV patients occur where there are more baseline PEEP prediction cases. The EXP set still yields the best prediction performance across various baseline PEEP levels, while 90 % of PIV errors are within 0.068 L, compared with 0.077 L and 0.078 L in PARA and CUMU sets respectively. Moreover, the median PIV error decreases to 0.019 L from 0.028 L while all errors are within 0.079 L for EXP if the maximum $\Delta PEEP$ for prediction narrows to 6 cmH₂O (3 prediction steps) from 12 cmH₂O (6 prediction steps), which is a more clinically realistic setting. In these clinically realistic cases, the R² values increase, with similar improvement in VCV predictions, as shown in Table 4.

For PCV prediction, the CUMU set has the lowest R² value, R² = 0.80, with 90 % of PIV prediction errors within 0.078 L. In EXP and PARA, 90 % of errors are lower than 0.068 L and 0.077 L, respectively. As shown in Fig. 8, comparing performance between EXP and CUMU sets, the latter has lower median PIV error, but more and larger outliers. Overall, the EXP set yields to the most robust prediction over all 3 basis function sets.

Knowing a patient's optimal elastance and recruitable volume allows clinicians to select an appropriate PEEP for optimal ventilation. Prediction models and algorithms would enable these clinicians with an assistive tool to indicate what the optimal ventilation settings are for that patient specifically by using patient-specific prediction models. Having the correct ventilator settings will minimise the likelihood of overdistension occurring and in turn minimise the occurrence of VILI in patients post ventilator therapy.

The efficacy of *k2end* is validated with prior work [72]. It is kept the same in this study across all three basis functions to predict the over-distension at higher PEEP levels. The PIP and PIV predictions bias and errors are possibly affected by both the applied basis function set and *k2end* function. However, the elastance predictions at lower baseline PEEP levels shown in Figs. 5 and 7, where over-distension is rarely seen, present the difference across basis function sets.

This model will be run through multiple different data sets before conclusively stating its complete ability. After using data sets McREM and Maastricht, the predictive model is showing large promise. Accuracy of the predictive software when looking at PIV (PCV), PIP (VCV) and *k2* is high, particularly for VCV mode (approx. 96 %). However, alterations to improve the accuracy of predictions to the PCV mode model are required and underway.

While predictive models have been increasingly developed and tested, integrating the proposed predictive model in the clinical control loop remains a challenge because the practical implementation of the proposed model in real patients would require rigorous clinical trials and assessment to ensure its robustness and safety [28,29,83,84]. In addition, engagement of clinical staff would still be required to ensure the oversight, planning and safety of the intervention. Therefore, beyond the technology factors, social factors should also be considered for appropriate change management processes in addition to workload management to enable appropriate levels of engagement with technology and training prior to the model use in real world.

In this work we have analysed three potential basis functions. These were chosen based off physiological compatibility and previous work within the same framework. However, this work does not preclude better basis functions or a different hysteretic model with different or similar basis functions from performing better.

In summary, the EXP set yields the best performance across various baseline PEEP levels and MV modes, VCV and PCV. Although the PARA and CUMU sets are not as good as the EXP set overall, they do show very promising ability, and might be further optimised. Overall, the results show the potential power of personalised models to predict outcomes to changes in care using physiologically relevant basis function sets. Model-based approaches to personalising care require far less added hardware, added data, or/and personnel costs, and require only relatively limited computation as found on bedside computers or cloud served computation. Moreover, the 3 basis function sets examined in this approach can still be improved with further tests and offer new insights for researchers to study and consider the inner correlation between elastance prediction and respiratory response prediction for model optimizing.

5. Conclusion

This study presents the prediction performance of 3 physiologically relevant basis function sets across 32 ventilated patients (18 VCV, 14 PCV) at a wide range of different baseline PEEP levels with $\Delta PEEP$ prediction intervals up to 12 cmH₂O. While all 3 sets yield very good predictions for both VCV and PCV, the exponential basis function set, EXP, has the best performance across both PCV and VCV modes, and the most robust prediction performance in both modes, thus providing a best balance of accuracy and robustness. The overall outcome shows all three physiologically relevant basis function sets offer the possibility for accurate and simpler lung mechanics prediction, and how otherwise similar basis function forms can lead to different prediction outcomes for

both elastance and pulmonary response. This latter outcome indicates the need to test robustness over basis function shapes when using this approach for any type of digital twin or virtual patient model, which has not been tested previously. Thus, the main results offer new insights into how to consider and optimize lung mechanics models with elastance evolution function forms for further studies, and the basis function shapes themselves create new potential hypotheses to better understanding the macro behaviour of lung tissue mechanics in mechanical ventilation.

Declaration of Competing Interest

The authors on this submission declare that there are no conflicts of interest on this paper, financial or otherwise.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.cmpb.2023.107988](https://doi.org/10.1016/j.cmpb.2023.107988).

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