Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Predicting prolonged hospital stay in children hospitalised with respiratory syncytial virus infection: model development, internal validation and a calendar-year transportability assessment

Ai Chen

zuoma78@163.com

Chengdu Second People's Hospital

Zhi Chen

Affiliated Hospital of Southwest Medical University

Pei lin Dai

Queen Mary School (Hainan), Beijing University of Posts and Telecommunications,

YunXiu Chen

Chengdu Second People's Hospital

Ying Pang

Sichuan Provincial Women's and Children's Hospital

Hui Zhu

Sichuan Provincial Women's and Children's Hospital

Fu Xiong

Sichuan Provincial Women's and Children's Hospital

Shuyao Zhu

Sichuan Provincial Women's and Children's Hospital

Yuanlin Zhou

Chengdu Second People's Hospital

Research Article

Keywords: respiratory syncytial virus, length of stay, prediction model, nomogram, paediatrics

Posted Date: November 12th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-11459742/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Predicting prolonged hospital stay in children hospitalised with respiratory syncytial virus infection: model development, internal validation and a calendar-year transportability assessment

Running title: Prolonged stay in paediatric RSV infection

Ai Chen [a*,b],*Zhi Chen* [d], *Peilin Dai* [e], *YunXiu Chen* [a], *Ying Pang* [c], Hui Zhu [c],Fu Xiong[C], Shuyao Zhu [c],Y*uanlin Zhou* [a*]

[a] West China School of Medicine, Sichuan University; Department of Pediatrics, Sichuan University Affiliated Chengdu Second People's Hospital, Chengdu Second People's Hospital,Chengdu,610000, China

[b] Neurological Disease Research Institute, Chengdu Second People's Hospital, Chengdu,610000, China

[c] Department of Pediatrics, Sichuan Provincial Women's and Children's Hospital / The Affiliated Women's and Children's Hospital of Chengdu Medical College, Chengdu, 610045,China

[d] Department of Emergency Medicine, Affiliated Meishan Hospital of Southwest Medical University, Meishan, 620010,China

[e] Media and Technology, Class of 2026, Queen Mary School (Hainan), Beijing University of Posts and Telecommunications, Beijing,100083, China

* Correspondence:

Ai Chen, Department of Pediatrics, West China School of Medicine, Sichuan University, Chengdu Second People's Hospital Affiliated to Sichuan University, No. 10 Qingyun South Street, Chengdu, Sichuan 610000, China E-mail: zuoma78@163.com

Y*uanlin Zhou* : Department of Pediatrics, West China School of Medicine, Sichuan University, Chengdu Second People's Hospital Affiliated to Sichuan University, No. 10 Qingyun South Street, Chengdu, Sichuan 610000, China E-mail:1935049810@qq.com

Word count (abstract): 300
Word count (main text): 6816
Tables: 6. Figures: 5. Supplementary tables: 5. References: 27.

Abstract

Background. Respiratory syncytial virus (RSV) is the commonest cause of lower respiratory tract infection in young children, and length of stay dominates cost. Published RSV models mostly predict intensive-care outcomes from variables unavailable on a ward. We developed a model for prolonged stay from routine admission data and examined its transport across years.

Methods. Retrospective cohort of children under 5 years admitted to general paediatric wards in Chengdu, China, with RSV confirmed by multiplex polymerase chain reaction, 2023–2025. Prolonged stay was 7 days or more. Fifteen admission variables were ranked by least absolute shrinkage and selection operator regression with 300 bootstrap resamples; retention required 95% selection frequency and stability across four specifications. Discrimination was assessed with 500-resample optimism correction, calibration by slope, intercept and Brier score against a constant-risk benchmark, and utility by decision curves. The primary model was refitted in 2023–2024 and applied unchanged to 2025.

Results. Of 494 admissions, 476 were analysed (median age 20.0 months; 57.6% boys); 106 (22.3%) stayed ≥ 7 days. Age (odds ratio 0.49 per 16.7 months, 95% CI 0.38–0.64), co-detection (1.73, 1.07–2.79) and lactate dehydrogenase (0.66 per 66.6 U/L, 0.51–0.86) were retained; AUC 0.708 (0.653–0.760), optimism-corrected 0.687, slope 1.00, Brier 0.158. Prolonged stay fell from 32.1% (62/193) to 15.5% (44/283) ($p < 0.001$). On transport discrimination was preserved (AUC 0.701, 0.623–0.772; slope 1.07) but risk was overestimated (intercept −0.82; predicted 28.3% vs observed 15.5%), and the Brier score (0.142) exceeded the constant-risk benchmark (0.131) until recalibrated (0.124). At a 20% threshold, 33.9% of 2025 admissions were low risk (negative predictive value 95.8%; 14 events missed per 1000).

Conclusions. Three routine admission variables predicted prolonged RSV stay with moderate discrimination, preserved across calendar years, whereas absolute risk was not and needs recalibration before use. The model suits ruling out a long stay, not escalation.

Keywords: respiratory syncytial virus; length of stay; prediction model; nomogram; paediatrics

Introduction

Respiratory syncytial virus (RSV) is the most frequent viral cause of acute lower respiratory tract infection in early childhood and the leading reason for paediatric hospital admission worldwide. Global analyses attribute approximately 33 million episodes and 3.6 million hospital admissions each year to children younger than five years, with the greatest burden concentrated in infants under six months [1–3]. In China, RSV activity follows a sharply seasonal pattern with a peak between November and March [4], so that winter bed occupancy in paediatric wards is determined to a large extent by RSV and by the duration of the admissions it causes [3,5].

For the individual child and for the ward that receives them, the decisive question is not whether the illness is RSV but how long the admission will last. Length of stay determines bed occupancy, the opportunity cost of blocked beds during the seasonal peak, the indirect costs borne by families, and the risk of hospital-acquired infection [5]. Seven days is the conventional boundary between an ordinary and a prolonged paediatric admission in China, and in our own cohort it lies at the 78th percentile of the length-of-stay distribution. A tool that identifies on the day of admission the children likely to remain in hospital beyond that boundary would allow discharge planning to begin early and would support cohorting and family counselling.

Most published RSV prediction models have been built to predict intensive-care outcomes — the need for respiratory support, mechanical ventilation or length of intensive-care stay —

and they typically rely on variables that become available only after a decision to escalate has been taken, such as blood gas indices, respiratory severity scores or natriuretic peptides [6,7]. Such models are useful in the emergency department or the intensive care unit but are not transportable to a general paediatric ward, where the information at hand is a full blood count, a liver and renal panel and the result of a multiplex respiratory panel. The one published model built specifically for prolonged RSV admission derived its predictors from a national administrative database — interhospital transfer, intubation, comorbidity and hospital characteristics — and reported an area under the curve of 0.73 in a United States sample of 9589 children, of whom 1054 (11.0%) stayed 7 days or more [8]. Those variables are informative, but they are not the variables a ward doctor in a middle-income country has in front of them at the moment the discharge question is first asked.

We therefore developed a model predicting prolonged hospital stay in children admitted with RSV infection, using only information obtainable within 24 hours of admission on a general ward, and we examined how its performance behaved when the same predictors were applied to a later calendar year in which the observed rate of prolonged stay was half as high. We deliberately restricted the model to variables whose association survived transformation of skewed laboratory values, on the reasoning that a predictor whose effect depends on the scale on which it is entered is unlikely to replicate. The study is reported in accordance with the TRIPOD+AI statement [9].

Methods

Study design and setting

This was a retrospective cohort study conducted in the general paediatric wards of Sichuan University affiliated Chengdu Second People's Hospital in Chengdu, Sichuan Province, China. Consecutive children admitted between 1 January 2023 and 31 December 2025 with laboratory-confirmed RSV infection were identified from the hospital information system.

The hospital serves as a regional referral centre and admits approximately 12,000 children to its general paediatric wards each year. The manuscript follows the TRIPOD+AI checklist for prediction model development [9].

Participants

Eligible children were younger than 5 years and had RSV detected in a nasopharyngeal specimen during the index admission. In this laboratory, RSV is detected exclusively by a 13-target multiplex respiratory polymerase chain reaction (PCR) panel that covers RSV, influenza A and B, adenovirus, human metapneumovirus, parainfluenza virus, bocavirus, rhinovirus, coronaviruses, Mycoplasma pneumoniae and Chlamydia pneumoniae; antigen-only testing was not used for any admission in the study period, so ascertainment of RSV was uniform across the cohort. Children were excluded if they were managed as outpatients or in the emergency observation unit without ward admission; if they were admitted to the neonatal ward or the neonatal intensive care unit, where discharge practice and normal physiological values differ substantially from the general ward; if the recorded length of stay was shorter than one day or was missing; or if the admission was a repeat admission of a child already included, in which case only the first admission was retained. Seven neonates aged less than 28 days who were managed on a general ward were retained, because their discharge decisions followed general ward practice.

Outcome

The outcome was prolonged hospital stay, defined as a length of stay of 7 days or more, calculated from admission and discharge timestamps and expressed in fractional days. The threshold was fixed before analysis because it is an integer that can be applied at the bedside, because it sits at the upper end of the normal range of paediatric inpatient stays in China, where tertiary children's hospitals report a mean of 6.3 days and tertiary general hospitals 7.6 days [10], and because it is the point at which case-based prospective payment stops

reimbursing the marginal bed-day. In this cohort the threshold falls at the 77.7th percentile of the length-of-stay distribution (75th percentile 6.96 days); the two differ by a few hours in 16 children (3.4%), who were discharged between 167.0 and 168.0 hours because times are recorded to the hour. A stay of 8 days or more, and the logarithm of length of stay as a continuous outcome, were analysed as alternative parameterisations.

Candidate predictors

Fifteen variables available within 24 hours of admission were considered: age, sex, winter admission, pathogen co-detection, and eleven laboratory measurements (creatine kinase MB isoenzyme, creatine kinase, lactate dehydrogenase, total and direct bilirubin, alanine and aspartate aminotransferases, creatinine, urea, procalcitonin and carbon dioxide combining power). Winter admission was defined as admission in December, January or February, and the definition was applied identically in all three years. Co-detection was defined as the identification of at least one additional respiratory pathogen in the same admission, either by the multiplex panel or by sputum culture; sputum culture was sent in 435 of 476 admissions (91.4%) and identified a bacterial pathogen in 31 of them. Because the multiplex panel was performed in every child but culture was not, co-detection was also defined a second time using nucleic acid results only, and all models were refitted under that narrower definition. Laboratory values were those of the first specimen drawn after admission. Availability of every candidate is given in Supplementary Table S1; completeness exceeded 94% for all variables except procalcitonin (86.1%).

Missing laboratory values were handled by multiple imputation with chained equations (20 imputations, 20 iterations), with all fifteen candidates and the outcome in the imputation model and coefficients pooled by Rubin’s rules [11]. Median imputation, complete-case analysis and log-transformed imputation were carried out as sensitivity analyses, because several analytes were strongly right-skewed and median replacement compresses variance.

Sample size

The final three-parameter model used all 476 admissions and 106 events, giving 35 events per parameter against a conventional minimum of ten [12]; the fifteen candidates provided only 7.1 events each, so selection was penalised and its stability was quantified rather than assumed. The transportability analysis used a model refitted in 193 admissions with 62 events (20.7 events per parameter) and applied to 283 admissions with 44 events, so all its estimates are reported with bootstrap confidence intervals.

Variable selection and specification stability

Candidates were first ranked by least absolute shrinkage and selection operator (LASSO) logistic regression with 10-fold cross-validation over a logarithmically spaced penalty grid [13]. Because a single penalised fit can be unstable in a modest sample, the entire selection was repeated in 300 bootstrap resamples and the proportion of resamples retaining each candidate was recorded as its selection frequency [14].

At the penalty minimising the cross-validated deviance ($\lambda = 0.0028$), LASSO retained 14 of the 15 candidates, so penalisation did not by itself produce a parsimonious model. Selection frequency was therefore used as a first, reproducible filter: seven candidates were retained in at least 95% of bootstrap resamples (age 99.7%, co-detection 99.7%, lactate dehydrogenase 99.0%, creatine kinase MB 98.3%, creatinine 98.3%, winter admission 97.0% and total bilirubin 96.7%). These seven formed the comparator model. A candidate entered the primary model only if, in addition, its odds ratio was materially unchanged in four specifications of the model: the raw scale; the natural-logarithmic scale (necessary because several analytes were strongly right-skewed — total bilirubin skewness 8.65, alanine aminotransferase 9.18, procalcitonin 13.25); winsorisation of values outside the 1st and 99th percentiles; and restriction to complete cases. No variable was excluded on the basis of a p value alone, and the comparator model is reported in full so that the cost of the restriction can be judged.

Model development and internal validation

Logistic regression was fitted by maximum likelihood. Continuous predictors were divided by their standard deviation so that odds ratios are expressed per standard deviation; the binary co-detection variable was left on its natural 0/1 scale so that its odds ratio compares co-detection with single RSV infection. The functional form of age, the dominant predictor, was checked by adding a three-knot restricted cubic spline (knots at the 10th, 50th and 90th percentiles) and comparing the spline model with the linear model by likelihood ratio test, Akaike information criterion and AUC [15].

Discrimination was summarised by the area under the receiver operating characteristic curve (AUC) with 95% confidence intervals from 1000 bootstrap resamples. Optimism was estimated from 500 bootstrap resamples in which the whole modelling sequence — standardisation, fitting and prediction — was repeated, and the optimism-corrected AUC was obtained by subtracting the mean optimism from the apparent AUC [16,17].

Calibration was assessed with three complementary measures, because none alone captures both the spread and the level of the predictions [18,19]. The calibration slope was obtained by regressing the outcome on the linear predictor (a slope of 1 indicates that the spread is correct); the calibration intercept, or calibration-in-the-large, was obtained by solving for the constant that makes the mean predicted probability equal the observed rate (0 indicates that the level is correct); and the Brier score summarised overall accuracy. Because a Brier score is uninterpretable in isolation, it was compared with that of a constant-risk model assigning every child the observed rate of the same cohort; a model that cannot beat that benchmark adds nothing to absolute risk prediction whatever its AUC [19]. The Hosmer–Lemeshow test with ten risk groups was also computed, although it is insensitive to uniform shifts in level [20]. Recalibration was performed in the evaluation cohort by correcting the intercept alone and then the intercept and slope [21].

Clinical utility was quantified by decision curve analysis, with net benefit calculated across threshold probabilities from 0.02 to 0.75 and compared with treating all and treating none [22]. Because net benefit computed on the fitting data is optimistic, curves were produced both in the full cohort (apparent) and in the 2025 admissions using the frozen 2023–2024 fit. Internal stability was additionally examined by stratified five-fold cross-validation.

Calendar-year transportability analysis

The final model reported in Table 2, the nomogram and the risk strata is the one fitted to all 476 admissions; its performance is therefore described by the optimism-corrected internal validation above, and the 2025 admissions are part of its development data. Separately, to examine how the same three predictors behaved across a change of calendar year, the model was refitted in admissions from 2023 and 2024 and applied without further modification to admissions in 2025. Selection of the three variables used the whole cohort, so this analysis is a transportability check rather than an independent external validation; it nonetheless shows what happens to discrimination, calibration slope, calibration intercept and Brier score when a model developed at one event rate is used at another [23]. The same procedure was repeated for a two-variable model without lactate dehydrogenase and for a model containing age alone.

Rule-out performance

Because the intended use is to identify children who will not stay beyond a week, performance was also expressed in the form relevant to that decision. A predicted risk of 20% was fixed in advance as the threshold below which a child would be regarded as low risk, because it corresponds to the boundary of the lowest third of predicted risk and because decision curve analysis showed positive net benefit there in both periods. At that threshold the sensitivity, specificity, positive and negative predictive value, positive and negative likelihood ratio, and the number of prolonged stays missed per 1000 admissions were

calculated with Wilson confidence intervals [24]; thresholds of 15%, 25% and 30% are given for comparison.

Nomogram

A nomogram was constructed from the primary model. Points were assigned so that the predictor with the largest contribution across its 5th-to-95th percentile range received 100 points; total points were mapped linearly onto the linear predictor and the linear predictor onto the predicted probability. The three variables were also divided into tertiles of predicted risk to compare predicted with observed rates. The full model equation is reported so that predictions can be reproduced without the figure.

Ethics and software

The study was approved by the Institutional Review Board of Sichuan University affiliated Chengdu Second People's Hospital (No. 2025030503303). The requirement for written informed consent was waived because the data were retrospective and anonymised before analysis. Analyses were performed in Python 3.13 (scikit-learn, statsmodels, matplotlib). Two-sided p values below 0.05 were considered statistically significant; p values are reported to three decimal places and odds ratios to two.

Results

Cohort assembly and calendar-year composition

Between January 2023 and December 2025, 494 admissions with laboratory-confirmed RSV infection were identified in 491 children. One admission was managed without ward admission, 13 were to the neonatal ward or neonatal intensive care unit, one had a length of stay shorter than one day, and three were repeat admissions of children already included; after these exclusions 476 admissions in 476 children remained for analysis (Figure 1). Median age was 20.0 months (IQR 8.0–38.6); 274 children (57.6%) were boys and 179

(37.6%) were younger than 12 months. Median length of stay was 6.3 days (IQR 5.0–7.0; range 1.1–15.9), and 106 admissions (22.3%) lasted 7 days or more.

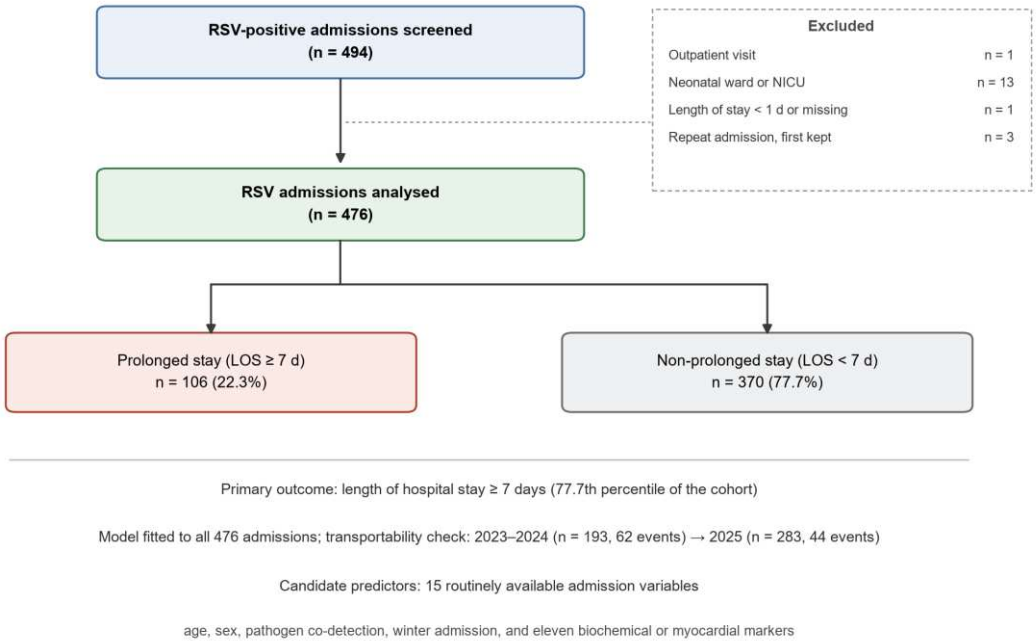


Figure 1. Selection of children admitted with respiratory syncytial virus (RSV) infection, 2023–2025. NICU, neonatal intensive care unit; LOS, length of stay.

The three years contributed 97, 96 and 283 admissions respectively, but the rate of prolonged stay was not stable across them: 30.9% (95% CI 22.6–40.7) in 2023, 33.3% (24.7–43.2) in 2024 and 15.5% (11.8–20.2) in 2025 (χ^2 $p < 0.001$). Comparing the two development years with 2025, the rate fell from 32.1% to 15.5% (crude odds ratio 0.39, 0.25–0.60). Only part of the fall is explained by case mix: children admitted in 2025 were older (median 23.1 vs 17.1 months), fewer were admitted in winter (23.7% vs 48.2%) because the 2025 season began earlier, and median length of stay was shorter (5.95 vs 6.86 days) (Supplementary Table S4). After adjustment for age, winter admission and co-detection the odds ratio for 2025 remained 0.50 (0.31–0.80).

Baseline characteristics

Children whose stay was prolonged were younger (median 9.3 vs 24.4 months, p < 0.001), more often had a co-detected pathogen (38.7% vs 27.0%, p = 0.028) and were more often admitted in winter (43.4% vs 30.8%, p = 0.021) (Table 1). Alanine aminotransferase was higher in that group (24 vs 19 U/L, p < 0.001), whereas lactate dehydrogenase (289 vs 302 U/L, p = 0.023) and creatinine (24 vs 26 μmol/L, p < 0.001) were lower; the remaining laboratory variables did not differ.

Table 1. Characteristics of children hospitalised with respiratory syncytial virus infection, by whether the stay was prolonged.

Characteristic	Prolonged stay (n = 106)	Not prolonged (n = 370)	P
Age (months)	9.3 (4.0–25.6)	24.4 (9.6–39.8)	<0.001
Male sex	69 (65.1)	205 (55.4)	0.095
Pathogen co-detection	41 (38.7)	100 (27.0)	0.028
Winter admission	46 (43.4)	114 (30.8)	0.021
CK-MB (U/L)	27.0 (23.0–35.0)	28.0 (22.0–35.0)	0.591
CK (U/L)	112.0 (77.0–153.0)	107.0 (80.5–152.0)	0.996
LDH (U/L)	289.0 (253.0–320.0)	302.0 (263.8–354.0)	0.023
Total bilirubin (μmol/L)	4.2 (2.8–6.5)	3.8 (2.8–5.1)	0.097
Direct bilirubin (μmol/L)	1.3 (0.8–2.1)	1.3 (1.0–1.7)	0.752
ALT (U/L)	24.0 (17.0–33.8)	19.0 (15.0–25.0)	<0.001
AST (U/L)	43.0 (35.0–53.0)	43.0 (35.0–51.0)	0.953
Creatinine (μmol/L)	24.0 (20.0–28.0)	26.0 (22.5–30.5)	<0.001
Urea (mmol/L)	2.7 (2.1–3.5)	2.9 (2.3–3.6)	0.305
PCT (ng/mL)	0.1 (0.1–0.1)	0.1 (0.1–0.2)	0.595
CO2 combining power (mmol/L)	21.0 (19.2–23.0)	20.7 (18.9–22.5)	0.226

Values are median (IQR) or n (%). Prolonged stay was defined as a length of stay of 7 days or more. P values are from the Mann–Whitney U test for continuous variables and the χ^2 or Fisher exact test for categorical variables. CK-MB, creatine kinase MB isoenzyme; CK, creatine kinase; LDH, lactate dehydrogenase; PCT, procalcitonin; CO2, carbon dioxide combining power.

Variable selection

At the penalty minimising the cross-validated deviance, LASSO retained 14 of the 15 candidates, excluding only aspartate aminotransferase, so the penalty did not produce parsimony (Figure 2A). Seven candidates were retained in at least 95% of 300 bootstrap resamples and formed the comparator model (Figure 2B).

The four-specification comparison then separated the candidates. Age, co-detection and lactate dehydrogenase were stable in every specification: age 0.49 (0.38–0.64) on the raw scale, 0.48 (0.39–0.60) on the log scale, 0.50 (0.39–0.64) after winsorisation and 0.54 (0.41–0.70) in complete cases; lactate dehydrogenase 0.66 (0.51–0.86) versus 0.72 (0.56–0.92) on the log scale; and co-detection 1.73 (1.07–2.79) to 1.79 (1.10–2.91) (Supplementary Table

S2). The other four failed. Total bilirubin was associated on the raw scale (1.44 (1.05–1.98), p = 0.024) but not on the log scale (0.98 (0.76–1.26), p = 0.870) and not in complete cases (1.07 (0.68–1.69)); its distribution was so skewed (median 3.9 µmol/L against a 99th percentile of 103.1) that the estimate was carried by a small number of high values, and it did not differ between groups on a rank test (p = 0.097). Creatinine (0.88 (0.65–1.19) on the raw scale but 0.70 (0.50–0.99) in complete cases), alanine aminotransferase (1.28 (0.98–1.65) to 1.34 (1.01–1.77)), creatine kinase MB (0.85 (0.61–1.18)) and winter admission (1.32 (0.82–2.11)) were inconsistent across specifications or were attenuated after adjustment. Age, co-detection and lactate dehydrogenase formed the primary model.

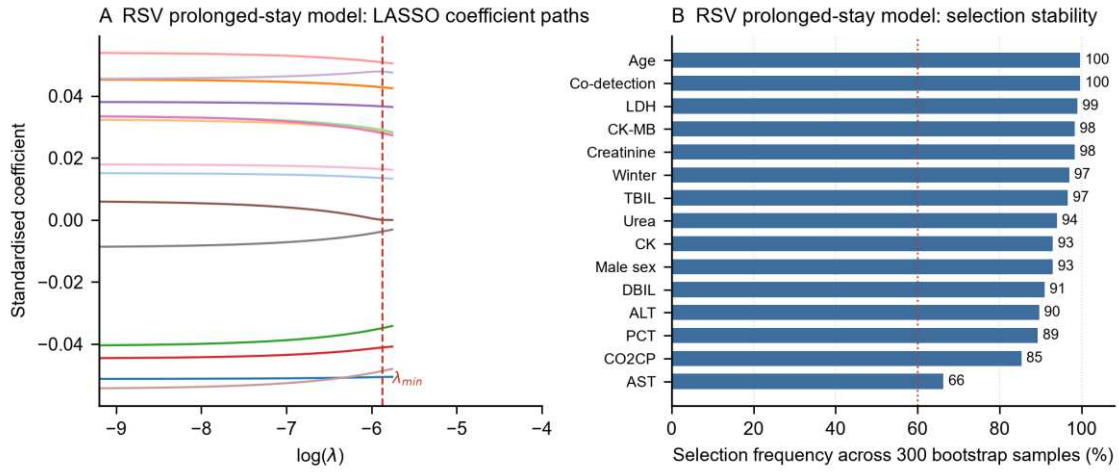


Figure 2. Variable selection for RSV prolonged stay. (A) LASSO coefficient paths for the 15 candidate predictors of prolonged hospital stay in children with RSV infection; the vertical line marks the penalty minimising the cross-validated deviance. (B) Selection frequency of each candidate in 300 bootstrap resamples of the RSV cohort.

Primary model

In the primary model, older age was associated with lower odds of a prolonged stay (odds ratio 0.49 per 16.7 months, 95% CI 0.38–0.64, p < 0.001), pathogen co-detection with higher odds (1.73, 1.07–2.79, p = 0.024) and lactate dehydrogenase with lower odds (0.66 per 66.6 U/L, 0.51–0.86, p = 0.002) (Table 2). Variance inflation factors were 1.03 for age, 1.01 for co-detection and 1.04 for lactate dehydrogenase, indicating no collinearity. Multiple imputation gave effectively the same estimates (age 0.50, 0.39–0.64; co-detection 1.73, 1.07–

2.79; lactate dehydrogenase 0.64, 0.50–0.83), so median imputation did not distort the coefficients. In the seven-variable comparator the first two estimates were preserved and slightly larger (age 0.68, 0.49–0.94; co-detection 1.88, 1.16–3.06), lactate dehydrogenase was attenuated (0.75, 0.55–1.02) and total bilirubin reached significance (1.53, 1.11–2.12, p = 0.010).

The fitted equation on the original scale is logit(p) = 1.308 − 0.0422 × age (months) + 0.5488 × co-detection (1 if present, 0 if not) − 0.00621 × lactate dehydrogenase (U/L), where p is the probability of a stay of 7 days or more. Age entered as age divided by 16.7 months and lactate dehydrogenase as the value divided by 66.6 U/L; the means were 23.2 months and 307.0 U/L respectively.

Table 2. Multivariable logistic models for prolonged hospital stay in children with respiratory syncytial virus infection (n = 476, 106 events).

Predictor	beta	OR (95% CI)	P	Scale
Primary model (3 variables)				
Age	-0.705	0.49 (0.38–0.64)	<0.001	per 16.7 months
Pathogen co-detection	+0.549	1.73 (1.07–2.79)	0.024	yes vs no
Lactate dehydrogenase	-0.414	0.66 (0.51–0.86)	0.002	per 66.6 U/L
Comparator model (7 variables meeting the frequency criterion)				
Age	-0.392	0.68 (0.49–0.94)	0.020	per 16.7 months
Pathogen co-detection	+0.632	1.88 (1.16–3.06)	0.011	yes vs no
Lactate dehydrogenase	-0.284	0.75 (0.55–1.02)	0.070	per 66.6 U/L
CK-MB	-0.197	0.82 (0.59–1.15)	0.248	per 15.4 U/L
Creatinine	-0.340	0.71 (0.51–1.00)	0.052	per 6.1 µmol/L
Winter admission	+0.349	1.42 (0.88–2.30)	0.156	yes vs no
Total bilirubin	+0.426	1.53 (1.10–2.12)	0.010	per 18.8 µmol/L

Continuous predictors are expressed per 1 SD; co-detection is expressed as yes versus no. beta, regression coefficient on the stated scale; OR, odds ratio; CI, confidence interval; CK-MB, creatine kinase MB isoenzyme. The intercept of the primary model is 1.308.

Model performance and internal validation

The primary model achieved an AUC of 0.708 (95% CI 0.653–0.760). The mean optimism over 500 bootstrap resamples was 0.021, giving an optimism-corrected AUC of 0.687. The calibration slope was 1.00, the calibration intercept 0.00 by construction, the Hosmer–Lemeshow statistic 9.76 (p = 0.282) and the Brier score 0.158 (Table 3, Figure 3B). Five-fold cross-validation gave an AUC of 0.698. The seven-variable comparator had a higher apparent AUC (0.728, 0.676–0.778) but greater optimism (0.045), so its corrected value (0.684) was

no better than that of the three-variable model; the fourteen-variable model corrected to 0.673, lower than either.

The functional form of age did not require a spline. Adding a three-knot restricted cubic spline changed the log-likelihood by 0.59 (likelihood ratio p = 0.443), left the AUC essentially unchanged (0.708 vs 0.709) and worsened the Akaike information criterion (468.8 vs 470.2). Age was therefore retained as a linear term.

Table 3. Discrimination, calibration and overall performance of the candidate models for prolonged stay in respiratory syncytial virus infection (n = 476, 106 events).

Model	k	AUC (95% CI)	Optimism	Corrected AUC	Slope	H-L p	Brier
Primary model, 3 variables	3	0.708 (0.653–0.760)	0.021	0.687	1.00	0.282	0.158
Comparator model, 7 variables	7	0.728 (0.676–0.778)	0.045	0.684	1.00	0.618	0.151
Full model, 14 variables	14	0.747 (0.696–0.801)	0.074	0.673	1.00	0.259	0.145

k, number of parameters; AUC, area under the receiver operating characteristic curve; CI, confidence interval; Optimism, mean optimism over 500 bootstrap resamples; Slope, calibration slope; H-L p, Hosmer–Lemeshow test with 10 risk groups; Brier, Brier score. The calibration intercept of a model fitted and evaluated in the same data is 0 by construction and is therefore not shown.

Transport to a later calendar year

In the development period (2023–2024, n = 193, 62 events) the primary model reached an AUC of 0.694. Applied unchanged to 2025, where the event rate was half as high (44/283, 15.5%), it achieved an AUC of 0.701 (0.623–0.772) and a calibration slope of 1.07 (0.64–1.60). Discrimination and the spread of the predictions therefore transported. The level of the predictions did not. The calibration intercept was −0.82 (95% CI −1.20 to −0.51), the mean predicted risk 28.3% against an observed rate of 15.5%, and the Brier score 0.142 (0.125–0.161), which is worse than the 0.131 obtained by assigning every child in that year the observed rate (Table 4, Figure 3B). The nine highest deciles of predicted risk are reported in Supplementary Table S5: in the top decile the observed rate was 27.6% against a predicted 52.6%.

The intercept deficit was the same whichever variables the model contained: −0.83 with age alone, −0.81 without lactate dehydrogenase and −0.82 with the full three-variable model. It therefore reflects the change in the event rate between the two periods, not any property of the predictors. Recalibrating the intercept alone restored agreement (Brier 0.124, below the

constant-risk benchmark of 0.131) and left the AUC unchanged at 0.701; adding a slope correction did not improve on this (0.124). Lactate dehydrogenase earned its place in the model on transport: without it the AUC fell to 0.656 and the calibration slope to 0.84, and with age alone they were 0.646 and 0.74 (Table 4).

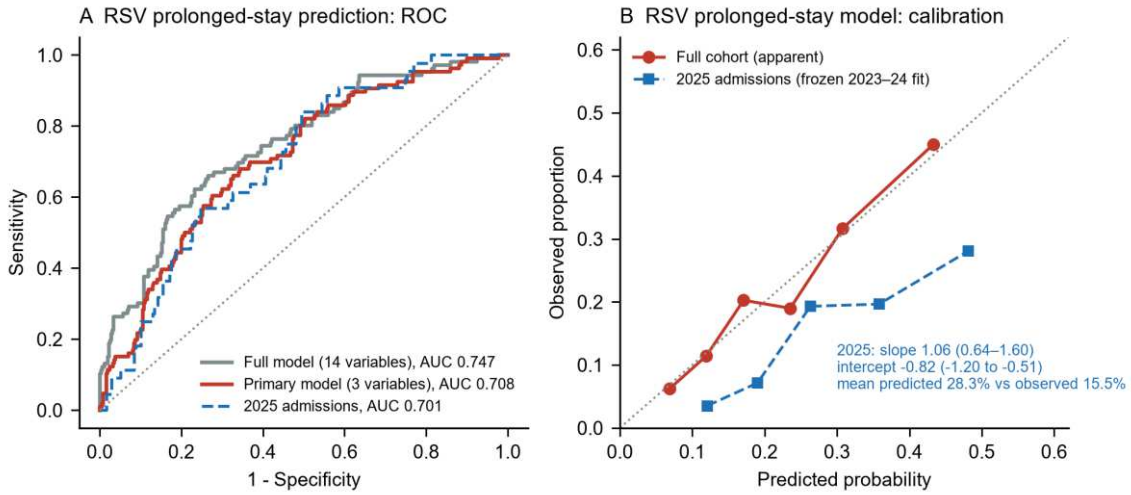


Figure 3. Discrimination and calibration of the RSV prolonged-stay model. (A) Receiver operating characteristic curves for the full model (14 variables), the primary model (3 variables) and the 2025 admissions analysed with the model fitted to 2023–2024. (B) Calibration of the primary model in the full cohort and in the 2025 admissions; the dotted line is the line of identity. The 2025 points lie below the identity line because the observed rate of prolonged stay in that year was lower than the rate at which the model had been fitted.

Table 4. Transport of the RSV prolonged-stay model from 2023–2024 (n = 193, 62 events) to 2025 (n = 283, 44 events; observed rate 15.5%).

Model	AUC in 2025 (95% CI)	Slope (95% CI)	Intercept (95% CI)	Brier	Recalibrated Brier
Primary model (age, co-detection, LDH)	0.701 (0.623–0.772)	1.06 (0.64–1.60)	−0.82 (−1.20, −0.51)	0.142	0.124
Without LDH (age, co-detection)	0.656 (0.597–0.716)	0.84 (0.51–1.17)	−0.81 (−1.11, −0.51)	0.145	0.126
Age alone	0.646 (0.586–0.706)	0.74 (0.41–1.07)	−0.83 (−1.13, −0.53)	0.149	0.128

Each model was refitted in admissions from 2023–2024 and applied without modification to 2025; variable selection, however, used the whole cohort, so the 2025 estimates are a transportability check rather than an independent external validation. Development AUCs were 0.694 (primary), 0.682 (without LDH) and 0.690 (age alone). The constant-risk Brier score in 2025 was 0.131 for every row; recalibration corrected the intercept only. Confidence intervals for the two reduced models are approximate. AUC, area under the curve; LDH, lactate dehydrogenase.

Rule-out performance and clinical utility

At the prespecified 20% threshold, the full-cohort model classified 49.6% of children as low risk, with a sensitivity of 71.7% and a negative predictive value of 87.3% (82.4–90.9); 63 prolonged stays per 1000 admissions would have been misclassified. Applied to 2025, the same threshold classified 33.9% as low risk with a negative predictive value of 95.8% (89.8–98.4) and 14 missed events per 1000; the negative likelihood ratio was 0.24 (Table 5). The

negative predictive value is higher in 2025 because the event rate was lower, which is a property of the prevalence and not of the model.

Table 5. Rule-out performance of the RSV prolonged-stay model at four predicted-risk thresholds.

Cohort	Threshold	Low risk (%)	Sensitivity (95% CI)	Specificity (%)	NPV (95% CI)	LR+	LR−	Missed per 1000
Full cohort	15%	35.5	85.8 (78.0–91.2)	41.6	91.1 (85.9–94.5)	1.47	0.34	32
Full cohort	20%	49.6	71.7 (62.5–79.4)	55.7	87.3 (82.4–90.9)	1.62	0.51	63
Full cohort	25%	62.0	62.3 (52.8–70.9)	68.9	86.4 (82.1–89.9)	2.00	0.55	84
Full cohort	30%	74.6	44.3 (35.2–53.8)	80.0	83.4 (79.2–86.9)	2.22	0.70	124
2025 admissions	15%	17.3	97.7 (88.2–99.6)	20.1	98.0 (89.3–99.6)	1.22	0.11	4
2025 admissions	20%	33.9	90.9 (78.8–96.4)	38.5	95.8 (89.8–98.4)	1.48	0.24	14
2025 admissions	25%	47.3	77.3 (63.0–87.2)	51.9	92.5 (86.8–95.9)	1.61	0.44	35
2025 admissions	30%	58.3	63.6 (48.9–76.2)	62.3	90.3 (84.8–93.9)	1.69	0.58	56

A child is classified low risk when the predicted probability of a stay of 7 days or more is below the threshold. Sensitivity and negative predictive value are shown with 95% Wilson confidence intervals; missed per 1000 is the number of prolonged stays that would fall below the threshold per 1000 admissions. NPV, negative predictive value; LR+ and LR−, positive and negative likelihood ratios. In the 2025 column the model was fitted to 2023–2024 and applied without recalibration; after recalibration the negative predictive value would be higher still.

Decision curve analysis was consistent with that reading. In the full cohort net benefit was positive and exceeded that of treating all children between thresholds of 0.04 and 0.38, and became negative at 0.40 (−0.006). In the 2025 admissions, using the frozen fit, net benefit was positive only between 0.07 and 0.22 and was negative beyond that (Figure 5A). That window is precisely the range in which a rule-out decision is made, and it does not extend to the thresholds at which a clinician would consider escalating care.

Nomogram and risk stratification

The nomogram assigned 100 points to age, 63.5 points to lactate dehydrogenase and 26.7 points to co-detection, giving a maximum of 190 points (Figure 4). A total of 101 points corresponds to a predicted risk of 20% and 127 points to 30%. For illustration, a 12-month-old child without co-detection and with a lactate dehydrogenase of 320 U/L scores about 111 points, corresponding to an estimated risk of 23%; a 3-month-old child with co-detection and a lactate dehydrogenase of 250 U/L scores about 177 points, corresponding to 54%.

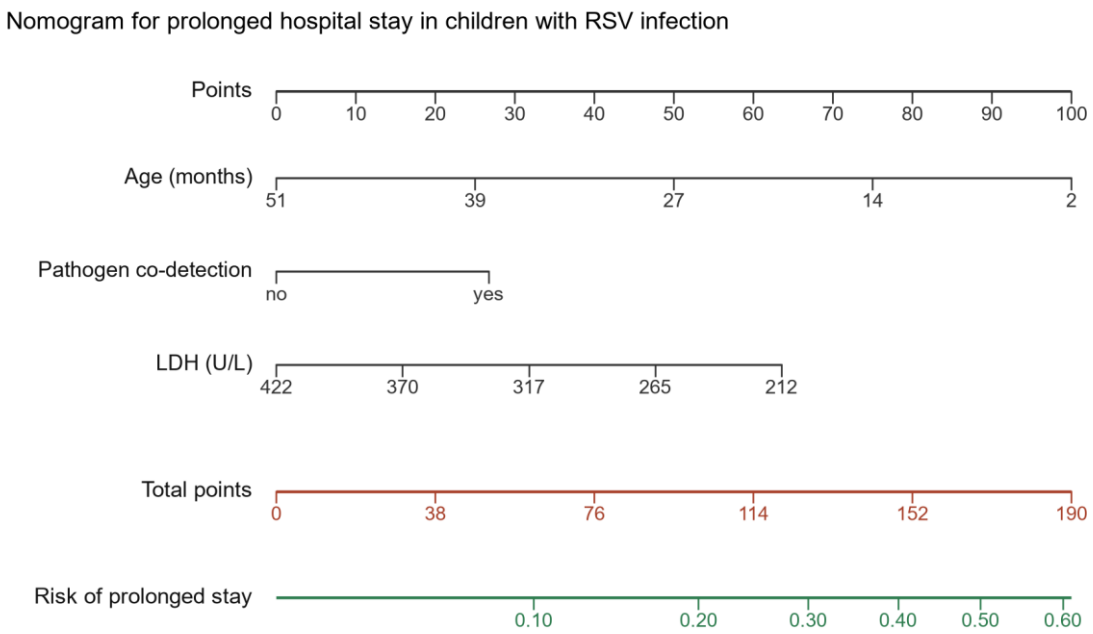


Figure 4. Nomogram for the predicted probability of prolonged hospital stay in children with respiratory syncytial virus infection. Points for each predictor are read on the top axis, summed on the total points axis, and translated into risk on the bottom axis.

Dividing the cohort into tertiles of predicted risk produced a monotonic gradient. Observed prolonged-stay rates were 8.8% (14/159) in the low tertile, 19.6% (31/158) in the intermediate tertile and 38.4% (61/159) in the high tertile, against predicted rates of 9.4%, 20.3% and 37.1% (Figure 5B).

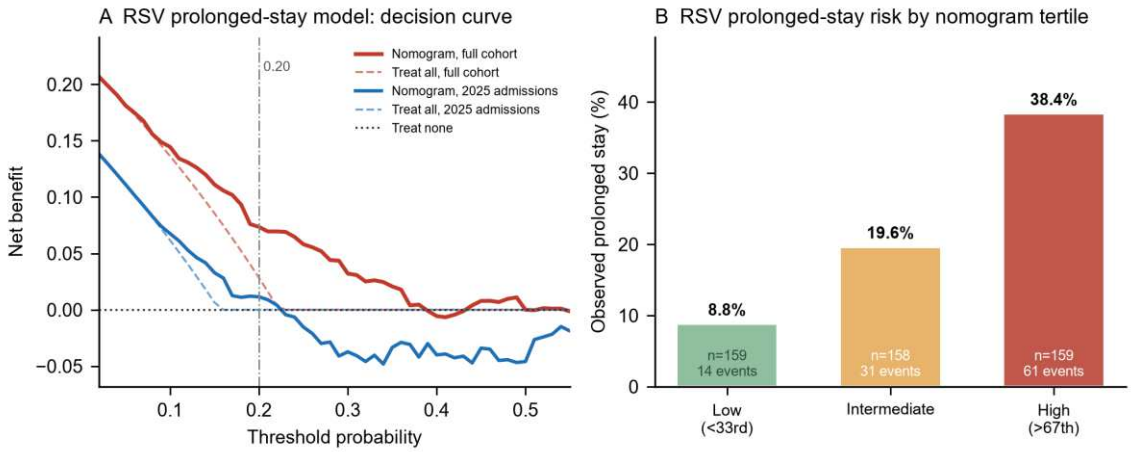


Figure 5. Clinical utility and risk stratification of the RSV prolonged-stay model. (A) Decision curve analysis in the full cohort and in the 2025 admissions; net benefit of the nomogram is compared with treating all children and treating none across threshold probabilities, and the vertical line marks the prespecified 20% threshold. (B) Observed rate of prolonged stay by tertile of nomogram-predicted risk.

Sensitivity analyses

Raising the threshold to 8 days or more (50 events) increased discrimination to 0.767 (0.701–0.827). Defining the outcome as a stay above the empirical 75th percentile rather than 7 days or more, which reclassifies the 16 children discharged in the hour before the seventh day, gave 0.708 (0.657–0.758). Restricting co-detection to nucleic acid results, which removes the 25 co-detections identified only by sputum culture, gave 0.707 (0.651–0.759) and an unchanged co-detection odds ratio of 1.75 (1.05–2.91); the interaction between co-detection and whether a culture was sent was not significant (p = 0.828). Modelling the logarithm of length of stay as a continuous outcome gave a linear model with $R^2 = 0.070$, the same three variables remaining associated. Multiple imputation gave an AUC of 0.712 and complete-case analysis 0.694 (0.631–0.750), essentially unchanged (Table 6).

Table 6. Sensitivity analyses of the primary model for prolonged stay in respiratory syncytial virus infection.

Analysis	n	Events	AUC (95% CI)
Primary definition (LOS ≥ 7 days)	476	106	0.708 (0.652–0.760)
LOS ≥ 8 days	476	50	0.767 (0.701–0.827)
LOS above the 75th percentile	476	119	0.708 (0.657–0.758)
Co-detection by nucleic acid only	476	106	0.707 (0.651–0.759)
Complete cases only	449	97	0.694 (0.631–0.750)
Multiple imputation (20 imputations)	476	106	0.712

AUC, area under the receiver operating characteristic curve; CI, confidence interval from 800 bootstrap resamples; LOS, length of stay. The primary analysis used median imputation; multiple imputation and complete-case analysis are shown as alternatives.

Discussion

In a three-year cohort of 476 children admitted to general paediatric wards with laboratory-confirmed RSV infection, three variables obtainable on the day of admission — age, pathogen co-detection and lactate dehydrogenase — predicted a stay of 7 days or more with an apparent AUC of 0.708, an optimism-corrected AUC of 0.687 and a Brier score of 0.158. Discrimination and the spread of the predictions were preserved when the same predictors were applied to a later year (AUC 0.701, slope 1.07); the absolute risks were not (intercept −0.82, Brier 0.142 against a constant-risk benchmark of 0.131). The model separates children into groups with a fourfold difference in risk, and at a 20% threshold it identifies a third of

admissions in which a long stay is unlikely. It does not identify individual children with the certainty that would justify a change in clinical management.

Age dominated the model. Each additional 16.7 months roughly halved the odds of a prolonged stay, and a model containing age alone reached an AUC of 0.678 in the whole cohort, against 0.708 for the three-variable model (0.690 against 0.694 in the 2023–2024 development subset). Most of the discriminative information therefore lies in how old the child is. This is consistent with the epidemiology of RSV: the burden of severe disease is concentrated in the first months of life, when narrower airways, lower functional residual capacity, predominantly nasal breathing and limited reserve for feeding all prolong recovery [2,25]. We checked whether the linear term was adequate, because a monotonic effect over the whole range from birth to five years is an assumption rather than a finding; a three-knot spline did not improve the fit (likelihood ratio $p = 0.443$), so the simpler form was kept. The dominance of age also explains why several laboratory associations disappeared on adjustment. Alanine aminotransferase and creatinine both vary systematically with age in childhood, and their univariable associations with prolonged stay in this cohort were largely explained by the younger age of the children who stayed longer. Reporting such associations without adjustment, as is common in single-centre RSV series, would have produced a model that appeared to be biochemically informative while resting almost entirely on age.

Pathogen co-detection was the only predictor that is not fixed at birth, with an adjusted odds ratio of 1.73. The direction is consistent with reports that multiple respiratory pathogens are associated with more severe illness and longer admission [26]. Three qualifications are needed. First, detection is not causation: in young children, rhinovirus and bocavirus are frequently present without contributing to the current illness, so co-detection may be a marker of a different exposure pattern rather than a direct cause of slower recovery. Second, co-detection is partly an artefact of ascertainment. The multiplex panel was performed in every

child, but the bacterial component of co-detection depends on sputum culture, which was sent in 91.4% of admissions; children in whom a culture was sent may differ from those in whom it was not. We therefore refitted the model with a nucleic-acid-only definition, which reduced the prevalence of co-detection from 29.6% to 24.4% but left the odds ratio unchanged (1.75, 1.05–2.91), and found no interaction with whether a culture was sent. Third, children in whom a full panel is requested and positive may be observed for longer regardless of their clinical course. The stability of the estimate across four specifications, and its persistence after adjustment for age and lactate dehydrogenase, argue against a purely artifactual association, but they cannot establish a mechanism.

The inverse association with lactate dehydrogenase was not anticipated. Higher admission lactate dehydrogenase was associated with a shorter rather than a longer stay, and the estimate was essentially identical on the raw and logarithmic scales (0.66 versus 0.72 per SD, both significant), and it persisted after adjustment for the other two variables. We are unable to offer a convincing biological explanation. Lactate dehydrogenase is a non-specific marker of cell turnover that rises with the acute cytopathic response and falls as it resolves; a high admission value may therefore identify children at the peak of an illness that will subsequently improve quickly, whereas a low value may accompany a more indolent course. Residual confounding by age, feeding difficulty or nutritional status cannot be excluded. Two further observations counsel caution. Lactate dehydrogenase was the least universally available of the three variables (94.3% complete), and its estimate weakened in the seven-variable model (0.75, 0.55–1.02; $p = 0.070$), in which total bilirubin became the strongest laboratory term. Against that, removing it cost discrimination (AUC 0.701 to 0.657) and slope (1.07 to 0.84) on transport, so it is doing statistical work even though we cannot say why. We therefore present it as an empirical contributor to prediction, and we would expect it

to be the first coefficient to fail in an external dataset. The nomogram should not be read as implying that modifying it would alter the length of stay.

The 7-day threshold deserves justification rather than convention, because the word "prolonged" is only meaningful relative to what is usual locally. Three reference points make the boundary defensible in this setting. First, the national averages: tertiary children's hospitals in China reported a mean length of stay of 6.3 days and tertiary general hospitals 7.6 days [10], so a 7-day admission sits at, not above, the prevailing system average; a stay that crosses it moves from the typical band into the right tail for the very condition that dominates paediatric inpatient demand. Second, the distribution within this cohort: median 6.3 days, 75th percentile 6.96 days, and the 7-day cut at the 77.7th percentile. Third, the payment architecture. Since 2019 China has progressively replaced fee-for-service reimbursement with prospective case-based payment, under which a hospital receives a fixed amount for a diagnostic group and bears the cost of bed-days beyond the group average itself [27]. In a system where paediatric beds are scarce and occupied at close to capacity through the respiratory season, the eighth day is therefore not a neutral statistical event: it is an unreimbursed cost to the ward and a bed unavailable to the next infant. That is why a threshold defined on calendar days, rather than a percentile, is the operationally meaningful one — and it is also why we retained the 7-day definition in the primary analysis even though the empirical 75th percentile lies a few hours below it.

The closest published comparator is the model of Wollny and colleagues, which used the United States National Inpatient Sample to predict a stay at or above the 90th percentile in 9589 children under two years, with development in 2016 and out-of-sample testing in 2017, and reported an AUC of 0.73 [8]. The two studies answer the same clinical question with different data. Wollny's predictors — interhospital transfer, intubation, comorbidity and hospital attributes — are recorded reliably in administrative data but are either unavailable or

uninformative at the moment of admission on a ward, and three of them are consequences of severity rather than antecedents of it. Our model uses only variables a ward doctor already has, in a single centre in a middle-income country, and we report the calibration intercept on transfer in addition to the AUC. The price of that restriction is a lower AUC (0.701 versus 0.73) and a much smaller sample. Neither model has been externally validated in the other's setting, and the comparison should be read as complementary rather than competitive. One point of convergence is worth noting: in the American sample the 90th percentile of length of stay also fell at 7 days, so the two studies defined "prolonged" as the same interval despite deriving it from different distributions.

The most important finding of this study is not the AUC but the behaviour of the absolute risks. Between 2023–2024 and 2025 the observed rate of prolonged stay fell from 32.1% to 15.5%, and the fall was only partly explained by case mix: after adjustment for age, season and co-detection the odds ratio for 2025 was still 0.50. Whatever its cause — a change in discharge practice, in bed pressure, or in the severity of the children referred — the consequence for a prediction model is the same. The calibration slope, which is the quantity usually reported, was 1.07 and would have been read as evidence of good calibration. It is not: a slope close to 1 says only that the spread of the predictions is right, and says nothing about their level. The calibration intercept was −0.82, the mean predicted risk was nearly double the observed rate, and the Brier score was worse than that of a model that assigns every child the same probability. The intercept deficit was identical (−0.81 to −0.83) whether the model contained one, two or three variables, which locates the problem unambiguously in the change of event rate rather than in the predictors. Recalibrating the intercept alone restored agreement (Brier 0.124) without touching discrimination. The practical lesson is that a model of this kind is transportable in its ranking but not in its numbers, and that a single intercept correction against local data is the minimum precondition for use [21,23].

That finding also determines how the model should be positioned. Calibration in the development cohort was good by construction; on transfer, the model that should be used is the recalibrated one, and the claim we are prepared to make is that discrimination and the ordering of risk are stable across calendar years, not that predicted probabilities can be taken at face value. Within that limit the model is a rule-out instrument. At a predicted risk below 20%, a third of the 2025 admissions were classified as unlikely to stay a week, with a negative predictive value of 95.8% and 14 missed events per 1000 admissions; in the development cohort the same threshold captured half the admissions with a negative predictive value of 87.3%. Those numbers, rather than the AUC, are what a discharge planner needs. The model should not be used to justify escalation: in the later year net benefit was positive only up to a predicted risk of 0.22, which is below the range in which a clinician would be considering escalation.

Several limitations should be weighed. The study was retrospective and single centre, and the analysis plan was not registered prospectively; the stability criteria were applied during analysis and are best regarded as exploratory rather than confirmatory. Variable selection used the whole cohort, so the 2023–2024 fit is not an independent development set and the 2025 estimates are a transportability check rather than an external validation; the 62 events available in that subset would in any case have been too few to support stable selection (no candidate reached 95% frequency when selection was repeated within it). Length of stay is a discharge-practice dependent outcome, and the fall in the event rate between the two periods shows how strongly it responds to factors outside the child. Co-detection cannot distinguish co-infection from colonisation and, for the bacterial component, depends on whether a culture was sent. We had no information on RSV subtype or viral load, on oxygen requirement, feeding support or other treatment, on socioeconomic status, or on the exact time of specimen collection. Laboratory values were missing in up to 14% of children for procalcitonin and

5.7% for lactate dehydrogenase; multiple imputation and complete-case analysis gave coefficients and discrimination close to the primary analysis, but informative missingness cannot be excluded. Finally, with 106 events the confidence interval around the AUC is wide, and in the 2025 subset, with 44 events, it is wider still.

Conclusions

Age, pathogen co-detection and admission lactate dehydrogenase predict, with moderate discrimination, which children admitted with RSV will remain in hospital for a week or more. In this cohort the ranking of risk transferred to a later year in which the event rate had halved, but the predicted probabilities did not, and the model was inferior to a constant-risk benchmark until its intercept was corrected. The model requires no test beyond those already ordered on admission, and at a 20% threshold it identifies a low-risk group in whom early discharge planning is reasonable. Prospective external validation in other hospitals, with recalibration to local incidence and explicit attention to discharge practice, is the necessary next step.

Declarations

Ethics approval and consent to participate. The study was conducted in accordance with the Declaration of Helsinki and was approved by the Institutional Review Board of the Sichuan University Affiliated Chengdu Second People's Hospital (approval No. 2025030503303). The requirement for individual informed consent was waived by the Institutional Review Board owing to the retrospective use of de-identified electronic medical records.

Consent for publication. Not applicable.

Availability of data and materials. The dataset analysed during the study, the analysis code and the fitted model coefficients are available from the corresponding author on reasonable request, subject to institutional data-sharing approval.

Competing interests. The authors declare that they have no competing interests.

Funding. This work was supported by the Project of Chengdu Municipal Health Commission (Project No. 2025669). Project of Chengdu Municipal Health Commission (Project No. 2026082).The funder was not involved in the study design, collection, analysis, interpretation of data, the writing of this article, or the decision to submit it for publication.

Authors' contributions. Ai Chen: Conceptualization, Methodology, Formal analysis, Data curation, Visualization, Writing – original draft. Zhi Chen : Methodology, Validation. Yuanlin Zhou: Data curation, Writing – review & editing.Peilin Dai: Data curation and statistical analysis, Investigation. YueXiu Chen: Data curation, Investigation. Ying Pang: Data curation, Resources. Hui Zhu: Data curation, Resources. Xiong Fu,Shuyao Zhu: Supervision. All authors critically revised the manuscript and approved the final version.

Acknowledgements.

The authors thank the clinical laboratory staff for pathogen testing and all the medical staff who admitted and treated the patients.

References

1. Li Y, Wang X, Blau DM, Caballero MT, Feikin DR, Gill CJ, et al. Global, regional, and national disease burden estimates of acute lower respiratory infections due to respiratory syncytial virus in children younger than 5 years in 2019: a systematic analysis. Lancet. 2022;399:2047–64.
2. Langedijk AC, Bont LJ. Respiratory syncytial virus infection and novel interventions. Nat Rev Microbiol. 2023;21:734–49.
3. Sun W, Duan Q, Guo L, Zhu A, Tang A, Miao Z, et al. The epidemiology and burden of respiratory syncytial virus and influenza infections in hospitalized children under 5 years old in Zhejiang, China (2018–2023). Front Public Health. 2025;13:1470770.

4. Li Y, Reeves RM, Wang X, Bassat Q, Brooks WA, Cohen C, et al. Global patterns in monthly activity of influenza virus, respiratory syncytial virus, parainfluenza virus, and metapneumovirus: a systematic analysis. Lancet Glob Health. 2019;7:e1031–45.

5. Miao Y, Xu X, Mao Z, Wang X, Li Y. Management cost of respiratory syncytial virus-associated hospitalisation episodes in children: a retrospective analysis of a regionally representative medical database in Eastern China. J Glob Health. 2026;16:04071.

6. Rodriguez H, Hartert TV, Gebretsadik T, Carroll KN, Larkin EK. A simple respiratory severity score that may help predict need for mechanical ventilation in respiratory syncytial virus infection. J Perinatol. 2017;37:933–8.

7. Sheikh Z, Potter E, Li Y, Cohen RA, Dos Santos G, Bont L, et al. Validity of clinical severity scores for respiratory syncytial virus: a systematic review. J Infect Dis. 2024;229(Suppl 1):S8–17.

8. Wollny K, Pitt T, Brenner D, Metcalfe A. Predicting prolonged length of stay in hospitalized children with respiratory syncytial virus. Pediatr Res. 2022;92:1780–6.

9. Collins GS, Moons KGM, Dhiman P, Riley RD, Beam AL, Van Calster B, et al. TRIPOD+AI statement: updated guidance for reporting clinical prediction models that use regression or machine learning methods. BMJ. 2024;385:e078378.

10. National Health Commission of the People's Republic of China. China Health Statistical Yearbook 2023. Beijing: China Union Medical College Press; 2023.

11. Austin PC, White IR, Lee DS, van Buuren S. Missing data in clinical research: a tutorial on multiple imputation. Can J Cardiol. 2021;37:1322–31.

12. Riley RD, Snell KI, Ensor J, Burke DL, Harrell FE Jr, Moons KGM, et al. Minimum sample size for developing a multivariable prediction model: Part II — binary and time-to-event outcomes. Stat Med. 2019;38:1276–96.

13. Riley RD, Snell KIE, Martin GP, Whittle R, Archer L, Sperrin M, et al. Penalization and shrinkage methods produced unreliable clinical prediction models especially when sample size was small. J Clin Epidemiol. 2021;132:88–96.

14. Meinshausen N, Bühlmann P. Stability selection. J R Stat Soc Series B. 2010;72:417–73.

15. Harrell FE Jr. Regression Modeling Strategies: With Applications to Linear Models, Logistic and Ordinal Regression, and Survival Analysis. 2nd ed. Cham: Springer; 2015.

16. Harrell FE Jr, Lee KL, Mark DB. Multivariable prognostic models: issues in developing models, evaluating assumptions and adequacy, and measuring and reducing errors. Stat Med. 1996;15:361–87.

17. Steyerberg EW. Clinical Prediction Models: A Practical Approach to Development, Validation, and Updating. 2nd ed. Cham: Springer; 2019.

18. Van Calster B, McLernon DJ, van Smeden M, Wynants L, Steyerberg EW. Calibration: the Achilles heel of predictive analytics. BMC Med. 2019;17:230.

19. Van Calster B, Nieboer D, Vergouwe Y, De Cock B, Pencina MJ, Steyerberg EW. A calibration hierarchy for risk models was defined: from utopia to empirical data. J Clin Epidemiol. 2016;74:167–76.

20. Hosmer DW Jr, Lemeshow S, Sturdivant RX. Applied Logistic Regression. 3rd ed. Hoboken: Wiley; 2013.

21. Janssen KJM, Moons KGM, Kalkman CJ, Grobbee DE, Vergouwe Y. Updating methods improved the performance of a clinical prediction model in new patients. J Clin Epidemiol. 2008;61:76–86.

22. Vickers AJ, Elkin EB. Decision curve analysis: a novel method for evaluating prediction models. Med Decis Making. 2006;26:565–74.

23. Riley RD, Archer L, Snell KIE, Collins GS, Dhiman P, Martin GP, et al. Evaluation of clinical prediction models (part 2): how to undertake an external validation study. BMJ. 2024;384:e074821.

24. Vergouwe Y, Steyerberg EW, Eijkemans MJC, Habbema JDF. Substantial effective sample sizes were required for external validation studies of predictive logistic regression models. J Clin Epidemiol. 2005;58:475–83.

25. Shi T, Vennard S, Mahdy S, Nair H; RESCEU Investigators. Risk factors for poor outcome or death in young children with respiratory syncytial virus–associated acute lower respiratory tract infection: a systematic review and meta-analysis. J Infect Dis. 2022;226(Suppl 1):S10–17.

26. Meskill SD, O'Bryant SC. Respiratory virus co-infection in acute respiratory infections in children. Curr Infect Dis Rep. 2020;22:3.

27. Chen YJ, Zhang XY, Tang X, Yan JQ, Qian MC, Ying XH. How do inpatients' costs, length of stay, and quality of care vary across age groups after a new case-based payment reform in China? An interrupted time series analysis. BMC Health Serv Res. 2023;23:160.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- BMCRSVSupplementarymaterial.docx
- RSV7Supplementarymaterial.docx