Predicting Young Bovine Slaughter Numbers Using Statistical Modelling

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Received 14.7.2025 (revisions received 1.11.2025, 2.2.2026), **Accepted** (reviewed) 12.2.2026, **Published** 12.6.2026

Abstract

The Statistical Office of the Republic of Slovenia (SURS) developed a predictive model to estimate the intended slaughter or breeding of young bovine animals using administrative data from the *Central Register of Bovine Animals (CRB)*. A binomial regression model with a logit link was employed to forecast slaughter rates, replacing the traditional, resource-intensive survey-based approach. Internal bootstrap validation and external calibration confirmed the model's robustness, ensuring that predictions align with real-world occurrences and are suitable for future forecasting. The model demonstrated a significant improvement in predictive accuracy, with a difference of around 2% between the model's estimates and the survey results, equating to approximately 3 000 animals per year. The model is now closely aligned with observed values, demonstrating that administrative data can effectively replace costly telephone surveys. This shift promises both cost savings and enhanced accuracy in official agricultural statistics, with potential for broader application in other agricultural sectors or regions.

Keywords	***DOI***	***JEL code***
Central Register of Bovine Animals, logistic regression, prediction, calibration, validation	*https://doi.org/10.54694/stat.2025.37*	*CQ18, C25, C53*

INTRODUCTION

The European Union (EU) has a longstanding commitment to agricultural statistics, with regulations dating back to 2004. Building on this foundation, the EU adopted the *Statistics on agricultural input and output (SAIO)* regulation, which aims to provide reliable, comparable, and timely data to support the *Common Agricultural Policy (CAP)* as well as other EU policies related to agriculture, food security, and rural development.

Regulation (EU) 2022/2379, adopted on 23 November 2022 and applicable from 1 January 2025, establishes a unified framework for collecting and reporting statistics on agricultural inputs and outputs

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across the European Union. The latest requirements for livestock statistics, discussed in this article, are closely linked to Commission Implementing Regulation (EU) 2023/2745, adopted on 8 December 2023. This regulation imposes rules for implementing Regulation (EU) 2022/2379, specifically concerning animal production statistics, and establishes clear deadlines for reporting livestock statistics. Slovenia is one of the countries obligated to report livestock data annually, with the reference date set as 1 December. According to the reporting schedule, the deadline for submitting the forecast of bovine animals is 15 May of the following year.

Regarding bovine animals, previous versions of the regulation required Member States to conduct livestock surveys. The new Regulation (EU) 2022/2379 introduces the possibility for significant methodological changes, aimed at increasing flexibility and reducing the administrative burden on respondents, national statistical institutes (NSIs), and other national authorities. In addition to statistical surveys, Member States are now allowed to use a variety of data sources and methods, including administrative records, and scientifically sound techniques such as imputation, estimation, and modelling. Nevertheless, the quality of the resulting statistics – particularly regarding accuracy, timeliness, and comparability – must be rigorously maintained.

The main bovine categories relevant to these analyses include bovine animals less than 1 year old (hereafter referred to as young bovines). This category is further disaggregated based on their intended purpose (i.e., for slaughter or not for slaughter). To determine the number of young bovine animals in each category, the previous methodology at the Statistical Office of Slovenia (SURS) – prior to the introduction of the model prediction – relied on the December livestock survey.

The general objective of this project was to develop a model to predict the number of slaughtered young bovines using administrative data from the CRB, thereby replacing the previous survey-based data acquisition method. Our goal was to build a parsimonious model that is likely to perform well on new datasets, particularly those to be used annually for forecasting slaughter numbers. To achieve this, we developed a predictive model based on the approach suggested by Hosmer et al. (2013), purposely selecting covariates by combining statistical methods, experience, and common sense. A detailed explanation of the model follows later.

1 LITERATURE SURVEY

1.1 December livestock survey vs Central Register of Bovine Animals (CRB)

In Slovenia, the *December Livestock Survey (KME-DEC)* is conducted annually using 1 December as the reference date. A sample is drawn from all farmers who own bovine animals on that date. These selected farmers are then contacted to report the status of their animals, including their final intentions, specifically, how many animals they plan to *slaughter* and how many they intend to *retain for breeding (not for slaughter)*.

This survey-based approach has advantages and disadvantages. One notable advantage is the ability to exercise full control over the collected variables. However, the survey incurs logistical and financial costs, including expenses related to employing and training enumerators. There is also a risk of miscommunication or misinterpretation between enumerators and respondents, which could affect the consistency and quality of the collected data.

On the other hand, *The Central Register of Bovine Animals* in Slovenia is a national database that monitors the entire bovine population in the country. It includes data on individual animals, such as births, imports, movements between farms (with separate records for departures and arrivals), deaths, slaughter, exports to the EU, and animal losses. This data set ensures that detailed information about each animal is always accessible. Animal owners are required by regulations to report data either directly through online applications or through a network of institutes.

According to the SAIO legislation, information on the purpose of breeding for each cohort group, specifically whether the animals are intended for slaughter or further breeding, must be reported in advance, no later than 15 May. This deadline is 165 days after the reference date and 200 days before the final classification of young bovines.

Since approximately 15 days are required for data processing and publication, we considered the status of the cohort group on the agreed date of 30 April. On that date, approximately 50% of the young bovines required prediction, while the rest were already classified. A prediction model is developed to classify animals not yet categorized as of 30 April each year.

2 METHODS

2.1 Overview of the data sets and timeline of events

In this section, the timeline of events is explained in detail. The study covers the entire population of young bovines in Slovenia, thus including both female and male bovines under one year of age, registered on Slovenian agricultural holdings as of the reference date. These animals are grouped into mutually exclusive cohorts, each corresponding to a specific annual reference date. For this project, data from two cohorts, registered on 1 December 2022 (N = 149 262) and 1 December 2023 (N = 144 655) were analysed. The model is trained using the 2022 cohort and subsequently applied to generate predictions for the 2023 cohort. In general, model calibration for each reference year relies on data from the immediately preceding year.

Cohort 2022 and Cohort 2023 were monitored longitudinally over a 365-day period from their respective reference dates, with the status of each animal recorded at two time points: 150 days and 365 days after the reference date. At the first time point (150 days after the reference date), approximately 50% of the animals had been classified, and by the second time point (365 days after the reference date), classification of all animals was complete.

As illustrated in Table 1, at the 150-day mark, animals within each cohort were classified into one of five categories. Those that had reached an age greater than one year by this time were classified as *not slaughtered*, indicating they had continued breeding (2022: 43.70%; 2023: 44.40%). Animals slaughtered during this period were classified as *slaughtered* (2022: 5.08%; 2023: 4.29%), whilst the animals that died or were exported were categorised as *losses* (2022: 1.12%; 2023: 1.19%) and *exports* (2022: 0.10%; 2023: 0.04%), respectively. Finally, animals still under one year of age and not slaughtered, dead, or exported

Table 1 Classification of young bovine animals 150 days after the reference date

		1 Dec 2022 (N = 149 262)				1 Dec 2023 (N = 144 655)			
		N	%	N	%	n	%	N	%
Classified				74 646	50.00			71 709	49.57
	Not slaughtered	65 232	43.70			63 713	44.40		
	Slaughtered	7 586	5.08			6,208	4.29		
	Losses	1 673	1.12			1,723	1.19		
	Exports	155	0.10			65	0.04		
Not classified				74 616	50.0			72 946	50.43

Source: Authors' estimations

were classified as *unclassified* (2022: 50.00%; 2023: 50.43%). At this point, about half of the animals had been assigned to one of the four definitive outcome categories (these being slaughtered, not for slaughter, losses, or exported), while others remained unclassified.

The primary objective of this project is to classify the animals that remained unclassified at the 150-day time point. In our example for the year 2023, 50.43% of the animals remained unclassified. Additionally, for the same year, two other groups present classification challenges: young bovines that died (1.19%) or were exported (0.04%) before the 150-day time point. These animals must also be classified. However, the absence of a system to monitor the status of exported young bovines presents a challenge. In practice, the same model will be applied to both the defined groups (i.e., exported or lost) and the unclassified animals. This approach involves predicting how many of these animals would have been slaughtered under a counterfactual scenario in which those that died or were exported had remained alive and present in Slovenia. The predictions will consider each animal's age at the time monitoring ceased, that is the date of death or export.

Table 2 presents the status of the cohort at the second time point, 365 days after the reference date, when all animals within each cohort were fully classified into one of four categories. Animals that had reached an age exceeding one year were classified as *not slaughtered* (2022: 91.90%; 2023: 92.93%;), indicating continued breeding. Those that were slaughtered were classified as *slaughtered* (2022: 6.62%, 2023: 5.60%), while animals that died or were exported were categorised as *losses* (2022: 1.35%, 2023: 1.40%) and *exports* (2022: 0.13%, 2023: 0.07%), respectively. At this stage, the exact number of animals in each category was determined, resulting in the complete classification of all individuals within the cohort. At the time of developing the model, the status of Cohort 2023 was not known in advance and had to be predicted. It is now known, and we are presenting the results.

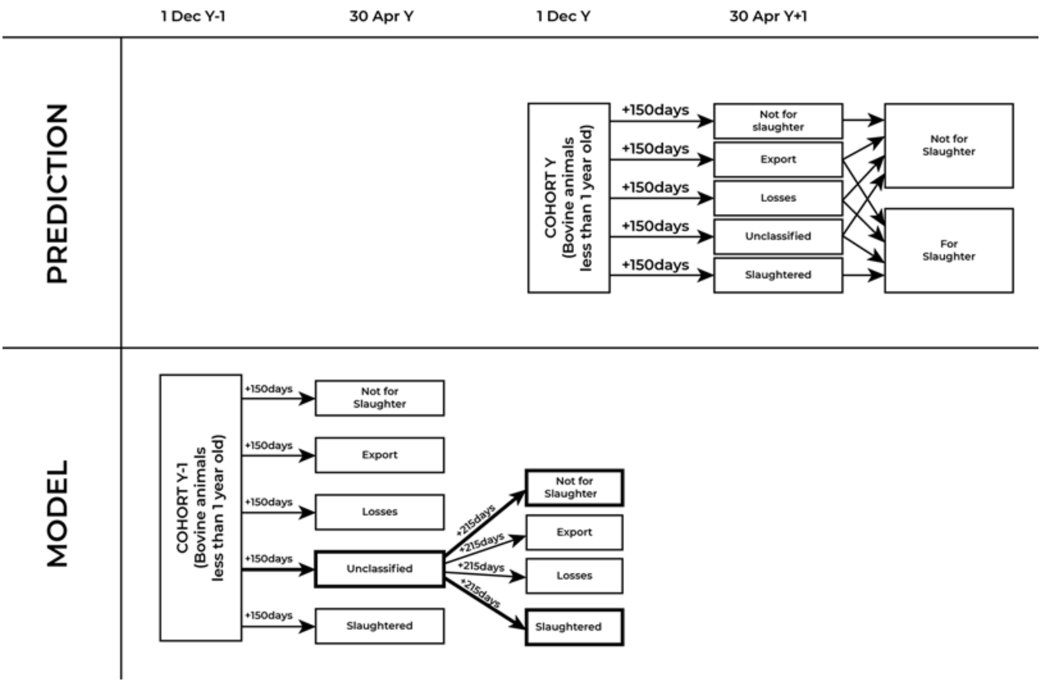
Table 2 Classification of young bovine animals 365 days after the reference date

		1 Dec 2022 (N = 149 262)				1 Dec 2023 (N = 144 655)			
		N	%	N	%	n	%	N	%
Classified				149 262	100.00%			144 655	100.00%
	Not slaughtered	137 165	91.90			134 433	92.93		
	Slaughtered	9 882	6.62			8 092	5.60		
	Losses	2 019	1.35			2 026	1.40		
	Exports	196	0.13			104	0.07		
Not classified				0.0%				0.0%	

Source: Authors' estimations

To estimate the coefficients of our model and predict the number of slaughtered and non-slaughtered animals, we trained the model using subgroup of animals from the previous year. The subgroup is visually represented and highlighted at the lower part of Figure 1. As an example, consider the cohort group with a reference date of 1 December 2022. To be included in the training data, bovine animals had to meet the following conditions: they had to be less than one year old on that date, registered with Slovenian agricultural holdings as of 1 December 2022, remain unclassified regarding slaughter status until 30 April 2023, and be definitively classified as either slaughtered or not slaughtered by 1 December 2023. This final classification served as the dependent variable (y), where a value of 1 was assigned to *slaughtered* animals and 0 to those *not slaughtered*.

Figure 1 Timeline of young bovines' categorization



Source: Authors' visualisation

2.2 Building the model

In this section, we outline the methodology used to select the variables that produce the "best" predictive model and describe how we assessed its adequacy, both for individual variables and overall performance. Our primary goal is to develop a model using a pseudo-out-of-sample evaluation, which will be used annually to estimate the probability of being slaughtered for the observed population. Estimating the effects of influencing factors (animal characteristics) is of secondary importance. The model was developed using *R Statistical Software* (R Core Team, 2025) with which the *Least Absolute Shrinkage and Selection Operator (LASSO)* method was applied by calling the glmnet package (Friedman et al., 2025), whilst the validation and calibration were conducted using the rms package (Harrell, 2025).

When we began building the model, we considered basic descriptive statistics about the animals, including their *age* on the reference date, *sex* (male = 1, female = 0), *region* (western = 1, eastern = 0), and *breed*. Our focus was on the four most common breeds in Slovenia: simmental (breed1), holstein (breed2), brown (breed3), and beef (breed4). All other 517 breeds were grouped under the category "other" (breed5). As Hosmer et al. (2013) noted, it is inappropriate to model a nominal variable as if it were an interval variable. To address this, we created a set of design variables to represent the different breed categories. Specifically, we introduced four dichotomous variables, each comparing one breed (i.e., holstein, brown, beef, and other) to the reference group, i.e., simmental, the most common and frequent breed found in Slovenia.

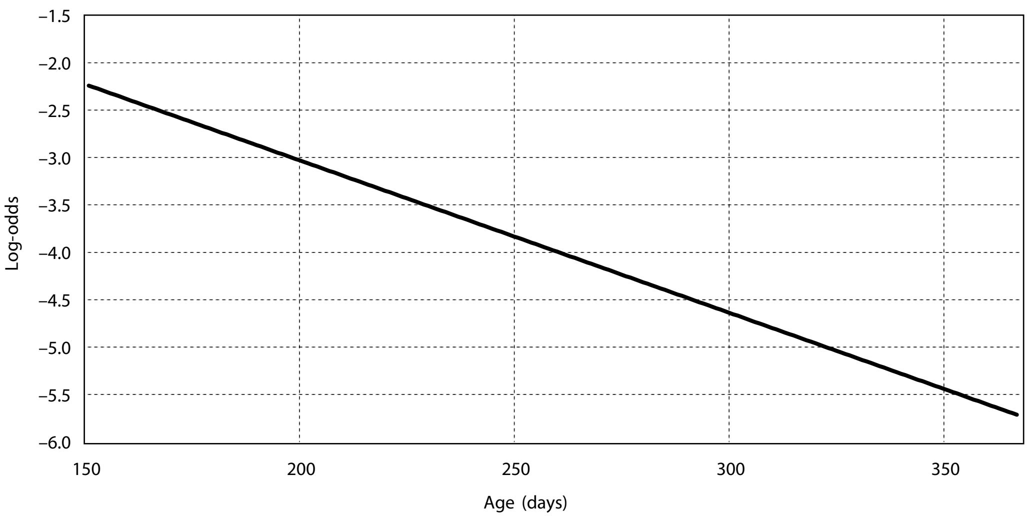
Additionally, we had information about the farm on which each animal was raised. Based on this data, a content specialist recommended creating a new variable that could be important for our predictions: the *type of farm*. To classify the farm type, we checked on which farm each animal was located as of 1 December 2022. We considered two key factors: the total number and the number of milking cows on the farm. If the proportion of milking cows exceeded 30%, the farm was classified as a dairy farm; otherwise, it was categorised as a beef farm (dairy = 0, beef = 1).

The dataset used to build the model consisted of data from 74 616 cattle, of which 2 296 had been slaughtered. Since the response variable is binary, the appropriate method for modelling the relationship is binomial logistic regression using logit link. Coefficients were estimated using maximum likelihood estimation. The covariates are as follows: *age* ranges from 150 to 365 days ($\bar{x}$ = 263.3, SD = 63.78), where *sex* is nearly equally distributed, with 51.13% female and 48.87% male. For *type of farm*, 45.59% are dairy and 54.41% are beef. *Region* distribution is 70.70% eastern and 29.30% western. *Breed* includes 40.65% simmental, 18.70% holstein, 3.60% brown, 15.48% beef, and 21.57% other.

With only five covariates and a large sample size, we followed Hosmer et al. (2013) recommendation to begin by fitting an initial model that included all covariates. The Wald test for all coefficients was significant ($p < 0.001$). Thus, our preliminary main effect model ("model_initial") contains eight covariates: *age*, *breed2*, *breed3*, *breed4*, *breed5*, *sex*, *type_farm*, *region*.

Furthermore, we assessed the assumption that the model is linear in the logit for the continuous variable age (days). To check this, we used a smoothed scatterplot, as suggested by Crawley (2012), with LOWESS smoothing providing a nonparametric description of the relationship between the logit (log-odds) and age. Visual inspection of the Figure 2 indicated that the logit decreases linearly as a function of age, confirming a clear linear relationship.

Figure 2 Lowess smooth on the log – odds scale of outcome slaughter, versus the covariate AGE, n = 74 229



Source: Authors' visualisation

The next step in the purposeful selection procedure is to explore possible interactions among the main effects. We fit models that individually added each of the 22 possible interactions to the main effect model. At this stage, the main effects are considered fixed and could not be removed. The results are summarized in Table 3.

We identified 15 interaction terms that were statistically significant at the p=0.10 level. To obtain a parsimonious model, we applied the Least Absolute Shrinkage and Selection Operator (LASSO) (Friedman et al., 2010) in R, further reducing the number of significant interaction terms identified in the previous step. Predictor variables included main effects and selected two-way interactions constructed

Table 3 Log-Likelihood, Likelihood Ratio (G, df = 1), and p-value for the addition of the interaction to the main effects model

Interaction	Log-likelihood	G	p
Main Effects Model			
age*breed2	−8,449.170	99.699	< 0.001*
age*breed3	−8,498.710	0.609	0.435
age*breed4	−8,497.195	3.651	0.056*
age*breed5	−8,495.108	7.823	0.005*
age*sex	−8,470.572	56.896	< .001*
age*type_farm	−8,474.738	48.565	< .001*
age*region	−8,498.923	0.194	0.659
sex*breed2	−8,154.567	688.905	< 0.001*
sex*breed3	−8,494.297	9.447	0.002*
sex*breed4	−8,434.204	129.632	< 0.001*
sex*breed5	−8,421.576	154.889	< 0.001*
sex*type_farm	−8,192.901	612.238	< 0.001*
sex*region	−8,494.017	10.007	0.002*
type_farm*breed2	−8,498.003	2.033	0.153
type_farm*breed3	−8,498.830	0.380	0.537
type_farm*breed4	−8,498.515	1.010	0.314
type_farm*breed5	−8,497.218	3.604	0.058*
type_farm*region	−8,479.428	39.184	< 0.001*
region*breed2	−8,495.943	6.154	0.013*
region*breed3	−8,497.846	2.347	0.126
region*breed4	−8,497.787	0.465	0.495
region*breed5	−8,497.028	3.983	0.046*

Source: Authors' estimations

with *model.matrix*. The penalty parameter (λ) was chosen by 10-fold cross-validation using *cv.glmnet*. We selected λ_min as the optimal value. All predictors were standardised before estimation. As stated by Kuhn and Johnson (2013), the practical implications of using this technique are significant. While the regression coefficients are shrunk towards 0, a consequence of penalising the absolute values is that some parameters are actually set to 0 for some values of *λ*. Thus, the LASSO yields models that simultaneously use regularisation to improve the model and to conduct feature selection.

The results of the LASSO regularisation revealed that 7 interactions had coefficients of zero, suggesting minimal contribution to the model. Interactions *age*breed2, age*breed4, age*breed5, age*sex, age*type_farm, type_farm*breed5, region*breed5* were therefore excluded from the final model. One interaction *sex*breed2,* had a coefficient of 0.19, suggesting a moderate contribution, and was retained in the model. The remaining 7 interactions showed small contributions, with coefficients ranging from 0.01 to 0.1. After consulting with a content expert and based on these coefficients, three additional interactions *sex*breed3, sex*type_farm,* and *region*type_farm* were included in the initial model.

The final model consists of one continuous variable, *age*, along with seven categorical dummy variables and four significant interactions: *sex*breed2, sex*breed3, sex*type_farm,* and *region*type_farm*. According to Hosmer et al. (2013), when an interaction term is statistically significant, but the corresponding main effect is not, both the main effect and the interaction should be retained in the model to ensure accurate calculation of the odds ratio. Therefore, the selected model includes a nonsignificant covariate (*breed3*).

The four-degree-of-freedom likelihood ratio test comparing the interactions model to the model consisting only of the main effects (eight covariates) resulted in a G value of 863.71 with $p < 0.001$, indicating that the model with interactions statistically reduces the deviance. Thus, in aggregate, the interactions contribute significantly to the model. The final model is presented in the Table 4.

Table 4 Results of fitting the Final multivariable model fit, n = 74,229

Variable	Coeff.	Std. Err.	*Z*	p	95% CI		OR
(Intercept)	–1.847	0.137	–13.480	< 0.001	–2.118	–1.581	0.158
age	–0.015	0.001	–34.069	< 0.001	–0.016	–0.014	0.985
breed2	0.437	0.141	3.101	< 0.001	0.159	0,711	1.548
breed3	–0.066	0.330	–0.199	.842	–0.778	0.529	0.937
breed4	0.688	0.090	7.674	< 0.001	0.511	0.863	1.989
breed5	1.177	0.071	16.613	< 0.001	1.038	1.316	3.243
sex	0.885	0.106	8.386	< 0.001	0.681	1.095	2.424
type_farm	1.267	0.111	11.448	< 0.001	1.052	1.487	3.550
Region	0.658	0.066	10.018	< 0.001	0.529	0.786	1.930
sex*breed2	2.300	0.147	15.631	< 0.001	2.013	2.590	9.972
sex*breed3	1.509	0.353	4.271	< 0.001	0.860	2.259	4.521
sex*type_farm	–1.140	0.119	–9.624	< 0.001	–1,374	–0,910	0.320
Region*type_farm	–0.636	0.095	–6.698	< 0.001	–0,823	–0,451	0.529

Source: Authors' estimations; Log-Likelihood = -7 903.203

The model is formally described by Formula 1.

$$\ln \frac{\pi}{1\text{-}\pi} = -1.847 - 0.015 * age + 0.437 * bred2 - 0.066 * bred3 + 0.688 * bred4 + 1.177 * bred5 + 0.885 * sex + 1.267 * type\_farm + 0.658 * region + 2.30 * sex * bred2 + 1.509 * sex * bred3 - 1.140 * sex * type\_farm - 0.636 * region * type\_farm \tag{1}$$

To better understand the results, we have presented the odds ratios for the significant groups.

Table 5 Estimated odds ratios and 95% Confidence interval for certain groups in the study CRB, n = 74,229

Variable	Subgroup	Odds ratio	95% CI	
age		0.638	0.618	0.651
breed4		1.989	1.667	2.370
breed5		3.243	2.825	3.730
male/female	breed2	24.067	16.960	34.630
male/female	breed3	10.957	5.330	22.53
male/female	dairy	2.423	1.970	2.980
male/female	beef	0.775	0.568	1.058
western/eastern	dairy	1.931	1.698	2.198
western/eastern	beef	3.624	2.650	4.970

Source: Authors' estimations

The estimated odds ratio for a positive difference of one month (30 days) is 0.638. This indicates that for each additional 30-day period, the odds of slaughter decrease by a factor of 0.638, representing a reduction in the odds of slaughter that could range from a 0.618-fold to a 0.651-fold decrease.

The analysis also reveals several key insights regarding the odds of slaughter across different *breeds* and *type of farms*. Firstly, the odds of slaughter for animals from the *beef breed* (*breed4*) are nearly twice as high – 1 989 times greater (95% CI: 1.667, 2.370) – compared to all *other breeds* in the study population. Similarly, the *other breed* (*breed5*), which consists of 517 less frequently occurring breeds, shows even higher odds of slaughter, with the odds being 3 243 times greater (95% CI: 2 825, 3 730) than those for the prevalent breed groups: *simmental, holstein, brown, and beef*.

When considering sex differences within specific breeds, male bovines from the *holstein breed* have 24 167 times higher odds of slaughter than females of the same breed (95% CI: 16 960, 34 630). A similar pattern is observed for the *brown breed*, where male bovines have 10 957 times greater odds of slaughter than their female counterparts (95% CI: 5 330, 22 530).

The *type of farm* also plays a critical role. On farms where more than 30% of cows are used for milking (classified as dairy farms), male bovines have 2 423 times greater odds of slaughter than females (95% CI: 1 970, 2 980). In contrast, on farms where fewer than 30% of cows are used for milking (classified as *beef farms*), male bovines face 0.775 times the odds of slaughter compared to females (95% CI: 0.568, 1.058).

Geography further influences these odds. Among *dairy farms* in Western Slovenia, the odds of slaughter are 1 931 times higher than those observed on *dairy farms* in Eastern Slovenia (95% CI: 1 698, 2 198). However, on *beef farms*, the odds of slaughter for animals in Western Slovenia are 3 624 times greater than those in Eastern Slovenia (95% CI: 2 650, 4 970). The confidence intervals for the interactions were estimated using the four-step method described by Hosmer et al. (2013).

These findings highlight significant differences in slaughter odds based on breed, sex, type of farm, and geographical location, with respect to the other variables in the model.

2.3 Assessment of model fit

To assess the accuracy and reliability of the model, we conducted both internal validation and external calibration. According to Hanley and McNeil (1982), there are two common methods for model validation: cross-validation and bootstrap validation, with the latter requiring fewer assumptions. For internal validation, we used bootstrap validation, in which samples were drawn with replacement from the original dataset, simulating the process of sampling from an underlying population. These bootstrap samples were the same size as the original dataset. As recommended by Steyerberg (2019), 100–200 bootstrap iterations are typically sufficient for stable estimates. In our analysis, we performed 200 bootstrap iterations to ensure robust performance estimates.

For each bootstrap sample, a prediction model was developed. The model was evaluated both within the bootstrap sample itself and on the original dataset. The difference in performance between the two reflects the "optimism" of the model – that is, how much better it performs on the bootstrap sample compared to the original data. This optimism is then subtracted from the apparent performance in the original sample to obtain a more accurate estimate of model fit (see Table 6).

Steyerberg (2019) claims that the advantages of bootstrap validation are numerous with the principal benefit being that the optimism-corrected performance estimate tends to be stable, as the same sample size is used for both model development and testing. This makes bootstrap validation a reliable method for assessing model performance in predictive modelling.

Model performance was assessed by calculating two of the many diagnostic measures suggested by Harrell (2015): Nagelkerke's coefficient of determination (R^2) and the Area Under the Receiver Operating Characteristic Curve (AUC). Both metrics range from 0 to 1, with higher values indicating better model fit and predictive accuracy. The model achieved a Nagelkerke's R^2 of 0.252. According to Field et al. (2012), Nagelkerke's R^2 values between 0.2 and 0.4 are considered acceptable.

Table 6 Bootstrap validation of model performance, as indicated by Nagelkerke's R2 in a subsample of the CRP dataset (n = 74,229)

	Original sample	Training sample	Test sample	Optimism	Corrected index	N
Dxy	0.680	0.680	0.679	0.001	0.678	200
R^2	0.253	0.254	0.253	0.001	0.252	200

Source: Authors' estimations

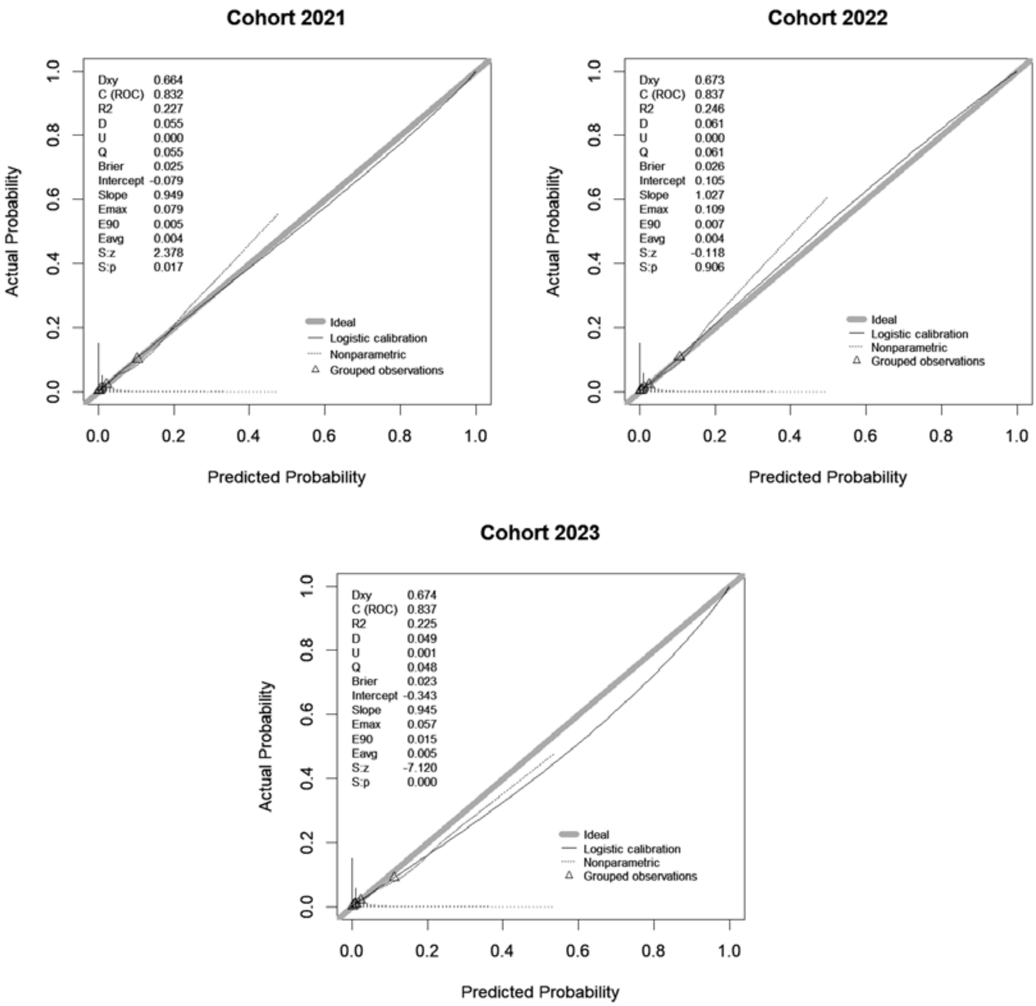
Regarding the second validation parameter (AUC; computed as $AUC = \frac{Dxy+1}{2}$), Hanley and McNeil (1982) provide basic guidelines for interpreting the AUC. Values between 0.8 and 0.9 suggest that the model has acceptable performance for many practical purposes. The model in our analysis achieved a validation AUC of 0.839.

Model calibration was evaluated using historical data, utilising the set from the immediately preceding year. Harrell (2015) stated that calibration refers to how well the predicted probabilities match the actual observed outcomes, reflecting the model's reliability in producing accurate predictions. To visually assess this calibration, we constructed three calibration plots for each dataset (see Figure 3).

In each plot, the predicted probabilities are plotted along the x-axis, while the observed outcomes are shown on the y-axis. The line of identity (the 45° diagonal line) serves as a reference point: perfectly calibrated predictions will fall along this line, indicating that the predicted probabilities align precisely with the actual outcomes.

The evaluation across three datasets – *Cohort2021*, *Cohort2022*, and *Cohort2023* –demonstrates consistent discriminatory ability in all models. Key metrics such as Dxy and C (ROC) provide clear evidence of the models' effectiveness in distinguishing between positive and negative outcomes. The Dxy values, ranging from 0.664 to 0.674, reflect a strong capacity that outcomes are correctly ranked, while a consistent range of C (ROC) values from 0.832 to 0.837 confirms the models' solid discriminatory power.

Figure 3 Calibration plot of actual outcome vs. predictions for three models, 2021 (n = 77,327), 2022 (n = 74,616), 2023 (n = 72,970)



Source: Authors' visualisation

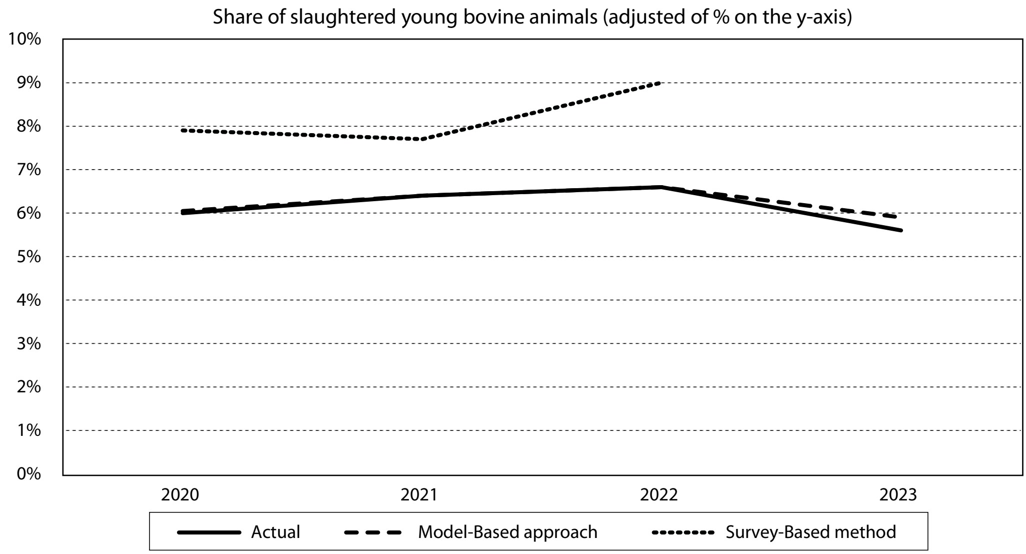
Regarding model calibration, the results demonstrate promising consistency in predictive performance. The models exhibit a reasonable fit, as indicated by moderate R^2 values ranging from 0.225 to 0.246. These values suggest that the models capture a meaningful portion of the data's variability, although they do not explain all of it. The relatively low residual deviance (D) values, between 0.049 and 0.061, suggest minimal unexplained error, supporting the conclusion that the models accurately reflect the underlying patterns in the data.

The Brier score values in this analysis range from 0.023 to 0.026, indicating strong predictive accuracy. The Brier score (Brier, 1950) ranges from 0 to 2, where 0 represents perfect predictions and 2 corresponds with the worst possible outcome. In practice, values typically fall between 0 and 1, with lower scores indicating better accuracy. These results suggest that the models are well-calibrated and perform effectively in probabilistic predictions. Furthermore, calibration slopes were consistently close to 1.0, which affirms that the predicted probabilities align closely with observed frequencies. This further reinforces the conclusion that the models are well-calibrated and their predictions reliably reflect real-world outcomes.

3 RESULTS

This chapter presents the practical perspective, comparing the estimated shares of slaughtered young bovines using the previous survey-based method with our new model-based approach.

Figure 4 Comparison of the share of slaughtered young bovines, computed from each year's cohort: survey-based method vs. model-based approach



Source: Authors' estimations

Figure 4 presents the actual and predicted shares of slaughtered young bovines by year, together with estimates from the previous survey-based method. According to data reported to Eurostat using the former method, the shares were 7.90% in 2020, 7.70% in 2021, and 9.00% in 2022. In contrast, the shares predicted by our model – 6.05% in 2020, 6.40% in 2021, and 6.60% in 2022 – are notably closer to the actual observed values: 6.00% in 2020, 6.40% in 2021, and 6.60% in 2022. This close alignment between predicted and actual shares highlights the model's strong predictive performance and its improvement over the previous methodology. Compared to the earlier approach, the difference between the survey results and the model's predictions is about 2%, or approximately 3 000 animals per year.

The graph also shows that in 2023, the predicted percentage was higher, likely because the model could not account for the unexpected decrease in the trend. Nevertheless, the difference between the observed and predicted percentages is minor. Since the survey was not conducted in 2023, there is no data point for that year on the graph.

4 DISCUSSION

The results indicate that the model demonstrates solid and consistent performance, exhibiting a strong ability to discriminate between outcomes, being suitably calibrated and showing low residual errors across all datasets.

From a practical perspective, the new model-based approach provides predicted slaughter shares for young bovines that closely align with the actual observed values. We have achieved our goal and have begun implementing the model in practice, as it outperforms the previous survey-based method reported to Eurostat and meets the expectations of our content specialists.

The model performs with high precision when external factors – such as weather conditions (droughts, floods, or extreme temperatures), crop yields, and disease or health factors – remain stable. However, when these external variables change, they can affect the percentage of slaughtered animals. For instance, it is often argued that if crop yields decrease, the number of slaughtered animals may increase, as farmers may have less feed available for their livestock. This concept was explored in a model developed by Breimyer (1952), where crop yields were treated as an external variable, making a significant contribution to the model's predictions.

The price of meat or livestock can significantly affect the number of animals slaughtered. Higher prices for meat may encourage producers to slaughter more animals to capitalise on profitable markets, while lower prices may reduce slaughter numbers. Many authors have analysed the factors that influence cattle prices (Gallardo et al., 2010; Goodwin, 1992; Kulshrestatha and Rosaasen, 1980; Weimar and Stillman, 1990; Tonsor and Schroeder, 2011; Zapata and Garcia, 1990) and have asserted in their research that potential additional elements to be incorporated in the model encompass supply and demand dynamics, production costs, weather and environmental conditions, market factors, economic conditions, government policies and trade, disease and health factors, technological improvements, and the influence of global markets and trade.

Although we are very pleased with the results, alternative approaches could be explored to simplify the methodology. Several researchers have forecasted meat production using time series approaches (Aujla and Sadiq, 2018; Duwalage et al., 2023; Gritsenko et al., 2023; Odru and Zengin, 2020), based on which a monthly time series of slaughtered animals could be created. This method would help mitigate seasonality effects (if present) and capture one-time events, such as disease outbreaks or droughts. While time series analysis is useful for generating estimates, it has limitations, as it does not account for the demographic characteristics of the animals or the influence of external factors like market fluctuations, weather patterns, or policy changes.

One promising approach is random forest prediction, a machine learning ensemble technique that does not rely on strict assumptions. For example, Ordu and Zengin (2020) proposed an interesting methodology for predicting animal production by comparing three forecasting approaches: Autoregressive integrated moving average (ARIMA), exponential smoothing (ES) and the function of the seasonal and trend decomposition using loess (STLF).

The percentage of slaughtered animals has been steadily increasing recently; however, in the coming years, content experts anticipate a decrease in the number of slaughtered animals. In this context, monitoring the model's performance will be necessary, as we will need to assess how accurately it predicts these shifting trends, and, if necessary, add more explanatory variables.

CONCLUSION

In this study, we demonstrated that the number of slaughtered animals can be predicted more accurately using administrative data. The findings indicate that employing detailed bovine data with statistical modelling can lead to more effective predictions and improved production outcomes. The methodology developed is directly applicable to the *Statistical Office of the Republic of Slovenia*. In conclusion, the model exhibited strong predictive performance, with a high AUC, a moderate Nagelkerke's R^2, and robust calibration diagnostics, reflecting both excellent predictive accuracy and reliable calibration.

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