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Project Milestone 3

**Module:** Business Intelligence 381  
**Project:** Health & Demographic Data Science using CRISP-DM – Modelling Phase  
**Milestone:** 3 Modelling (CRISP-DM Phase 4)

Petrus Human 577842

Frederik Knoetze 600965

Teleki Shai 601377

Moloko Rakumako 601352

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# 1. Introduction (CRISP-DM Phase 4: Modelling)

This milestone advances our project from **CRISP-DM Phase 2–3 (Data Understanding & Preparation)** into **Phase 4 (Modelling)**. In Milestone 1, we framed the **business understanding** around public-health questions (e.g., access to care, coverage, and risk indicators). In Milestone 2, we prepared twelve national health/demographic datasets (cleaning, harmonising codes, creating features and splitting data), delivering reproducible R scripts and a data dictionary.

Now, Milestone 3 specifies, justifies and implements **candidate models** appropriate for our (mostly tabular) health survey data, with attention to **interpretability**, **robustness**, and **evaluation design**. We follow CRISP-DM’s guidance to:

* select algorithms consistent with our data types and goals
* document assumptions
* design tests (splits/CV/metrics)
* evaluate results before Phase 5 (Evaluation) and Phase 6 (Deployment).

While CRISP-DM is a complete framework, recent work highlights its continued relevance and agile adaptations for modern data science projects. We adopt in our workflow (iterating between preparation and modelling as data quality/feature needs emerge) (Silva and Viana, 2024).

Given our targets are primarily **classification** (e.g., coverage yes/no, high-risk vs not), and our predictors mix **categorical** and **numeric** variables with potential non-linearities and interactions, we shortlist four algorithms widely used in health analytics: **Logistic Regression**, **Decision Trees (CART/C5.0)**, **Random Forest**, and **Naïve Bayes**. These offer a spectrum from **high interpretability** (logistic, trees) to **strong predictive robustness** (random forest), plus a **simple baseline** (naïve Bayes). That 4 algorithms is commonly recommended for tabular health data benchmarking. Evidence from recent healthcare studies supports these choices and clarifies their trade-offs in accuracy, interpretability and robustness (Balendran et al., 2025; Harris, Yang and Hardin, 2021; Nguyen et al., 2023; Rahmati et al., 2024; Wallace, Diez Roux and Greven, 2023).

# 2. Modelling Techniques: Rationale & Assumptions

## 2.1 Rationale narrative (why these four)

* **Logistic Regression (GLM, logit link).**   
  Standard for binary clinical outcomes and risk prediction. Provides odds ratios and clear coefficient interpretation. Assumptions are explicit (linearity of log-odds, no perfect multicollinearity, independent observations) and well-documented in recent clinical reviews. This transparency is valuable for public-health stakeholders (Harris, Yang and Hardin, 2021; Hua and Zhang, 2025).
* **Decision Trees (CART/C5.0).**   
  Highly interpretable (human-readable rules/paths), handle mixed types and capture non-linearities & interactions without manual feature engineering. Recent health studies show effective use for population surveillance and COVID-19 mortality risk segmentation (Nguyen et al., 2023; Rahmati et al., 2024).
* **Random Forest.**   
  An ensemble of trees (bagging + random feature subspace) that typically improves generalisation and robustness on tabular health data. Resilient to outliers and noise, with strong performance reported in current healthcare applications (e.g., discharge risk, costs). Ongoing work in digital medicine stresses robustness considerations in clinical ML (Tran, Nguyen and Le, 2024; Balendran et al., 2025; Wallace, Diez Roux and Greven, 2023).
* **Naïve Bayes.**   
  A lightweight baseline with a simple probabilistic assumption (conditional independence). Despite its naive assumption, it is often surprisingly competitive on high-dimensional tabular data, fast to train, and useful as a calibration point for more complex models (ScienceDirect Topics, 2025).

## 2.2 Technique–Assumption–Use-case table

|  |  |  |  |
| --- | --- | --- | --- |
| Algorithm | Why we chose it (fit to our data/goals) | Key assumptions / caveats | Typical health use-cases & notes |
| **Logistic Regression** | Transparent coefficients/Ors. Strong baseline for binary outcomes. Easy to communicate to policy teams (Harris, Yang and Hardin, 2021). | Linearity of log-odds; no perfect multicollinearity; independent observations; adequate events per variable. Model misspecification reduces calibration (Hua and Zhang, 2025). | Clinical risk models, coverage yes/no, program targeting; use interactions/splines if needed; check VIFs & calibration (Hua and Zhang, 2025). |
| **Decision Trees (CART/C5.0)** | Interpretable rules, handle mixed types, missingness heuristics, capture non-linearities/interactions (Nguyen et al., 2023). | Greedy splits can overfit, unstable to small data changes; control with pruning/minsplit/CP. | Population segmentation (e.g., youth mental health), triage pathways, mortality risk stratification incl. COVID-19 (Rahmati et al., 2024). |
| **Random Forest** | Robust predictive performance on tabular health data. Reduces variance via bagging; handles many variables, variable importance for signal-finding (Tran, Nguyen and Le, 2024). | Less interpretable than single tree, variable importance must be interpreted carefully, tune mtry, ntree, class balance. Robustness must still be verified across shifts (Wallace, Diez Roux and Greven, 2023). | Discharge/LOS risk, cost prediction, multi-factor risk indices, good default when accuracy is a priority (Balendran et al., 2025). |
| **Naïve Bayes** | Fast baseline, performs well when independence holds approximately, good with many categorical features, serves as sanity check (ScienceDirect Topics, 2025). | Conditional independence assumption, often over-confident probabilities and may underperform when features interact strongly. | Screening/triage baselines, text/categorical-heavy data; compare against logistic/tree/forest to judge added value. |

## 2.3 Metrics & evaluation note (for continuity with Person 2)

Because our targets are mostly binary, we will prioritise **ROC-AUC, F1, Precision/Recall, and calibration**. AUC is widely used to compare classifiers across thresholds and has strong support in recent methodology literature (Li, Zhao and Xu, 2024).

# 3. Generation of the test parameters and train test split

Because of the limitations for the data being only two years with corresponding data the only train test split available is a 50/50. This can still be used but there is no way to generate an accurate model. The model will fir one year exactly. If both are used to train the model the model will be more accurate for a wider range of scenarios. Both will need to be tested. Thus there is a 50/50 train test split available alongside the full dataset.

## Classification Metrics

ROC-AUC (Receiver Operating Characteristic - Area Under the Curve)

What it is: The AUC score represents the model's ability to distinguish between positive and negative classes. It is the area under the ROC curve, which plots the true positive rate against the false positive rate at various threshold settings. A score of 0.5 indicates a model with no discriminative ability (equivalent to random guessing), while a score of 1.0 represents a perfect model.

Relevance: For predicting health indicators, AUC is valuable because it provides a single, aggregate measure of performance across all possible classification thresholds.

Success Metric:

* > 0.9: Outstanding
* 0.8 - 0.9: Excellent
* 0.7 - 0.8: Acceptable
* < 0.7: Poor

F1 Score

What it is: The F1 score is the harmonic mean of precision and recall. It is a good measure to use when you want to find a balance between precision and recall and when there is an uneven class distribution.

Relevance: In health data, we might have imbalanced classes (e.g., a rare disease). The F1 score provides a more useful measure than accuracy in such cases.

* Success Metric: The F1 score is highly dependent on the specific problem and the balance of the classes. However, a general guideline is:
* > 0.7: Generally considered a good score.
* > 0.9: Excellent score.

Precision & Recall

What they are:

* Precision: Answers the question: "Of all the instances the model predicted to be positive, how many were actually positive?"
* Recall (Sensitivity): Answers the question: "Of all the actual positive instances, how many did the model correctly identify?"

Relevance:

* High Precision is important when the cost of a false positive is high. For example, wrongly identifying a region as "high-risk" might lead to unnecessary resource allocation.
* High Recall is important when the cost of a false negative is high. For example, failing to identify a region with low vaccination coverage could have serious public health consequences.

Success Metric: The trade-off between precision and recall needs to be considered. A good model should have a reasonable balance or be tuned to prioritize one over the other based on the specific business problem. A score above 0.7 for both is often a good starting point.

Calibration

What it is: Calibration measures how well the predicted probabilities from a model match the actual observed frequencies of the positive class. For example, if a model predicts a 30% chance of a certain outcome for a group of instances, then approximately 30% of those instances should actually have that outcome.

Relevance: In healthcare, well-calibrated probabilities are crucial for risk assessment and decision-making. If a model is used to estimate the risk of disease in a population, the predicted probabilities must be reliable.

How to Measure:

* Calibration Plots (Reliability Diagrams): These plots show the predicted probabilities against the observed frequencies. A perfectly calibrated model will have a plot that follows the diagonal line.
* Brier Score: A numerical score where a lower value indicates better calibration. A perfect model has a Brier score of 0.

Success Metric:

* Calibration Plot: The calibration curve should be as close to the main diagonal as possible.
* Brier Score: A score below 0.25 is generally considered good, with scores closer to 0 being better.

Summary of Success Metrics

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Metric | Poor | Acceptable | Good | Excellent |
| ROC-AUC | 0.7 | 0.7-0.8 | 0.8-0.9 | >0.9 |
| F1 Score | <0.6 | 0.6 - 0.7 | 0.7 - 0.9 | >0.9 |
| Precision | <0.6 | 0.6 - 0.7 | > 0.7 | >0.9 |
| Recall | <0.6 | 0.6 - 0.7 | > 0.7 | >0.9 |
| Brier Score | >0.35 | 0.25-0.35 | 0.1-25 | <0.1 |

# 3. How this guides the rest of Milestone 3

Person 2 (Test Design): will implement stratified 70/15/15 splits and 10-fold CV, selecting metrics per outcome (classification vs any regression), and documenting thresholds/operating points that meet our business success criteria.

Person 3 (Build): will implement each algorithm with sensible defaults plus minimal tuning (e.g., Logistic with logit link; Trees with cp/pruning; Random Forest with ntree/mtry; Naïve Bayes with Laplace option), saving models and predictions.

Person 4 (Assessment): will compare models via confusion matrices, ROC-AUC curves, and policy-relevant interpretation (e.g., which features drive risk/coverage), feeding the Evaluation phase of CRISP-DM and recommendations to stakeholders.

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