NutriScore ML Predictor using OpenFoodFacts Data

Jacopo Parretti, Cesare Fraccaroli
Student IDs: VR536104, VR533061
MsC in Artificial Intelligence - Machine Learning course
Academic Year 2025-26

Contents

1 Motivation and Rationale

1.1 Contextual Framework

Non-Communicable Diseases (NCDs) linked to modern diets are important nowadays. People need access to nutritional information, but interpreting nutritional tables is not so easy. Front-of-Pack labels like Nutri-Score help by giving an immediate visual for healthier choices. Predicting these grades accurately matters because today's food landscape is dominated by ultra-processed foods. The increased availability of these foods has changed how the world eats and drinks, with lots of negative effects on health [1].

1.2 Problem Statement

The task we are trying to solve is the prediction of the Nutri-Score grade given some data about food and culinary products. The dataset we are using is obtained from the Open Food Facts (https://it.openfoodfacts.org/) website. The food dataset (https://static.openfoodfacts.org/data/en.openfoodfacts.org.products.csv.gz) is a vast crowd-sourced dataset. It is large but prone to many errors, invalid and missing data, and different languages.

The Nutri-Score is usually calculated using a deterministic formula that uses fiber, fruits, protein, etc. However, all this data is not always present in the dataset. When not all of these nutrients are present, we are left with unclassified products.

1.3 Rationale

We want to use Machine Learning in order to solve the problem of unclassified products. Machine learning can act as an approximator capable of predicting the grade based on partial macronutrient data or pattern handling missing or wrong values. We want to try filling the gap in the dataset by automating the classification.

1.4 Significance

We, as MSc students, want to try investigating classification performance in a highly noisy, real-world dataset. The classification can maybe help the usage of the Open Food Facts dataset for third-party applications or for research.

2 State of the Art (SOTA)

Research on crowded nutritional databases like this shows two main problems: data sparsity and the non-linear nature of quality indices like Nutri-Score.

Traditional approaches used linear models, but these don't work well. They can't preserve macronutrient correlations or capture the thresholds in the Nutri-Score calculation. Logistic Regression has limitations because it can't model the decision rules that Nutri-Score uses.

Current state-of-the-art methods use multivariate imputation via KNN to keep the local data structure, combined with non-linear ensemble models. Ensemble models handle outliers well and can model complex relationships in imbalanced datasets [4].

In this project, we explore Random Forest and XGBoost as state-of-the-art ensemble models. Research suggests that better solutions exist for missing data imputation: Non-Negative Matrix Factorization (NMF), Multiple Imputations by Chained Equations (MICE), Nonparametric Missing Value Imputation using Random Forest (MissForest), and K-Nearest Neighbors (KNN). These methods perform better than simple approaches like using mean or median [2].

3 Objectives

The main objective of the project is to develop a robust machine learning framework capable of predicting the Nutri-Score grade (classes A through E) for products in the Open Food Facts database. The main problem is the issue of incomplete nutritional metadata, which in most cases, as we will see, prevents the deterministic calculation of the score for a significant portion of the samples. To achieve this, the project tries:

- **Algorithmic Benchmarking:** Conduct a comparative analysis between linear models (Logistic Regression), distance-based algorithms (KNN), non-linear methods (SVM with RBF kernel), and ensemble tree methods (Random Forest, XGBoost). The goal is to identify the best model for the approximation of the Nutri-Score.
- **Optimization for Class Imbalance:** To maximize the F1-Macro score rather than simple Accuracy as the primary success criterion. This ensures the model performs reliably across all nutritional grades.
- **Efficiency Analysis:** To evaluate the trade-off between predictive performance and computational cost (training time), identifying a model that is both accurate and scalable.

4 Methodology

The project uses and elaborates data from the Open Food Facts dataset. The dataset is open source and under the Open Database License. We use the dataset URL to download with a simple Python script.

4.1 Loading and Filtering

The total number of rows is over 4 million. Since the size is very large (over 9 GB), we decided to adopt a chunk-based solution: we first split into chunks and then open each chunk to filter the data. First, we delete the entries that do not have the target variable Nutri-Score grade. After this operation, we have around 1 million products. We decided to keep this set of columns:

```
'nutriscore_grade', 'code', 'product_name', 'brands', 'categories', 'countries',
'energy_100g', 'energy-kcal_100g', 'fat_100g', 'saturated-fat_100g',
'carbohydrates_100g', 'sugars_100g', 'fiber_100g', 'proteins_100g',
'salt_100g', 'sodium_100g', 'fruits-vegetables-nuts_100g',
'fruits-vegetables-nuts-estimate_100g', 'additives_n', 'ingredients_n',
'nutrition_grade_fr', 'pnns_groups_1', 'pnns_groups_2', 'main_category'
```

After filtering, we proceed with a sampling of 250,000 products with a set random state to ensure reproducibility. After this, we performed an exploratory data analysis to check the data.

4.2 Exploratory Data Analysis

To better understand the dataset, an exploratory data analysis on the 250k samples is needed. The project focuses on the prediction of the target variable Nutri-Score grade. Nutri-Score Grade does not appear evenly across all possible values A, B, C, D, E. The random sampling we conducted should guarantee that this can represent well the distribution in all of the dataset (see Figure 1).

Class imbalance:

- **A = 14.4%**
- **B = 11.6%** (least common)

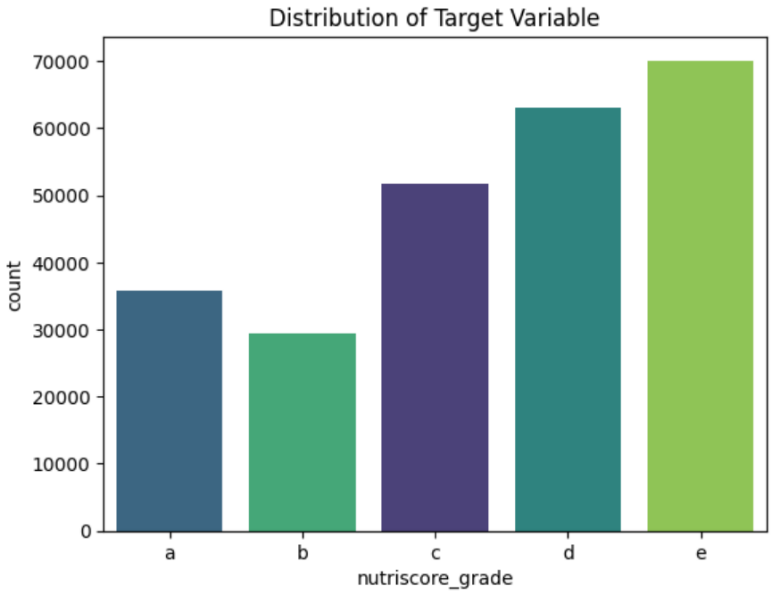


Figure 1: Distribution of the Nutri-Score grades (A-E) showing class imbalance.

- **C = 20.5%**
- **D = 25.2%**
- **E = 28.2%** (most common)

Then we analyze the missing percentages in the features we selected (Figure 2).

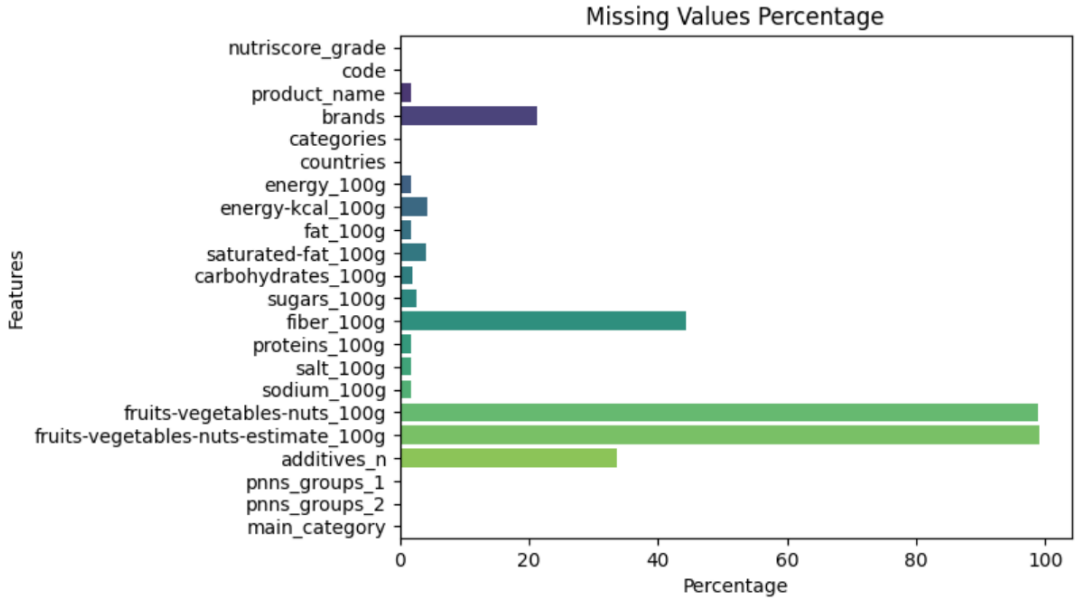


Figure 2: Percentages of missing values in the selected features.

It appears that `fruits-vegetables-nuts` and `fruits-vegetables-nuts-estimate` have more than **95 percent** of missing values (see Figure 2).

We now try plotting the skewness of the other features (Figure 3). There are some features that have a high skew value. A skew value of over 300 means that there are some extreme outliers, maybe some invalid or out-of-range data that should be removed.

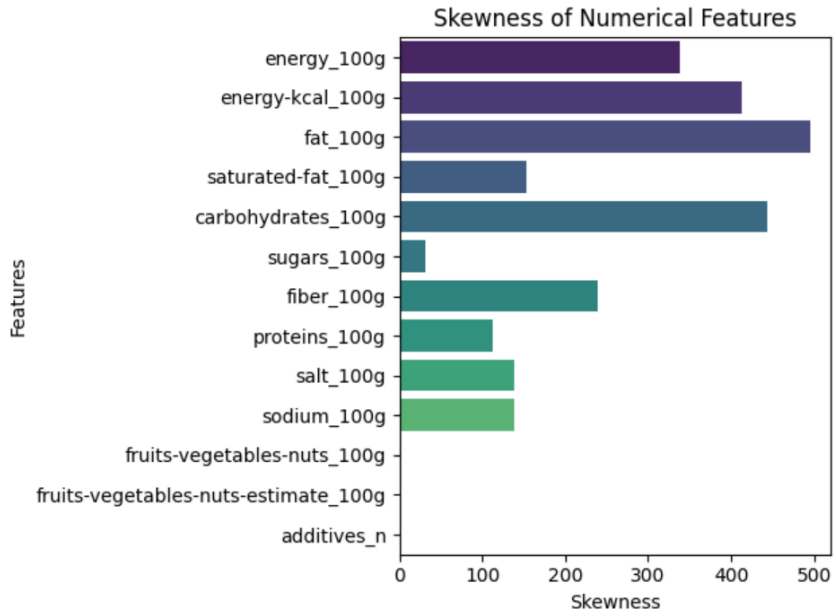


Figure 3: Skewness values of features before outlier removal. Extreme right-skewed values indicate strong zero-inflation and outliers.

`energy_100g`	134000.00
`energy-kcal_100g`	32100.00
`fat_100g`	90937.00
`saturated-fat_100g`	992276.00
`carbohydrates_100g`	8761109.00
`sugars_100g`	765433221122.00
`fiber_100g`	938364.00
`proteins_100g`	8578293.00
`salt_100g`	3625.00
`sodium_100g`	1450.00
`fruits-vegetables-nuts_100g`	100.00
`fruits-vegetables-nuts-estimate_100g`	100.00
`additives_n`	36.00

After a check on the values, we can clearly see some inconsistencies in the data.

Positive skewness is a structural characteristic of nutritional data. The distribution typically shows high near zero values (**zero-inflation**) and an elongated right tail (see Figure 4).

In the nutritional domain, this pattern is common: the vast majority of products have minimal amounts of specific nutrients (e.g., `salt` or `fiber`), while only a small part of specific categories (e.g., **concentrated sauces** or **whole-grain cereals**) possess high concentrations.

Now we plot each feature singularly against the target variable to get some insights (Figure 5). Some features like fat, energy, sugars, and saturated fat clearly impact negatively on the Nutri-Score. The ones that seem to have a positive correlation with the Nutri-Score are fruit, vegetables, and nuts; however, as we stated before, they have over 95% of missing values.

We can now plot the features against each other to see if they have a correlation. To better visualize this, we plot the correlation matrix (Figure 6).

As shown in Figure 6, Salt and Sodium have perfect correlation, and so do `energy_100g` and `energy-kcal_100g` (logically it's just a difference in unit measure). Some other features have some degree of correlation like `fat_100g` and `saturated_fat_100g` (one is a subset of the other).

We now proceed to check categorical features. The categorical features we take into exam are

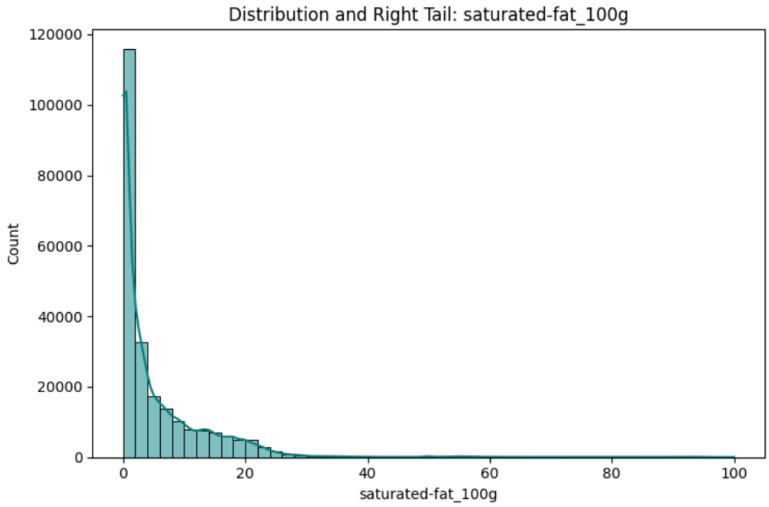


Figure 4: Example of right tail: distribution of a nutrient showing zero-inflation and a long right tail.

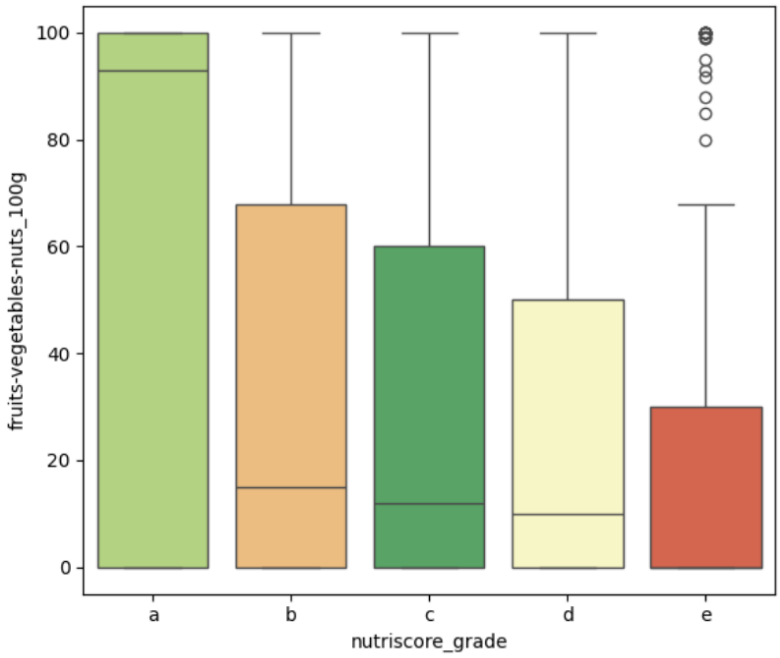


Figure 5: Distribution and importance of the fruits, vegetables, and nuts feature, which suffers from high missingness.

Brands, Product Name, Countries, `pnns_group_1`, `pnns_group_2`, categories, and `main_category`. Of these features, most of them have very high cardinality with a lot of unique values. For our models, we can mainly focus on the ones with acceptable cardinality.

- `pnns_groups_1` (10 unique)
- `pnns_groups_2` (40 unique)
- `countries` (3000 unique)

The countries feature has high cardinality and contains acronyms, country names in multiple languages, and inconsistent syntactical formats. Furthermore, many entries consist of multi-label strings where products are associated with several countries simultaneously. To address this, we

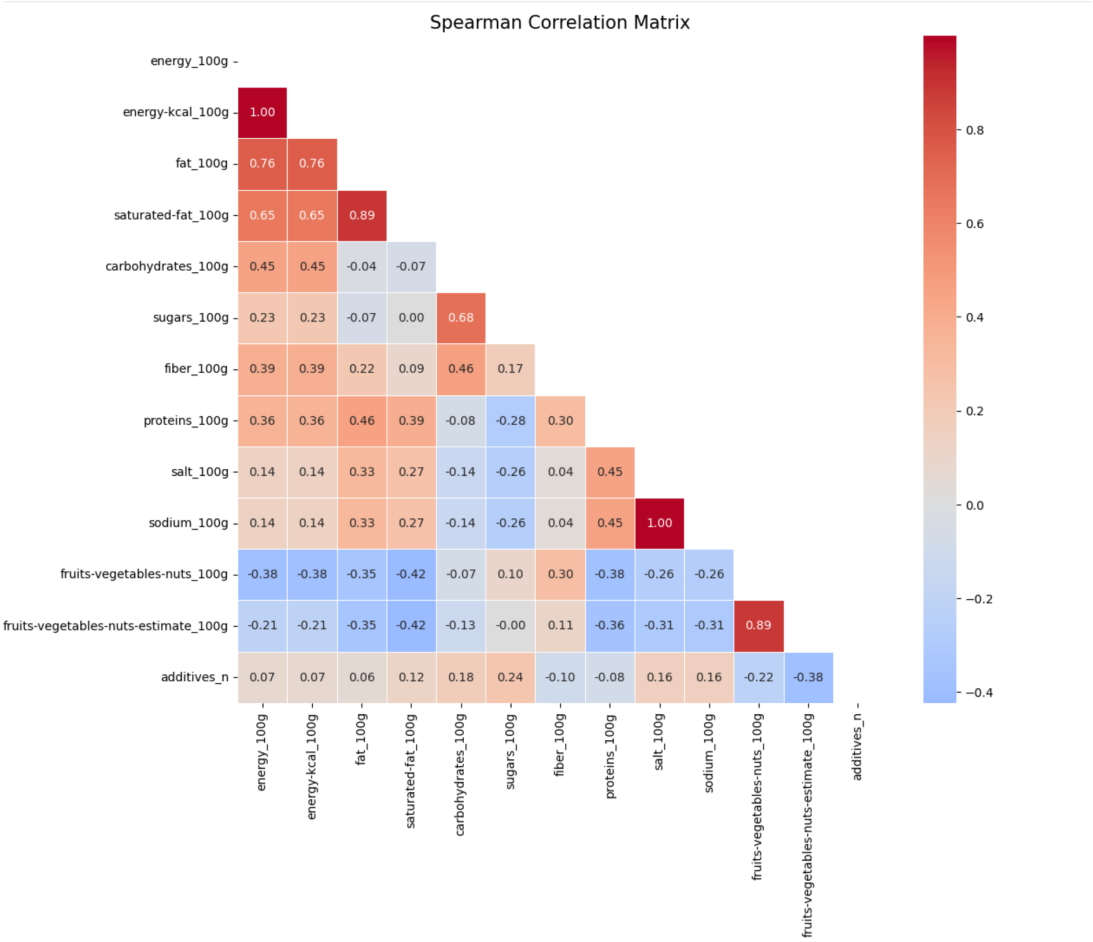


Figure 6: Correlation matrix among the main nutritional features. Highly correlated pairs such as salt/sodium and energy (kcal)/energy (kJ) are evident.

will subsequently implement a targeted approach to standardize these strings and achieve an effective encoding.

Now that we have gained some insights, we can proceed to the preprocessing stage.

4.3 Preprocessing

The preprocessing is done through a scikit-learn transformation pipeline [3]. The pipeline is composed of the following steps:

1. Missing Value Handling
2. Outlier Detection and Removal
3. Categorical Feature Encoding
4. Feature Engineering
5. Feature Scaling
6. Dimensionality Reduction (PCA)
7. Data Splitting

4.3.1 Missing Value Handling

First we drop the features with more than 95% of missing values (see Figure 7). In our case, we dropped the features `fruits-vegetables-nuts-estimate_100g` and `fruits-vegetables-nuts_100g`. Remembre that these features are important for the calculation of the Nutri- Score with the deterministic formula, so their absence is the exact challenge we are trying to solve with this project. The missing value handling is done through a median imputation. The median imputation is done for the numerical features. For the categorical features, the missing values are labeled as 'unknown'.

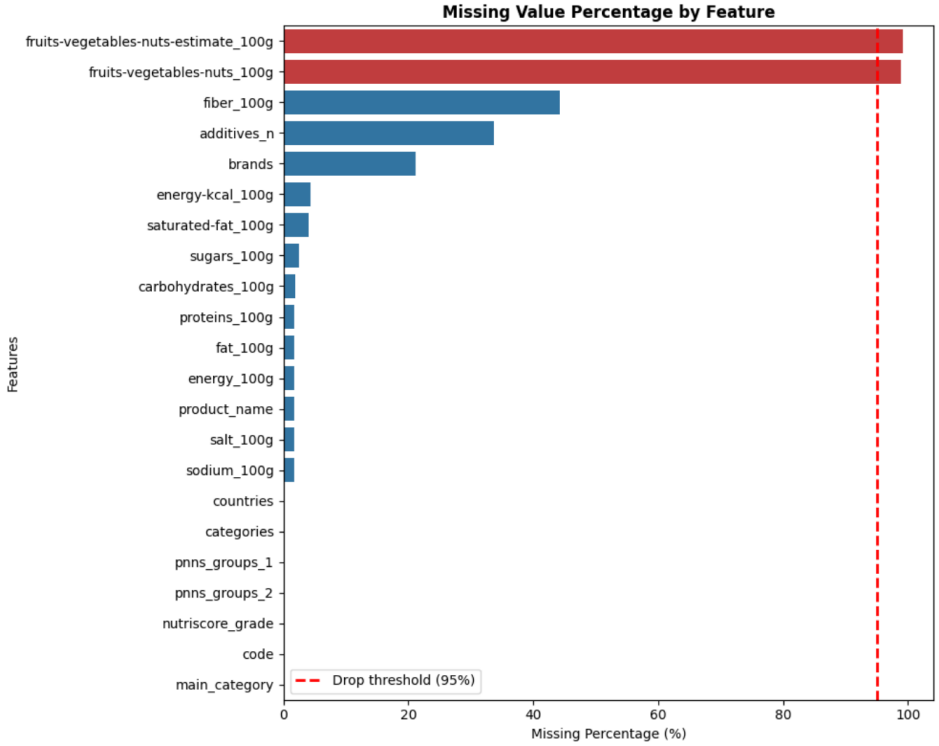


Figure 7: Feature missing values: reasons for dropping 'fruits-vegetables-nuts' and its estimate.

4.3.2 Outlier Detection and Removal

The outlier detection and removal is done through a domain-based and an optional statistical outlier detection. The domain-based outlier detection is done for the numerical features, invalid values such as negative values or values outside the valid range(200g in the column `saturated-fat_100g`). The project also implements a statistical outlier removal method. However this method did not produce good results because the domain of nutritional values is made of highly skewed values with a lot of outliers that should not be removed. For example olive oil is made almost entirely of fats while other foods don't have fat at all, this is not a valid reason to remove olive oil from the dataset. If the statistical outlier is implemented it removes around 25% of data from the samples and models give worse performances overall.

4.3.3 Categorical Feature Encoding

The categorical feature encoding operates on the features `countries`, `pnns_groups_1`, and `pnns_groups_2`. The `pnns_groups_1` feature is encoded using a one-hot encoding, while The `pnns_groups_2` feature is encoded using a target encoding. The target encoding is used because it is a high cardinality feature with a lot of unique values. Target encoding replaces each categorical label with the mean of the target variable for that specific category, effectively converting

discrete strings into numerical values based on their statistical relationship with the output. The `countries` feature presents a more complex case. The feature is a multi-label feature, and it has a lot of acronyms and country names in multiple languages. To address this, we implement a mapping of the country names to a canonical form. This is done by using a generated mapping and the PyCountry library [5]. After this, we apply a multi-label binarization and we choose the top 15 countries by frequency (the top 15 represent 98% of the data) and the other is set to 'unknown' (see Figure 8).

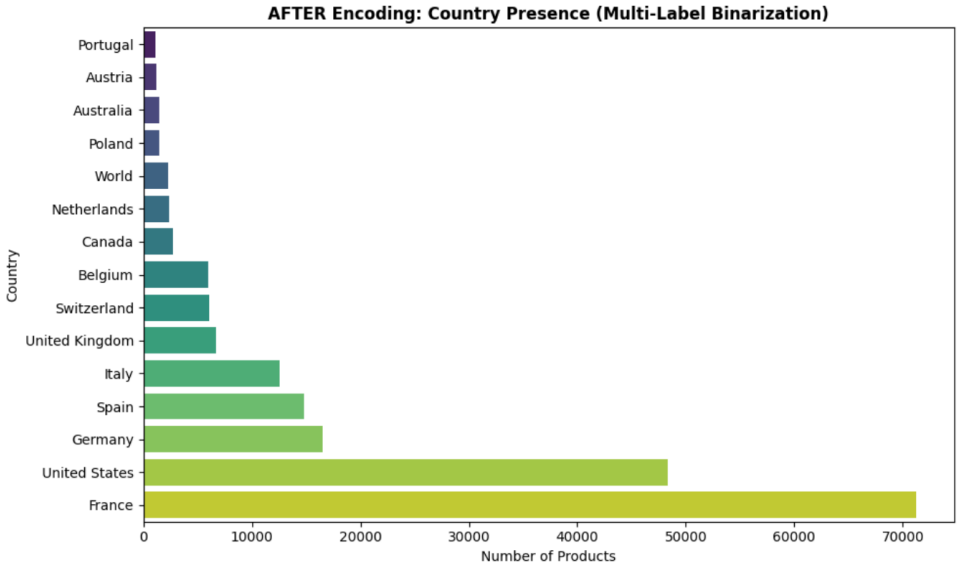


Figure 8: Visualizing the countries feature after cleaning, mapping, and binarization.

4.3.4 Feature Engineering

The feature engineering is done through a transformer that creates the following types of features:

- **Nutritional Ratios:** 4 features:
  - `fat_to_protein_ratio`
  - `sugar_to_carb_ratio`
  - `saturated_to_total_fat_ratio`
  - `energy_density`
- **Energy Decomposition:** 4 features:
  - `calories_from_fat`
  - `calories_from_carbs`
  - `calories_from_protein`
  - `energy_density`
- **Health Threshold Flags:** 3 features:
  - `high_sugar`
  - `high_salt`
  - `high_fat`

4.3.5 Feature Scaling

The feature scaling implements three different scalers: StandardScaler, MinMaxScaler, and RobustScaler. Some features that are highly skewed are transformed with a log1p transformation before the scaling.

The log $1p$ transformation is applied to highly skewed features before scaling, which helps reduce the impact of extreme outliers and normalizes the distribution. The mathematical formula for the log $1p$ transformation is:

$$x' = \log(1 + x) \tag{1}$$

where x is the original feature value and x' is the transformed value. This transformation is numerically stable for small x and prevents issues with zeros in the data while solving the problem of very big data (example the engineered feature `fat_to_protein_ratio` if the product has a small value of protein like 0.01 it will explode).

Through numerous testing of the models, we found that the StandardScaler is the best scaler for the dataset. This is probabilly because of the nutritional data distributions. Outliers are important so RobustScaler is not the best choice and MinMaxScaler is not the best choice with high skewness.

4.3.6 Dimensionality Reduction

The dimensionality reduction is done through Principal Component Analysis (PCA). The wrapper class first filters all numerical features and sets aside the metadata features (`product name`, `brands`, `code`). The variance threshold is set to 0.95. This means that the PCA will retain the features that explain 95% of the variance in the data. This is done to reduce the dimensionality of the data and to reduce the number of features. The reduction is around 25% of the features (lower variance threshold have been proven to be not good for the model performance), as shown in Figure 9.

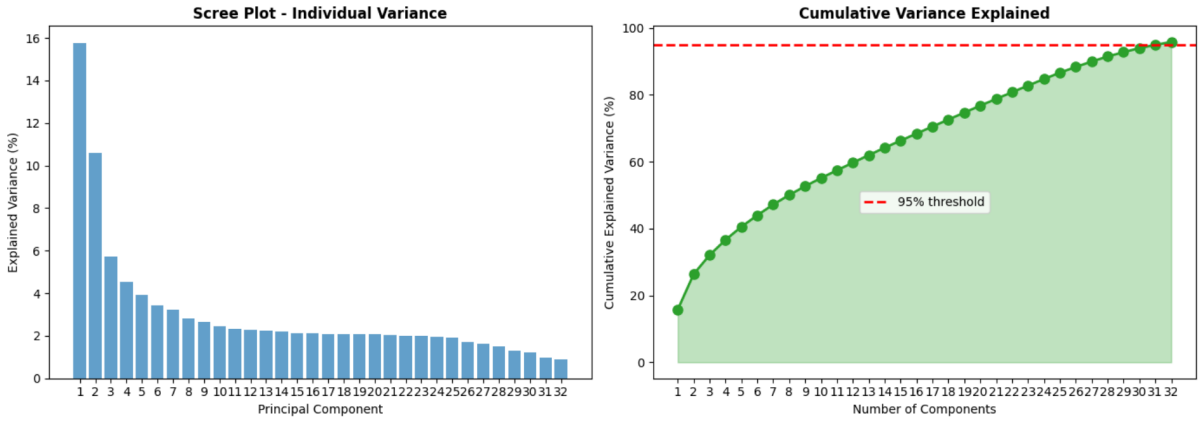


Figure 9: PCA: Explained variance ratio and feature reduction by principal component analysis.

4.3.7 Data Splitting

The data splitting is done through a train, validation, and test split. The split is stratified by the target variable to ensure its distribution is the same in all sets [3]. is the same in all sets. The split is done using a 70/15/15 ratio. The splits are necessary to evaluate the model performance. We used the explicit validation set to match performances between the models. Later we will also use Cross-Validation to tune the hyperparameters. The usage of both explicit validation and cross-validation was a deliberate choice to avoid data snooping bias and to get

a more accurate performance estimation (we use the big explicit validation set for performance so we can use test set only one time at the end for final evaluation). To prevent data leakage and avoid data snooping bias, we strictly isolate the training set for model development and parameter estimation, ensuring that both the test sets remain completely unseen during the entire development and tuning process.

4.4 Models

In this project we explored the following models:

- **Logistic Regression**
- **K-Nearest Neighbors**
- **Support Vector Machine**
- **Random Forest**
- **XGBoost**

Each model is encapsulated in its own wrapper class, all of which refer to a common BaseModel abstract class interface. The wrapper class is responsible for the training, prediction, and evaluation of the models. This approach allows for easy addition of new models and greatly helped us during the development of the project.

4.4.1 Logistic Regression

The logistic regression is the linear model we use as a baseline. It is a simple model that is easy to understand and to interpret and helped us with the initial testing of the project structure and the preprocessing pipeline. Logistic Regression computes the probability of a product of being in a certain Nutri-Score grade using a linear combination of the features. It is quite simple and does not perform very well in the presence of non-linear relationships.

4.4.2 K-Nearest Neighbors

The K-Nearest Neighbors is a non-parametric model based on the distance. We decided to use the K-Nearest Neighbors to try a distance-based model with our dataset. Later we decide the best model parameters for our dataset.

4.4.3 Support Vector Machine

The Support Vector Machine is a kernel-based model that is used to find the best hyperplane to separate the data. Since we wanted to explore a non-linear model, we decided to use the Support Vector Machine with a RBF kernel. SVM is a very powerful model that is able to find the best hyperplane to separate the data. Its training time is quite long, but the results are quite good.

4.4.4 Random Forest

The Random Forest is an ensemble learning model. It uses multiple decision trees and the bagging technique to improve the performance and stability. Each decision tree is trained on a random subset of the data and the trees are then used to make a prediction. Studies have shown that Random Forest and gradient boosting models (LightGBM, Catboost, XGBoost) work very well with imbalanced food datasets [4]. As we will see in the results section, Random Forest performed well with our dataset even though it presented some overfitting.

4.4.5 XGBoost

XGBoost (eXtreme Gradient Boosting) is an open-source, distributed machine learning library that implements gradient-boosted decision trees—a supervised boosting algorithm based on gradient descent. It is known for its speed, efficiency, and its ability to scale effectively to large datasets [6].

5 Model Tuning

5.1 GridCV Search

In order to find the best hyperparameters for the models, we used a grid cross validation search (Scikit-Learn GridSearchCV). Since the target variable is imbalanced, we used a stratified cross-validation (StratifiedKFold). We used the F1-Macro as our main metric. F1-Macro is used when multiple classes are present. It is calculated as the average of the F1 scores of each class. The formula for F1-Macro is:

$$F1 - Macro = 1/N * \sum_{i=1}^{N} F1_i \tag{2}$$

where N is the number of classes and $F1_i$ is the F1 score of the i-th class.

We created a python script that takes as arguments the model name and using the custom wrapper class of the model automaticaly searches for the best hyperparameters and saves the model result in a json file.

5.1.1 Logistic Regression

Hyperparameter	**Grid Values**
`C`	[0.001, 0.01, 0.1, 1.0, 10.0, 100.0, 1000.0]

Table 1: Logistic Regression: grid search hyperparameter ranges.

For logistic regression we decided to use the lbfgs solver because it is a good solver and it is a good solver for large datasets. We also decided to use the balanced class weight to handle the imbalance of the data. The hyperparameter we tuned is the C hyperparameter (see Table 1). The C hyperparameter is the regularization parameter. In logistic regression, the regularization is l2 by default. The best results are achieved with a C value of 1.0 (see Figure 10).

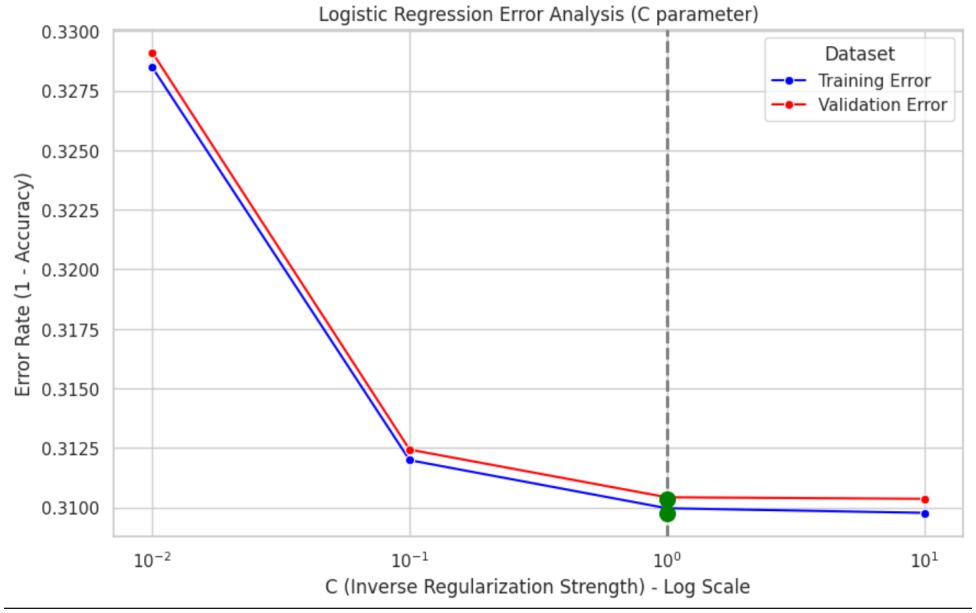


Figure 10: Logistic Regression: tuning results for C.

5.1.2 K-Nearest Neighbors

Hyperparameter	**Grid Values**
`n_neighbors`	[3, 5, 7, 9, 11, 15, 31, 63, 127]
`weights`	[uniform, distance]
`metric`	[euclidean, manhattan]

Table 2: K-Nearest Neighbors: grid search hyperparameter ranges.

For K-Nearest Neighbors we decided to try euclidean and manhattan distances and we decided to try both uniform and distance weights (see Table 2). We searched for the best k value combined with the best metric and the best weights. The manhattan distance had poor results, and the distance weight had a very high overfitting gap between the train and the validation f1 macro (see Figure 11). The best results are achieved with a k value of 15, a euclidean distance and a uniform weight.

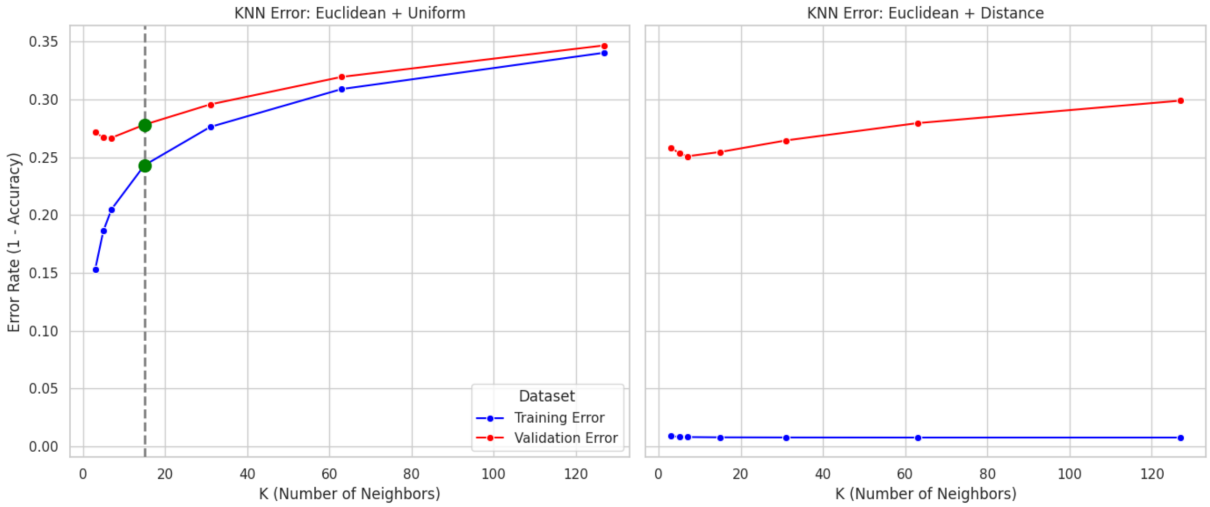


Figure 11: K-Nearest Neighbors: difference in overfitting between uniform and distance weights.

5.1.3 Support Vector Machine

Hyperparameter	Grid Values
`C`	$[2^{-5}, 2^{0}, 2^{5}, 2^{10}, 2^{15}]$
`gamma`	$[2^{-15}, 2^{-10}, 2^{-5}, 2^{0}, 2^{5}]$

Table 3: SVM: grid search hyperparameter ranges.

For SVM we decided beforehand to use the rbf kernel because we wanted to try a non-linear kernel that could handle some non-linear relationships between the features and the target. We set class weight to balanced to handle the imbalance of the data. Then we did a grid search over the C and gamma hyperparameters (see Table 3). The best results are achieved with a C value of 32 and a gamma value of 0.03125 (see Figure 12). We had to limit the search because the training time was too long for each fold.

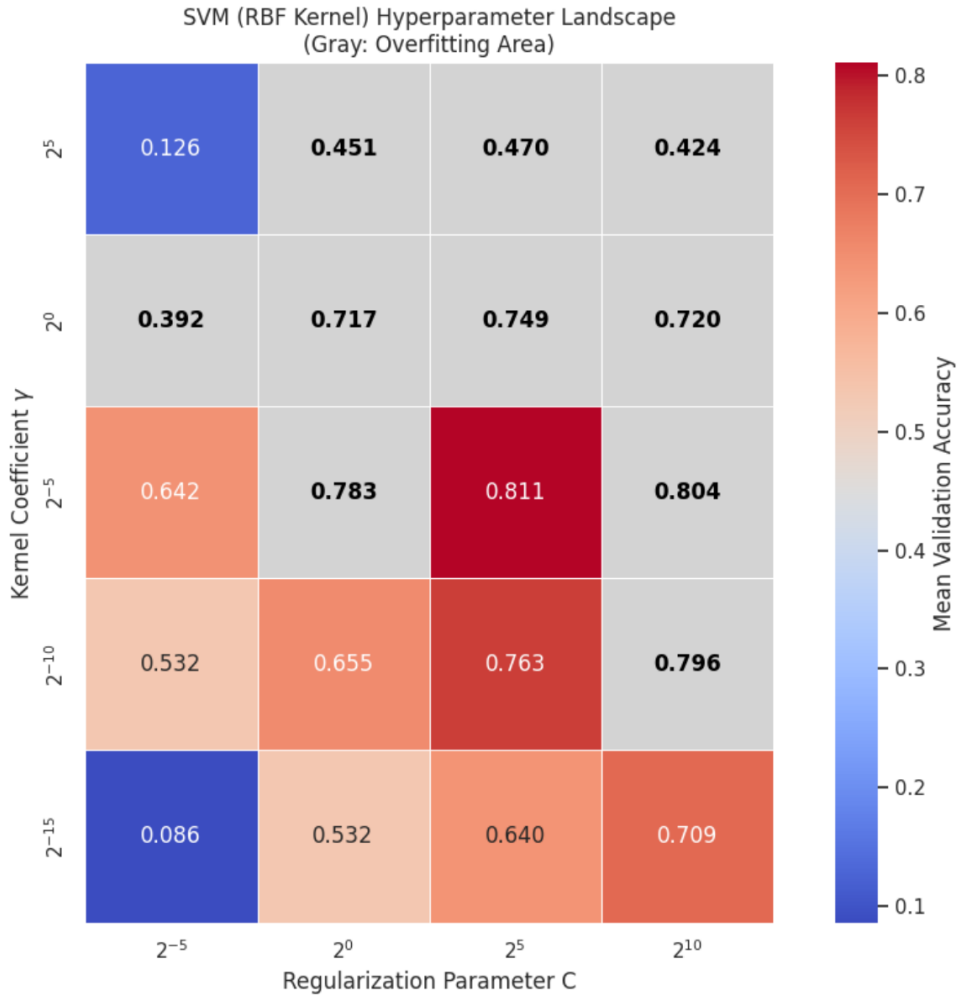


Figure 12: Support Vector Machine: tuning results with RBF kernel for C and gamma.

5.1.4 Random Forest

Hyperparameter	Grid Values
`n_estimators`	[100, 200, 300]
`max_depth`	[10, 15, 20]
`min_samples_split`	[2, 5]
`min_samples_leaf`	[1, 2]

Table 4: Random Forest: grid search hyperparameter ranges.

For random forest we searched for the best `n_estimators`, `max_depth`, `min_samples_split` and `min_samples_leaf` hyperparameters (see Table 4). We had to be careful because `n_estimators` and `max_depth` if set too high often caused overfitting. `min_samples_split` is used to control the minimum number of samples while `min_samples_leaf` is used to control the minimum number of samples required to be at a leaf node. The best results are achieved with a `n_estimators` value of 200, a `max_depth` value of 15, a `min_samples_split` value of 2 and a `min_samples_leaf` value of 2 (see Figure 13).

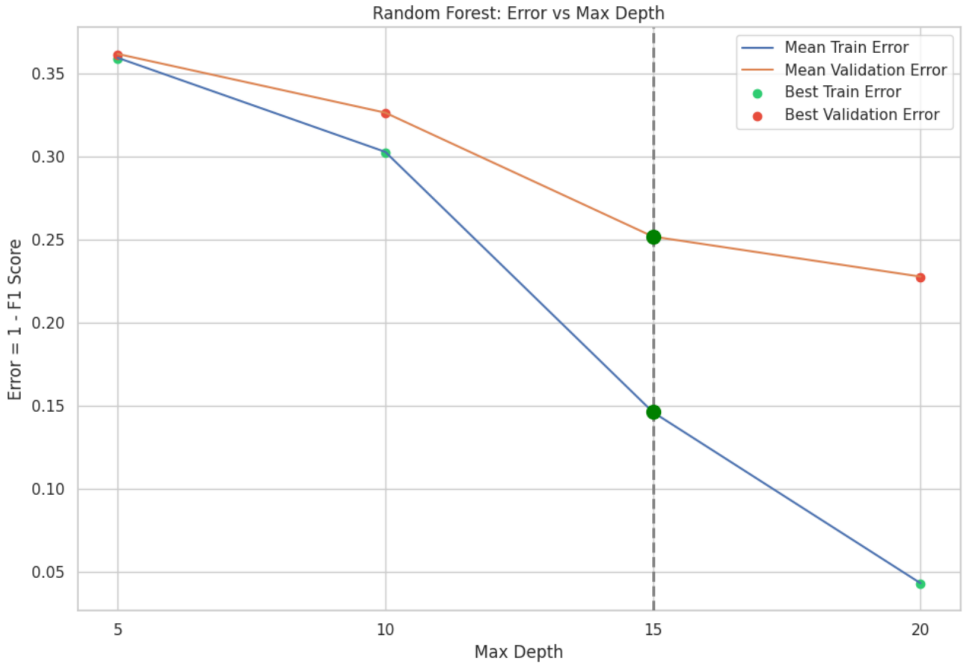


Figure 13: Random Forest: tuning results.

5.1.5 XGBoost

Hyperparameter	Grid Values
`n_estimators`	[200, 300, 400]
`max_depth`	[3, 6, 7]
`learning_rate`	[0.05, 0.1, 0.2]
`min_child_weight`	[3, 5]

Table 5: XGBoost: grid search hyperparameter ranges.

For XGBoost we searched for the best hyperparameters (see Table 5): `n_estimators`, `max_depth`, `learning_rate` and `min_child_weight` . Since XGBoost is a very fast model, we could afford to search for more hyperparameters and more values for each hyperparameter. Since it uses decision trees, we had to be careful like in random forest because `max_depth` if set too high often caused overfitting. The best results are achieved with `n_estimators`=400, `max_depth`=7, `learning_rate`=0.2 and `min_child_weight`=3 (see Figure 14).

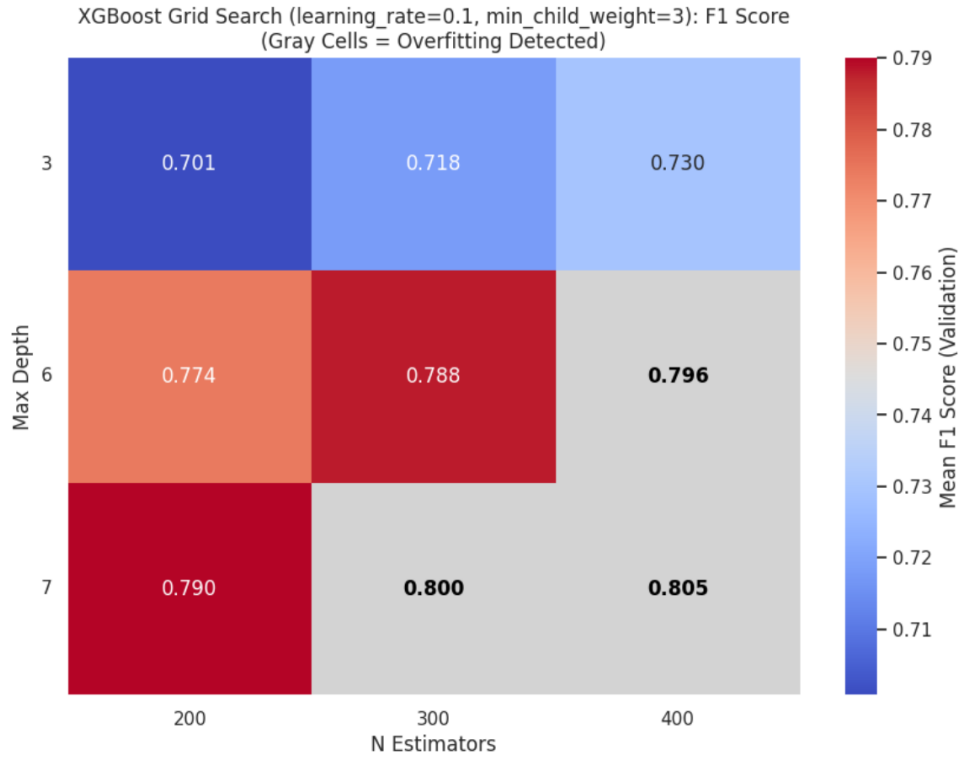


Figure 14: XGBoost: tuning results.

6 Experiments & Results

6.1 Experimental Setup

We trained all five models on the preprocessed dataset of 250,000 samples with a 70/15/15 train/validation/test split. We used stratified splitting to keep the class distribution consistent across sets, which matters because of the imbalance in our data (class E: 28.2% vs. class B: 11.6%).

We noticed that accuracy wasn't enough to evaluate performance. Because of the imbalance, a model could get decent accuracy just by doing good on the majority classes (D and E) while failing on minority classes. We chose F1-Macro as our main metric because it weights all classes equally.

We started with default hyperparameters and then tuned based on validation results. The F1-Macro scores for all models are shown in Figure 15.

6.2 Performance Metrics

Table 6 shows the results for each model on the validation set.

Model	F1 Macro	Accuracy	Precision Macro	Recall Macro	Time (s)
SVM	**0.8223**	**0.8423**	**0.8191**	**0.8268**	**1699.15**
XGBoost	0.7741	0.8001	0.7835	0.7713	11.55
Random Forest	0.7709	0.7923	0.7712	0.7717	45.97
KNN	0.7276	0.7509	0.7313	0.7269	42.23
Logistic Regression	0.6855	0.7079	0.6836	0.6896	4.24

Table 6: Validation set performance metrics and training time for all models.

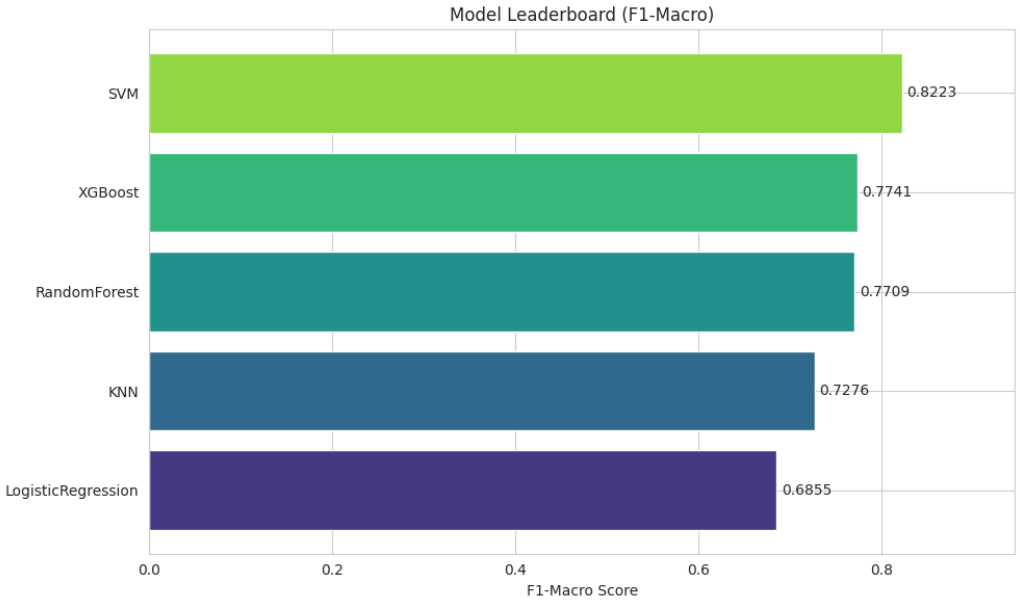


Figure 15: F1-Macro scores of all models on the validation set.

Figure 16: Training time (seconds) for each model.

SVM with RBF kernel got the best results: 84.2% accuracy and 82.3% F1-Macro (see Table 6). Precision and recall are balanced (82.0% and 82.7%), showing no bias toward false positives or negatives. However, training took 1699 seconds (about 28 minutes), which was a bit problematic during the experiments (see Figure 16).

6.3 Model-Specific Analysis

Logistic Regression. We started with Logistic Regression as a baseline. It got 70.8% F1-Macro, which confirmed that the relationship between features and Nutri-Score is non-linear (see Section 4.2 and Figure 6). The model had difficulty with middle classes (B and C), often confusing them with the ones close to them. This makes sense because the Nutri-Score uses step

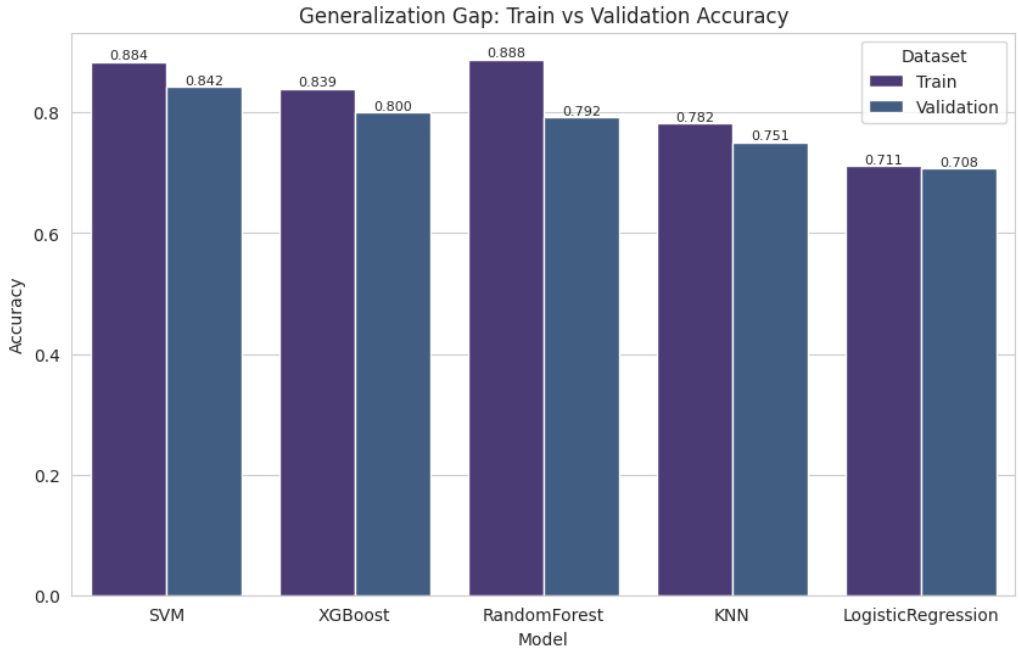


Figure 17: Train versus validation accuracy per model, showing the generalization gap (e.g., KNN overfitting).

functions and thresholds, not smooth transitions.

K-Nearest Neighbors. For KNN, validation F1-Macro was good at 75.1%, but training accuracy reached 99.3% versus only 75.1% on validation a 24% gap, indicating severe overfitting in case of distance weights (see Figure 17). If we choose uniform weights, we get a much lower gap and we avoid overfitting. We tested k values from 3 to 127 and selected k=15 based on the tuning results (see Table 2 and Figure 11).

Support Vector Machine. SVM with RBF kernel had the best performance at 82.2% F1-Macro (see Table 6). It was very good at handling class B (the smallest class), where the others failed. The RBF kernel works well because it can model complex decision boundaries. The Nutri-Score formula has different thresholds for different nutrients plus interaction effects (like fruits/vegetables / sugar), and RBF captures these (see Figure 12). However, 1699 seconds (about 28 minutes) training time was too long (see Figure 16). We had to limit hyperparameter search because of this (see Table 3). We tried LinearSVC as a faster option, but it got only 0.67 F1-Macro, worse than Logistic Regression so we discarded it. For a real system that needs online updating on new Open Food Facts data, this training time isn't practical.

Random Forest. Random Forest got 77.1% F1-Macro in about 46 seconds (see Table 6 and Figure 16). Random Forest handled class imbalance well. The main issue was that it preferred middle classes (C and D) over extremes (A and E). This happens because when trees disagree, averaging pulls predictions toward the center. The best hyperparameters found through grid search are shown in Table 4 and Figure 13.

XGBoost. For practical use, XGBoost was the best. It got 77.4% F1-Macro in 12 seconds – the best performance-to-speed ratio (see Table 6 and Figure 16). We tuned hyperparameters and found learning rate was critical (see Table 5 and Figure 14). 0.3 caused overfitting, 0.01 underfit even with 500 rounds. Best results came from learning rate 0.2 with max_depth=7 and n_estimators=400. XGBoost also handled missing values well during prediction.

6.4 Test Set Results

To confirm that the validation results generalize well, we evaluated all five models on the held-out test set (36,960 samples), which was never used during training or hyperparameter tuning.

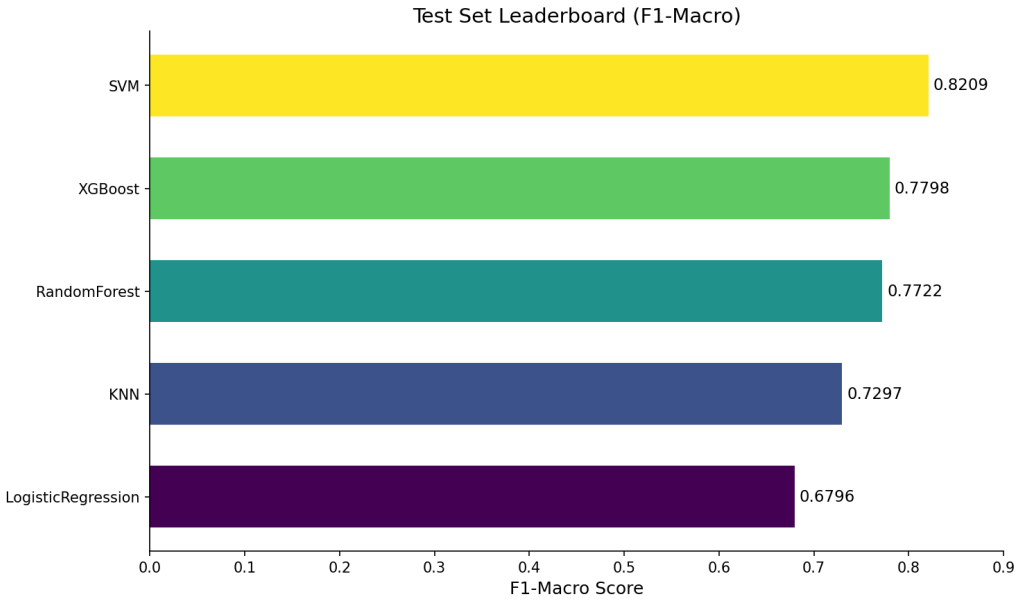


Figure 18: F1-Macro scores of all models on the test set.

Table 7 reports the detailed results.

Model	F1 Macro	Accuracy	Precision Macro	Recall Macro
SVM	**0.8209**	**0.8403**	**0.8176**	**0.8255**
XGBoost	0.7798	0.8038	0.7890	0.7766
Random Forest	0.7722	0.7927	0.7727	0.7730
KNN	0.7297	0.7511	0.7334	0.7293
Logistic Regression	0.6796	0.7005	0.6771	0.6844

Table 7: Test set performance metrics for all models.

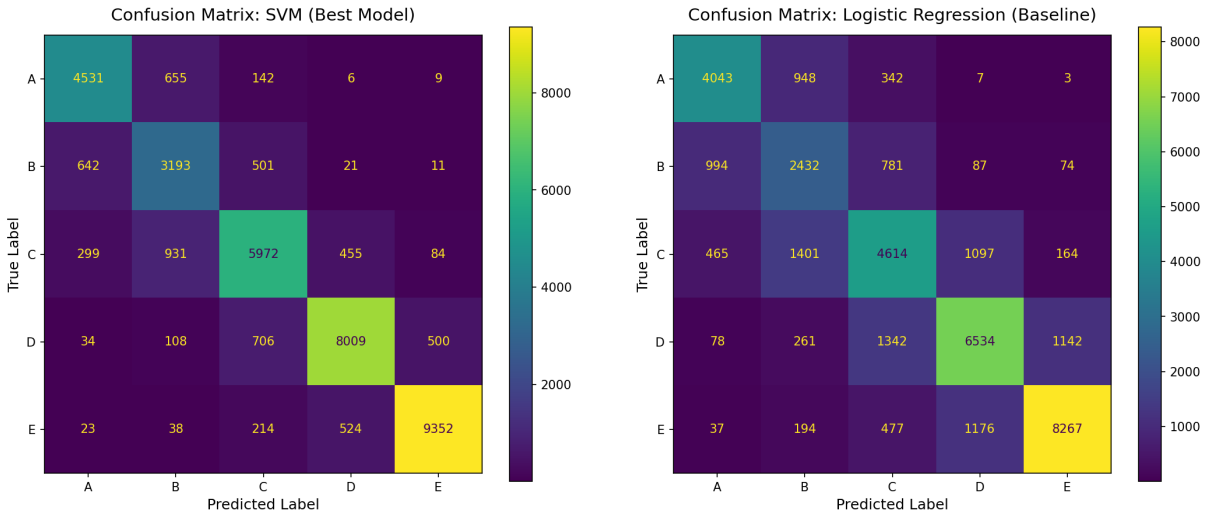
The test set metrics are very close to the validation results across all models, with differences below 0.5% in F1-Macro. This confirms that the models generalize well and that no data leakage occurred during training or tuning. SVM remains the top performer on the test set with 82.1% F1-Macro, while XGBoost maintains the best performance-to-speed trade-off at 78.0% F1-Macro.

6.5 Error Analysis

Looking at confusion matrices, all models showed similar error patterns. They often confused close grades (C as D, B as C). Big errors (predicting E for an A product) were rare but more common with Logistic Regression and KNN. Class B was the harder to predict it's both the smallest class (11.6%) and has a large nutritional range between A and C.

To illustrate the difference between the best and worst performing models, we compare the confusion matrices of SVM and Logistic Regression on the test set (Figure 19a and Figure 19b).

SVM correctly classifies 3,193 out of 4,368 class B samples (73.1%), while Logistic Regression only gets 2,432 (55.7%). The improvement is also visible in the middle classes: SVM correctly predicts 5,972 C samples versus 4,614 for Logistic Regression. Logistic Regression spreads its



(a) SVM (F1-Macro: 0.8209)

(b) Logistic Regression (F1-Macro: 0.6796)

Figure 19: Confusion matrices on the test set: SVM (best) vs Logistic Regression (baseline). SVM shows a much stronger diagonal with fewer off-diagonal errors, especially for class B.

errors more broadly, with significant confusion between adjacent classes (e.g., 1,401 C samples misclassified as B, 1,342 D samples as C), confirming its inability to capture the non-linear thresholds of the Nutri-Score formula.

6.6 Observations

Non-linearity matters. The gap between Logistic Regression (68.1%) and non-linear models is a lot. Nutri-Score uses thresholds and interactions that linear models can't handle well.

Ensemble methods balance performance and speed. SVM performed the best, but Random Forest and XGBoost were very close with much lower cost. The 500x speed difference between XGBoost (37s) and SVM (6588s) is important, thinking of real-deployment use cases.

Feature engineering is important. Our project showed that engineered features added a lot of importance. Nutritional ratios provide context 10g sugar means different things if total carbs are 80g rather than 15g.

Missing fruit/vegetable data limits performance. This feature is important, especially for distinguishing A from B. We had to drop it (95%+ missing), which probably caused errors in healthy products grades.

7 Conclusions

This project predicts Nutri-Score grades for products in Open Food Facts. We tested five models and found that SVM performed best (81.6% F1-Macro), but XGBoost offered the most practical solution with 78.9% F1-Macro in just 37 seconds.

The results confirmed that non-linear models are best for this project. Logistic Regression only reached 68.1% F1-Macro because Nutri-Score uses thresholds and interactions, not linear relationships. Feature engineering was important ratio features gave models information they couldn't get from raw nutrient values as they were originally.

The main limitation is missing fruits/vegetables/nuts data (95%+ missing). This feature is important for separating grade A from B, and without it, models had problems with these classes. Class B was the hardest to predict it's the smallest class (11.6%). Our 250k sample was also a limitation; smaller than the full 1M+ products available from the dataset, but hardware gave us a limit.

For future work, advanced methods could handle missing nutrients better than just dropping them. Testing on the full dataset would show if performance is the same even if the scale is larger. Category-specific models (beverages vs. dairy) might perform better than one general model.

8 References

References

[1] NCD Alliance. *Unhealthy Diets.* https://ncdalliance.org/explore-ncds/risk-factors/unhealthy-diets

[2] ResearchGate. *Evaluating missing value imputation methods for food composition databases.* https://www.researchgate.net/publication/341157370_Evaluating_missing_value_imputation_methods_for_food_composition_databases

[3] Aurélien Géron. *Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow: Concepts, Tools, and Techniques to Build Intelligent Systems*, 3rd Edition. O'Reilly Media, 2022.

[4] Nalin Arora, Aviral Chauhan, Siddhant Rana, Mahansh Aditya, Sumit Bhagat, Aditya Kumar, Akash Kumar, Akanksh Semar, Ayush Vikram Singh, Ganesh Bagler. *Application of machine learning to predict food processing level using Open Food Facts*, 2025. https://arxiv.org/abs/2512.17169

[5] Flying Circus. *pycountry: ISO country, subdivision, language, currency and script definitions and translations* (Python package version 22.3.5), 2023. https://github.com/flyingcircusio/pycountry

[6] Tianqi Chen and Carlos Guestrin. *XGBoost: A Scalable Tree Boosting System.* Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD '16), 2016, pp. 785-794. ACM, New York, NY, USA. http://doi.acm.org/10.1145/2939672.2939785