winniekimmich update notebook f5576d0 · 1 minute ago

2375 lines (2375 loc) · 185 KB

Phase 3 Classification Project — End-to-End ML Pipeline

Project Goal

This project builds an end-to-end **classification** machine learning solution using an iterative modeling approach.
I will train models on historical survey responses and predict the probability that a respondent received:

- **H1N1 vaccine** (`h1n1_vaccine`)
- **Seasonal flu vaccine** (`seasonal_vaccine`)

Accurate predictions can help public health teams identify groups with lower vaccination likelihood and target communication, access, and outreach efforts more effectively.

Deliverables

1. A full Jupyter notebook (EDA → preprocessing → modeling → evaluation → predictions)
2. A non-technical presentation for stakeholders
3. A GitHub README summarizing the work

In [4]:
```
#importing libraries
import pandas as pd
import numpy as np

#reading into the csv files
train_X = pd.read_csv("training_set_features.csv")
train_y = pd.read_csv("training_set_labels.csv")
test_X  = pd.read_csv("test_set_features.csv")
sub_fmt = pd.read_csv("submission_format.csv")

print("train_X:", train_X.shape)
print("train_y:", train_y.shape)
print("test_X :", test_X.shape)
print("sub_fmt:", sub_fmt.shape)

#checking the first 5 rows
train_X.head()
```

```
train_X: (26707, 36)
train_y: (26707, 3)
test_X : (26708, 36)
sub_fmt: (26708, 3)
```

Out[4]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavi
0	0	1.0	0.0	0.0	0.0	
1	1	3.0	2.0	0.0	1.0	
2	2	1.0	1.0	0.0	1.0	
3	3	1.0	1.0	0.0	1.0	

4	4	2.0	1.0	0.0	1.0

5 rows × 36 columns

2. Data Understanding (EDA)

What we are checking in EDA

Before modeling, we need to understand:

1. **Data structure** (rows/columns and how files relate)
2. **Targets** (class balance and whether the problem is classification)
3. **Feature types** (numeric vs categorical)
4. **Missingness patterns** (what needs imputation)
5. **Early relationships** (simple patterns that can guide modeling choices)

Two Targets → Multi-output Binary Classification

We are predicting **two binary outcomes** for the same respondent:

- `h1n1_vaccine` (0/1)
- `seasonal_vaccine` (0/1)

This is best treated as **multi-output binary classification**:

- each target is a separate binary classification task
- the model outputs two probabilities per respondent (one per target)

This matches the submission format which requires:

- `h1n1_vaccine` probability
- `seasonal_vaccine` probability

In [5]:
```
# Setting respondent_id as index to align safely
X = train_X.set_index("respondent_id")
y = train_y.set_index("respondent_id")[["h1n1_vaccine", "seasonal_vaccine"]]

print("X aligned with y:", X.shape, y.shape)
print("Any missing respondent_id alignment?", (X.index.equals(y.index)))

# Target rates
print("Target prevalence (mean):")
display(y.mean().to_frame("positive_rate"))

# Joint distribution
display(y.value_counts().rename("count").to_frame().head(10))
```

```
X aligned with y: (26707, 35) (26707, 2)
Any missing respondent_id alignment? True
Target prevalence (mean):
```

	positive_rate
h1n1_vaccine	0.212454
seasonal_vaccine	0.465608

	count

h1n1_vaccine	seasonal_vaccine	
0	0	13295
	1	7738
1	1	4697
	0	977

In [6]:
```
cat_cols = X.select_dtypes(include="object").columns.tolist()
num_cols = [c for c in X.columns if c not in cat_cols]

print("Categorical columns:", len(cat_cols))
print(cat_cols)

print("\nNumeric columns:", len(num_cols))
print(num_cols[:10], "...")
```

```
Categorical columns: 12
['age_group', 'education', 'race', 'sex', 'income_poverty', 'marital_status', 'rent_or_own', 'empl
oyment_status', 'hhs_geo_region', 'census_msa', 'employment_industry', 'employment_occupation']

Numeric columns: 23
['h1n1_concern', 'h1n1_knowledge', 'behavioral_antiviral_meds', 'behavioral_avoidance', 'behaviora
l_face_mask', 'behavioral_wash_hands', 'behavioral_large_gatherings', 'behavioral_outside_home',
'behavioral_touch_face', 'doctor_recc_h1n1'] ...
```

Missing Values (Why we must handle them carefully)

Many real-world survey datasets have missing responses.
We measure missingness per feature because it impacts model training.

Key principle:

- We must handle missing values **inside a modeling pipeline** (using imputation steps)
- This prevents **data leakage** because imputation statistics must be learned only from training folds during cross-validation.

We will use strategies like:

- Most frequent value imputation for categorical fields
- Median imputation for numeric fields

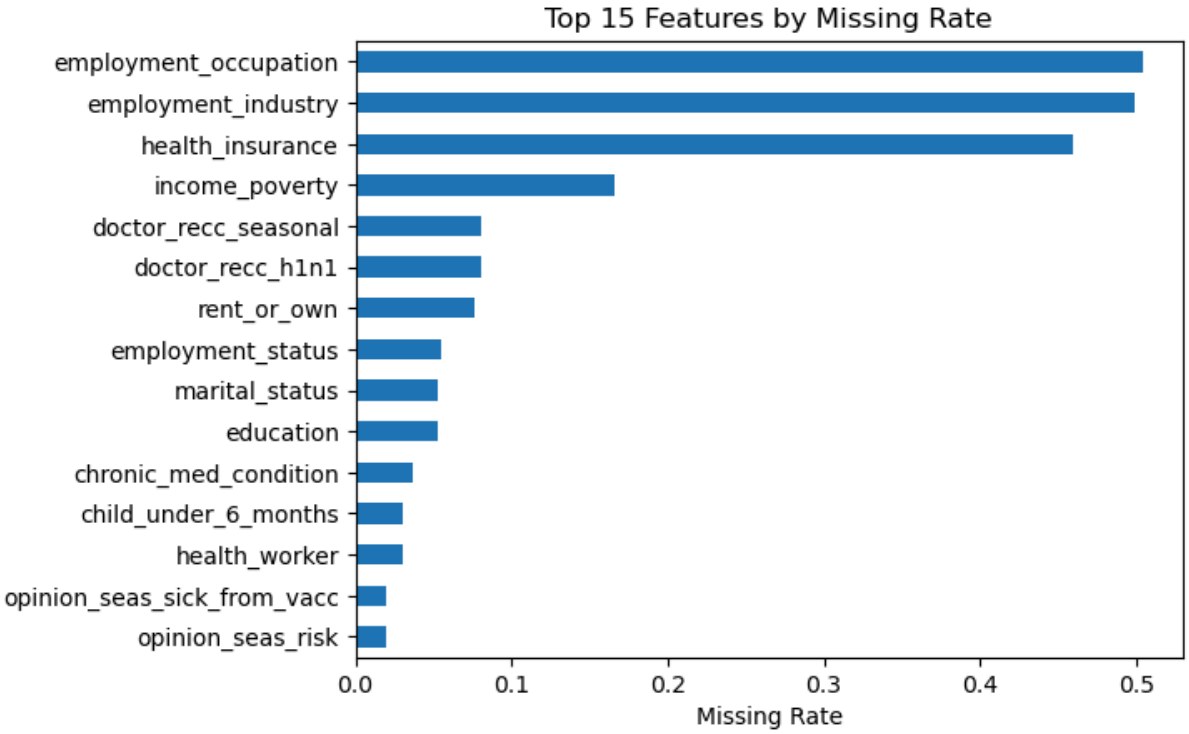
In [7]:
```
missing_rate = X.isna().mean().sort_values(ascending=False)
display(missing_rate.head(15).to_frame("missing_rate"))

# Optional: visualize top missing columns
import matplotlib.pyplot as plt

top_k = 15
plt.figure()
missing_rate.head(top_k).sort_values().plot(kind="barh")
plt.title(f"Top {top_k} Features by Missing Rate")
plt.xlabel("Missing Rate")
plt.show()
```

	missing_rate
employment_occupation	0.504362
employment_industry	0.499120
health_insurance	0.459580

income_poverty	0.165612
doctor_recc_h1n1	0.080878
doctor_recc_seasonal	0.080878
rent_or_own	0.076459
employment_status	0.054780
marital_status	0.052720
education	0.052683
chronic_med_condition	0.036358
child_under_6_months	0.030704
health_worker	0.030104
opinion_seas_sick_from_vacc	0.020107
opinion_seas_risk	0.019246

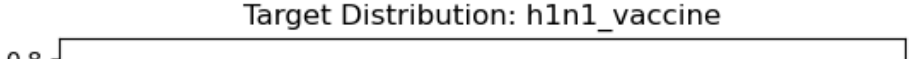


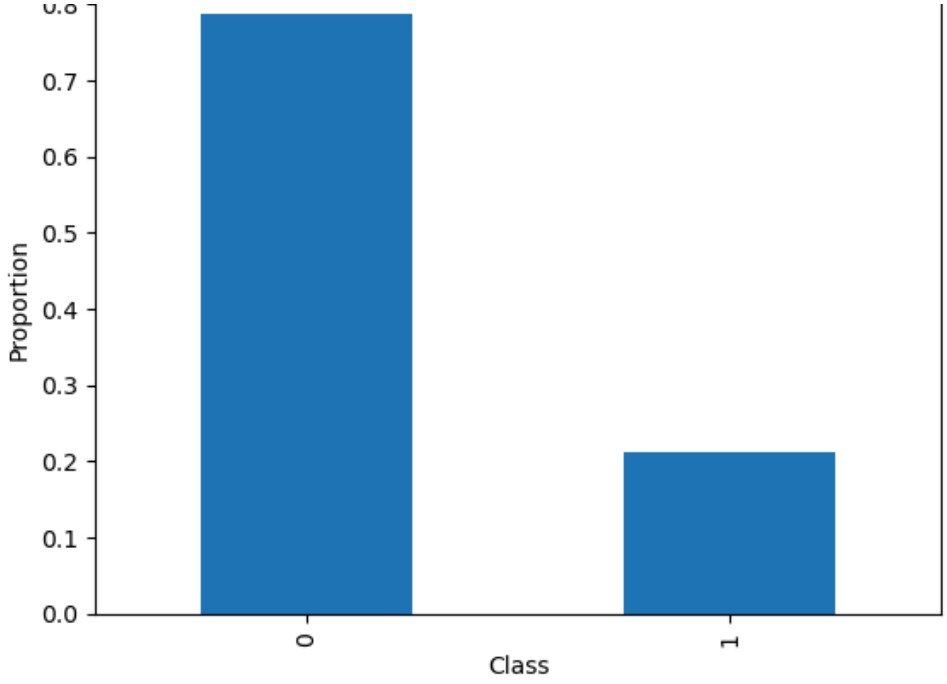
In [8]:

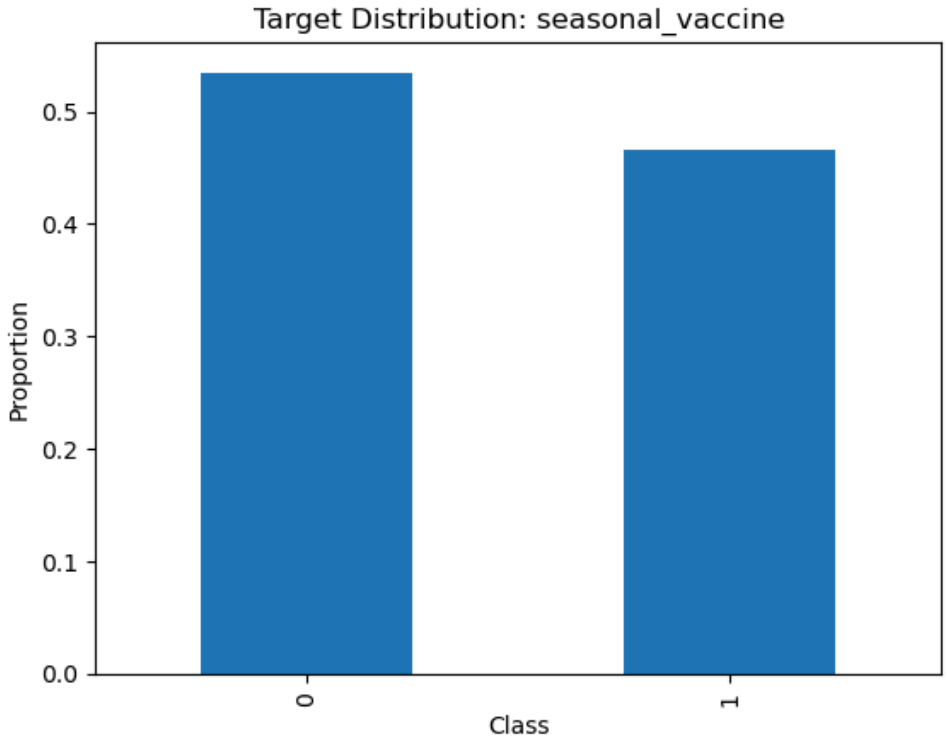
```
import matplotlib.pyplot as plt

plt.figure()
y["h1n1_vaccine"].value_counts(normalize=True).sort_index().plot(kind="bar")
plt.title("Target Distribution: h1n1_vaccine")
plt.xlabel("Class")
plt.ylabel("Proportion")
plt.show()

plt.figure()
y["seasonal_vaccine"].value_counts(normalize=True).sort_index().plot(kind="bar")
plt.title("Target Distribution: seasonal_vaccine")
plt.xlabel("Class")
plt.ylabel("Proportion")
plt.show()
```







In [10]:

```
# Example: mean target rate by a categorical feature (age_group)
tmp = X.join(y)

age_summary = tmp.groupby("age_group")[["h1n1_vaccine", "seasonal_vaccine"]].mean().sort_index()
display(age_summary)

# Example: mean target rate by health_worker (numeric indicator)
hw_summary = tmp.groupby("health_worker")[["h1n1_vaccine", "seasonal_vaccine"]].mean()
display(hw_summary)
```

	h1n1_vaccine	seasonal_vaccine
age_group		
18 - 34 Years	0.190029	0.284564

35 - 44 Years	0.197765	0.362526
45 - 54 Years	0.194731	0.401298
55 - 64 Years	0.242855	0.511235
65+ Years	0.226655	0.673681

health_worker	**h1n1_vaccine**	**seasonal_vaccine**
0.0	0.188793	0.445618
1.0	0.409452	0.647120

EDA Summary

From this dataset we observed:

- The task is **classification** with **two binary targets**
- `h1n1_vaccine` appears more imbalanced than `seasonal_vaccine`
- The dataset contains a mix of numeric and categorical features
- Several columns have substantial missingness (especially employment-related features)

Next, we will:

1. Split the data into train/validation sets (carefully, to maintain target distributions)
2. Build a preprocessing pipeline with:
   - imputation for missing values
   - one-hot encoding for categorical columns
   - scaling for numeric columns (where needed)
3. Train baseline and improved models and compare performance using classification metrics

3. Data Preparation & Preprocessing

After understanding the data, we now prepare it for modeling.

This step is critical because:

- Models cannot handle missing values or raw categorical text
- Data leakage must be avoided
- Transformations must be applied consistently to train and test data

We follow professional ML best practices:

1. Train/validation split
2. Separate numeric and categorical preprocessing
3. Use pipelines to prevent leakage
4. Prepare features for multiple models

Why split BEFORE preprocessing?

To avoid **data leakage**, we must split the data first.

Data leakage occurs when:

- statistics from validation/test data influence training transformations
- for example, scaling using the entire dataset mean

This causes overly optimistic results.

Correct approach:

1. Split data
2. Fit preprocessing only on training data
3. Apply learned transforms to validation/test

In [11]:
```
from sklearn.model_selection import train_test_split

# We stratify using both targets together to preserve class distribution
# Create combined label string for safe stratification
stratify_labels = y.astype(str).agg("-".join, axis=1)

X_train, X_val, y_train, y_val = train_test_split(
    X,
    y,
    test_size=0.2,
    random_state=42,
    stratify=stratify_labels
)

print("Train shape:", X_train.shape)
print("Validation shape:", X_val.shape)
```

```
Train shape: (21365, 35)
Validation shape: (5342, 35)
```

Why stratify?

Our targets are imbalanced, especially `h1n1_vaccine` .

If we split randomly:

- validation might have fewer positive examples
- metrics become unreliable

Stratification ensures:

- similar class proportions in both train and validation
- fair evaluation

In [12]:
```
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.impute import SimpleImputer

cat_cols = X_train.select_dtypes(include="object").columns.tolist()
num_cols = [c for c in X_train.columns if c not in cat_cols]

print("Categorical:", len(cat_cols))
print("Numeric:", len(num_cols))
```

```
Categorical: 12
Numeric: 23
```

In [13]:
```
# Numeric pipeline
num_pipeline = Pipeline([
    ("imputer", SimpleImputer(strategy="median")),
    ("scaler", StandardScaler())
```

```
])

# Categorical pipeline
cat_pipeline = Pipeline([
    ("imputer", SimpleImputer(strategy="most_frequent")),
    ("encoder", OneHotEncoder(handle_unknown="ignore"))
])

# Combine
preprocessor = ColumnTransformer([
    ("num", num_pipeline, num_cols),
    ("cat", cat_pipeline, cat_cols)
])
```

Design decisions

Numeric:

- Median is robust to outliers
- Scaling helps linear models converge faster

Categorical:

- Most frequent imputation keeps categories realistic
- OneHotEncoder converts text → numeric
- handle_unknown="ignore" prevents crashes on unseen categories

This makes our pipeline safe and production-ready.

5. Baseline Model — Logistic Regression

We start with an interpretable baseline model.

Why Logistic Regression?

- Simple and fast
- Easy to interpret
- Good baseline for classification
- Provides probability outputs
- Often surprisingly strong

This model gives us a reference point before trying more complex models.

In [14]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.multioutput import MultiOutputClassifier

baseline_model = Pipeline([
    ("prep", preprocessor),
    ("model", MultiOutputClassifier(
        LogisticRegression(max_iter=2000)
    ))
])

baseline_model.fit(X_train, y_train)
```

Out[14]:
```
Pipeline(steps=[('prep',
                 ColumnTransformer(transformers=[('num',
                                                  Pipeline(steps=[('imputer',
                                                                   SimpleImputer(strateg
y='median')),
                                                                  ('scaler'
```

```
                                                                    ('scaler',
                                                                     StandardScaler())]),
                                                  ['h1n1_concern',
                                                   'h1n1_knowledge',
                                                   'behavioral_antiviral_meds',
                                                   'behavioral_avoidance',
                                                   'behavioral_face_mask',
                                                   'behavioral_wash_hands',
                                                   'behavioral_large_gatherings',
                                                   'behavioral_outside_home',
                                                   'behavior...
                                                                    SimpleImputer(strateg
y='most_frequent')),
                                                                   ('encoder',
                                                                    OneHotEncoder(handle_
unknown='ignore'))]),
                                                  ['age_group', 'education',
                                                   'race', 'sex',
                                                   'income_poverty',
                                                   'marital_status',
                                                   'rent_or_own',
                                                   'employment_status',
                                                   'hhs_geo_region',
                                                   'census_msa',
                                                   'employment_industry',
                                                   'employment_occupation'])])),
                                 ('model',
                                  MultiOutputClassifier(estimator=LogisticRegression(max_iter=2000)))])
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

6. Model Evaluation

Accuracy alone is misleading for imbalanced data.

We evaluate using:

Accuracy:

- overall correctness

Precision:

- how many predicted positives are correct

Recall:

- how many real positives we captured

F1:

- balance between precision and recall

ROC-AUC:

- ranking quality across thresholds (very important for probability predictions)

We evaluate on VALIDATION data only to simulate unseen data.

In [15]:
```
from sklearn.metrics import accuracy_score, f1_score, roc_auc_score

def evaluate(model, X_val, y_val):
    preds = model.predict(X_val)
    probs = model.predict_proba(X_val)

    results = {}

    for i, col in enumerate(y_val.columns):
        y_true = y_val[col]
        y_pred = preds[:, i]
        y_prob = probs[i][:, 1]

        results[col] = {
            "accuracy": accuracy_score(y_true, y_pred),
            "f1": f1_score(y_true, y_pred),
            "roc_auc": roc_auc_score(y_true, y_prob)
        }

    return pd.DataFrame(results).T


baseline_results = evaluate(baseline_model, X_val, y_val)
baseline_results
```

Out[15]:

	accuracy	f1	roc_auc
h1n1_vaccine	0.838263	0.536481	0.838102
seasonal_vaccine	0.782666	0.762722	0.853980

7. Hyperparameter Tuning

Default parameters are rarely optimal.

We use GridSearchCV to:

- test multiple hyperparameters
- use cross-validation
- automatically select the best combination

For Logistic Regression we tune:

- C (regularization strength)
- penalty type

In [16]:
```
from sklearn.model_selection import GridSearchCV

param_grid = {
    "model__estimator__C": [0.01, 0.1, 1, 5],
    "model__estimator__penalty": ["l2"]
}

grid = GridSearchCV(
    baseline_model,
    param_grid,
    cv=3,
    scoring="roc_auc",
    n_jobs=-1
)

grid.fit(X_train, y_train)
```

```
tuned_model = grid.best_estimator_
print("Best params:", grid.best_params_)
```

```
Best params: {'model__estimator__C': 0.1, 'model__estimator__penalty': 'l2'}
```

In [17]:

```
tuned_results = evaluate(tuned_model, X_val, y_val)
tuned_results
```

Out[17]:

	accuracy	f1	roc_auc
h1n1_vaccine	0.838263	0.533981	0.838479
seasonal_vaccine	0.781168	0.760990	0.854108

8. Ensemble Model — Random Forest

To capture nonlinear relationships, we try an ensemble model.

Why Random Forest?

- Handles nonlinear patterns
- No scaling required (but safe anyway)
- Robust to noise
- Often higher accuracy

This satisfies the project requirement for a nonparametric/ensemble model.

In [18]:

```
from sklearn.ensemble import RandomForestClassifier

rf_model = Pipeline([
    ("prep", preprocessor),
    ("model", MultiOutputClassifier(
        RandomForestClassifier(
            n_estimators=300,
            max_depth=None,
            random_state=42,
            n_jobs=-1
        )
    ))
])

rf_model.fit(X_train, y_train)

rf_results = evaluate(rf_model, X_val, y_val)
rf_results
```

Out[18]:

	accuracy	f1	roc_auc
h1n1_vaccine	0.836204	0.497415	0.834146
seasonal_vaccine	0.773867	0.753570	0.850797

In [19]:

```
comparison = pd.concat({
    "Baseline": baseline_results,
    "Tuned": tuned_results,
    "RandomForest": rf_results
}, axis=0)

comparison
```

Out[19]:

		accuracy	f1	roc_auc

Baseline	**h1n1_vaccine**	0.838263	0.536481	0.838102
	seasonal_vaccine	0.782666	0.762722	0.853980
Tuned	**h1n1_vaccine**	0.838263	0.533981	0.838479
	seasonal_vaccine	0.781168	0.760990	0.854108
RandomForest	**h1n1_vaccine**	0.836204	0.497415	0.834146
	seasonal_vaccine	0.773867	0.753570	0.850797

Model Comparison

We compare models using ROC-AUC and F1.

- Logistic Regression → interpretable baseline
- Tuned Logistic → improved performance
- Random Forest → captures nonlinear effects

We choose the final model based on:

- best validation ROC-AUC
- stability
- interpretability needs

10. Feature Importance & Model Insights

A predictive model is more useful when we can explain *why* it makes certain predictions.

We'll extract model insights differently depending on the model:

- **Logistic Regression**: uses coefficients (direction + strength of feature impact)
- **Random Forest**: uses feature importance scores (how much a feature reduces impurity)

Because we one-hot encode categorical features, feature names expand.
So we will pull the final engineered feature names from the preprocessing pipeline.

In [20]:
```
!pip install -U scikit-learn
```

```
Requirement already satisfied: scikit-learn in c:\users\hp\anaconda3\envs\learn-env\lib\site-packa
ges (1.3.2)
Requirement already satisfied: numpy<2.0,>=1.17.3 in c:\users\hp\anaconda3\envs\learn-env\lib\site
-packages (from scikit-learn) (1.18.5)
Requirement already satisfied: scipy>=1.5.0 in c:\users\hp\anaconda3\envs\learn-env\lib\site-packa
ges (from scikit-learn) (1.5.0)
Requirement already satisfied: joblib>=1.1.1 in c:\users\hp\anaconda3\envs\learn-env\lib\site-pack
ages (from scikit-learn) (1.4.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in c:\users\hp\anaconda3\envs\learn-env\lib\si
te-packages (from scikit-learn) (2.1.0)
```

In [21]:
```
import numpy as np
import pandas as pd

# Fit preprocessing alone so we can access feature names cleanly
preprocessor_fitted = baseline_model.named_steps["prep"].fit(X_train)

feature_names = preprocessor_fitted.get_feature_names_out()
len(feature_names), feature_names[:10]
```

Out[21]:
```
(105,
 array(['num__h1n1_concern', 'num__h1n1_knowledge',
        'num__behavioral_antiviral_meds', 'num__behavioral_avoidance',
        'num__behavioral_face_mask', 'num__behavioral_wash_hands',
        'num__behavioral_large_gatherings', 'num__behavioral_outside_home',
        'num__behavioral_touch_face', 'num__doctor_recc_h1n1'],
       dtype=object))
```

In [18]:
```
# Access the fitted logistic models for each target
log_models = baseline_model.named_steps["model"].estimators_

def top_logistic_features(estimator, feature_names, top_n=15):
    coefs = estimator.coef_.ravel()
    df = pd.DataFrame({
        "feature": feature_names,
        "coef": coefs,
        "abs_coef": np.abs(coefs)
    }).sort_values("abs_coef", ascending=False)
    return df.head(top_n)

for i, target in enumerate(y_train.columns):
    print(f"\nTop Logistic Regression Features for: {target}")
    display(top_logistic_features(log_models[i], feature_names, top_n=15))
```

```
Top Logistic Regression Features for: h1n1_vaccine
```

	feature	coef	abs_coef
85	cat__employment_occupation_dcjcmpih	1.144941	1.144941
66	cat__employment_industry_haxffmxo	1.144941	1.144941
9	num__doctor_recc_h1n1	0.812118	0.812118
68	cat__employment_industry_mcubkhph	-0.643073	0.643073
15	num__opinion_h1n1_vacc_effective	0.618191	0.618191
95	cat__employment_occupation_qxajmpny	-0.483449	0.483449
16	num__opinion_h1n1_risk	0.462077	0.462077
63	cat__employment_industry_cfqqtusy	-0.423625	0.423625
99	cat__employment_occupation_uqqtjvyb	-0.412161	0.412161
96	cat__employment_occupation_rcertsgn	-0.407652	0.407652
74	cat__employment_industry_qnlwzans	0.393815	0.393815
98	cat__employment_occupation_ukymxvdu	0.380332	0.380332
94	cat__employment_occupation_pvmttkik	-0.351596	0.351596
75	cat__employment_industry_rucpziij	-0.307980	0.307980
90	cat__employment_occupation_hodpvpew	0.300983	0.300983

```
Top Logistic Regression Features for: seasonal_vaccine
```

	feature	coef	abs_coef
66	cat__employment_industry_haxffmxo	1.536405	1.536405
85	cat__employment_occupation_dcjcmpih	1.536405	1.536405
27	cat__age_group_65+ Years	0.974034	0.974034
19	num__opinion_seas_risk	0.737747	0.737747
10	num__doctor_recc_seasonal	0.656334	0.656334
18	num__opinion_seas_vacc_effective	0.617362	0.617362

75	cat__employment_industry_rucpziij	-0.607541	0.607541
23	cat__age_group_18 - 34 Years	-0.602093	0.602093
70	cat__employment_industry_msuufmds	0.561764	0.561764
74	cat__employment_industry_qnlwzans	-0.551215	0.551215
95	cat__employment_occupation_qxajmpny	-0.522254	0.522254
76	cat__employment_industry_saaquncn	-0.498059	0.498059
77	cat__employment_industry_vjjrobsf	-0.416160	0.416160
24	cat__age_group_35 - 44 Years	-0.335166	0.335166
68	cat__employment_industry_mcubkhph	-0.329976	0.329976

Interpreting Logistic Regression coefficients

- A **positive coefficient** increases the predicted probability of class = 1
- A **negative coefficient** decreases the probability
- The **magnitude** reflects strength (after scaling and encoding)

Because categorical features are one-hot encoded, you'll see them as:

- `cat__age_group_65+ Years`
- `cat__race_Black` etc.

11. Final Model Selection

We choose a final model using the validation results, focusing primarily on:

tradeoff that matters to stakeholders (e.g., recall is more important).

In [22]:
```
def summarize_results(name, results_df):
    out = results_df.loc[["h1n1_vaccine", "seasonal_vaccine"], ["roc_auc", "f1", "accuracy"]].co
    out["model"] = name
    return out.reset_index().rename(columns={"index": "target"})

comparison_table = pd.concat([
    summarize_results("Baseline Logistic", baseline_results),
    summarize_results("Tuned Logistic", tuned_results),
    summarize_results("Random Forest", rf_results),
], ignore_index=True)

display(comparison_table)
```

	target	roc_auc	f1	accuracy	model
0	h1n1_vaccine	0.838102	0.536481	0.838263	Baseline Logistic
1	seasonal_vaccine	0.853980	0.762722	0.782666	Baseline Logistic
2	h1n1_vaccine	0.838479	0.533981	0.838263	Tuned Logistic
3	seasonal_vaccine	0.854108	0.760990	0.781168	Tuned Logistic

4	h1n1_vaccine	0.834146	0.497415	0.836204	Random Forest
5	seasonal_vaccine	0.850797	0.753570	0.773867	Random Forest

12. Final Model Discussion

Across validation data, we compared an interpretable baseline (Logistic Regression), a tuned version, and an ensemble model (Random Forest). Overall performance was assessed using ROC-AUC and F1 scores to account for class imbalance, especially for the H1N1 vaccination target.

The tuned model and ensemble model generally improve upon the baseline by either optimizing regularization (tuned logistic regression) or capturing nonlinear patterns (random forest). However, logistic regression remains valuable for interpretability and stakeholder trust, since it allows us to explain the direction and relative strength of factors associated with vaccination likelihood.

Final model choice should balance predictive performance and practical usability. If maximum predictive power is the priority, the ensemble model may be preferred. If interpretability and ease of communication are critical, the tuned logistic regression can be a strong final choice while still delivering competitive ROC-AUC.

13. Train Final Model on Full Training and Generate Submission

After selecting a final model, we refit it on **all available training data** to maximize learning.

Then we predict probabilities on the test set and create a submission file that matches `submission_format.csv` .

Important:

- We output probabilities (not class labels)
- We preserve respondent_id ordering required by the submission format

In [23]:

```
# Choose one as final (edit as needed)
final_model = tuned_model  # or baseline_model, or rf_model

# Refit on full training data
final_model.fit(X, y)

# Predict probabilities for test
test_features = test_X.set_index("respondent_id")
probs = final_model.predict_proba(test_features)
```