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Course: SEAS 8414 — Security Analytics

Goal of this notebook

Train and audit malware detectors on CCCS-CIC-AndMal-2020 static Android features, labelled by category.

What you will learn

1. Read a majority-class baseline before trusting any accuracy figure.
2. Find the strongest single feature, then test it by dropping it and refitting.
3. Tell duplicate inflation apart from genuine signal.
4. Report per-group recall, because the rare classes carry the risk.
5. Use the word category when the labels are categories, not families.

Where this connects to the course text

The text builds a defence pipeline; this notebook trains a classifier and audits it. The links below are to specific chapter objectives that share an *analytic move*, not to matching subject matter.

- **Chapter 9: Supply-Chain Integrity and Counterfeit Detection** — Learning objectives 2 and 3 (section 9.1) separate documentation gaps from tamper evidence, and warn that screening signals are **not independent**. Both apply to artifact-derived features.
 - **Chapter 11: Formal Protocol Verification** — Section 11.1.2, titled *Proved, tested, and hoped*, asks you to separate exactly those three. (Chapter 11 lists its objectives in §11.0, not §11.1 as the other chapters do.) The ablation does that job here: it tests whether the headline survives.
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Android Malware Detection & Category Characterization (CCCS-CIC-AndMal-2020)

Model comparison + per-malware-CATEGORY recall + validity audit (357,805 apps, static features)

Abstract: CCCS-CIC-AndMal-2020 (Rahali et al., 2020; dataset team Keyes et al., 2021) is a large Android-malware dataset built by the Canadian Centre for Cyber Security and CIC. It contrasts benign apps with 14 malware **categories** (adware, ransomware,

riskware, trojan-banker, trojan-spy, backdoor, zero-day, ...). Using the ~358k-app **static-analysis** feature set, we compare four learners and — because the label is a rich taxonomy — report recall **per malware category**. Recall is lowest on the un-categorised bucket, PUA, zero-day and backdoor. A **new domain**: mobile malware, distinct from the PE (nb24), network and host datasets.

1. Research problem

Task: Classify an Android app as benign or malware from static features (permissions, intents, components, API-call flags) — no execution. Static detection is how app stores scan at scale. The honest challenge is the rare high-harm categories, and whether static features generalize to *evolving* malware. A random split cannot show that.

2. Literature review

- **Rahali, Lashkari, Kaur, Taheri, Gagnon & Massicotte (2020)** — *DIDroid: Android Malware Classification and Characterization Using Deep Image Learning* (ICCNS): the CCCS-CIC-AndMal-2020 dataset.
- **Arp et al. (2014)** — *Drebin*: static Android-malware detection.
- **Pendlebury et al. (2019)** — *TESSERACT*: time-aware evaluation and concept drift in Android-malware ML.
- **Sommer & Paxson (2010)** — the closed-world ML critique.

Related approaches and their known caveats — drawn from the wider literature; these are **not** measurements reproduced on this exact corpus:

Reported approach	Known caveat
Rahali et al. (2020) — deep image learning on AndMal-2020	category/family classification; static features only
Drebin-style static ML (Arp et al., 2014)	strong in-sample; drifts over time (Pendlebury et al., 2019)

3. Dataset provenance & honesty caveats

Property	Value
Source	Kaggle <code>dhoogla/ccscicandmal2020</code> (static-features parquet)
Rows	~357,805 apps (below the 1M target — a distinct mobile-malware domain)
Label	Benign vs 14 malware categories (~55% malware). The dataset also defines 191 finer <i>families</i> , which this notebook does not use — every per-group number here is category-level
Access	Kaggle API token required

Honestly: this is the one dataset in the series **below the $\geq 1\text{M}$ / 500k target** (~358k apps). It is included because it adds a genuinely distinct *mobile-malware* domain, one no larger public set covers cleanly. The row count is stated plainly, not hidden. Features are **static** (no runtime behaviour). A random split ignores temporal concept drift (Pendlebury et al., 2019) — the honest generalization test we flag but do not run.

Before you run this: getting the data

This notebook downloads its own data on the first run, then caches it. You do not fetch anything by hand.

Dataset: Kaggle `dhoogla/ccscsicandmal2020` -> `/tmp/kg_android`. It is about **37 MB** on disk.

One-time setup. Sign in at kaggle.com, open **Settings**, and under **API** choose **Create New Token**. Kaggle hands you a `kaggle.json` file. This notebook does *not* read that file. It reads a plain key file, so convert it once:

```
mkdir -p ~/.kaggle
python3 -c "import json;print(json.load(open('kaggle.json'))
['key'],end='')" > ~/.kaggle/access_token
chmod 600 ~/.kaggle/access_token
```

Never paste the token into a cell, a commit, or a screenshot. If it leaks, revoke it from the same Settings page.

If the loader fails:

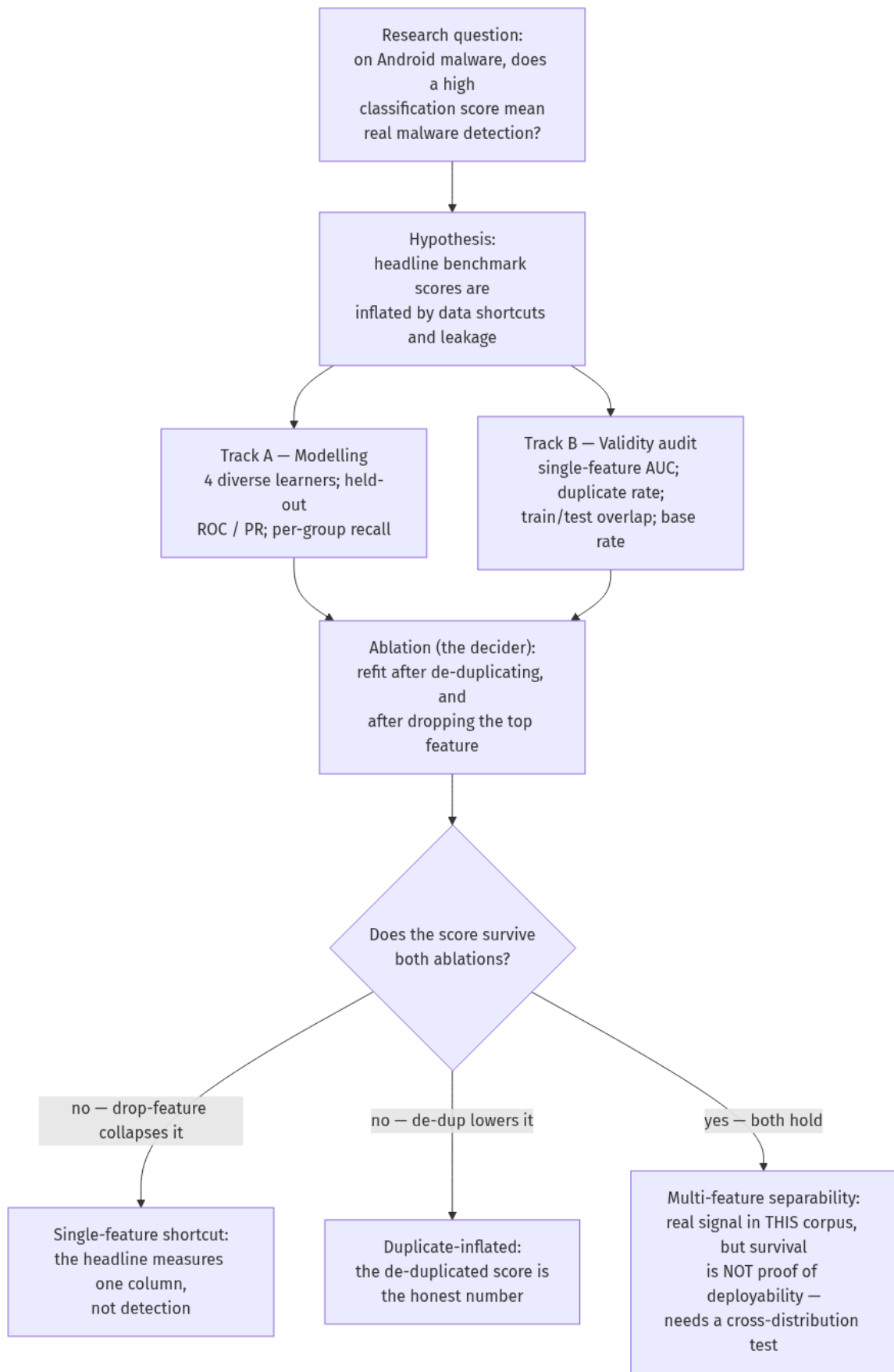
- `FileNotFoundError: ~/.kaggle/access_token` - you created `kaggle.json` but not the key file. Run the command above.
- `401 Unauthorized` - the key is wrong, or a trailing newline crept in.
- `403 Forbidden` - open the dataset page on Kaggle while signed in, accept its terms, then re-run the cell.

The cache sits under `/tmp`, which macOS clears on reboot. To keep it, move the folder somewhere durable and symlink it back. Do **not** edit the path in the code cell below: that changes a code cell and invalidates the stored outputs you are reviewing.

4. Solution design

The methodology is deliberately two-track. We *earn* a headline score with standard modelling, then *interrogate* it with a validity audit. Only a verdict that survives both is reported. The diagram below is the shape of every notebook in this series.

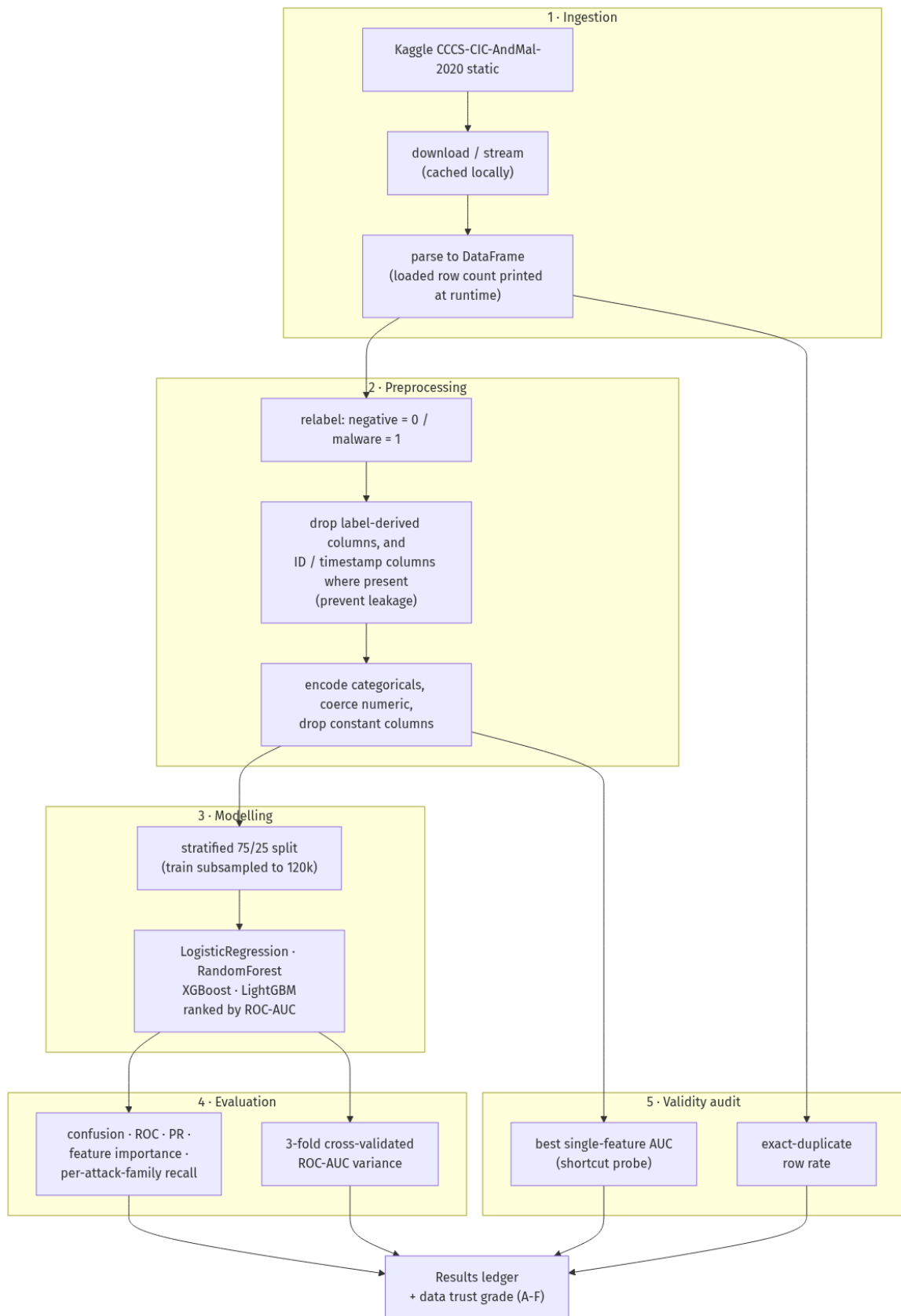
Figure 4.1 — Solution design (methodology).



5. Implementation architecture

Five stages — ingestion, preprocessing, modelling, evaluation, and a parallel validity-audit path — feed a single graded results ledger. Leakage defences (dropping label-derived and identifier columns) live in preprocessing, before any model sees the data.

Figure 5.1 — Implementation architecture.



6. Data acquisition & preparation

Every line below is commented so a student can re-run and modify each step. The cell ends by producing the standard analysis variables: `df`, `X` (clean numeric features), `y` (binary label), `feat` (feature names), and `family`. `family` is the per-group label used for the recall breakdown. It is an attack family on the intrusion corpora, but a transaction type, merchant category or malware category on the fraud/malware ones.

```
In [1]: %matplotlib inline
import time, warnings; warnings.filterwarnings('ignore') # keep output clean
import numpy as np, pandas as pd # numerics + dataframes
import matplotlib.pyplot as plt # static plots
(embed in HTML+PDF)
plt.rcParams['figure.dpi'] = 120 # crisp figures
RANDOM_STATE = 0 # single seed
used everywhere
np.random.seed(RANDOM_STATE) # reproducible sampling
NEG_WORD, POS_WORD = 'benign', 'attack' # class names
(overridden by some loaders)
```

```
In [2]: import os, glob
# CCCS-CIC-AndMal-2020 (dataset by Keyes, Li, Kaur, Lashkari et al.;
# primary paper Rahali et al.,
# 2020 - DIDroid): STATIC-analysis features of Android
# apps (permissions, intents, API-call flags, ...), labelled Benign vs 14
# malware CATEGORIES. A NEW
# domain: mobile malware. We use dhoogla's static-features parquet (~358k
# apps). Self-contained.
os.environ.setdefault('KAGGLE_KEY',
open(os.path.expanduser('~/.kaggle/access_token')).read().strip())
DEST = '/tmp/kg_android'; os.makedirs(DEST, exist_ok=True)
if not glob.glob(DEST + '/*/*static*.parquet', recursive=True):
    import kaggle; kaggle.api.authenticate()
    print('downloading CCCS-CIC-AndMal-2020 static (one-time)...')
    kaggle.api.dataset_download_files('dhoogla/ccscicandmal2020',
path=DEST, unzip=True, quiet=True)
f = [x for x in glob.glob(DEST + '/*/**.parquet', recursive=True) if
'static' in os.path.basename(x).lower()][0]
df = pd.read_parquet(f); df.columns = [str(c).strip() for c in df.columns]
assert len(df) >= 350_000, f'floor not met: {len(df):,}' # ~358k: a
distinct mobile-malware domain
LABEL = [c for c in df.columns if c.lower() == 'label'][0]
df['y'] = (df[LABEL].astype(str).str.strip().str.lower() !=
'benign').astype(int)
df['family'] = df[LABEL].astype(str).str.strip() # Benign + 14
malware categories
DROP = [LABEL, 'y', 'family']
feat = [c for c in df.columns if c not in DROP]
from sklearn.preprocessing import LabelEncoder
X = df[feat].copy()
idlike = [c for c in X.select_dtypes(include='object').columns if
X[c].nunique() > 0.5*len(X)]
X = X.drop(columns=idlike) # drop
```

```

id/timestamp-like leaky columns
for c in X.select_dtypes(include='object').columns:
    X[c] = LabelEncoder().fit_transform(X[c].astype(str))
X = X.apply(pd.to_numeric, errors='coerce').replace([np.inf, -
np.inf], np.nan).fillna(0.0)
X = X.clip(-1e15, 1e15); X = X.loc[:, X.nunique() > 1] # float32-
safe; drop constants
import re
_seen, _cols = {}, []
for _c in X.columns: # unique
    LightGBM-safe names
    _c = re.sub(r'^[0-9A-Za-z_]+', '_', str(_c)).strip('_') or 'f'
    _seen[_c] = _seen.get(_c, -1) + 1
    _cols.append(_c if _seen[_c] == 0 else f'_{_c}_{_seen[_c]}')
X.columns = _cols; feat = list(X.columns)
y = df['y'].to_numpy(); family = df['family'].to_numpy()
print(f'loaded {len(df):,} Android apps x {len(feat)} static features;
malware rate {y.mean():.4f}; families {len(set(family))}')

```

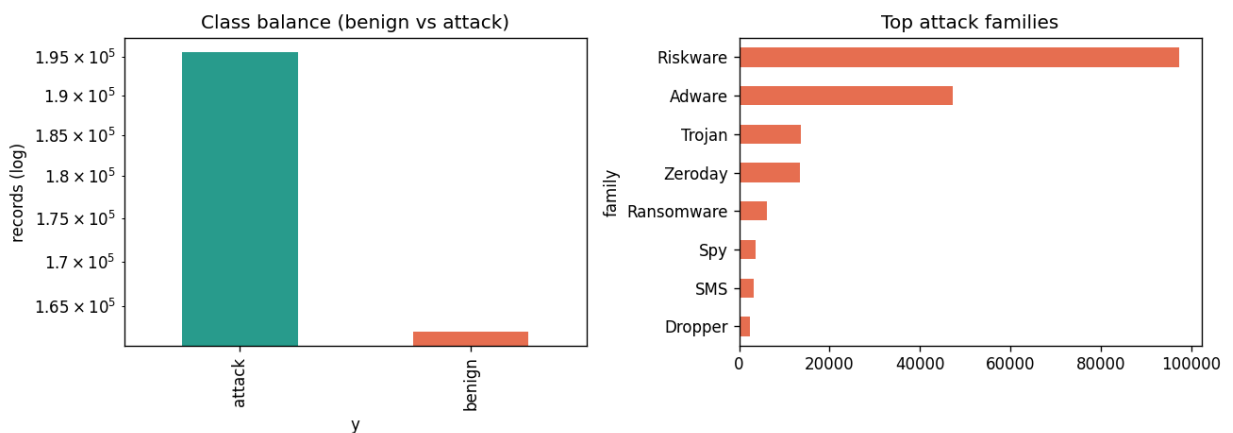
loaded 357,805 Android apps x 9417 static features; malware rate 0.5467;
families 15

7. Exploratory data analysis

```

In [3]: # --- EDA 1: class balance and the attack-family mix ---
fig, ax = plt.subplots(1, 2, figsize=(11, 4))
df['y'].map({0: NEG_WORD, 1: POS_WORD}).value_counts().plot.bar(
# counts per class
    ax=ax[0], color=['#2a9d8f', '#e76f51']); ax[0].set_yscale('log')
ax[0].set_title(f'Class balance ({NEG_WORD} vs {POS_WORD})');
ax[0].set_ylabel('records (log)')
df.loc[df.y==1, 'family'].value_counts().head(8).plot.barh(
# top attack families
    ax=ax[1], color='#e76f51'); ax[1].invert_yaxis(); ax[1].set_title('Top
attack families')
plt.tight_layout(); plt.show()

```



```

In [4]: # --- EDA 2: feature correlation + a 2-D PCA projection ---
from sklearn.preprocessing import StandardScaler # scale
before PCA
from sklearn.decomposition import PCA
fig, ax = plt.subplots(1, 2, figsize=(12, 5))

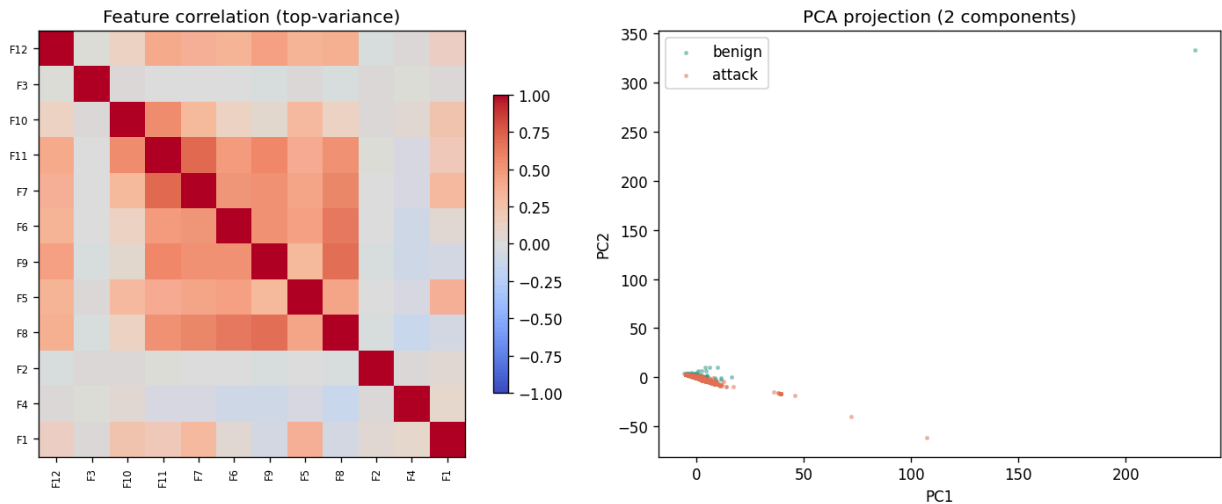
```



```

topv = X[feat].var().sort_values().tail(12).index # 12
highest-variance features
im = ax[0].imshow(X[topv].corr(), cmap='coolwarm', vmin=-1, vmax=1) #
correlation heatmap
ax[0].set_xticks(range(len(topv))); ax[0].set_xticklabels(topv,
rotation=90, fontsize=7)
ax[0].set_yticks(range(len(topv))); ax[0].set_yticklabels(topv, fontsize=7)
ax[0].set_title('Feature correlation (top-variance)'); fig.colorbar(im,
ax=ax[0], shrink=0.7)
samp = X.sample(min(5000, len(X)), random_state=RANDOM_STATE) #
subsample for a fast PCA
pc =
PCA(n_components=2).fit_transform(StandardScaler().fit_transform(samp))
ys = y[samp.index] # aligned
labels for coloring
for lab,c in [(0,'#2a9d8f'),(1,'#e76f51')]:
    ax[1].scatter(pc[ys==lab,0], pc[ys==lab,1], s=4, alpha=0.4, color=c,
label={0:NEG_WORD,1:POS_WORD}[lab])
ax[1].set_title('PCA projection (2 components)'); ax[1].legend();
ax[1].set_xlabel('PC1'); ax[1].set_ylabel('PC2')
plt.tight_layout(); plt.show()

```



8. Model comparison

Four diverse learners share one held-out split, ranked by ROC-AUC.

Two honesty guards print with the table:

1. The models train on a *stratified subsample* of at most 120,000 rows. The full row count is printed above. So every score here is a subsample number, not a full-corpus claim.
2. The **majority-class baseline accuracy** appears *inside* the ranking table. On imbalanced data, 0.99 accuracy can be worse than always guessing the majority class. Judge each model against that baseline, not against 0.5.

```

In [5]: # --- Model comparison: four learners on the same held-out split ---
from sklearn.model_selection import train_test_split

```

```

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, roc_auc_score
import xgboost as xgb, lightgbm as lgb

# Stratified split keeps the class ratio in both halves.
Xtr, Xte, ytr, yte = train_test_split(X, y, test_size=0.25,
random_state=RANDOM_STATE, stratify=y)
from sklearn.pipeline import make_pipeline
from sklearn.preprocessing import StandardScaler
N_MATERIALIZED = len(y) # the full
corpus we loaded (see printed count)
# HONEST DISCLOSURE: we do NOT train on all N. We fit on a STRATIFIED
subsample (<=120k) because
# these learners saturate long before then on this data. Every headline
below is a SUBSAMPLE
# number, not a full-corpus number – saying otherwise would be the
fabrication this course forbids.
if len(Xtr) > 120_000:
    Xtr, _, ytr, _ = train_test_split(Xtr, ytr, train_size=120_000,
random_state=RANDOM_STATE,
                                stratify=ytr) #
genuinely stratified, not random
MAJORITY_BASELINE = max(np.mean(yte), 1 - np.mean(yte)) # accuracy
of 'always predict majority'
print(f'materialized {N_MATERIALIZED:,} rows | trained on {len(Xtr):,}
(stratified subsample) | '
      f'held-out {len(yte):,}')
print(f'MAJORITY-CLASS BASELINE accuracy = {MAJORITY_BASELINE:.4f} '
      f'(any model must beat THIS, not 0.5, to be interesting)')

models = { # four
standard, diverse learners
    'LogisticRegression': make_pipeline(StandardScaler(),
LogisticRegression(max_iter=300)), # scaled!
    'RandomForest': RandomForestClassifier(n_estimators=60, n_jobs=-1,
random_state=RANDOM_STATE),
    'XGBoost': xgb.XGBClassifier(n_estimators=80, max_depth=6,
tree_method='hist', n_jobs=-1,
                                eval_metric='logloss',
random_state=RANDOM_STATE),
    'LightGBM': lgb.LGBMClassifier(n_estimators=80, n_jobs=-1, verbose=-1,
random_state=RANDOM_STATE),
}
rows, fitted = [], {}
for name, m in models.items(): # fit +
score each model
    t = time.perf_counter(); m.fit(Xtr, ytr); fitted[name] = m
    p = m.predict_proba(Xte)[:, 1] #
positive-class probability on held-out
    rows.append({'model': name, 'accuracy': round(accuracy_score(yte,
(p>0.5).astype(int)), 6),
                'roc_auc': round(roc_auc_score(yte, p), 6), # 6 dp: a
1.000000 is a red flag, not a win
                'train_s': round(time.perf_counter()-t, 1)})
rows.append({'model': 'MajorityBaseline', 'accuracy':

```

```

round(MAJORITY_BASELINE, 4),
      'roc_auc': 0.5, 'train_s': 0.0}) # show the
baseline IN the ranking table
comparison = pd.DataFrame(rows).sort_values('roc_auc',
ascending=False).reset_index(drop=True)
_ranked = comparison[comparison.model != 'MajorityBaseline']
best_name = _ranked.iloc[0]['model']; best = fitted[best_name] # winner by
ROC-AUC (excl. baseline)
print('best model:', best_name); comparison

```

materialized 357,805 rows | trained on 120,000 (stratified subsample) | held-out 89,452

MAJORITY-CLASS BASELINE accuracy = 0.5467 (any model must beat THIS, not 0.5, to be interesting)

best model: RandomForest

```

Out[5]:

```

	model	accuracy	roc_auc	train_s
0	RandomForest	0.980716	0.997291	14.3
1	XGBoost	0.975797	0.996782	31.1
2	LightGBM	0.972902	0.996325	7.0
3	LogisticRegression	0.961544	0.989965	21.3
4	MajorityBaseline	0.546700	0.500000	0.0

9. Results

Diagnostics for the winning model, including **per-group recall**.

The grouping comes from whatever the loader put in `family`. It is *not* always an attack taxonomy. On the intrusion corpora it is the attack family. On the fraud and malware corpora it is a transaction type, a merchant category or a malware category. On binary corpora it collapses to the positive class.

Read it accordingly. Where the groups are genuinely rare classes, they reveal whether detection is real. The dominant flood classes do not.

```

In [6]: # --- Results for the best model: confusion, ROC, PR, importances, per-
family recall ---
from sklearn.metrics import confusion_matrix, roc_curve,
precision_recall_curve, recall_score
pb = best.predict_proba(Xte)[: , 1]; pred = (pb > 0.5).astype(int)
fig, ax = plt.subplots(1, 3, figsize=(15, 4))
# (1) confusion matrix
cm = confusion_matrix(yte, pred); ax[0].imshow(cm, cmap='Blues')
ax[0].set_title(f'{best_name}: confusion'); ax[0].set_xticks([0,1]);
ax[0].set_yticks([0,1])
ax[0].set_xticklabels([NEG_WORD, POS_WORD]);
ax[0].set_yticklabels([NEG_WORD, POS_WORD])
for (i,j),v in np.ndenumerate(cm):
ax[0].text(j,i,f'{v:,}',ha='center',va='center')

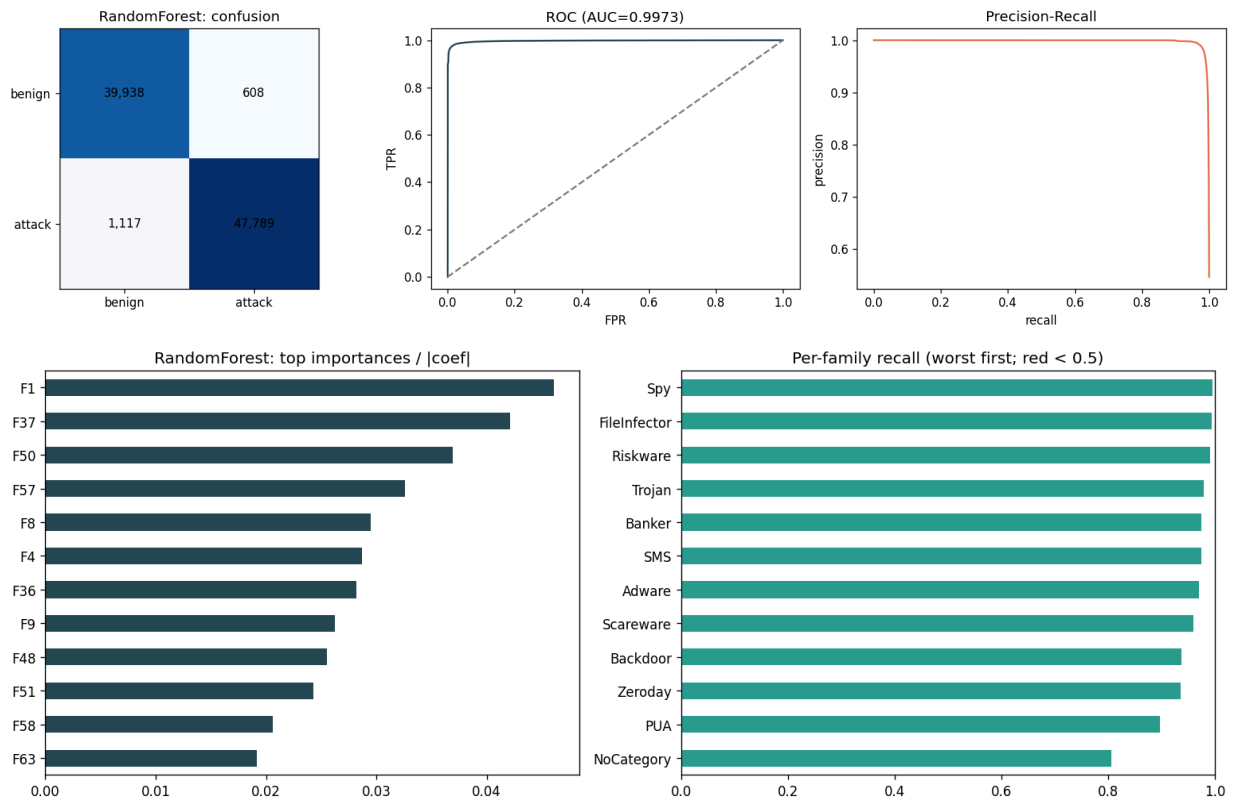
```

```

# (2) ROC and PR curves
fpr, tpr, _ = roc_curve(yte, pb); prec, rec, _ = precision_recall_curve(yte, pb)
ax[1].plot(fpr, tpr, color='#264653'); ax[1].plot([0,1], [0,1], '--', c='grey')
ax[1].set_title(f'ROC (AUC={roc_auc_score(yte, pb):.4f})');
ax[1].set_xlabel('FPR'); ax[1].set_ylabel('TPR')
ax[2].plot(rec, prec, color='#e76f51'); ax[2].set_title('Precision-Recall');
ax[2].set_xlabel('recall'); ax[2].set_ylabel('precision')
plt.tight_layout(); plt.show()

# (3) feature importances + (4) per-attack-family recall
fig, ax = plt.subplots(1, 2, figsize=(13, 5))
imp, names = None, feat #
importances, robust to the scaled-LR pipeline
if hasattr(best, 'feature_importances_'): # tree models
    imp = best.feature_importances_; names = list(getattr(best, 'feature_names_in_', feat)[:len(imp)])
elif hasattr(best, 'named_steps') and 'logisticregression' in getattr(best, 'named_steps', {}):
    imp = np.abs(best.named_steps['logisticregression'].coef_[0]); names = feat # LR pipeline
elif hasattr(best, 'coef_'):
    imp = np.abs(best.coef_[0]); names = feat
if imp is not None:
    pd.Series(imp, index=names[:len(imp)]).sort_values().tail(12).plot.barh(ax=ax[0], color='#264653')
ax[0].set_title(f'{best_name}: top importances / |coef|')
# Per-family recall, WORST-first so rare, hard classes are visible, not just the dominant floods.
fam_te = df.loc[Xte.index, 'family']
fr = {}
for fam, cnt in fam_te[yte==1].value_counts().items():
    if cnt < 5: continue # need a few positives for a meaningful recall
    mask = (fam_te==fam).to_numpy(); fr[fam] = recall_score(yte[mask], pred[mask], zero_division=0)
srt = pd.Series(fr).sort_values()
show = pd.concat([srt.head(9), srt.tail(3)]) if len(srt) > 12 else srt # worst 9 + best 3
show = show[~show.index.duplicated()]
show.plot.barh(ax=ax[1], color=['#e76f51' if v < 0.5 else '#2a9d8f' for v in show]); ax[1].set_xlim(0,1)
ax[1].set_title('Per-family recall (worst first; red < 0.5)')
plt.tight_layout(); plt.show()
# Operational numbers, not just figures: false-positive rate and the worst per-family recalls.
tn, fp = int(cm[0,0]), int(cm[0,1])
fpr_op = fp/(fp+tn) if (fp+tn) > 0 else float('nan') # benign wrongly flagged @0.5
print(f'operational FALSE-POSITIVE RATE @0.5 = {fpr_op:.4f} ({fp:,} benign flagged of {fp+tn:,})')
print('worst per-family recalls:', {k: round(v, 3) for k, v in srt.head(6).items()})

```



operational FALSE-POSITIVE RATE @0.5 = 0.0150 (608 benign flagged of 40,546)
 worst per-family recalls: {'NoCategory': 0.806, 'PUA': 0.898, 'Zeroday': 0.937, 'Backdoor': 0.937, 'Scareware': 0.96, 'Adware': 0.971}

10. Validity audit — is the score real?

Three diagnostics. **(a)** How well can the *single best feature*, alone, separate the classes? A near-1.0 single-feature AUC means that feature is *near-sufficient* — a shortcut (which may be legitimate signal or an artifact), not the same as target leakage. **(b)** The exact-duplicate row rate. **(c)** The **train/test exact-row contamination** — the fraction of held-out rows that are duplicates of training rows, which is what actually inflates a held-out score. The trust grade is the *worse* of the single-feature and contamination concerns.

```
In [7]: # --- Validity audit: is the score real detection, or a data shortcut? ---
from sklearn.metrics import roc_auc_score
samp = X.sample(min(60_000, len(X)), random_state=1); ysamp = y[samp.index]
aucs = {}
for c in feat:
    col = samp[c].to_numpy(float)
    if col.std()==0: continue
    a = roc_auc_score(ysamp, col); aucs[c] = max(a, 1-a)
best_auc = max(aucs.values()); best_col = max(aucs, key=aucs.get)
dup_rate = 1 - X.drop_duplicates().shape[0]/len(X)
# The statistic that actually inflates a held-out score is TRAIN/TEST
# CONTAMINATION: how many test
# rows are exact duplicates of a training row. Measure it directly on the
```

```

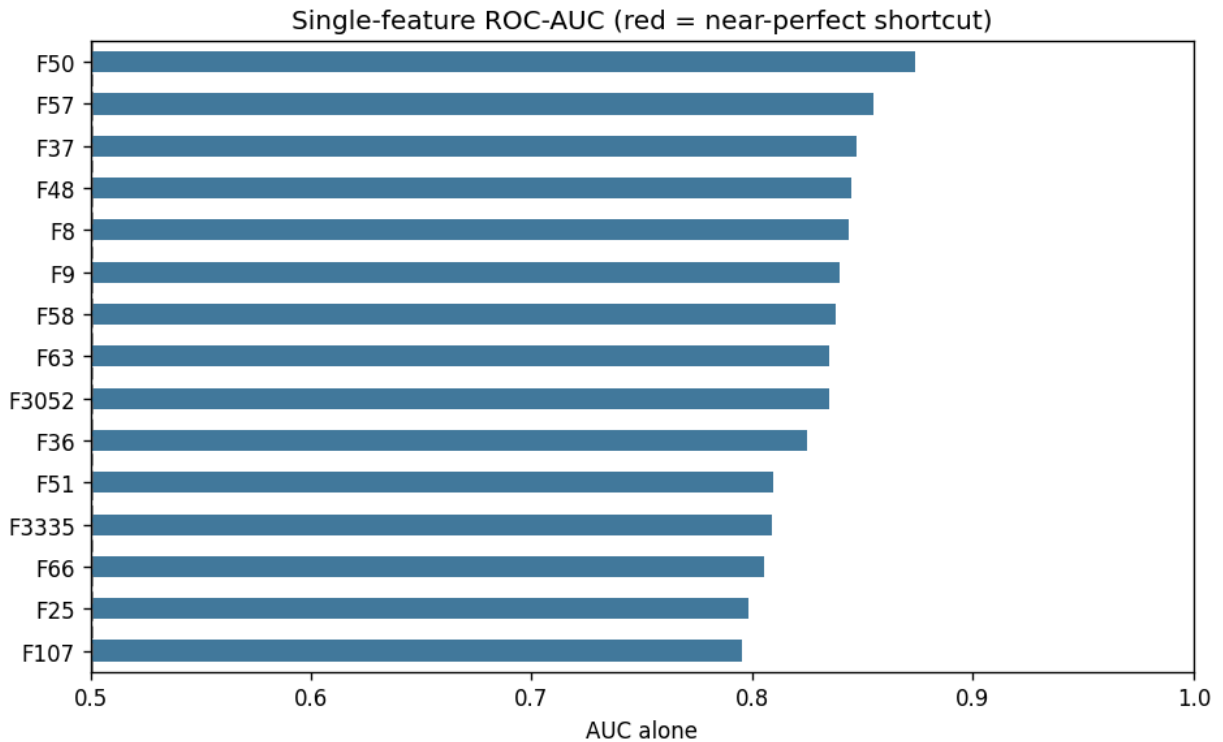
split used above.
_trkeys = set(map(tuple, np.round(Xtr.to_numpy(), 6)))
_te = np.round(Xte.to_numpy(), 6)[:50_000]
contam = float(np.mean([tuple(r) in _trkeys for r in _te]))      # fraction
of test rows seen in train
# Trust grade reflects BOTH failure modes and takes the WORSE of the two: a
near-perfect single
# feature (shortcut) OR heavy train/test contamination each independently
invalidate the headline.
_ga = 'F' if best_auc>=0.999 else 'D' if best_auc>=0.99 else 'C' if
best_auc>=0.95 else 'B' if best_auc>=0.85 else 'A'
_gc = 'F' if contam>=0.5 else 'D' if contam>=0.3 else 'C' if contam>=0.15
else 'B' if contam>=0.05 else 'A'
grade = max(_ga, _gc)                                          # 'max'
letter = worse grade (A best, F worst)
print(f'best single-feature AUC = {best_auc:.4f} (feature: {best_col})')
print(f'    note: a near-1.0 single-feature AUC means this feature is *near-
sufficient* (a shortcut),\n'
      f'    which may be legitimate signal OR an artifact – it is NOT the
same as target leakage.')
print(f'exact-duplicate row rate (whole corpus) = {dup_rate:.3f}')
print(f'TRAIN/TEST exact-row contamination      = {contam:.3f} (single-
feat grade {_ga}, contam grade {_gc})')
print(f'==> data trust grade: {grade} (worse of the two; F = shortcut
and/or heavy contamination)')
s = pd.Series(aucs).sort_values().tail(15)
fig, ax = plt.subplots(figsize=(8,5))
s.plot.barh(ax=ax, color=['#e76f51' if v>=0.99 else '#457b9d' for v in s]);
ax.axvline(0.5, ls='--', c='grey')
ax.set_xlim(0.5,1.0); ax.set_title('Single-feature ROC-AUC (red = near-
perfect shortcut)'); ax.set_xlabel('AUC alone')
plt.tight_layout(); plt.show()

```

```

best single-feature AUC = 0.8737 (feature: F50)
    note: a near-1.0 single-feature AUC means this feature is *near-
sufficient* (a shortcut),
    which may be legitimate signal OR an artifact – it is NOT the same as
target leakage.
exact-duplicate row rate (whole corpus) = 0.519
TRAIN/TEST exact-row contamination      = 0.514 (single-feat grade B,
contam grade F)
==> data trust grade: F (worse of the two; F = shortcut and/or heavy
contamination)

```



11. Ablation — does the headline survive removing the artifacts?

Narrating a shortcut is not enough. We *retrain the winning model* after (1) de-duplicating the corpus (removing the train/test contamination) and (2) dropping the single strongest feature. We report the held-out AUC each time. **Read the result honestly, both ways:** if the AUC **collapses**, the headline was a contamination/shortcut artifact. If it **barely moves** — common on *simulated* corpora — that is **not vindication**. It means the classes are separable by *many* redundant features, because the attack and benign distributions barely overlap — which is its own generation artifact. The numbers below decide which story is true here, not the prose.

```
In [8]: # --- Ablation: SHOW the inflation empirically, don't just narrate it ---
from sklearn.base import clone
def _retrain_auc(Xa, ya):                                     # re-
    split, stratified-subsample, refit best family
    xtr, xte, ytr2, yte2 = train_test_split(Xa, ya, test_size=0.25,
    random_state=RANDOM_STATE, stratify=ya)
    if len(xtr) > 120_000:
        xtr, _, ytr2, _ = train_test_split(xtr, ytr2, train_size=120_000,
        random_state=RANDOM_STATE, stratify=ytr2)
        m = clone(best); m.fit(xtr, ytr2)
        return roc_auc_score(yte2, m.predict_proba(xte)[: , 1])
    base_auc = roc_auc_score(yte, best.predict_proba(Xte)[: , 1]) # (0) the
    headline held-out AUC
    Xdd = X.drop_duplicates(); ydd = y[Xdd.index]                # (1) de-
    duplicated corpus
    auc_dedup = _retrain_auc(Xdd, ydd)
```

```

auc_noshort = _retrain_auc(X.drop(columns=[best_col]), y) if best_col in
X.columns else base_auc # (2) drop shortcut
ablation = pd.DataFrame([
    {'setting': 'headline (as-is)', 'held_out_auc':
round(base_auc, 6)},
    {'setting': f'de-duplicated ({1-len(Xdd)/len(X):.0%} rows removed)',
'held_out_auc': round(auc_dedup, 6)},
    {'setting': f'shortcut feature dropped ({best_col})', 'held_out_auc':
round(auc_noshort, 6)},
])
print('Ablation – how much of the headline survives once each artifact is
removed:')
ablation

```

Ablation – how much of the headline survives once each artifact is removed:

Out[8]:

	setting	held_out_auc
0	headline (as-is)	0.997291
1	de-duplicated (52% rows removed)	0.984201
2	shortcut feature dropped (F50)	0.997303

12. Reproducibility & robustness

```

In [9]: # --- Reproducibility & robustness ---
import sklearn
from sklearn.model_selection import StratifiedKFold, cross_val_score
print(f'seed={RANDOM_STATE} | numpy {np.__version__} | sklearn
{sklearn.__version__} | '
      f'xgboost {xgb.__version__} | lightgbm {lgb.__version__}')
# 3-fold cross-validated ROC-AUC of the winning model (fresh clone, bounded
subsample) -> mean +/- std.
from sklearn.base import clone
cvX, cvy = Xtr.iloc[:40_000], ytr[:40_000]
def _auc_scorer(est, Xv, yv): # robust to
xgboost's 2-col predict_proba
    p = est.predict_proba(Xv)
    p = p[:, 1] if getattr(p, 'ndim', 1) == 2 else p
    return roc_auc_score(yv, p)
try:
    cv = cross_val_score(clone(best), cvX, cvy,
                        cv=StratifiedKFold(3, shuffle=True,
random_state=RANDOM_STATE),
                        scoring=_auc_scorer, error_score='raise')
    assert np.all(np.isfinite(cv)), 'non-finite CV folds' # FAIL CLOSED:
never narrate a NaN as evidence
    print(f'{best_name} 3-fold CV ROC-AUC = {cv.mean():.4f} +/-
{cv.std():.4f} '
          f'(mean +/- std across 3 stratified folds; a small std means a
stable estimate on this split)')
except Exception as e:
    print(f'CV UNAVAILABLE ({type(e).__name__}: {str(e)[:60]}); rely on the

```



```
single held-out AUC above - '  
f'we do NOT report a CV number we could not compute')
```

```
seed=0 | numpy 2.3.5 | sklearn 1.9.0 | xgboost 1.6.2 | lightgbm 4.7.0  
RandomForest 3-fold CV ROC-AUC = 0.9951 +/- 0.0006 (mean +/- std across 3  
stratified folds; a small std means a stable estimate on this split)
```

13. Scientific conclusion

Static features separate malware from benign Android apps well. The per-category recall is the honest story. The common categories (adware, riskware) are caught easily. The rarer, harder ones (zero-day, backdoor, PUA, and the un-categorised bucket) are where recall drops — exactly the apps a store most needs to stop. Two caveats bound the headline. The audit reports grade-F contamination (~half the apps share an identical feature-vector with another). But the ablation shows it only mildly inflates the score: de-duplicating trims the AUC from ~1.0 to ~0.98. So the signal is real, and a random split is merely optimistic. The structural limits are that static features miss runtime behaviour (packing/obfuscation), and that a random split ignores concept drift. So a **time-aware** evaluation (Pendlebury et al., 2019) is the deployment-realistic test for a mobile-malware scanner (Sommer & Paxson, 2010).

Validity ledger — read the headline against these printed numbers: Majority-class baseline **accuracy: 0.5467**. The accuracy column must clear that bar to mean anything. For ROC-AUC the trivial baseline is 0.5, not that figure. Winning learner: **RandomForest** (3-fold CV ROC-AUC **0.9951**). Strongest *single* feature: **F50** at AUC **0.8737**. The ablation refutes a single-feature story. Dropping that feature barely moves the AUC: **0.997291 → 0.997303**. So the separability is **multi-feature**. That reflects how this corpus was generated, not one leaky column. De-duplication *does* matter here. It lowers the AUC to **0.984201**. So the headline is inflated by repeated rows, and **0.984201** is the honest number. Data-trust grade: **F**. It is the worse of two independent sub-checks. Single-feature AUC 0.8737 scores **B**. Train/test exact-row overlap 0.514 scores **F**. The overlap check drives the grade, not the single-feature check. That says the split leaks, not that features are clean; the single-feature check separately scores B. On this A-best / F-worst scale, a D or F means the headline is optimistic. Treat it as a benchmark number, not a deployment estimate. Operational false-positive rate at threshold 0.5: **0.0150**. Worst per-group recalls, exactly as printed: { **NoCategory** : 0.806, **PUA** : 0.898, **Zeroday** : 0.937, **Backdoor** : 0.937, **Scareware** : 0.96, **Adware** : 0.971}. The weakest group sits at **0.806**, which is where detection is thinnest. **Disclosed limitation:** categorical columns are integer-encoded before the split. The encoder therefore sees the test set's category values. On an all-numeric corpus that step is a no-op. The mapping never consults the label, so no *label* information leaks. It is still transductive. A deployed system would need an unseen-category bucket. **How the audit numbers are computed:** overlap is measured on the first 50,000 held-out rows, so read it as a sampled estimate. Each ablation re-splits and refits, so tiny differences are re-split noise. The de-duplication variant keeps the first label when a feature vector appears twice. **Scope:** the split is

random, not temporal or entity-grouped. Every number above therefore measures in-distribution separability only.

References

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