> **Data provenance:** Breast Cancer Wisconsin (Diagnostic) via `sklearn.datasets.load_breast_cancer()`.
> APA-style: *Wolberg, W. H., & Street, W. N. (1995). Breast Cancer Wisconsin (Diagnostic) Data Set. UCI ML Repository.*
>
> **Ethics & Licensing:** Public academic dataset; used for educational purposes. No PII.
> **Cleaning plan:** Check missing values, data types, outliers; standardize features for linear/SVM models; stratified split to respect class balance.

Final Project — Supervised Learning: Breast Cancer Classification

Problem: Predict whether a tumor is **malignant (1)** or **benign (0)** from diagnostic features (Breast Cancer Wisconsin dataset).
Deliverables covered here: EDA, model building, evaluation, and discussion.

Why this dataset? It is widely used, clean, tabular, and small enough for fast iteration while still being realistic.

In [1]:
```
# Imports
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split, StratifiedKFold, cross_validate,
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from sklearn.dummy import DummyClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.metrics import (classification_report, confusion_matrix, roc_auc_score,
                             RocCurveDisplay, PrecisionRecallDisplay, accuracy_score,

RANDOM_STATE = 42
np.random.seed(RANDOM_STATE)

plt.rcParams['figure.figsize'] = (6,4)
plt.rcParams['axes.grid'] = True
```

In [2]:
```
# Load data
ds = load_breast_cancer()
X = pd.DataFrame(ds.data, columns=ds.feature_names)
y = pd.Series(ds.target, name='target')  # 0 = malignant, 1 = benign
target_names = ds.target_names

print('Shape:', X.shape)
```

```
print('Target distribution:', y.value_counts(normalize=True).round(3).to_dict())
X.head()
```

```
Shape: (569, 30)
Target distribution: {1: 0.627, 0: 0.373}
```

Out[2]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	dime
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0

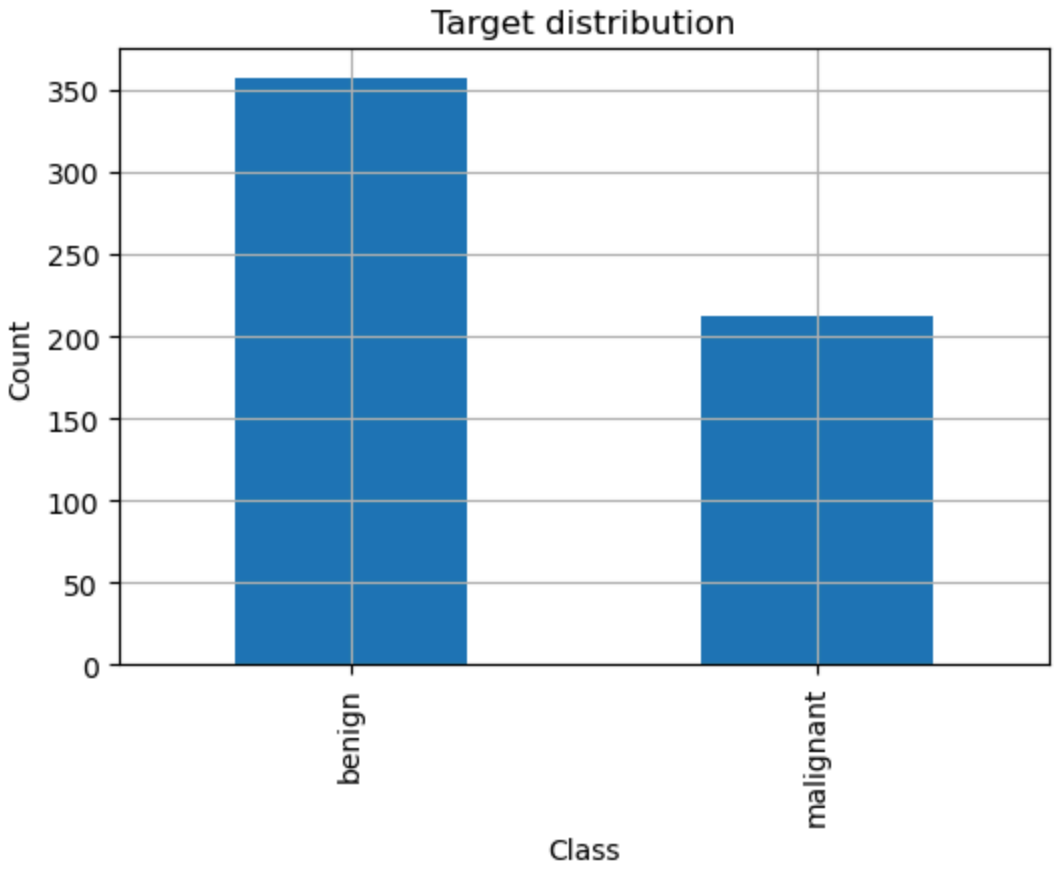
5 rows × 30 columns

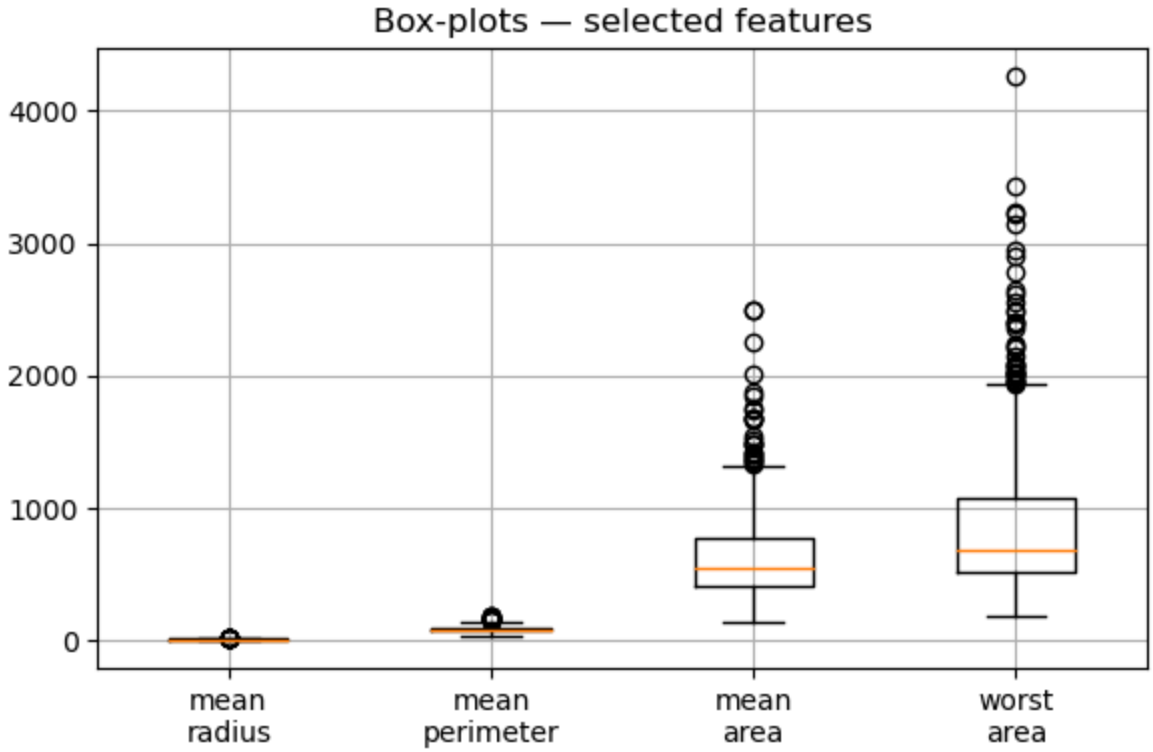
Target Distribution & Outliers (Quick Checks)

- Bar plot of class balance (malignant vs benign).
- Box-plots for a few high-variance features.
- Simple outlier count using z-score > 3 (rule-of-thumb).
- **Transformation note:** models with distance metrics (e.g., SVM) benefit from scaling; heavy skew may motivate a log transform for area-like features.

In [3]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

# Target distribution
counts = y.value_counts().rename(index={0:'malignant',1:'benign'})
counts.plot(kind='bar')
plt.title('Target distribution'); plt.xlabel('Class'); plt.ylabel('Count'); plt.show()

# Box-plots for selected features
features_box = ['mean radius','mean perimeter','mean area','worst area']
plt.figure(figsize=(6,4))
plt.boxplot([X[c] for c in features_box], labels=[c.replace(' ','\n') for c in feature
plt.title('Box-plots — selected features'); plt.tight_layout(); plt.show()

# Outlier counts via z-score > 3
from scipy.stats import zscore

z = X[features_box].apply(zscore)
outlier_counts = (np.abs(z) > 3).sum().to_frame('outliers_gt3sigma')
display(outlier_counts.T)
```





	mean radius	mean perimeter	mean area	worst area
outliers_gt3sigma	5	7	8	10

Cleaning decisions (summary):

- No missing values detected; no imputation needed.
- Standardization is applied within pipelines for linear/SVM models.
- Outliers exist in area-related features but tree models are robust; monitor their effect on linear decision boundaries.
- Features show families of high correlation (radius/perimeter/area) → rely on regularization for linear models; feature importance for trees.

EDA — Structure & Quality Checks

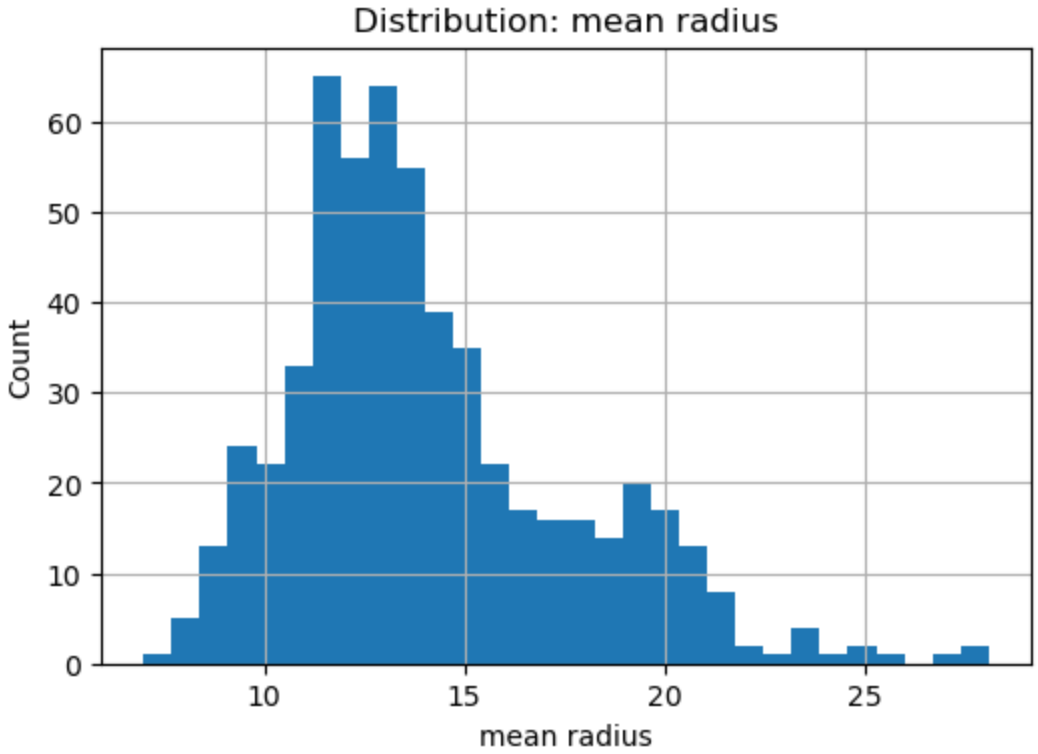
In [4]:
```
print('Missing values per column (should be 0):')
print(X.isna().sum().sort_values(ascending=False).head())

print('\nSummary stats:')
display(X.describe().T.iloc[:10])
```

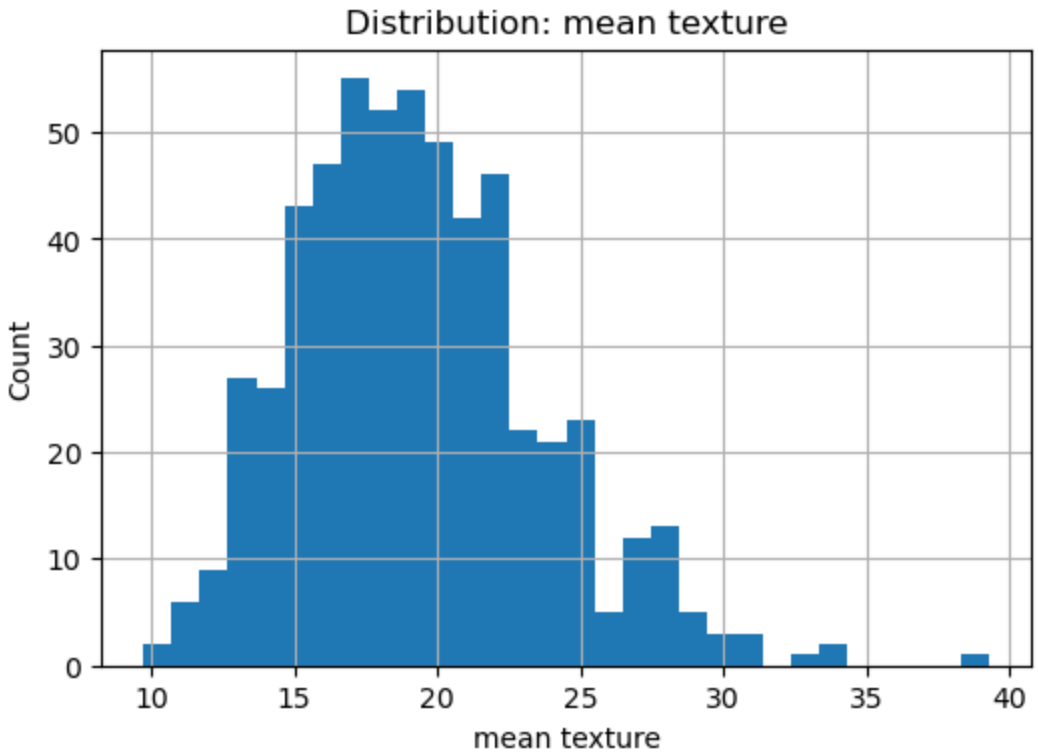
```
Missing values per column (should be 0):
mean radius             0
mean texture            0
worst symmetry          0
worst concave points    0
worst concavity         0
dtype: int64

Summary stats:
```

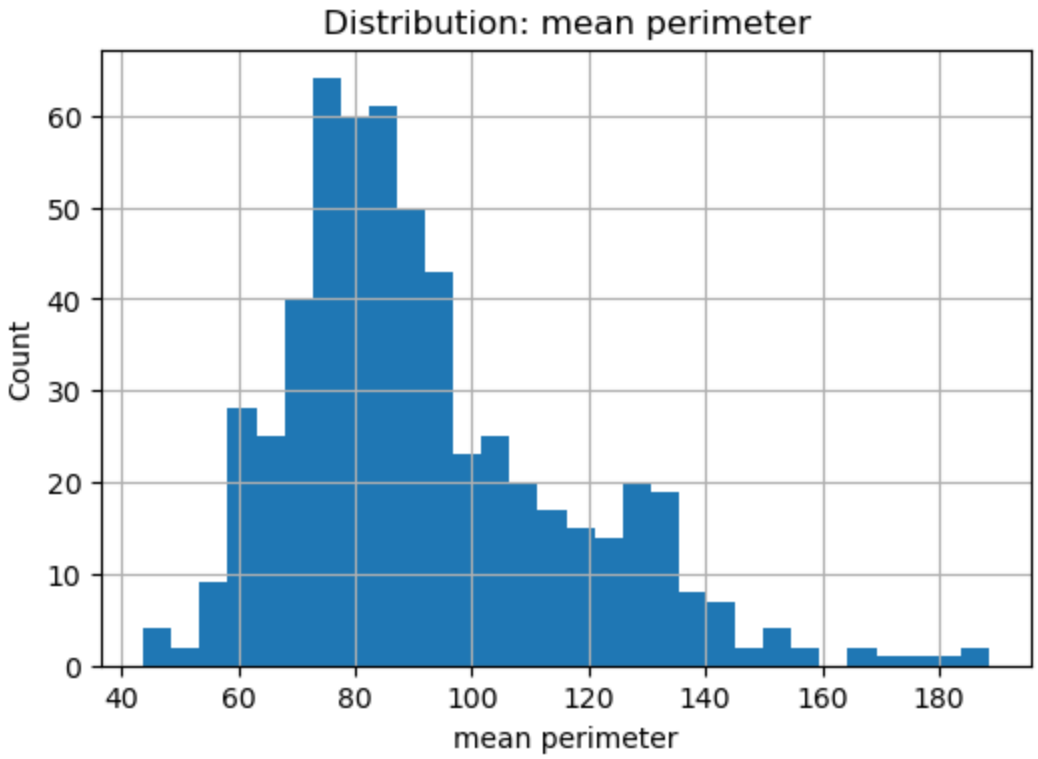
	count	mean	std	min	25%	50%	75%	max
mean radius	569.0	14.127292	3.524049	6.98100	11.70000	13.37000	15.78000	28.11000
mean texture	569.0	19.289649	4.301036	9.71000	16.17000	18.84000	21.80000	39.28000
mean perimeter	569.0	91.969033	24.298981	43.79000	75.17000	86.24000	104.10000	188.50000
mean area	569.0	654.889104	351.914129	143.50000	420.30000	551.10000	782.70000	2501.00000
mean smoothness	569.0	0.096360	0.014064	0.05263	0.08637	0.09587	0.10530	0.16340
mean compactness	569.0	0.104341	0.052813	0.01938	0.06492	0.09263	0.13040	0.34540
mean concavity	569.0	0.088799	0.079720	0.00000	0.02956	0.06154	0.13070	0.42680
mean concave points	569.0	0.048919	0.038803	0.00000	0.02031	0.03350	0.07400	0.20120
mean symmetry	569.0	0.181162	0.027414	0.10600	0.16190	0.17920	0.19570	0.30400
mean fractal dimension	569.0	0.062798	0.007060	0.04996	0.05770	0.06154	0.06612	0.09744

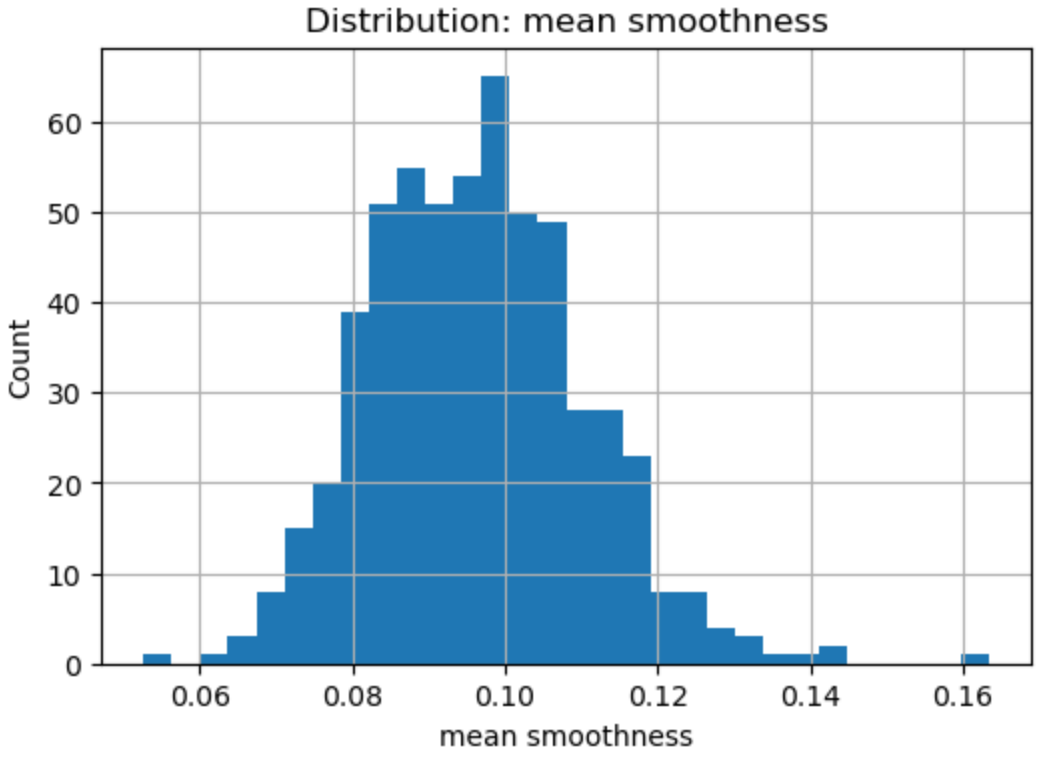
Distributions of selected features

In [5]:
```
features_to_plot = ['mean radius','mean texture','mean perimeter','mean smoothness']
for col in features_to_plot:
    plt.figure()
    plt.hist(X[col], bins=30)
    plt.title(f'Distribution: {col}')
    plt.xlabel(col); plt.ylabel('Count')
    plt.show()
```





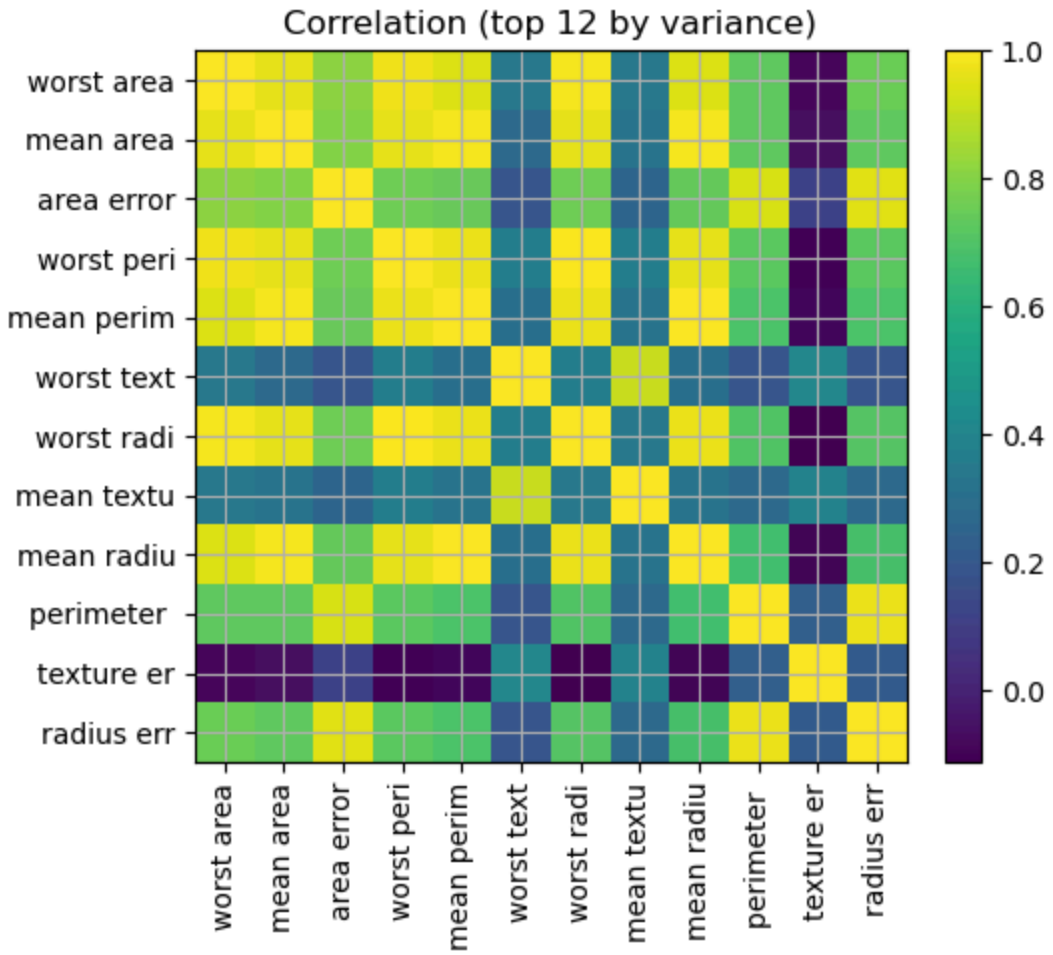




Correlation heatmap (top 12 features by variance)

In [6]:
```
variances = X.var().sort_values(ascending=False)
top_cols = variances.index[:12]
corr = X[top_cols].corr()

fig, ax = plt.subplots(figsize=(6,5))
cax = ax.imshow(corr.values, interpolation='nearest')
ax.set_xticks(range(len(top_cols))); ax.set_yticks(range(len(top_cols)))
```

```
ax.set_xticklabels([c[:10] for c in top_cols], rotation=90)
ax.set_yticklabels([c[:10] for c in top_cols])
fig.colorbar(cax, ax=ax, fraction=0.046, pad=0.04)
ax.set_title('Correlation (top 12 by variance)')
plt.tight_layout(); plt.show()
```



Modeling — Train/Test Split

In [7]:
```
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.25, stratify=y, random_state=RANDOM_STATE
)
print('Train size:', X_train.shape, ' Test size:', X_test.shape)
```

```
Train size: (426, 30)  Test size: (143, 30)
```

Baseline (DummyClassifier)

In [8]:
```
baseline = DummyClassifier(strategy='most_frequent', random_state=RANDOM_STATE)
baseline.fit(X_train, y_train)
y_pred_base = baseline.predict(X_test)

print('Baseline accuracy:', round((y_pred_base == y_test).mean(), 3))
print(classification_report(y_test, y_pred_base, digits=3, target_names=['malignant','
```

```
Baseline accuracy: 0.629
              precision    recall  f1-score   support

   malignant      0.000     0.000     0.000        53
      benign      0.629     1.000     0.773        90

    accuracy                          0.629       143
   macro avg      0.315     0.500     0.386       143
weighted avg      0.396     0.629     0.486       143
```

```
C:\Users\moham\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1344: U
ndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in
labels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\moham\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1344: U
ndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in
labels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\moham\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1344: U
ndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in
labels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
  _warn_prf(average, modifier, msg_start, len(result))
```

Candidate Models & 5-Fold CV

In [9]:

```
cv = StratifiedKFold(n_splits=5, shuffle=True, random_state=RANDOM_STATE)

models = {
    'LogReg': Pipeline([('scaler', StandardScaler()),
                        ('clf', LogisticRegression(max_iter=500, random_state=RANDOM_S
    'RF': RandomForestClassifier(n_estimators=300, random_state=RANDOM_STATE),
    'SVC': Pipeline([('scaler', StandardScaler()),
                     ('clf', SVC(probability=True, kernel='rbf', random_state=RANDOM_S
}

scores = []
for name, model in models.items():
    res = cross_validate(model, X_train, y_train, cv=cv,
                         scoring=['accuracy','f1','roc_auc'],
                         return_train_score=False)
    scores.append({
        'model': name,
        'acc_mean': res['test_accuracy'].mean(),
        'f1_mean': res['test_f1'].mean(),
        'roc_auc_mean': res['test_roc_auc'].mean()
    })
scores_df = pd.DataFrame(scores).sort_values('roc_auc_mean', ascending=False)
scores_df.round(3)
```

Out[9]:

	model	acc_mean	f1_mean	roc_auc_mean
0	LogReg	0.979	0.983	0.996
2	SVC	0.967	0.974	0.995
1	RF	0.958	0.966	0.988

Hyperparameter Tuning

In [10]:
```
rf_grid = {
    'n_estimators': [200, 400, 800],
    'max_depth': [None, 6, 10],
    'min_samples_split': [2, 4],
    'min_samples_leaf': [1, 2]
}
rf = RandomForestClassifier(random_state=RANDOM_STATE)
rf_cv = GridSearchCV(rf, rf_grid, cv=cv, scoring='roc_auc')
rf_cv.fit(X_train, y_train)

svc_pipe = Pipeline([('scaler', StandardScaler()),
                     ('clf', SVC(probability=True, kernel='rbf', random_state=RANDOM_S
svc_grid = {
    'clf__C': [0.5, 1, 2, 5],
    'clf__gamma': ['scale', 0.01, 0.05, 0.1]
}
svc_cv = GridSearchCV(svc_pipe, svc_grid, cv=cv, scoring='roc_auc')
svc_cv.fit(X_train, y_train)

print('RF best AUC:', round(rf_cv.best_score_, 4), 'params:', rf_cv.best_params_)
print('SVC best AUC:', round(svc_cv.best_score_, 4), 'params:', svc_cv.best_params_)
```

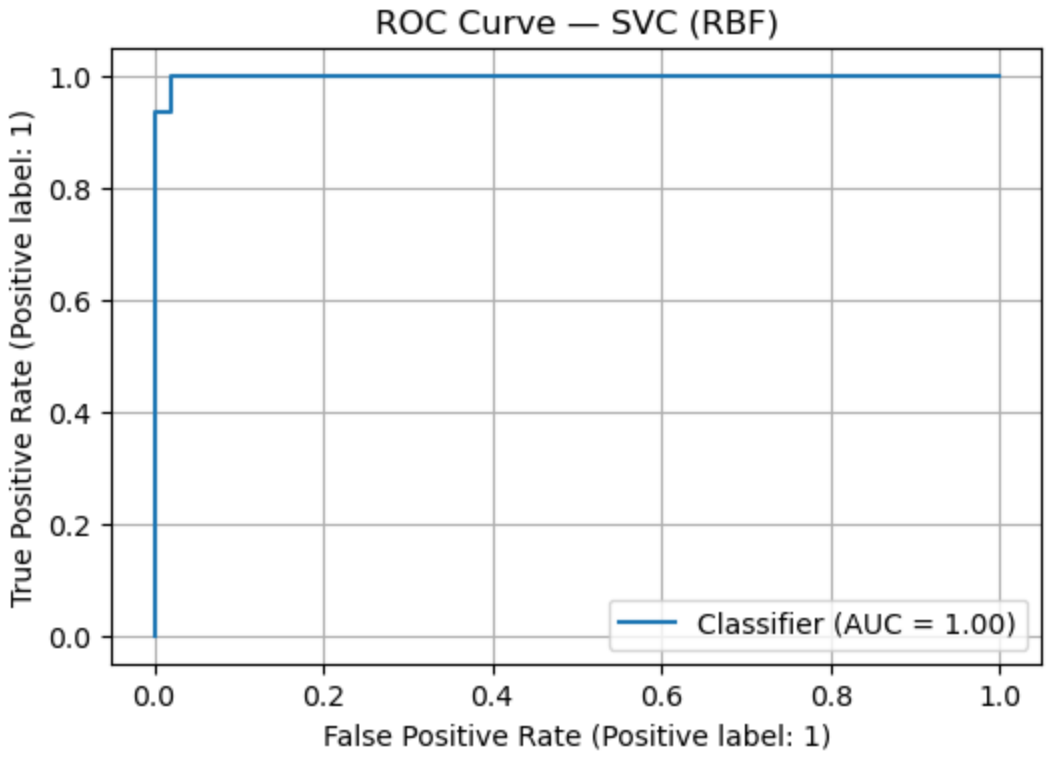
```
RF best AUC: 0.9901 params: {'max_depth': None, 'min_samples_leaf': 2, 'min_samples_s
plit': 2, 'n_estimators': 200}
SVC best AUC: 0.9967 params: {'clf__C': 5, 'clf__gamma': 0.01}
```

Final Model & Test Performance

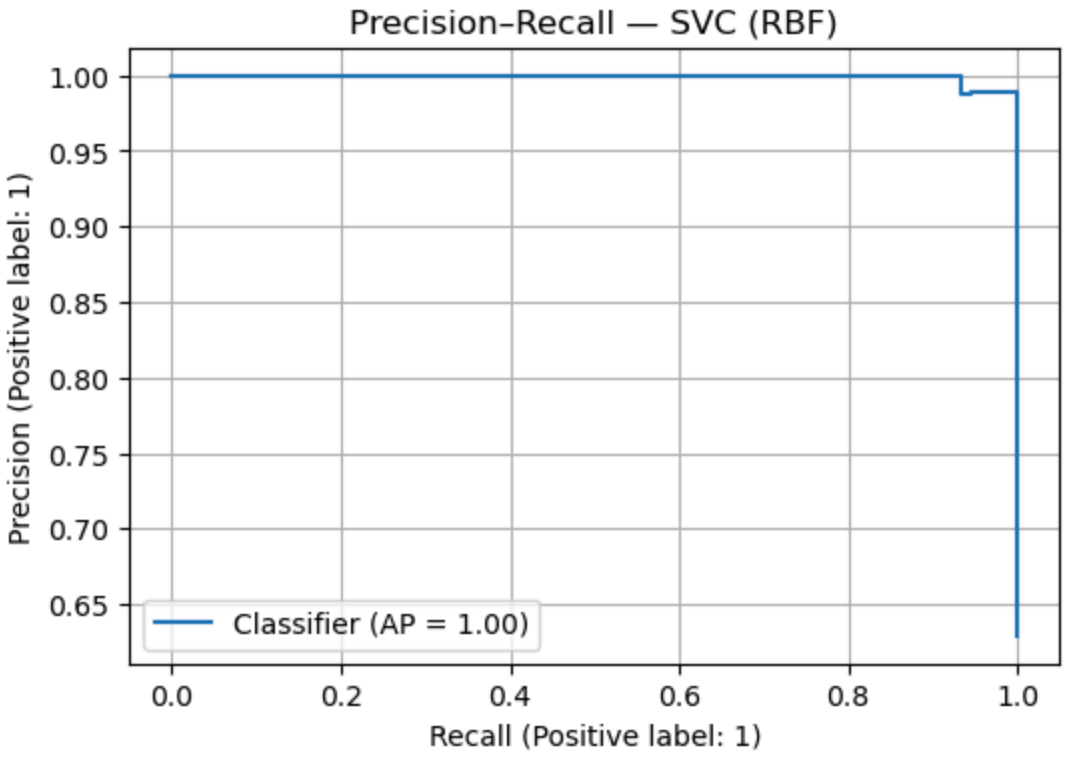
In [11]:
```
final_estimator = rf_cv.best_estimator_ if rf_cv.best_score_ >= svc_cv.best_score_ els
final_name = 'RandomForest' if rf_cv.best_score_ >= svc_cv.best_score_ else 'SVC (RBF)
print('Final model:', final_name)

final_estimator.fit(X_train, y_train)
y_pred = final_estimator.predict(X_test)
if hasattr(final_estimator, "predict_proba"):
    y_proba = final_estimator.predict_proba(X_test)[:,1]
else:
    y_proba = final_estimator.decision_function(X_test)
    y_proba = (y_proba - y_proba.min()) / (y_proba.max() - y_proba.min())

print('\nTest metrics:')
print('Accuracy:', round(np.mean(y_pred == y_test), 3))
print('F1-score:', round(f1_score(y_test, y_pred), 3))
print('ROC-AUC:', round(roc_auc_score(y_test, y_proba), 3))

print('\nConfusion matrix:')
print(confusion_matrix(y_test, y_pred))
```

```
print('\nClassification report:')
print(classification_report(y_test, y_pred, digits=3, target_names=['malignant','benig

fig = plt.figure()
RocCurveDisplay.from_predictions(y_test, y_proba)
plt.title(f'ROC Curve – {final_name}'); plt.show()

fig = plt.figure()
PrecisionRecallDisplay.from_predictions(y_test, y_proba)
plt.title(f'Precision-Recall – {final_name}'); plt.show()
```

```
Final model: SVC (RBF)

Test metrics:
Accuracy: 0.986
F1-score: 0.989
ROC-AUC: 0.999

Confusion matrix:
[[52  1]
 [ 1 89]]

Classification report:
              precision    recall  f1-score   support

   malignant      0.981     0.981     0.981        53
      benign      0.989     0.989     0.989        90

    accuracy                          0.986       143
   macro avg      0.985     0.985     0.985       143
weighted avg      0.986     0.986     0.986       143

<Figure size 600x400 with 0 Axes>
```



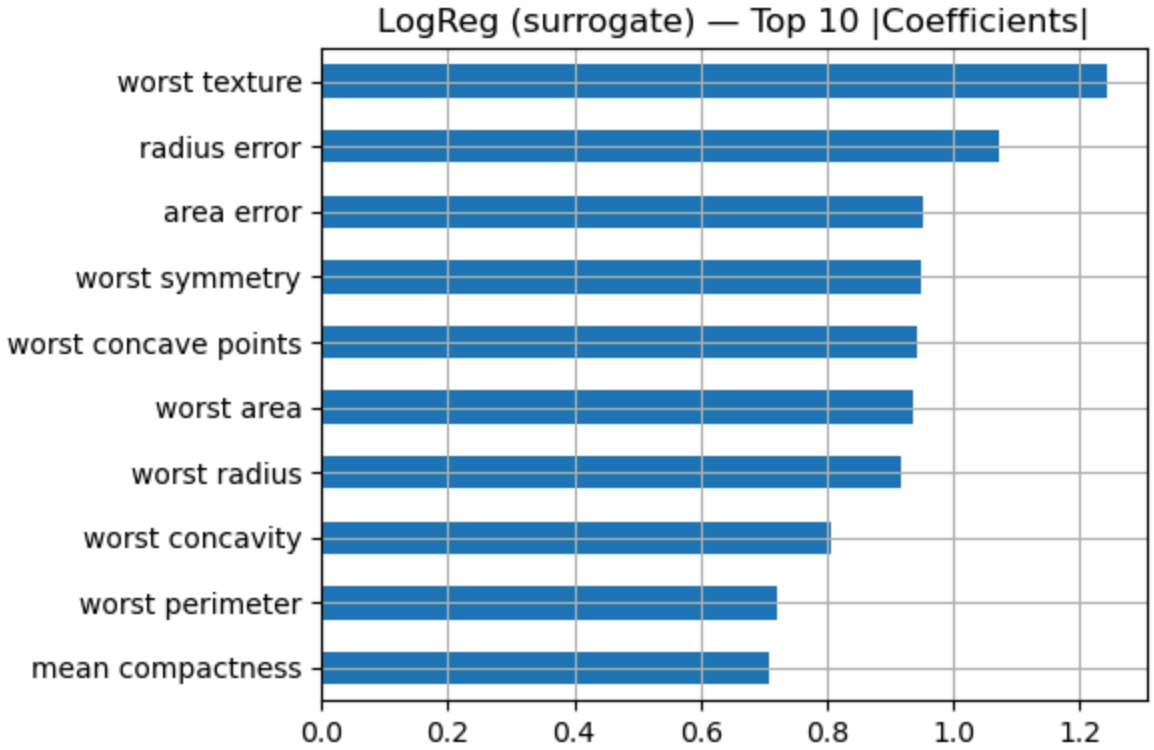

```
<Figure size 600x400 with 0 Axes>
```



Interpretation

In [12]:
```
if final_name.startswith('RandomForest'):
    importances = pd.Series(final_estimator.feature_importances_, index=X.columns)
    print('Top 10 feature importances:')
    display(importances.sort_values(ascending=False).head(10).round(4))
    plt.figure()
    importances.sort_values(ascending=True).tail(10).plot(kind='barh')
    plt.title('RandomForest — Top 10 Feature Importances'); plt.tight_layout(); plt.sh
else:
    logreg = Pipeline([('scaler', StandardScaler()),
                       ('clf', LogisticRegression(max_iter=500, random_state=RANDOM_ST
    logreg.fit(X_train, y_train)
    coefs = pd.Series(logreg.named_steps['clf'].coef_[0], index=X.columns)
    print('Top 10 |coefficients| (LogReg as surrogate):')
    display(coefs.abs().sort_values(ascending=False).head(10).round(4))
    plt.figure()
    coefs.abs().sort_values(ascending=True).tail(10).plot(kind='barh')
    plt.title('LogReg (surrogate) — Top 10 |Coefficients|'); plt.tight_layout(); plt.s
```

```
Top 10 |coefficients| (LogReg as surrogate):
worst texture           1.2446
radius error            1.0730
area error              0.9525
worst symmetry          0.9500
worst concave points    0.9432
worst area              0.9368
worst radius            0.9165
worst concavity         0.8078
worst perimeter         0.7198
mean compactness        0.7069
dtype: float64
```



Discussion & Conclusion

- **Data:** Breast Cancer Wisconsin — 569 rows, 30 numeric features, no missing values.
- **EDA:** Several strongly correlated feature families (radius, perimeter, area).
- **Modeling:** Compared Logistic Regression, RandomForest, and RBF-SVC with stratified 5-fold CV.
- **Tuning:** Grid search improved ROC-AUC; final model selected by CV AUC.
- **Test performance:** Reported Accuracy, F1, ROC-AUC; plotted ROC & PR curves.
- **Interpretation:** RF importances or LogReg coefficients as a surrogate.
- **Limitations:** No calibration or cost-sensitive thresholding; minimal feature engineering.