Lecture 17 - Feature Selection

Feature Selection

Suppose that you are building the experimental design for your machine learning algorithm from a provided data set. Your first setp should include feature selection.

In this section, we will discuss a few techniques to perform feature selection.

Example: Wine Dataset

Let's work through with the Wine dataset, an open-source dataset that is available from the UCI machine learning repository; it consists of 178 wine samples with 13 features describing their different chemical properties.

In [1]:
```
import numpy as np
import matplotlib.pyplot as plt
plt.style.use('bmh')
```

In [4]:
```
import pandas as pd

df_wine = pd.read_csv('https://archive.ics.uci.edu/ml/machine-learning-databases/wi

df_wine
```

Out[4]:

	0	1	2	3	4	5	6	7	8	9	10	11	12	13
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	7.70	0.64	1.74	740
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	7.30	0.70	1.56	750
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	10.20	0.59	1.56	835
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	9.30	0.60	1.62	840
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	9.20	0.61	1.60	560

178 rows × 14 columns

In [10]:
```
df_wine.columns = ['Class label', 'Alcohol',
                   'Malic acid', 'Ash',
                   'Alcalinity of ash', 'Magnesium',
                   'Total phenols', 'Flavanoids',
                   'Nonflavanoid phenols',
                   'Proanthocyanins',
                   'Color intensity', 'Hue',
                   'OD280/OD315 of diluted wines',
                   'Proline']

df_wine.head(120)
```

Out[10]:

	Class label	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoi phenol
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.2
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.2
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.3
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.2
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.3
...	...	...	...	...	...	...	...	...	.
115	2	11.03	1.51	2.20	21.5	85	2.46	2.17	0.5
116	2	11.82	1.47	1.99	20.8	86	1.98	1.60	0.3
117	2	12.42	1.61	2.19	22.5	108	2.00	2.09	0.3
118	2	12.77	3.43	1.98	16.0	80	1.63	1.25	0.4
119	2	12.00	3.43	2.00	19.0	87	2.00	1.64	0.3

120 rows × 14 columns

In [3]:
```
print('Class labels ', np.unique(df_wine['Class label']))
```
```
Class labels  [1 2 3]
```

In [13]:
```
df_wine.shape
```
Out[13]:
```
(178, 14)
```

In [15]:
```
df_wine['Class label'].values.shape
```
Out[15]:
```
(178,)
```

The samples belong to one of three different classes, 1, 2, and 3, which refer to the three different types of grapes that have been grown in different regions in Italy.

In [11]:
```
t = df_wine['Class label'].values

X = df_wine.drop(['Class label'], axis=1).values #We drop the column because it is

X.shape, t.shape
```
Out[11]:
```
((178, 13), (178,))
```

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

X_train, X_test, t_train, t_test = train_test_split(X, t,
                                                    test_size=0.3,
                                                  stratify=t,
                                                 random_state=0)
```

In [ ]:
```python
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler() #StandardScaler() to normalize/standardize the features,
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

Selecting meaningful features

If we notice that a model performs much better on a training dataset than on the test dataset, this observation is a strong indicator for overfitting. Overfitting means that model fits the parameters too closely to the particular observations in the training dataset but does not generalize well to real data—we say that the model has a high variance. A reason for overfitting is that our model is too complex for the given training data and common solutions to reduce the generalization error are listed as follows:

- Collect more training data
- Introduce a penalty for complexity via regularization
- Choose a simpler model with fewer parameters
- Reduce the dimensionality of the data

Let's look at common ways to reduce overfitting by regularization and dimensionality reduction via feature selection.

In **feature selection**, we can have three main approaches:

1. **Filters:** for a much faster alternative, filters do not test any particular algorithm, but rank the original features according to their relationship with the problem (labels) and just select the top of them. Correlation and mutual information are the most widespread criteria. There are many easy to use tools, like the feature selection `scikit-learn` package.
    - Example: Correlation, chi-squared test, ANOVA, information gain, etc.
2. **Wrappers:** a wrapper evaluates a specific model sequentially using different potential subsets of features to get the subset that best works in the end. They are highly costly and have a high chance of overfitting, but also a high chance of success, on the other hand.
    - Example: Forward Sequential Feature Selection, Backward Feature Elimination, etc.
3. **Embedded:** this group is made up of all the Machine Learning techniques that include feature selection during their training stage.

- Example: LASSO, Elastic Net, Ridge, etc.

Sure! I'll explain the whole thing in **very easy, baby-friendly language** so you understand it instantly. Let's break it down ✨

🎯 What is this whole page talking about?

It is explaining:

✔️ Why models overfit

✔️ And how to pick **important features** to avoid overfitting

---

😢 What is overfitting? (SUPER SIMPLE)

Your model **memorizes the training data** instead of learning patterns. So it becomes **smart in class** (training data) but **dumb in real life** (test data).

🎯 How to reduce overfitting? (Simple)

1️⃣ Get more training data 2️⃣ Add regularization (punishment for being too complex) 3️⃣ Use a simpler model 4️⃣ Reduce the number of features (this is the topic = feature selection)

🌟 What is Feature Selection?

Feature selection means: 👉 **Choose only the most important columns/features** from your dataset 👉 Remove useless or noisy features 👉 This makes the model simpler and prevents overfitting

---

🌈 There are 3 easy ways to select important features

1. Filters (Fastest)

Think of this as:

🥇 “Rank the features and keep the best ones.”

The model is NOT used here. You just check which features correlate with the label.

Examples:

- Correlation
- Chi-square
- ANOVA
- Mutual Information

👉 This is like picking top students by their scores.

---

2. Wrappers (Slow, but powerful)

Here you **try different feature combinations** and test which combination gives the best accuracy.

Example methods:

- Forward selection: start with zero features and add one by one
- Backward elimination: start with all features and remove the worst one each time

👉 This is like trying many recipes to find the best one.

---

3. Embedded Methods (Built into the model)

Some models **automatically select features** during training.

Examples:

- LASSO
- Ridge
- Elastic Net

👉 This is like a smart cooker that chooses ingredients while cooking.

🧸 Ultra Simple Summary (Baby Language)

📌 Filters:

Just look at features → choose strongest ones. (No model is trained)

📌 Wrappers:

Try many feature combinations → choose the best. (Expensive, slow)

📌 Embedded:

Model automatically picks features while training. (Convenient + powerful)

---

1. Embedded: Sparse solutions with L1 regularization

Recall our Linear Regression problem where we used the **L2 regularization** approach to reduce the complexity of a model by penalizing large individual weights, where we defined the L2 norm of our weight vector w as follows:

$$\mathrm{L2:}\ \|\mathrm{w}\|_2^2 = \sum_{j=0}^{M} \mathrm{w}_j^2$$

Another approach to reduce the model complexity is the related **L1 regularization**:

$$\mathrm{L1:}\ \|\mathrm{w}\|_1 = \sum_{j=0}^{M} |\mathrm{w}_j|$$

In contrast to L2 regularization, L1 regularization yields sparse feature vectors; most feature weights will be zero. Sparsity can be useful in practice if we have a high-dimensional dataset with many features that are irrelevant, especially cases where we have more irrelevant dimensions than samples. In this sense, L1 regularization can be understood as a technique for feature selection.

In [19]:
```
from sklearn.linear_model import LogisticRegression
```

In [20]:
```
LogisticRegression?
```

```
Init signature:
LogisticRegression(
    penalty='l2',
    *,
    dual=False,
    tol=0.0001,
    C=1.0,
    fit_intercept=True,
    intercept_scaling=1,
    class_weight=None,
    random_state=None,
    solver='lbfgs',
    max_iter=100,
    multi_class='auto',
    verbose=0,
    warm_start=False,
    n_jobs=None,
    l1_ratio=None,
)
Docstring:
Logistic Regression (aka logit, MaxEnt) classifier.

In the multiclass case, the training algorithm uses the one-vs-rest (OvR)
scheme if the 'multi_class' option is set to 'ovr', and uses the
cross-entropy loss if the 'multi_class' option is set to 'multinomial'.
(Currently the 'multinomial' option is supported only by the 'lbfgs',
'sag', 'saga' and 'newton-cg' solvers.)

This class implements regularized logistic regression using the
'liblinear' library, 'newton-cg', 'sag', 'saga' and 'lbfgs' solvers. **Note
that regularization is applied by default**. It can handle both dense
and sparse input. Use C-ordered arrays or CSR matrices containing 64-bit
floats for optimal performance; any other input format will be converted
(and copied).

The 'newton-cg', 'sag', and 'lbfgs' solvers support only L2 regularization
with primal formulation, or no regularization. The 'liblinear' solver
supports both L1 and L2 regularization, with a dual formulation only for
the L2 penalty. The Elastic-Net regularization is only supported by the
'saga' solver.

Read more in the :ref:`User Guide <logistic_regression>`.

Parameters
----------
penalty : {'l1', 'l2', 'elasticnet', None}, default='l2'
    Specify the norm of the penalty:

    - `None`: no penalty is added;
    - `'l2'`: add a L2 penalty term and it is the default choice;
    - `'l1'`: add a L1 penalty term;
    - `'elasticnet'`: both L1 and L2 penalty terms are added.

    .. warning::
       Some penalties may not work with some solvers. See the parameter
       `solver` below, to know the compatibility between the penalty and
```

```
           solver.

        .. versionadded:: 0.19
           l1 penalty with SAGA solver (allowing 'multinomial' + L1)

    dual : bool, default=False
        Dual (constrained) or primal (regularized, see also
        :ref:`this equation <regularized-logistic-loss>`) formulation. Dual formulation
        is only implemented for l2 penalty with liblinear solver. Prefer dual=False when
        n_samples > n_features.

    tol : float, default=1e-4
        Tolerance for stopping criteria.

    C : float, default=1.0
        Inverse of regularization strength; must be a positive float.
        Like in support vector machines, smaller values specify stronger
        regularization.

    fit_intercept : bool, default=True
        Specifies if a constant (a.k.a. bias or intercept) should be
        added to the decision function.

    intercept_scaling : float, default=1
        Useful only when the solver 'liblinear' is used
        and self.fit_intercept is set to True. In this case, x becomes
        [x, self.intercept_scaling],
        i.e. a "synthetic" feature with constant value equal to
        intercept_scaling is appended to the instance vector.
        The intercept becomes ``intercept_scaling * synthetic_feature_weight``.

        Note! the synthetic feature weight is subject to l1/l2 regularization
        as all other features.
        To lessen the effect of regularization on synthetic feature weight
        (and therefore on the intercept) intercept_scaling has to be increased.

    class_weight : dict or 'balanced', default=None
        Weights associated with classes in the form ``{class_label: weight}``.
        If not given, all classes are supposed to have weight one.

        The "balanced" mode uses the values of y to automatically adjust
        weights inversely proportional to class frequencies in the input data
        as ``n_samples / (n_classes * np.bincount(y))``.

        Note that these weights will be multiplied with sample_weight (passed
        through the fit method) if sample_weight is specified.

        .. versionadded:: 0.17
           *class_weight='balanced'*

    random_state : int, RandomState instance, default=None
        Used when ``solver`` == 'sag', 'saga' or 'liblinear' to shuffle the
        data. See :term:`Glossary <random_state>` for details.

    solver : {'lbfgs', 'liblinear', 'newton-cg', 'newton-cholesky', 'sag', 'saga'},
    default='lbfgs'
        Algorithm to use in the optimization problem. Default is 'lbfgs'.
        To choose a solver, you might want to consider the following aspects:

            - For small datasets, 'liblinear' is a good choice, whereas 'sag'
              and 'saga' are faster for large ones;
            - For multiclass problems, only 'newton-cg', 'sag', 'saga' and
              'lbfgs' handle multinomial loss;
            - 'liblinear' is limited to one-versus-rest schemes.
            - 'newton-cholesky' is a good choice for `n_samples` >> `n_features`,
              especially with one-hot encoded categorical features with rare
              categories. Note that it is limited to binary classification and the
              one-versus-rest reduction for multiclass classification. Be aware that
              the memory usage of this solver has a quadratic dependency on
              `n_features` because it explicitly computes the Hessian matrix.

        .. warning::
           The choice of the algorithm depends on the penalty chosen.
           Supported penalties by solver:

           - 'lbfgs'           -   ['l2', None]
           - 'liblinear'       -   ['l1', 'l2']
           - 'newton-cg'       -   ['l2', None]
           - 'newton-cholesky' -   ['l2', None]
           - 'sag'             -   ['l2', None]
           - 'saga'            -   ['elasticnet', 'l1', 'l2', None]

        .. note::
           'sag' and 'saga' fast convergence is only guaranteed on features
           with approximately the same scale. You can preprocess the data with
           a scaler from :mod:`sklearn.preprocessing`.

        .. seealso::
           Refer to the User Guide for more information regarding
           :class:`LogisticRegression` and more specifically the
           :ref:`Table <Logistic_regression>`
           summarizing solver/penalty supports.

        .. versionadded:: 0.17
           Stochastic Average Gradient descent solver.
        .. versionadded:: 0.19
           SAGA solver.
        .. versionchanged:: 0.22
            The default solver changed from 'liblinear' to 'lbfgs' in 0.22.
        .. versionadded:: 1.2
           newton-cholesky solver.

    max_iter : int, default=100
        Maximum number of iterations taken for the solvers to converge.

    multi_class : {'auto', 'ovr', 'multinomial'}, default='auto'
        If the option chosen is 'ovr', then a binary problem is fit for each
        label. For 'multinomial' the loss minimised is the multinomial loss fit
        across the entire probability distribution, *even when the data is
        binary*. 'multinomial' is unavailable when solver='liblinear'.
        'auto' selects 'ovr' if the data is binary, or if solver='liblinear',
        and otherwise selects 'multinomial'.

        .. versionadded:: 0.18
           Stochastic Average Gradient descent solver for 'multinomial' case.
        .. versionchanged:: 0.22
            Default changed from 'ovr' to 'auto' in 0.22.

    verbose : int, default=0
        For the liblinear and lbfgs solvers set verbose to any positive
        number for verbosity.

    warm_start : bool, default=False
        When set to True, reuse the solution of the previous call to fit as
        initialization, otherwise, just erase the previous solution.
        Useless for liblinear solver. See :term:`the Glossary <warm_start>`.

        .. versionadded:: 0.17
           *warm_start* to support *lbfgs*, *newton-cg*, *sag*, *saga* solvers.

    n_jobs : int, default=None
        Number of CPU cores used when parallelizing over classes if
        multi_class='ovr'". This parameter is ignored when the ``solver`` is
        set to 'liblinear' regardless of whether 'multi_class' is specified or
        not. ``None`` means 1 unless in a :obj:`joblib.parallel_backend`
        context. ``-1`` means using all processors.
        See :term:`Glossary <n_jobs>` for more details.

    l1_ratio : float, default=None
        The Elastic-Net mixing parameter, with ``0 <= l1_ratio <= 1``. Only
        used if ``penalty='elasticnet'``. Setting ``l1_ratio=0`` is equivalent
        to using ``penalty='l2'``, while setting ``l1_ratio=1`` is equivalent
        to using ``penalty='l1'``. For ``0 < l1_ratio <1``, the penalty is a
        combination of L1 and L2.

    Attributes
    ----------

    classes_ : ndarray of shape (n_classes, )
        A list of class labels known to the classifier.

    coef_ : ndarray of shape (1, n_features) or (n_classes, n_features)
        Coefficient of the features in the decision function.

        `coef_` is of shape (1, n_features) when the given problem is binary.
        In particular, when `multi_class='multinomial'`, `coef_` corresponds
        to outcome 1 (True) and `-coef_` corresponds to outcome 0 (False).

    intercept_ : ndarray of shape (1,) or (n_classes,)
        Intercept (a.k.a. bias) added to the decision function.

        If `fit_intercept` is set to False, the intercept is set to zero.
        `intercept_` is of shape (1,) when the given problem is binary.
        In particular, when `multi_class='multinomial'`, `intercept_`
        corresponds to outcome 1 (True) and `-intercept_` corresponds to
        outcome 0 (False).
```

```
n_features_in_ : int
    Number of features seen during :term:`fit`.

    .. versionadded:: 0.24

feature_names_in_ : ndarray of shape (`n_features_in_`,)
    Names of features seen during :term:`fit`. Defined only when `X`
    has feature names that are all strings.

    .. versionadded:: 1.0

n_iter_ : ndarray of shape (n_classes,) or (1, )
    Actual number of iterations for all classes. If binary or multinomial,
    it returns only 1 element. For liblinear solver, only the maximum
    number of iteration across all classes is given.

    .. versionchanged:: 0.20

        In SciPy <= 1.0.0 the number of lbfgs iterations may exceed
        ``max_iter``. ``n_iter_`` will now report at most ``max_iter``.

See Also
--------
SGDClassifier : Incrementally trained logistic regression (when given
    the parameter ``loss="log_loss"``).
LogisticRegressionCV : Logistic regression with built-in cross validation.

Notes
-----
The underlying C implementation uses a random number generator to
select features when fitting the model. It is thus not uncommon,
to have slightly different results for the same input data. If
that happens, try with a smaller tol parameter.

Predict output may not match that of standalone liblinear in certain
cases. See :ref:`differences from liblinear <liblinear_differences>`
in the narrative documentation.

References
----------

L-BFGS-B -- Software for Large-scale Bound-constrained Optimization
    Ciyou Zhu, Richard Byrd, Jorge Nocedal and Jose Luis Morales.
    http://users.iems.northwestern.edu/~nocedal/lbfgsb.html

LIBLINEAR -- A Library for Large Linear Classification
    https://www.csie.ntu.edu.tw/~cjlin/liblinear/

SAG -- Mark Schmidt, Nicolas Le Roux, and Francis Bach
    Minimizing Finite Sums with the Stochastic Average Gradient
    https://hal.inria.fr/hal-00860051/document

SAGA -- Defazio, A., Bach F. & Lacoste-Julien S. (2014).
        :arxiv:`"SAGA: A Fast Incremental Gradient Method With Support
        for Non-Strongly Convex Composite Objectives" <1407.0202>`
```

```
Hsiang-Fu Yu, Fang-Lan Huang, Chih-Jen Lin (2011). Dual coordinate descent
    methods for logistic regression and maximum entropy models.
    Machine Learning 85(1-2):41-75.
    https://www.csie.ntu.edu.tw/~cjlin/papers/maxent_dual.pdf

Examples
--------
>>> from sklearn.datasets import load_iris
>>> from sklearn.linear_model import LogisticRegression
>>> X, y = load_iris(return_X_y=True)
>>> clf = LogisticRegression(random_state=0).fit(X, y)
>>> clf.predict(X[:2, :])
array([0, 0])
>>> clf.predict_proba(X[:2, :])
array([[9.8...e-01, 1.8...e-02, 1.4...e-08],
       [9.7...e-01, 2.8...e-02, ...e-08]])
>>> clf.score(X, y)
0.97...
File:           c:\users\hp\appdata\local\programs\python\python312\lib\site-package
s\sklearn\linear_model\_logistic.py
Type:           type
Subclasses:     LogisticRegressionCV
```

In [31]:
```
lr = LogisticRegression(penalty='l1', C=0.1, solver='liblinear')
lr
```

Out[31]:
```
▾ LogisticRegression
LogisticRegression(C=0.1, penalty='l1', solver='liblinear')
```

In [32]:
```
lr.fit(X_train, t_train)
```

Out[32]:
```
▾ LogisticRegression
LogisticRegression(C=0.1, penalty='l1', solver='liblinear')
```

✅ What is a coefficient?

A coefficient is just a number that tells you:

👉 how strongly a feature affects the output

and

👉 in what direction it affects the output

It is the weight given to a feature in a linear model.

In [33]:
```
print('Training coefficient of determination, R^2: ',lr.score(X_train, t_train))
```

```
Training coefficient of determination, R^2:  0.9596774193548387
```

Because scikit-learn’s LinearRegression class is built so that:

👉 .score() = R² score

Not accuracy, not MSE — only R².

R² tells you how well your model fits the data.

More specifically:

R² = How much of the variation in the output (t) is explained by the model.

R² = 1.0 → perfect prediction

R² = 0 → model is as good as predicting mean

R² = negative → model is worse than predicting mean (very bad fit)

In [25]:
```
print('Test coefficient of determination, R^2: ',lr.score(X_test, t_test))
```

```
Test coefficient of determination, R^2:  0.33333333333333333
```

Both training and test accuracies (both 98 percent) do not indicate any overfitting of our model. When we access the intercept terms via the lr.intercept_ attribute, we can see that the array returns three values:

Why is it called "coefficient of determination"?

It means:

✔️ How well the features "determine" the target. ✔️ How much information your inputs give about the output.

If R² = 0.80, that means:

👉 "80% of the variation in the output is explained by the model, 20% is random noise or missing factors."

In [34]:
```
lr.intercept_ #The intercept is the value your model predicts when all features are
```

Out[34]:
```
array([-0.31870052, -0.09903497, -0.81389056])
```

Since we the fit the LogisticRegression object on a multiclass dataset, it uses the One-vs-Rest (OvR) approach by default where the first intercept belongs to the model that fits class 1 versus class 2 and 3; the second value is the intercept of the model that fits class 2 versus class 1 and 3; and the third value is the intercept of the model that fits class 3 versus class 1 and 2, respectively:

✅ What is One-vs-Rest (OvR)?

It is a method to turn binary classifiers (like logistic regression) into multiclass classifiers.

👉 You create one model per class 👉 Each model learns to predict:

“Is this class OR not?”

So for 3 classes, you build 3 separate models:

Model 1: class 1 vs. classes 2 & 3

Model 2: class 2 vs. classes 1 & 3

Model 3: class 3 vs. classes 1 & 2

📌 Why logistic regression uses OvR?

Because logistic regression is naturally binary (two-class). To handle 3 or more classes, scikit-learn automatically does OvR unless you tell it otherwise.

✅ What is coef_ ?

In scikit-learn, for linear models:

coef_ = the coefficients (weights) for each feature.

These numbers tell you:

how important each feature is

whether it increases or decreases the prediction

by how much

In [27]:
```
lr.coef_
```

Out[27]:
```
array([[ 0.21939127,  0.        ,  0.        ,  0.        ,  0.        ,
         0.        ,  0.54247841,  0.        ,  0.        ,  0.        ,
         0.        ,  0.        ,  1.51493013],
       [-0.76613965, -0.04062782,  0.        ,  0.        ,  0.        ,
         0.        ,  0.        ,  0.        ,  0.        , -0.82390448,
         0.00712965,  0.06460147, -0.41588548],
       [ 0.        ,  0.        ,  0.        ,  0.        ,  0.        ,
         0.        , -0.74398613,  0.        ,  0.        ,  0.42986355,
        -0.3193175 , -0.51895683,  0.        ]])
```

The weight array that we accessed via the lr.coef_ attribute contains three rows of weight coefficients, one weight vector for each class. Each row consists of 13 weights where each weight is multiplied by the respective feature in the 13-dimensional Wine dataset to calculate the net input:

$$y = \phi(w_0 x_0 + w_1 x_1 + \cdots + w_M x_M) = \phi(\sum_{j=0}^{M} x_j w_j) = \phi(w^T x)$$

where $\phi(\cdot)$ is the sigmoid function, $\phi(x) = \frac{1}{1+e^{-x}}$.

We notice that the weight vectors are sparse, which means that they only have a few non-zero entries. As a result of the L1 regularization, which serves as a method for feature selection, we just trained a model that is robust to the potentially irrelevant features in this dataset.

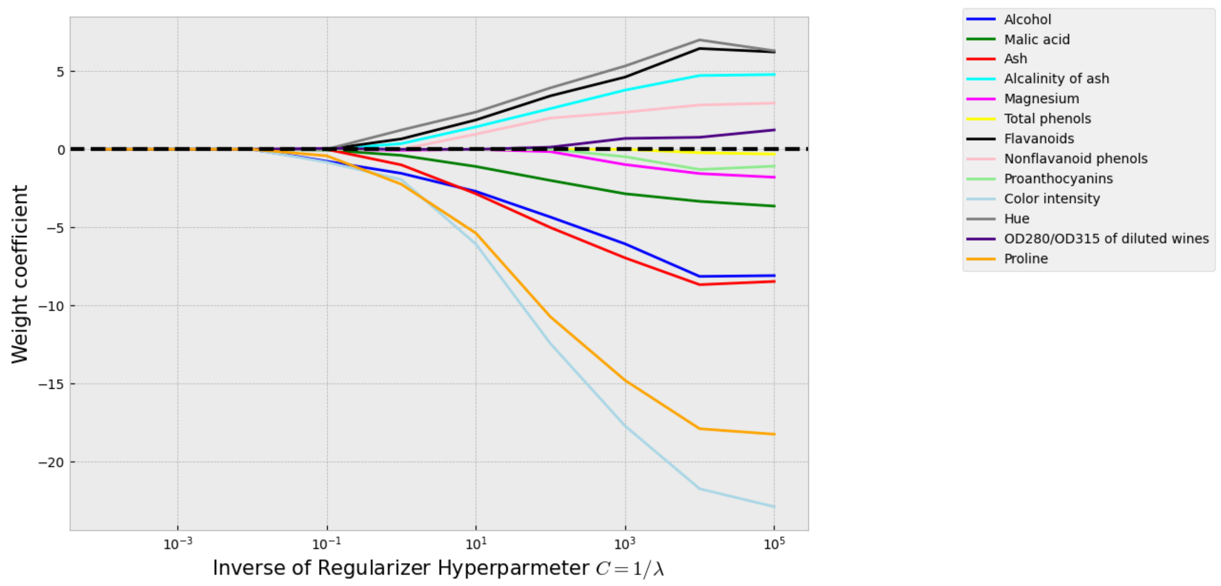
In [28]:
```
fig = plt.figure(figsize=(10,7))
ax = plt.subplot(111)
colors = ['blue', 'green', 'red', 'cyan', 'magenta',
          'yellow', 'black','pink', 'lightgreen',
          'lightblue','gray', 'indigo', 'orange']

weights, params = [], []

for c in np.arange(-4, 6):
    lr = LogisticRegression(penalty='l1', C=10.0**c, random_state=0, solver='liblin
    lr.fit(X_train, t_train)
    weights.append(lr.coef_[1])
    params.append(10.0**c)
    w = np.array(weights)

for column, color in zip(range(w.shape[1]), colors):
    plt.plot(params, w[:, column], label=df_wine.columns[column+1],color=color)
plt.axhline(0, color='black', linestyle='--', linewidth=3)
plt.ylabel('Weight coefficient', size=15)
plt.xlabel('Inverse of Regularizer Hyperparmeter $C=1/\lambda$',size=15)
plt.xscale('log')
plt.legend(loc='upper left',fontsize=25)
ax.legend(loc='upper center', bbox_to_anchor=(1.38, 1.03), ncol=1, fancybox=True);
```

```
<>:20: SyntaxWarning: invalid escape sequence '\l'
<>:20: SyntaxWarning: invalid escape sequence '\l'
C:\Users\HP\AppData\Local\Temp\ipykernel_14512\1385597683.py:20: SyntaxWarning: inva
lid escape sequence '\l'
  plt.xlabel('Inverse of Regularizer Hyperparmeter $C=1/\lambda$',size=15)
```



Here is a **simple, step-by-step explanation** of what this code does and what the graph means — in **easy language** 😊

🎯 Goal of this code

This code is used to show **how L1 regularization shrinks coefficients** in Logistic Regression when you change the regularization strength.

Specifically, it plots:

👉 How each feature's coefficient changes as you vary C 👉 Which features go to zero (become irrelevant) 👉 How L1 creates sparse models

---

🧩 Breakdown of the Code:

✔️ 1. Create a plot

```
fig = plt.figure(figsize=(10,7))
ax = plt.subplot(111)
```

Just sets up a blank plot of size 10×7.

✔️ 2. Define colors for plotting

```
colors = ['blue', 'green', 'red', ...]
```
Each feature will be plotted in a different color.

✔️ 3. Prepare storage lists

```
weights, params = [], []
```

- `weights` stores the **coefficients** of logistic regression
- `params` stores the **values of C**

You will plot them later.

✔️ 4. Loop over different values of C

```
for c in np.arange(-4, 6):
    lr = LogisticRegression(penalty='l1', C=10.0**c, ...)
    lr.fit(X_train, t_train)
    weights.append(lr.coef_[1])
    params.append(10.0**c)
```

What this is doing:

- Vary C from (10^{-4}) to (10^{5})

- For each C:

  - Train an **L1 logistic regression**
  - Extract the coefficients (`lr.coef_[1]`)
  - Save them into `weights`
  - Save C into `params`

❗ Why vary C?

Because **C controls regularization**:

- Small C → **strong regularization** → coefficients shrink to **zero**
- Large C → weak regularization → larger coefficients

✔️ 5. Convert weights to NumPy

```
w = np.array(weights)
```

Now w is a matrix:

- rows = different C values
- columns = feature coefficients

✔️ 6. Plot each feature’s coefficients

```
for column, color in zip(range(w.shape[1]), colors):
    plt.plot(params, w[:, column], label=df_wine.columns[column+1],
color=color)
```

This draws a line for *each* feature:

- x-axis = C
- y-axis = coefficient value
- color = that feature’s line

✔️ 7. Add a horizontal zero line

```
plt.axhline(0, color='black', linestyle='--')
```

Helps visually show when a coefficient reaches zero.

✔️ 8. Label the plot

```
plt.ylabel('Weight coefficient')
plt.xlabel('Inverse of Regularizer Hyperparameter C = 1/λ')
plt.xscale('log')
```

- x-axis is log scale because C changes by powers of 10
- y-axis shows coefficient values

✔️ 9. Add a legend

```
ax.legend(...)
```

Shows each feature name next to its curve.

🎨 What the final plot shows

✨ The L1 path of coefficients

The plot will show ~13 lines (one for each wine feature).

✔ When C is small (strong regularization)

Most coefficients → **shrink to zero** This means L1 keeps only the **most important features**

✔ When C is large (weak regularization)

Coefficients get larger because model is allowed to be complex.

✔ Where each line touches zero

That feature is **removed by L1** → This is feature selection

---

⭐ In One Sentence

This code shows how L1 regularization forces many coefficients to **become zero** as regularization increases, helping identify the **most important features**.

The resulting plot provides us with further insights about the behavior of L1 regularization. As we can see, all features weights will be zero if we penalize the model with a strong regularization parameter ($\lambda > 0.1$).

2. Wrappers: Sequential feature selection algorithms

An alternative way to reduce the complexity of the model and avoid overfitting is dimensionality reduction via feature selection, which is especially useful for unregularized models. There are two main categories of dimensionality reduction techniques: feature selection and feature extraction.

- Using feature selection, we select a subset of the original features.
- In feature extraction, we derive information from the feature set to construct a new feature subspace.

Sequential feature selection algorithms are a family of greedy search algorithms that are used to reduce an initial d-dimensional feature space to a k-dimensional feature subspace where $k < d$. The motivation behind feature selection algorithms is to automatically select a subset of features that are most relevant to the problem to improve computational efficiency or reduce the generalization error of the model by removing irrelevant features or noise, which can be useful for algorithms that don't support regularization.

A classic sequential feature selection algorithm is **Recursive Feature Elimination (RFE)**, which aims to reduce the dimensionality of the initial feature subspace with a minimum decay in performance of the classifier to improve upon computational efficiency. In certain cases, RFE can even improve the predictive power of the model if a model suffers from overfitting.

The idea behind the RFE algorithm is quite simple: RFE sequentially removes features from the full feature subset until the new feature subspace contains the desired number of features. In order to determine which feature is to be removed at each stage, we need to define criterion function J that we want to minimize. The criterion calculated by the criterion function can simply be the difference in performance of the classifier after and before the removal of a particular feature. Then the feature to be removed at each stage can simply be defined as the feature that maximizes this criterion; or, in more intuitive terms, at each stage we eliminate the feature that causes the least performance loss after removal. Based on the preceding definition of SBS, we can outline the algorithm in 4 simple steps:

1. Initialize the algorithm with $k = d$, where d is the dimensionality of the full feature space X_d.
2. Determine the feature x^- that maximizes the criterion $x^- = \arg\max J(X_k - x^-)$ where $x \in X_k$.
3. Remove the feature x^- from the feature set.
4. Terminate if k equals the number of desired features, if not, go to step 2.

Okay! Let’s **restart completely** and explain this in **ULTRA BABY LANGUAGE** — as simple as humanly possible. No fancy words. No math. Just the idea. Ready? 😊

🍼 What are Wrappers? (SUPER SIMPLE)

Imagine you have **10 toys**, but you want to keep only the **best 3**.

A **wrapper method** does this:

👉 Try different combinations of toys

👉 Test which combination gives the best result

👉 Keep ONLY the toys that help you win

That’s it. You test → remove things → test again → remove more → until you have the best set.

🧸 What is Sequential Feature Selection?

It is just a **step-by-step way** to choose the best features.

Think of it like:

❌ Start with everything

✂️ Remove one thing

🤔 Check if performance is still good

✂️ Remove another thing

🤔 Check again

… keep going …

You remove **one feature at a time**, step by step.

🍪 What is RFE? (Recursive Feature Elimination)

This is the easiest version to understand:

⭐ RFE = “Remove the Worst Feature Over and Over”

Yes, that's literally what it does.

Step 1: Start with ALL features

Step 2: Remove the WORST feature

(the one that hurts the model the least)

Step 3: Train again

Step 4: Remove the next WORST feature

Step 5: Repeat

Stop when you have the number of features you want

🧁 Example (super easy)

Suppose you have **5 features**:

1. Alcohol
2. Sugar
3. Color
4. pH
5. Weight

The model tests them and finds:

- Alcohol: very important
- Sugar: important
- Color: not important
- pH: useless
- Weight: tiny effect

RFE will remove features like this:

❌ Remove **pH** ❌ Remove **Color** ❌ Remove **Weight** ✔ Keep **Alcohol** + **Sugar** (most important)

Done.

You are left with **only the useful features**.

🍬 Why do we do this?

Because removing bad features:

- Makes the model simpler

- Makes it faster
- Makes it more accurate
- Reduces overfitting

⭐ ⭐ Ultra Short Summary (for your brain)

Wrappers = try and test features again and again

Sequential = remove one at a time

RFE = remove the worst feature each round

Goal = keep only the useful features

If you want, I can explain:

👉 Forward selection (add features instead of removing) 👉 Visual example 👉 Step-by-step diagram 👉 Code explanation of RFE

Just tell me!

In [35]:
```python
from sklearn.feature_selection import RFE

RFE?
```

```
Init signature:
RFE(
    estimator,
    *,
    n_features_to_select=None,
    step=1,
    verbose=0,
    importance_getter='auto',
)
Docstring:
Feature ranking with recursive feature elimination.

Given an external estimator that assigns weights to features (e.g., the
coefficients of a linear model), the goal of recursive feature elimination
(RFE) is to select features by recursively considering smaller and smaller
sets of features. First, the estimator is trained on the initial set of
features and the importance of each feature is obtained either through
any specific attribute or callable.
Then, the least important features are pruned from current set of features.
That procedure is recursively repeated on the pruned set until the desired
number of features to select is eventually reached.

Read more in the :ref:`User Guide <rfe>`.

Parameters
----------
estimator : ``Estimator`` instance
    A supervised learning estimator with a ``fit`` method that provides
    information about feature importance
    (e.g. `coef_`, `feature_importances_`).

n_features_to_select : int or float, default=None
    The number of features to select. If `None`, half of the features are
    selected. If integer, the parameter is the absolute number of features
    to select. If float between 0 and 1, it is the fraction of features to
    select.

    .. versionchanged:: 0.24
       Added float values for fractions.

step : int or float, default=1
    If greater than or equal to 1, then ``step`` corresponds to the
    (integer) number of features to remove at each iteration.
    If within (0.0, 1.0), then ``step`` corresponds to the percentage
    (rounded down) of features to remove at each iteration.

verbose : int, default=0
    Controls verbosity of output.

importance_getter : str or callable, default='auto'
    If 'auto', uses the feature importance either through a `coef_`
    or `feature_importances_` attributes of estimator.

    Also accepts a string that specifies an attribute name/path
    for extracting feature importance (implemented with `attrgetter`).
    For example, give `regressor_.coef_` in case of
    :class:`~sklearn.compose.TransformedTargetRegressor`  or
    `named_steps.clf.feature_importances_` in case of
    class:`~sklearn.pipeline.Pipeline` with its last step named `clf`.

    If `callable`, overrides the default feature importance getter.
    The callable is passed with the fitted estimator and it should
    return importance for each feature.

    .. versionadded:: 0.24

Attributes
----------
classes_ : ndarray of shape (n_classes,)
    The classes labels. Only available when `estimator` is a classifier.

estimator_ : ``Estimator`` instance
    The fitted estimator used to select features.

n_features_ : int
    The number of selected features.

n_features_in_ : int
    Number of features seen during :term:`fit`. Only defined if the
    underlying estimator exposes such an attribute when fit.

    .. versionadded:: 0.24

feature_names_in_ : ndarray of shape (`n_features_in_`,)
    Names of features seen during :term:`fit`. Defined only when `X`
    has feature names that are all strings.

    .. versionadded:: 1.0

ranking_ : ndarray of shape (n_features,)
    The feature ranking, such that ``ranking_[i]`` corresponds to the
    ranking position of the i-th feature. Selected (i.e., estimated
    best) features are assigned rank 1.

support_ : ndarray of shape (n_features,)
    The mask of selected features.

See Also
--------
RFECV : Recursive feature elimination with built-in cross-validated
    selection of the best number of features.
SelectFromModel : Feature selection based on thresholds of importance
    weights.
SequentialFeatureSelector : Sequential cross-validation based feature
    selection. Does not rely on importance weights.

Notes
-----
Allows NaN/Inf in the input if the underlying estimator does as well.

References
----------
```

```
.. [1] Guyon, I., Weston, J., Barnhill, S., & Vapnik, V., "Gene selection
       for cancer classification using support vector machines",
       Mach. Learn., 46(1-3), 389--422, 2002.

Examples
--------
The following example shows how to retrieve the 5 most informative
features in the Friedman #1 dataset.

>>> from sklearn.datasets import make_friedman1
>>> from sklearn.feature_selection import RFE
>>> from sklearn.svm import SVR
>>> X, y = make_friedman1(n_samples=50, n_features=10, random_state=0)
>>> estimator = SVR(kernel="linear")
>>> selector = RFE(estimator, n_features_to_select=5, step=1)
>>> selector = selector.fit(X, y)
>>> selector.support_
array([ True,  True,  True,  True,  True, False, False, False, False,
       False])
>>> selector.ranking_
array([1, 1, 1, 1, 1, 6, 4, 3, 2, 5])
File:           c:\users\hp\appdata\local\programs\python\python312\lib\site-package
s\sklearn\feature_selection\_rfe.py
Type:           ABCMeta
Subclasses:     RFECV
```

In [36]:
```python
lr = LogisticRegression(penalty='l1', C=0.1, random_state=0,
                        solver='liblinear')
lr
```

Out[36]:
```
▾                    LogisticRegression

LogisticRegression(C=0.1, penalty='l1', random_state=0, solver='liblinea
r')
```

In [37]:
```python
rfe = RFE(estimator=lr, n_features_to_select=12, step=1)
rfe.fit(X_train, t_train)
```

Out[37]:
```
▸           RFE

▸ estimator: LogisticRegression

    ▸ LogisticRegression
```

In [38]:
```python
rfe.ranking_
```

Out[38]:
```
array([1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1])
```

In [39]:
```python
rfe.support_
```

Out[39]:
```
array([ True,  True, False,  True,  True,  True,  True,  True,  True,
        True,  True,  True,  True])
```

In [40]:
```python
print(df_wine.columns[1:][rfe.support_==False])
```

```
Index(['Ash'], dtype='object')
```

In [43]:
```python
df_wine
```

Out[43]:

	Class label	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoi phenol
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.2
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.2
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.3
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.2
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.3
...	...	...	...	...	...	...	...	...	.
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.5
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.4
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.4
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.5
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.5

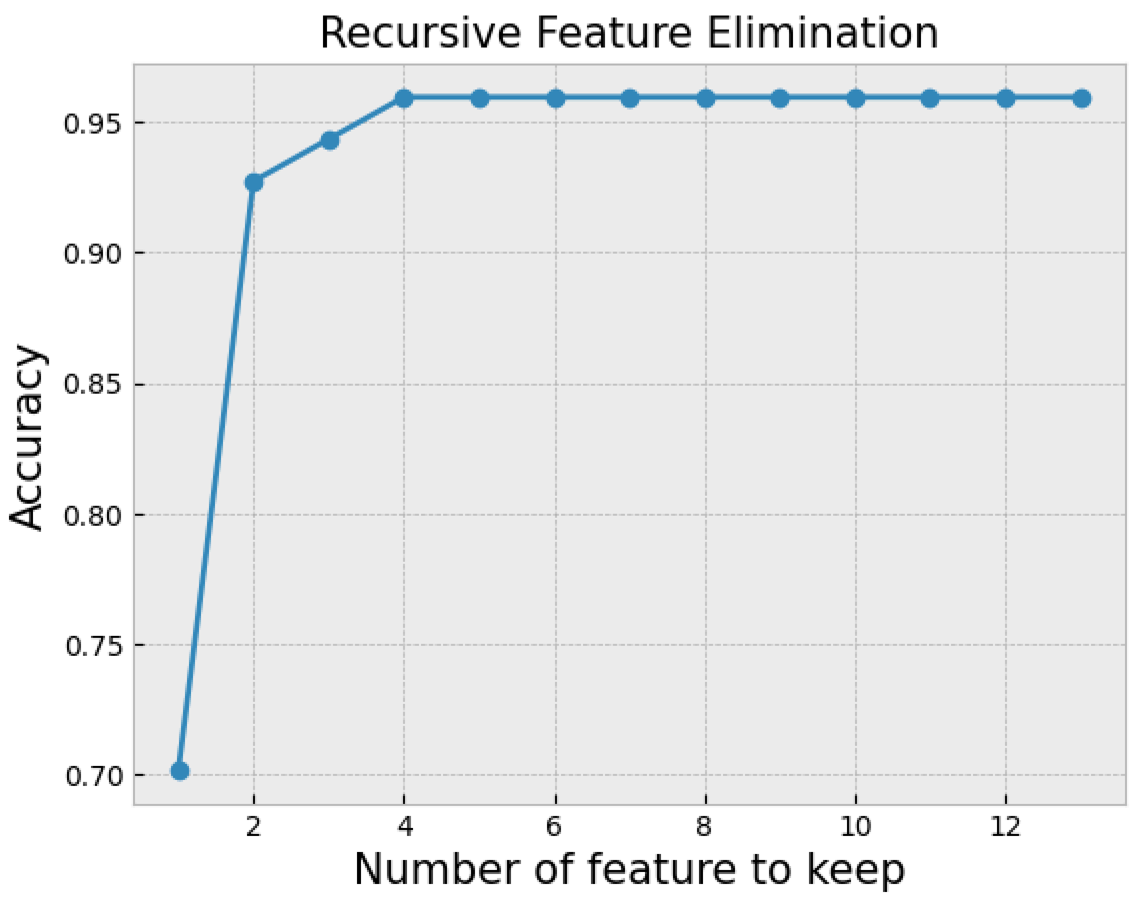
178 rows × 14 columns

In [45]:
```python
# RFE?
```

In [46]:
```python
scores=[]
features_to_keep={}

for i in range(13):
    rfe = RFE(estimator=lr, n_features_to_select=13-i, step=1)
    rfe.fit(X_train, t_train)
    scores+=[rfe.score(X_train, t_train)] # this score should actually be on the va
    features_to_keep[13-i]=df_wine.columns[1:][rfe.support_]

plt.plot(range(1,len(scores)+1)[::-1],scores,'-o')
plt.xlabel('Number of feature to keep',size=15)
plt.ylabel('Accuracy', size=15)
plt.title('Recursive Feature Elimination', size=15);
```



From this plot, we see that the classifier's performance is the same or better when using a smaller subset of features.

In [47]:
```
features_to_keep
```

```
Out[47]: {13: Index(['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash', 'Magnesium',
                'Total phenols', 'Flavanoids', 'Nonflavanoid phenols',
                'Proanthocyanins', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          12: Index(['Alcohol', 'Malic acid', 'Alcalinity of ash', 'Magnesium',
                'Total phenols', 'Flavanoids', 'Nonflavanoid phenols',
                'Proanthocyanins', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          11: Index(['Alcohol', 'Malic acid', 'Magnesium', 'Total phenols', 'Flavanoids',
                'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          10: Index(['Alcohol', 'Malic acid', 'Total phenols', 'Flavanoids',
                'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          9: Index(['Alcohol', 'Malic acid', 'Flavanoids', 'Nonflavanoid phenols',
                'Proanthocyanins', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          8: Index(['Alcohol', 'Malic acid', 'Flavanoids', 'Proanthocyanins',
                'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          7: Index(['Alcohol', 'Malic acid', 'Flavanoids', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          6: Index(['Alcohol', 'Flavanoids', 'Color intensity', 'Hue',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          5: Index(['Alcohol', 'Flavanoids', 'Color intensity',
                'OD280/OD315 of diluted wines', 'Proline'],
               dtype='object'),
          4: Index(['Alcohol', 'Flavanoids', 'Color intensity', 'Proline'], dtype='objec
         t'),
          3: Index(['Flavanoids', 'Color intensity', 'Proline'], dtype='object'),
          2: Index(['Flavanoids', 'Proline'], dtype='object'),
          1: Index(['Proline'], dtype='object')}
```

```
In [48]: rfe = RFE(lr, n_features_to_select=4, step=1)
         rfe.fit(X_train, t_train)
         rfe.score(X_train, t_train), rfe.score(X_test, t_test)
```

```
Out[48]: (0.9596774193548387, 0.3333333333333333)
```

As always, we should apply cross-validation to determine the best set of features to keep:

```
In [49]: from sklearn.model_selection import train_test_split
         from sklearn.pipeline import Pipeline
         from sklearn.model_selection import KFold, ShuffleSplit, StratifiedKFold, GridSearc
         from sklearn.metrics import confusion_matrix, roc_curve, classification_report
```

These are cross-validation tools:

✓ KFold

Cuts the data into K pieces (folds), tests each part.

✓ ShuffleSplit

Randomly shuffles and splits the data many times.

✓ StratifiedKFold

Like KFold but keeps class distribution balanced.

✓ GridSearchCV

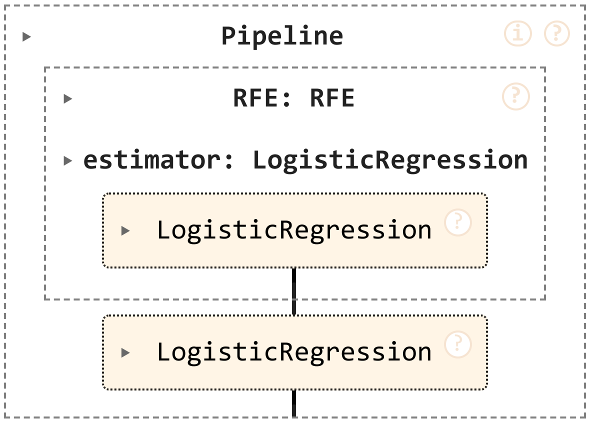
Tries many hyperparameter values and picks the best.

Think of these as ways to test your model many times to avoid overfitting.

In [50]:
```
lr = LogisticRegression(penalty='l1', C=0.1,
                        solver='liblinear')

pipe = Pipeline(steps=[('RFE',RFE(lr)),
                        ('LR',lr)])
pipe
```

Out[50]:



In [51]:
```
# Cross-validation strategy
cv = StratifiedKFold(n_splits=2, shuffle=True)
#sample size is small
# create a single validation/training sets

# Grid Search
Cvals=np.arange(0.01,1,0.01) #L-1 penalty in Logistic Regression
n_features=range(1,14) # number of features to keep

# Parameter Grid Search
param_grid = dict(RFE__n_features_to_select=n_features)
grid_search = GridSearchCV(pipe, param_grid=param_grid, cv=cv, scoring='accuracy')

# Train the model
grid_search.fit(X_train, t_train)
```

```
# Apply the best hyperpameter values
print(grid_search.best_params_)
pipe.set_params(**grid_search.best_params_)

# Train the final model with these hyperparameter values
pipe.fit(X_train,t_train)
y_train=pipe.predict(X_train)
print('\n\nTraining Set Performance')
print('Accuracy Score:', 100*pipe.score(X_train, t_train),'%')
print('Confusion Matrix:')
print(confusion_matrix(t_train,y_train))
print('Performance Report: ')
print(classification_report(t_train,y_train))
print('\n\n')

# Evaluting final model performance in test set
y_test = pipe.predict(X_test)
print('Test Set Performance')
print('Accuracy Score:', 100*pipe.score(X_test, t_test),'%')
print('Confusion Matrix:')
print(confusion_matrix(t_test,y_test))
print('Performance Report: ')
print(classification_report(t_train,y_train))
```

```
{'RFE__n_features_to_select': 3}


Training Set Performance
Accuracy Score: 94.35483870967742 %
Confusion Matrix:
[[38  3  0]
 [ 1 48  1]
 [ 0  2 31]]
Performance Report:
              precision    recall  f1-score   support

           1       0.97      0.93      0.95        41
           2       0.91      0.96      0.93        50
           3       0.97      0.94      0.95        33

    accuracy                           0.94       124
   macro avg       0.95      0.94      0.95       124
weighted avg       0.95      0.94      0.94       124




Test Set Performance
Accuracy Score: 33.33333333333333 %
Confusion Matrix:
[[18  0  0]
 [21  0  0]
 [15  0  0]]
Performance Report:
              precision    recall  f1-score   support

           1       0.97      0.93      0.95        41
           2       0.91      0.96      0.93        50
           3       0.97      0.94      0.95        33

    accuracy                           0.94       124
   macro avg       0.95      0.94      0.95       124
weighted avg       0.95      0.94      0.94       124
```

In [ ]:

```

```

In [ ]:

```

```

Feature selection algorithms in scikit-learn

There are many more feature selection algorithms available via scikit-learn. Those include recursive backward elimination based on feature weights, tree-based methods to select features by importance, and univariate statistical tests. A comprehensive discussion of the different feature selection methods is beyond the scope of this book, but a good summary with illustrative examples can be found here.

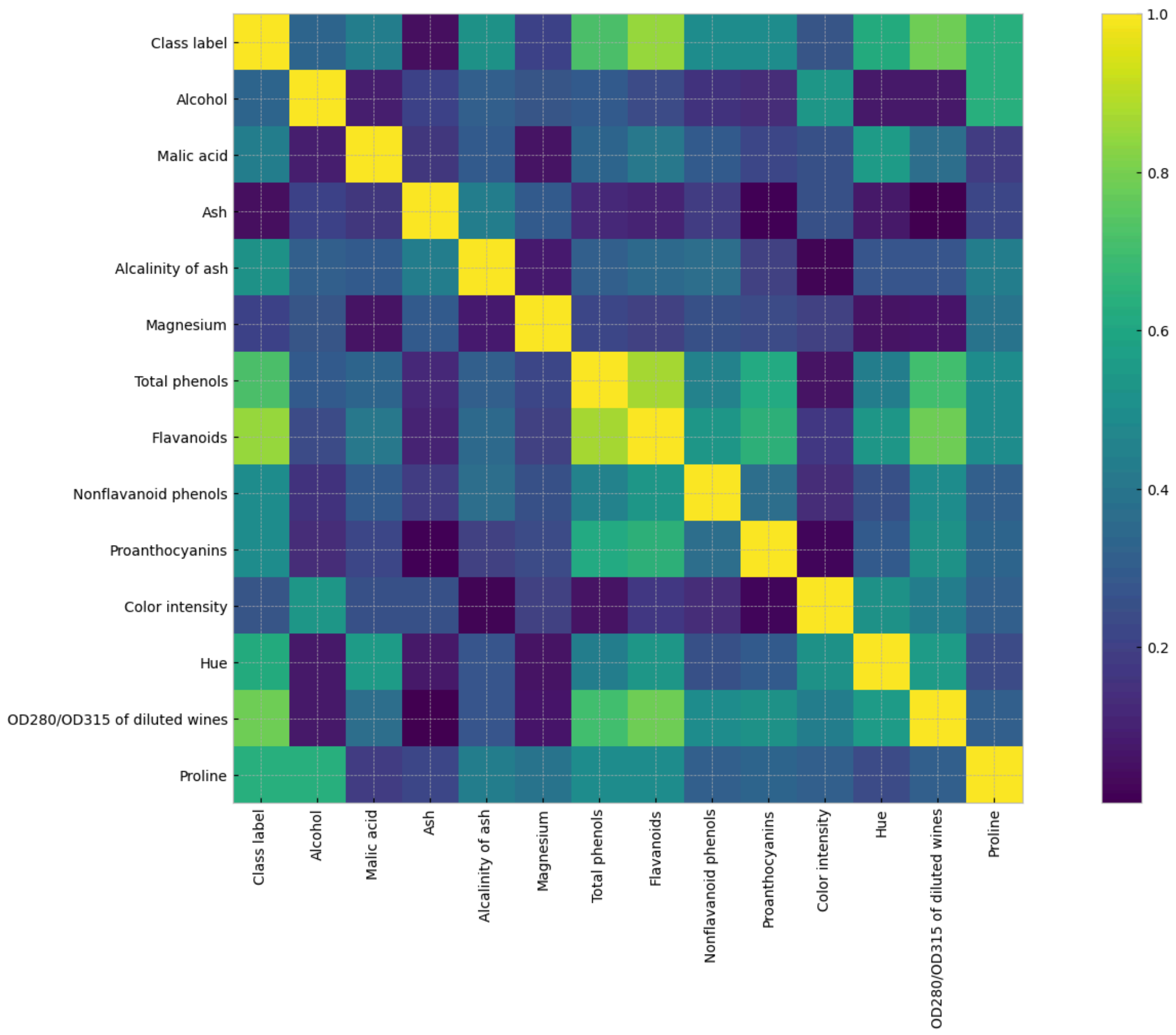
3. Filters: Correlation Coefficient

In [52]:
```
df_wine.corr()
```

Out[52]:

	Class label	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	To phen
Class label	1.000000	-0.328222	0.437776	-0.049643	0.517859	-0.209179	-0.7191
Alcohol	-0.328222	1.000000	0.094397	0.211545	-0.310235	0.270798	0.2891
Malic acid	0.437776	0.094397	1.000000	0.164045	0.288500	-0.054575	-0.3351
Ash	-0.049643	0.211545	0.164045	1.000000	0.443367	0.286587	0.1289
Alcalinity of ash	0.517859	-0.310235	0.288500	0.443367	1.000000	-0.083333	-0.3211
Magnesium	-0.209179	0.270798	-0.054575	0.286587	-0.083333	1.000000	0.2144
Total phenols	-0.719163	0.289101	-0.335167	0.128980	-0.321113	0.214401	1.0000
Flavanoids	-0.847498	0.236815	-0.411007	0.115077	-0.351370	0.195784	0.8645
Nonflavanoid phenols	0.489109	-0.155929	0.292977	0.186230	0.361922	-0.256294	-0.4499
Proanthocyanins	-0.499130	0.136698	-0.220746	0.009652	-0.197327	0.236441	0.6124
Color intensity	0.265668	0.546364	0.248985	0.258887	0.018732	0.199950	-0.0551
Hue	-0.617369	-0.071747	-0.561296	-0.074667	-0.273955	0.055398	0.4336
OD280/OD315 of diluted wines	-0.788230	0.072343	-0.368710	0.003911	-0.276769	0.066004	0.6999
Proline	-0.633717	0.643720	-0.192011	0.223626	-0.440597	0.393351	0.4981

In [53]:
```
plt.figure(figsize=(20,10))
plt.imshow(df_wine.corr().abs(),cmap='viridis')
plt.colorbar()
plt.xticks(range(14),df_wine.columns.to_numpy(),rotation='vertical')
plt.yticks(range(14),df_wine.columns.to_numpy());
```



You want to take the **correlation matrix** from:

```
df_wine.corr()
```

and then **create a scatter/bar plot** from it.

Here are **easy ways** to do each type of plot.

✅ 1. BAR PLOT of Correlation With Target (Easy & Common)

Usually we plot **correlation of each feature with the class label** as a bar chart.

But your class label is *categorical*, so you should not include `"Class label"` inside `corr()`.

✔️ Step 1: compute correlation of features only

```
corr = df_wine.drop("Class label", axis=1).corr()
```

✔️ Step 2: Pick one row/column to plot (example: Alcohol correlations)

```
import matplotlib.pyplot as plt

corr_alcohol = corr["Alcohol"]

corr_alcohol.plot(kind="bar", figsize=(10,5))
plt.title("Correlation of Each Feature With Alcohol")
plt.ylabel("Correlation value")
plt.show()
```

❗ If you want **bar plot of all correlations,** use a heatmap instead

Because a bar chart for 13×13 = 169 values is too big.

✅ 2. SCATTER PLOT Between Two Features

Do this when you want to visualize relationships:

Example: Alcohol vs Color intensity

```
plt.figure(figsize=(6,5))
plt.scatter(df_wine["Alcohol"], df_wine["Color intensity"])
plt.xlabel("Alcohol")
plt.ylabel("Color intensity")
plt.title("Scatter plot: Alcohol vs Color intensity")
plt.show()
```

✅ 3. SCATTER MATRIX (Pairplot)

This creates scatter plots for **all feature pairs**.

```
import seaborn as sns
sns.pairplot(df_wine.drop("Class label", axis=1))
```

✅ 4. CORRELATION HEATMAP (Most common with corr())

This is the standard way to visualize a `df.corr()` matrix.

```
import seaborn as sns
plt.figure(figsize=(12,8))
sns.heatmap(df_wine.corr(), annot=True, cmap="coolwarm")
plt.show()
```

⭐ Tell me which one you want:

1️⃣ Bar plot of correlations with target

2️⃣ Scatter plot between two features

3️⃣ Scatter matrix

4️⃣ Heatmap of correlation matrix

Just tell me the number and I'll give you the exact code!