In [1]:

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

In [2]:

```
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
```

In [3]:

```
from matplotlib import font_manager, rc
import matplotlib as plt

plt.rcParams['axes.unicode_minus'] = False
font_name = font_manager.FontProperties(fname="C:/Windows/Fonts/malgun.ttf").get_name()
rc('font', family=font_name)

plt.rcParams['axes.unicode_minus'] = False
```

In [4]:

```
X = np.array([[0, 1, 0, 1],
              [1, 0, 1, 1],
              [0, 0, 0, 1],
              [1, 0, 1, 0]])
y = np.array([0, 1, 0, 1])
```

In [5]:

```
counts = {}

for label in np.unique(y):
    counts[label] = X[y == label].sum(axis=0)

print("특성 카운트:₩n{}".format(counts))
```

```
특성 카운트:
{0: array([0, 1, 0, 2]), 1: array([2, 0, 2, 1])}
```

복잡도 제어하기

In [7]:

```
from sklearn.tree import DecisionTreeClassifier

cancer = load_breast_cancer()

X_train, X_test, y_train, y_test = train_test_split(
    cancer.data, cancer.target, stratify=cancer.target, random_state = 42)

tree = DecisionTreeClassifier(random_state=0)
tree.fit(X_train, y_train)

print("훈련 세트 정확도: {:.3f}".format(tree.score(X_train, y_train)))
print("테스트 세트 정확도: {:.3f}".format(tree.score(X_test, y_test)))
```

```
훈련 세트 정확도: 1.000
테스트 세트 정확도: 0.937
```

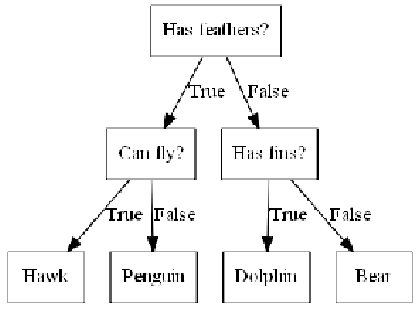
In [8]:

```
tree = DecisionTreeClassifier(max_depth=4, random_state=0)
tree.fit(X_train, y_train)

print("훈련 세트 정확도: {:.3f}".format(tree.score(X_train, y_train)))
print("테스트 세트 정확도: {:.3f}".format(tree.score(X_test, y_test)))
```

```
훈련 세트 정확도: 0.988
테스트 세트 정확도: 0.951
```

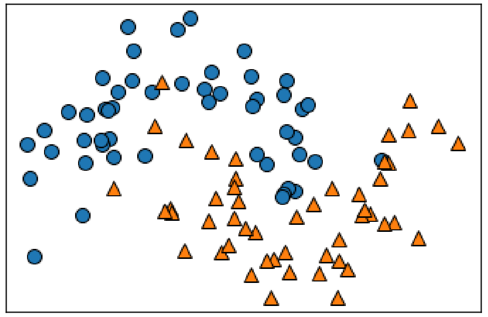
In [12]:

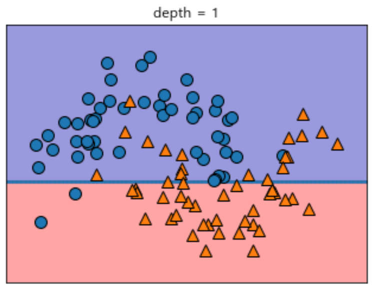
```
mglearn.plots.plot_animal_tree()
```

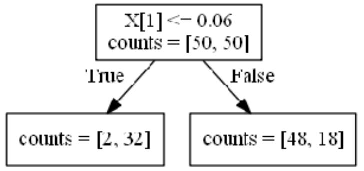


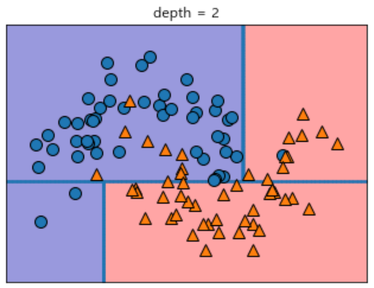
In [13]:

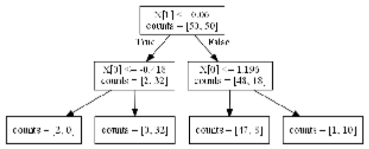
```
mglearn.plots.plot_tree_progressive()
```

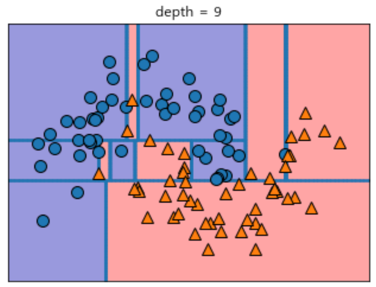


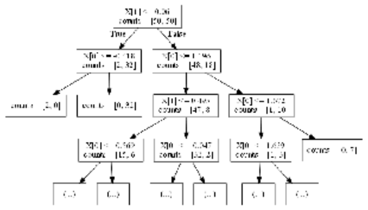










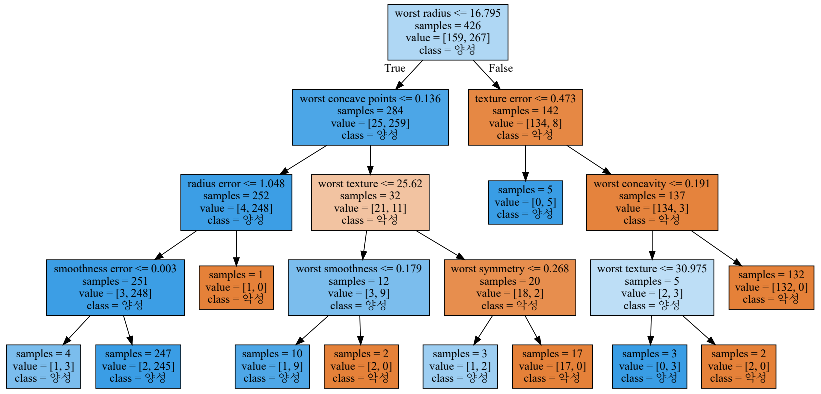


In [9]:

```
from sklearn.tree import export_graphviz
export_graphviz(tree, out_file="tree.dot", class_names=["악성", "양성"], feature_names=cancer.fe
ature_names, impurity=False,
                filled=True)
```

In [11]:

```
import graphviz

with open("tree.dot", encoding="utf-8") as f:
    dot_graph = f.read()

display(graphviz.Source(dot_graph))
```



특성 중요도

In [14]:

```
print("특성 중요도:\n", tree.feature_importances_)
```

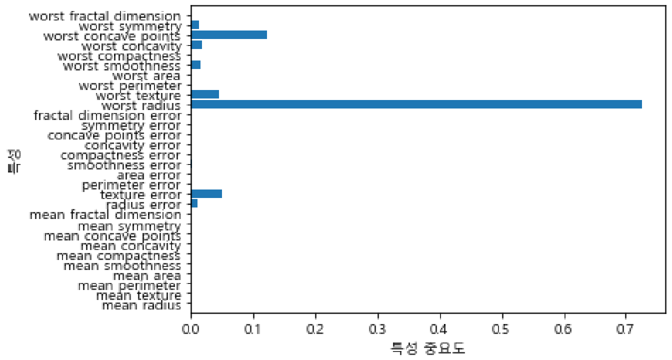
```
특성 중요도:
 [0.         0.         0.         0.         0.         0.
 0.         0.         0.         0.         0.01019737 0.04839825
 0.         0.         0.0024156  0.         0.         0.
 0.         0.         0.72682851 0.0458159  0.         0.
 0.0141577  0.         0.018188   0.1221132  0.01188548 0.        ]
```

In [19]:

```
import matplotlib.pyplot as plt
```

In [20]:

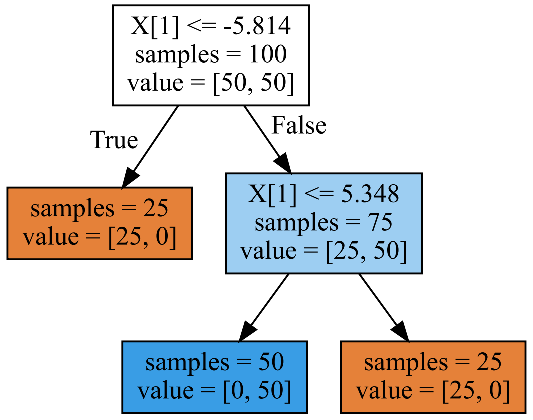
```
def plot_feature_importances_cancer(model):
    n_features = cancer.data.shape[1]
    plt.barh(range(n_features), model.feature_importances_, align='center')
    plt.yticks(np.arange(n_features), cancer.feature_names)
    plt.xlabel("특성 중요도")
    plt.ylabel("특성")
    plt.ylim(-1, n_features)

plot_feature_importances_cancer(tree)
```

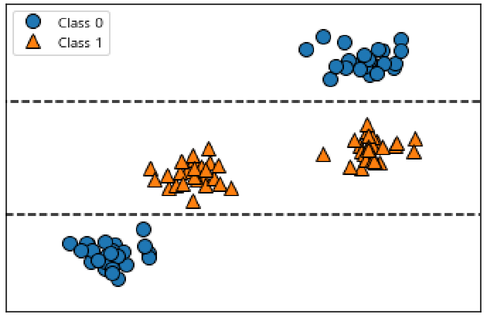


In [23]:

```
tree = mglearn.plots.plot_tree_not_monotone()
display(tree)
```

```
Feature importances: [0. 1.]
```





In [27]:

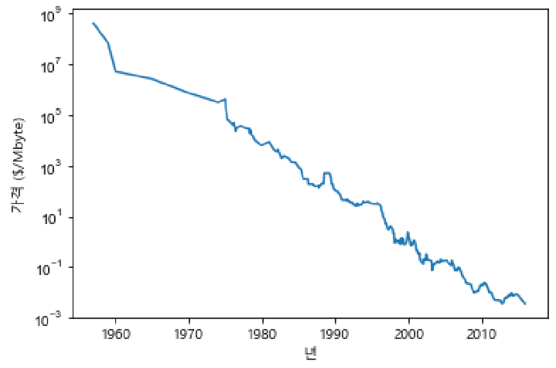
```
import os
```

In [28]:

```
ram_prices = pd.read_csv(os.path.join(mglearn.datasets.DATA_PATH, "ram_price.csv"))

plt.yticks(fontname = "Arial")
plt.semilogy(ram_prices.date, ram_prices.price)
plt.xlabel("년")
plt.ylabel("가격 ($/Mbyte)")
```

Out[28]:

```
Text(0, 0.5, '가격 ($/Mbyte)')
```



In [30]:

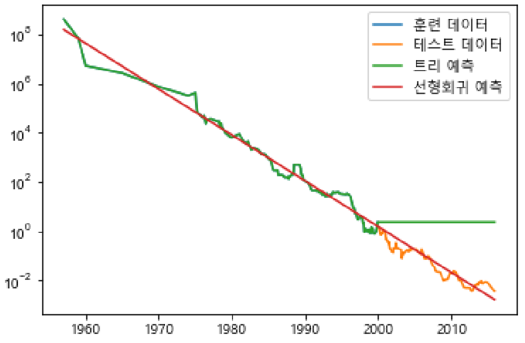
```
from sklearn.tree import DecisionTreeRegressor
from sklearn.linear_model import LinearRegression

data_train = ram_prices[ram_prices.date < 2000]
data_test = ram_prices[ram_prices.date >= 2000]

X_train = data_train.date[:, np.newaxis]
y_train = np.log(data_train.price)

tree = DecisionTreeRegressor().fit(X_train, y_train)
linear_reg = LinearRegression().fit(X_train, y_train)

X_all = ram_prices.date[:, np.newaxis]

pred_tree = tree.predict(X_all)
pred_lr = linear_reg.predict(X_all)

price_tree = np.exp(pred_tree)
price_lr = np.exp(pred_lr)
```

In [31]:

```
plt.yticks(fontname = "Arial")
plt.semilogy(data_train.date, data_train.price, label="훈련 데이터")
plt.semilogy(data_test.date, data_test.price, label="테스트 데이터")
plt.semilogy(ram_prices.date, price_tree, label="트리 예측")
plt.semilogy(ram_prices.date, price_lr, label="선형회귀 예측")
plt.legend()
```

Out[31]:

```
<matplotlib.legend.Legend at 0x236ba5ef550>
```



랜덤 포레스트

In [33]:

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.datasets import make_moons

X, y = make_moons(n_samples=100, noise=0.25, random_state=3)
X_train, X_test, y_train, y_test = train_test_split(
    X, y, stratify=y, random_state=42)

forest = RandomForestClassifier(n_estimators=5, random_state=2)
forest.fit(X_train, y_train)
```

Out[33]:

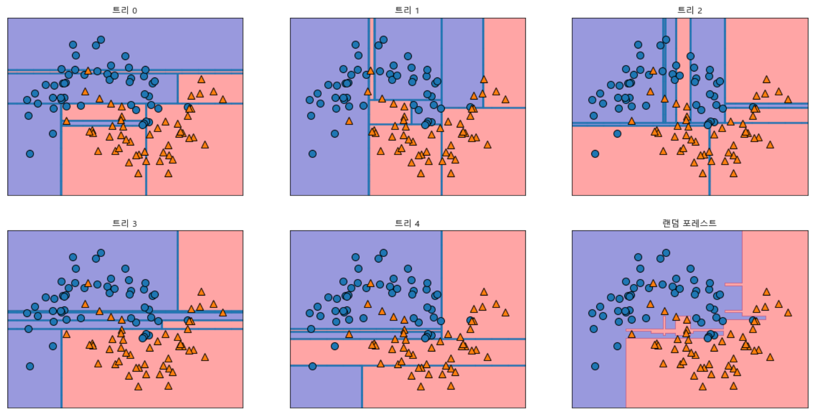
```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
            max_depth=None, max_features='auto', max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, n_estimators=5, n_jobs=None,
            oob_score=False, random_state=2, verbose=0, warm_start=False)
```

In [34]:

```
fig, axes = plt.subplots(2, 3, figsize=(20, 10))

for i, (ax, tree) in enumerate(zip(axes.ravel(), forest.estimators_)):
    ax.set_title("트리 {}".format(i))
    mglearn.plots.plot_tree_partition(X, y, tree, ax=ax)

mglearn.plots.plot_2d_separator(forest, X, fill=True, ax=axes[-1, -1], alpha=.4)
axes[-1, -1].set_title("랜덤 포레스트")
mglearn.discrete_scatter(X[:, 0], X[:, 1], y)
```

Out[34]:

```
[<matplotlib.lines.Line2D at 0x236bcad49e8>,
 <matplotlib.lines.Line2D at 0x236bf15ff98>]
```



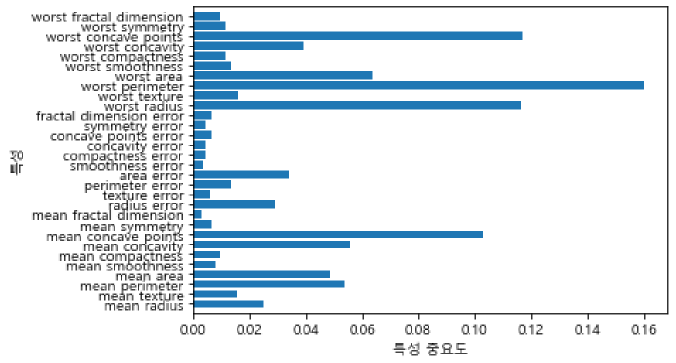
In [35]:

```
X_train, X_test, y_train, y_test = train_test_split(
    cancer.data, cancer.target, random_state=0)

forest = RandomForestClassifier(n_estimators=100, random_state=0)
forest.fit(X_train, y_train)

print("훈련 세트 정확도: {:.3f}".format(forest.score(X_train, y_train)))
print("테스트 세트 정확도: {:.3f}".format(forest.score(X_test, y_test)))
```

```
훈련 세트 정확도: 1.000
테스트 세트 정확도: 0.972
```

In [36]:

```
plot_feature_importances_cancer(forest)
```



In [ ]:

```
```