(Edited by David I. Inouye for classroom use) The text has been removed and the code has been edited and reordered as seemed appropriate.

This notebook contains an excerpt from the [Python Data Science Handbook (http://shop.oreilly.com/product/0636920034919.do)](http://shop.oreilly.com/product/0636920034919.do) by Jake VanderPlas; the content is available [on GitHub (https://github.com/jakevdp/PythonDataScienceHandbook)](https://github.com/jakevdp/PythonDataScienceHandbook).

In [24]:

```
%matplotlib inline
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns; sns.set()
from sklearn.decomposition import PCA
```

PCA for visualization: Hand-written digits

In [25]:

```
from sklearn.datasets import load_digits
digits = load_digits()
digits.data.shape
X = digits.data
X = X - np.mean(X, axis=0)
y = digits.target
print(X.shape)
```

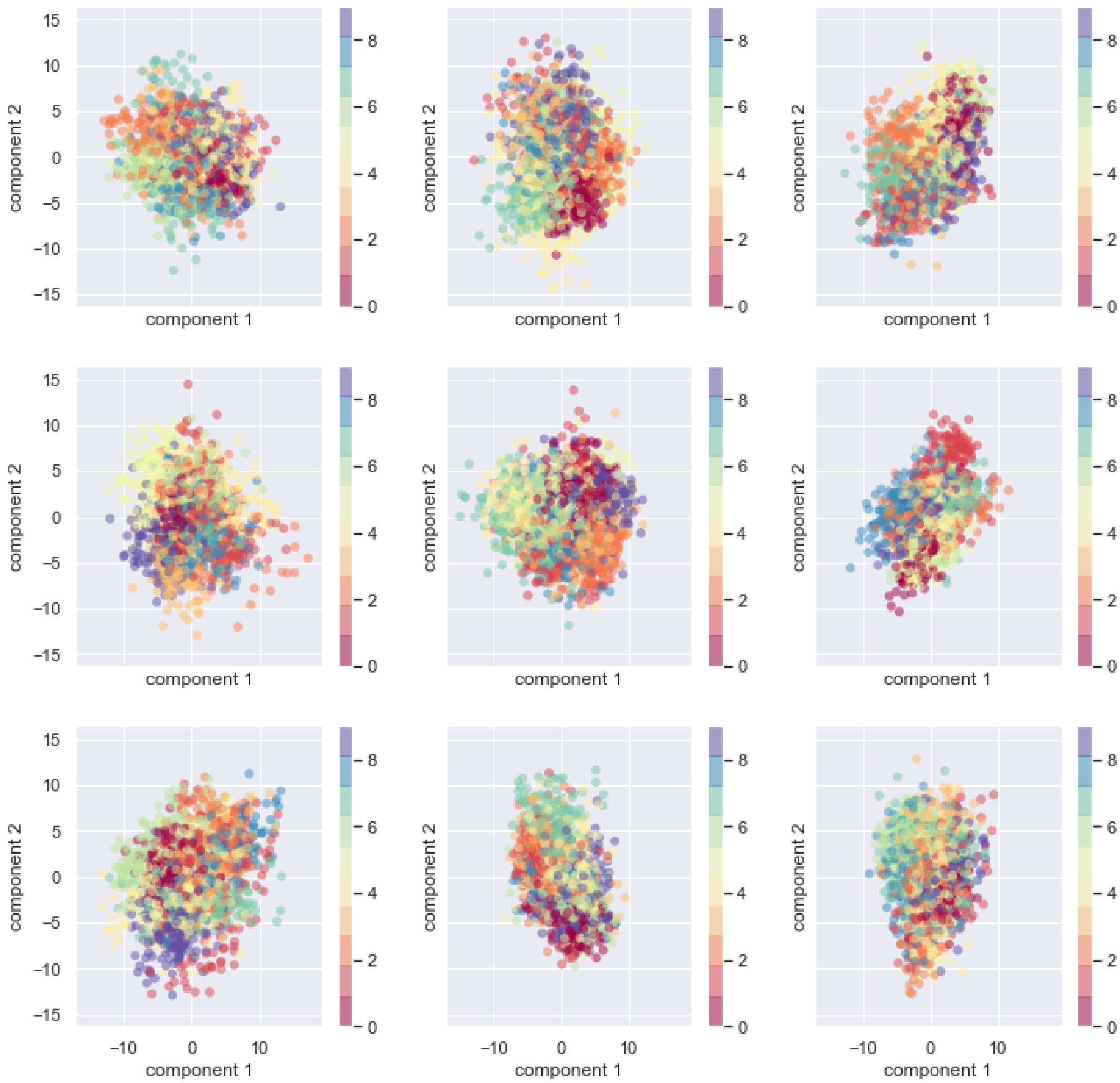
```
(1797, 64)
```

Let's try some random projections of the data

In [26]:

```
def show_projected(projected, y, ax=None):
    if ax is None:
        ax = plt.gca()
    sc = ax.scatter(projected[:, 0], projected[:, 1],
                c=y, edgecolor='none', alpha=0.5,
                cmap=plt.cm.get_cmap('Spectral', 10))
    ax.set_xlabel('component 1')
    ax.set_ylabel('component 2')
    plt.colorbar(sc, ax=ax)
    return sc
```

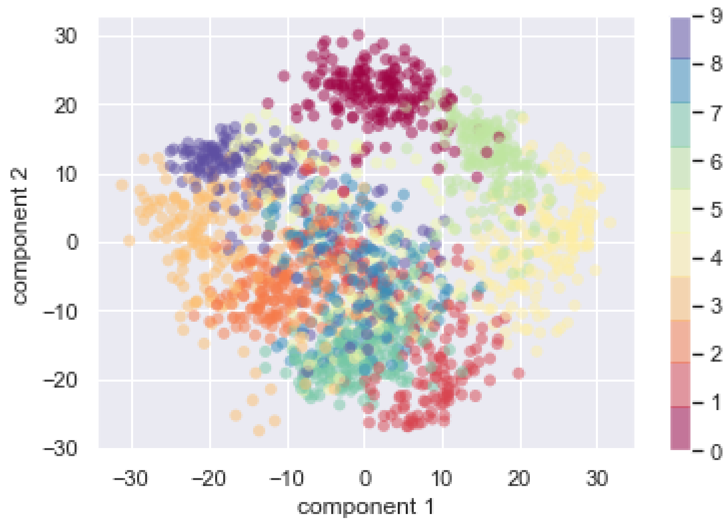
In [27]:
```python
rng = np.random.RandomState(0)
n_rows, n_cols = 3, 3
fig, axes = plt.subplots(n_rows, n_cols, figsize=(12, 12), sharex=True, sharey=True)
for ax in axes.ravel():
    # Generate random projection matrix
    A = rng.randn(X.shape[1], 2)
    Q, _ = np.linalg.qr(A)
    Z = np.dot(X, Q)
    sc = show_projected(Z, y, ax=ax)
#plt.colorbar(sc)
```



Now let's use Principal Component Analysis (PCA)

```
In [28]: pca = PCA(2)  # project from 64 to 2 dimensions
projected = pca.fit_transform(digits.data)
print(digits.data.shape)
print(projected.shape)

plt.scatter(projected[:, 0], projected[:, 1],
            c=digits.target, edgecolor='none', alpha=0.5,
            cmap=plt.cm.get_cmap('Spectral', 10))
plt.xlabel('component 1')
plt.ylabel('component 2')
plt.colorbar();
```

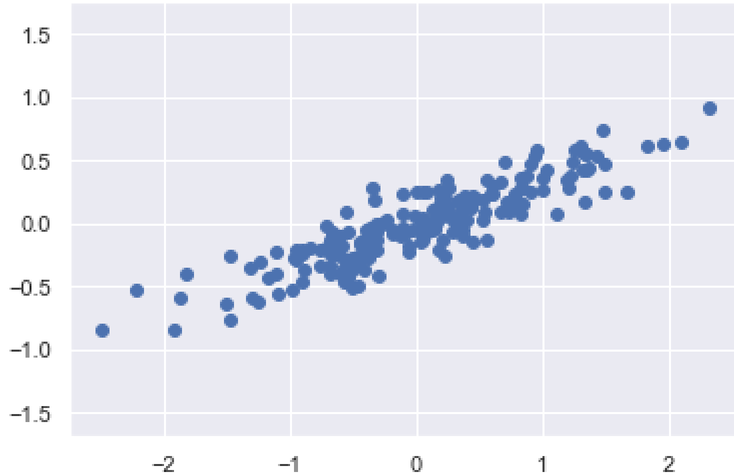
```
(1797, 64)
(1797, 2)
```



Notice that the limits of the component are [-30, 30] rather than [-10, 10]

Minimum reconstruction error / dimensionality reduction viewpoint of PCA

In [30]:
```
rng = np.random.RandomState(1)
X = np.dot(rng.rand(2, 2), rng.randn(2, 200)).T
plt.scatter(X[:, 0], X[:, 1])
plt.axis('equal');
```



In [32]:
```
pca = PCA(n_components=1)
pca.fit(X)
X_pca = pca.transform(X)
print("original shape:    ", X.shape)
print("transformed shape:", X_pca.shape)

X_new = pca.inverse_transform(X_pca)
plt.scatter(X[:, 0], X[:, 1], alpha=0.8, label='Original')
plt.scatter(X_new[:, 0], X_new[:, 1], alpha=0.8, label='Dimension Reduce
d')
plt.axis('equal');
plt.legend()
```

```
original shape:    (200, 2)
transformed shape: (200, 1)
```

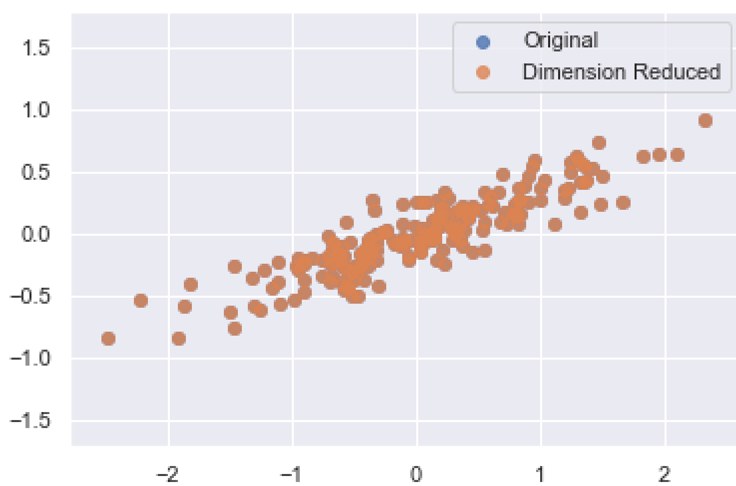
Out[32]: <matplotlib.legend.Legend at 0x1a1ff00ef0>

If we keep all components, then we get perfect reconstruction

In [33]:
```
pca = PCA(n_components=2)
pca.fit(X)
X_pca = pca.transform(X)
print("original shape:   ", X.shape)
print("transformed shape:", X_pca.shape)

X_new = pca.inverse_transform(X_pca)
plt.scatter(X[:, 0], X[:, 1], alpha=0.8, label='Original')
plt.scatter(X_new[:, 0], X_new[:, 1], alpha=0.8, label='Dimension Reduce
d')
plt.axis('equal');
plt.legend()
```

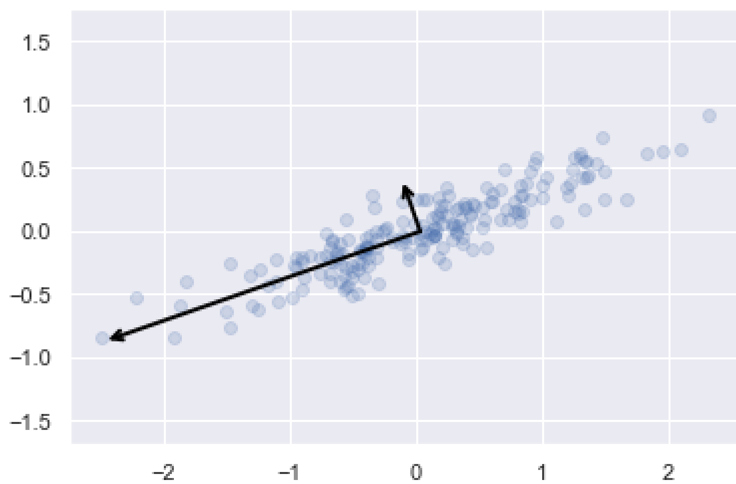
```
original shape:    (200, 2)
transformed shape: (200, 2)
```

Out[33]: `<matplotlib.legend.Legend at 0x1a217f0208>`



Maximum variance of projected data viewpoint of PCA

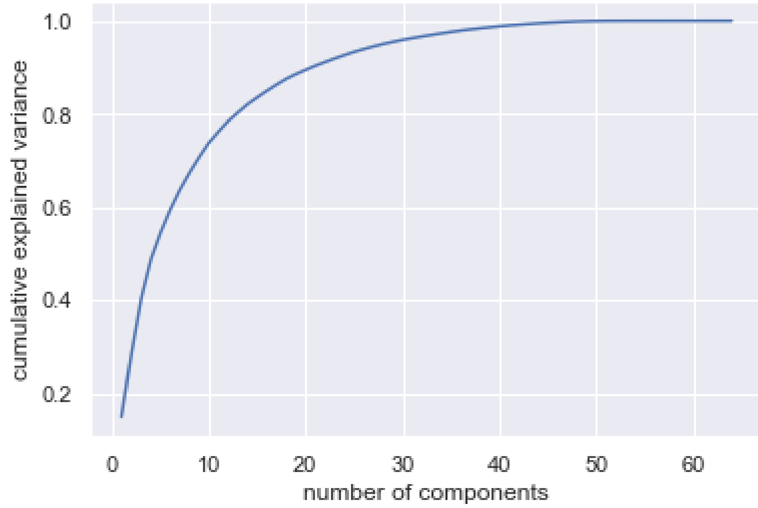
In [31]:
```
pca = PCA(n_components=2)
pca.fit(X)

#print(pca.components_)
#print(pca.explained_variance_)

def draw_vector(v0, v1, ax=None):
    ax = ax or plt.gca()
    arrowprops=dict(arrowstyle='->',
                    linewidth=2,
                    shrinkA=0, shrinkB=0, color='black')
    ax.annotate('', v1, v0, arrowprops=arrowprops)

# plot data
plt.scatter(X[:, 0], X[:, 1], alpha=0.2)
for length, vector in zip(pca.explained_variance_, pca.components_):
    v = vector * 3 * np.sqrt(length)
    draw_vector(pca.mean_, pca.mean_ + v)
plt.axis('equal');
```



Amount of variance explained (first components are most interesting)

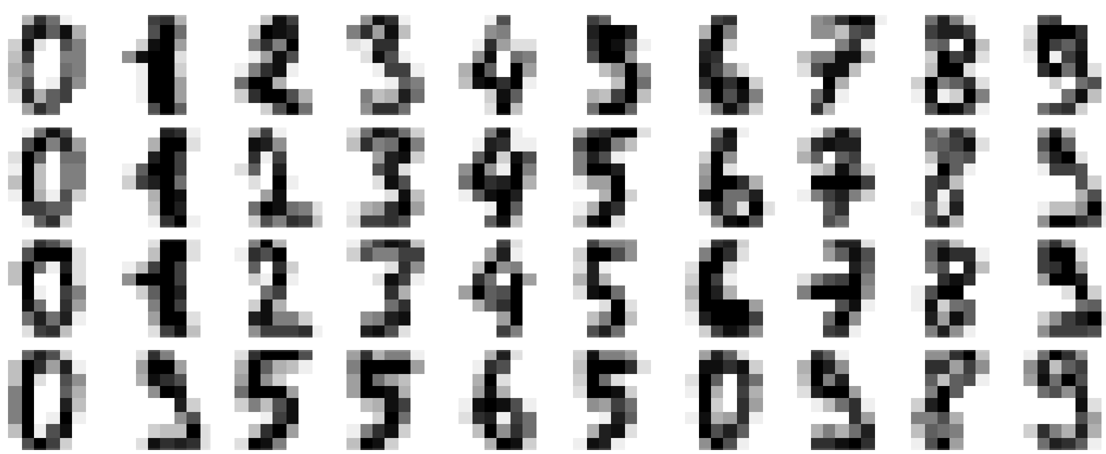
(On digits data)

In [23]:
```
pca = PCA().fit(digits.data)
plt.plot(np.arange(64)+1, np.cumsum(pca.explained_variance_ratio_))
plt.xlabel('number of components')
plt.ylabel('cumulative explained variance');
```

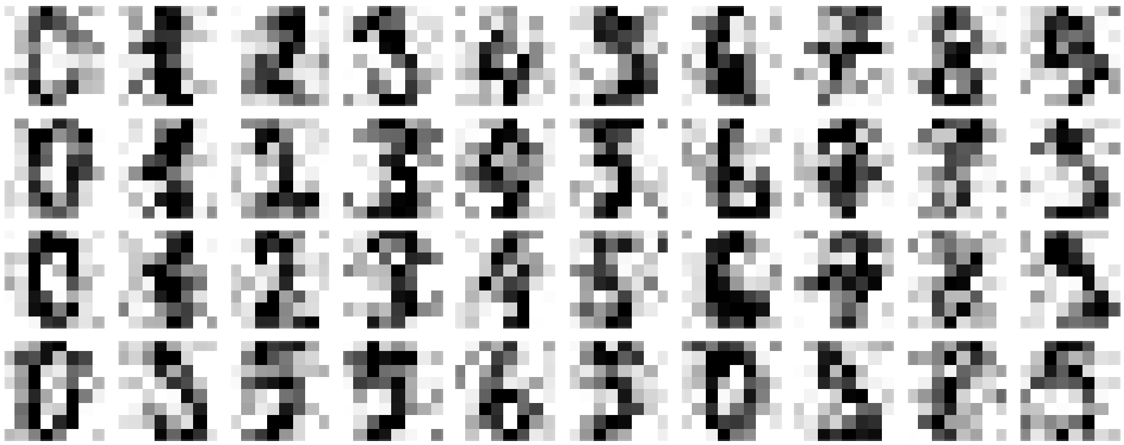


Example: PCA as Noise Filtering

In [6]:
```
def plot_digits(data):
    fig, axes = plt.subplots(4, 10, figsize=(10, 4),
                             subplot_kw={'xticks':[], 'yticks':[]},
                             gridspec_kw=dict(hspace=0.1, wspace=0.1))
    for i, ax in enumerate(axes.flat):
        ax.imshow(data[i].reshape(8, 8),
                  cmap='binary', interpolation='nearest',
                  clim=(0, 16))
plot_digits(digits.data)
```

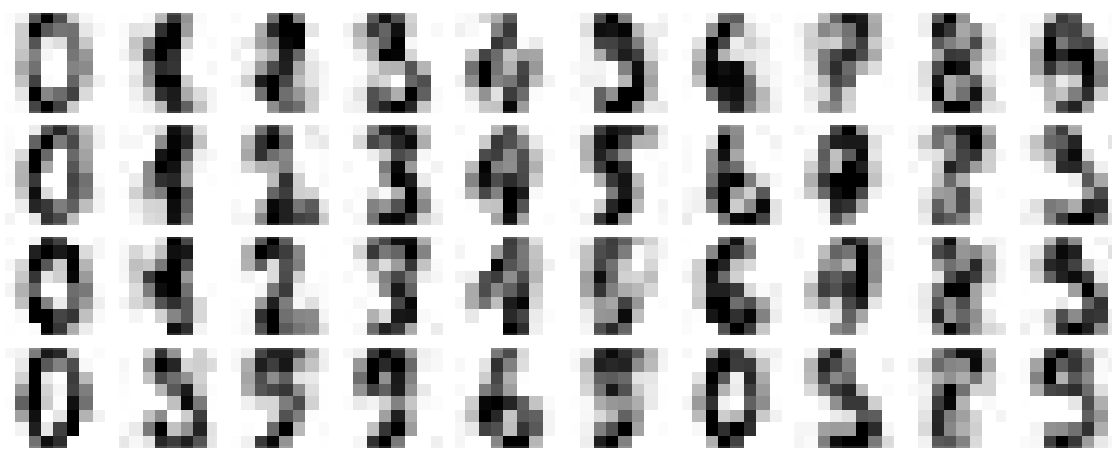


In [7]:
```
np.random.seed(42)
noisy = np.random.normal(digits.data, 4)
plot_digits(noisy)
```



In [8]:
```
pca = PCA(12).fit(noisy)
print(noisy.shape)
scores = pca.transform(noisy)
print(scores.shape)
filtered = pca.inverse_transform(scores)
print(filtered.shape)
plot_digits(filtered)
```

```
(1797, 64)
(1797, 12)
(1797, 64)
```



Example: Eigenfaces

In [34]:
```
from sklearn.datasets import fetch_lfw_people
faces = fetch_lfw_people(min_faces_per_person=60)
print(faces.target_names)
print(faces.images.shape)
```

```
['Ariel Sharon' 'Colin Powell' 'Donald Rumsfeld' 'George W Bush'
 'Gerhard Schroeder' 'Hugo Chavez' 'Junichiro Koizumi' 'Tony Blair']
(1348, 62, 47)
```

In [35]:
```
pca = PCA(n_components=150, svd_solver='randomized', whiten=True)
pca.fit(faces.data)
```

Out[35]:
```
PCA(copy=True, iterated_power='auto', n_components=150, random_state=No
ne,
    svd_solver='randomized', tol=0.0, whiten=True)
```

Eigenfaces are the principal components of the faces dataset

In [36]:
```
fig, axes = plt.subplots(3, 8, figsize=(9, 4),
                         subplot_kw={'xticks':[], 'yticks':[]},
                         gridspec_kw=dict(hspace=0.1, wspace=0.1))
for i, ax in enumerate(axes.flat):
    ax.imshow(pca.components_[i].reshape(62, 47), cmap='bone')
```

In [37]:
```
# Compute the components and projected faces
scores = pca.transform(faces.data)
projected = pca.inverse_transform(scores)
```

In [38]:
```python
# Plot the results
fig, ax = plt.subplots(2, 10, figsize=(10, 2.5),
                       subplot_kw={'xticks':[], 'yticks':[]},
                       gridspec_kw=dict(hspace=0.1, wspace=0.1))
for i in range(10):
    ax[0, i].imshow(faces.data[i].reshape(62, 47), cmap='binary_r')
    ax[1, i].imshow(projected[i].reshape(62, 47), cmap='binary_r')

ax[0, 0].set_ylabel('full-dim\ninput')
ax[1, 0].set_ylabel('150-dim\nreconstruction');
```