Single-sample PCA

In this notebook, we apply PCA to single audio samples. We'll use the following pipelines for analyzing single samples:

```
In [1]: | %matplotlib inline
       %load_ext autoreload
       %autoreload 2
       from pathlib import Path
       # Enter the locations of the sample directories
       CELLO_PATH = Path("/home/lukas/BA/philharmonia-samples/cello")
       GUITAR PATH = Path("/home/lukas/BA/philharmonia-samples/guitar")
       # Output directories for figures and wavfiles
       GFX_PATH = Path("/home/lukas/BA/report/gfx/")
       WAVS_PATH = Path("/home/lukas/BA/report/wavs/")
       # Whether to generate graphs for all samples. Image files will be
       # written to the dataset directories.
       GENERATE_ALL_GRAPHS = False
In [2]: # Initialization
       import pandas as pd
       import numpy as np
       import matplotlib.pyplot as plt
       from sklearn.decomposition import PCA
       import librosa
       import pya
       import random
       import principal_harmonics as ph
       for path in [GFX_PATH, WAVS_PATH]:
           if path.exists() and not path.is_dir():
               raise NotADirectoryError(path)
           if not path.exists():
               path.mkdir()
In [3]: | def plot_single_pca(coefs, pipeline, fig, n_vecs,
                           filename, logscale_explained_variance=False):
           fig.suptitle(filename)
           left_fig, right_fig = fig.subfigures(1, 2)
           var_ax, vec_ax = left_fig.subplots(2, 1)
           alpha_axs = right_fig.subplots(n_vecs, 1, sharex=True)
           trans = pipeline.fit_transform(np.abs(coefs))
           pca = pipeline[-1]
           var_ax.set_title("Explained Variance Ratio")
           var_ax.plot(pca.explained_variance_ratio_, ds='steps-post')
           var_ax.set_xlabel("Eigenvector index $i$")
           var_ax.set_ylabel("$\lambda_i / \sum_k \lambda_k$")
           if logscale_explained_variance:
               var_ax.semilogy()
               var_ax.set_ylim(bottom=1e-7)
           vec_ax.set_title("Eigenvectors")
           vec_ax.set_xlabel("Vector component index $j$")
           vec_ax.set_ylabel("$u_{i,j}$")
           for i, vec in enumerate(pca.components_[:n_vecs]):
               vec_ax.plot(vec, label=f'$u_{i}$', ds='steps-post')
           vec_ax.legend(loc='right')
           left_fig.align_ylabels()
           alpha_axs[0].set_title("Resulting control parameters")
           alpha_axs[-1].set_xlabel("Frame index $n$")
           for i, (alpha, color, ax) in enumerate(zip(trans.T[:n_vecs],
                                                     colors,
                                                     alpha_axs)):
               ax.plot(alpha, color=color)
               ax.set_ylabel(f'$\\alpha_{i}[n]$')
           right_fig.align_ylabels()
```

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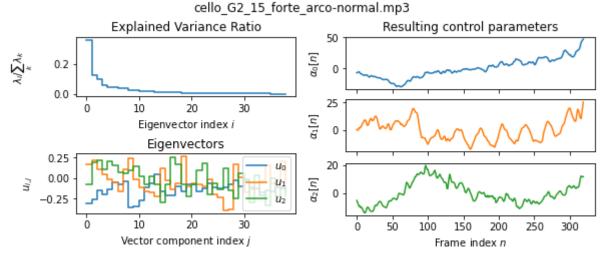
Let's try the Cello first:

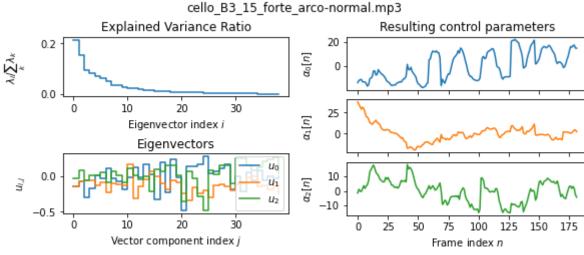
```
In [5]: cello_df = ph.dataset.open_dataset(CELLO_PATH)
# let's exclude the degraded samples (See section 3.3 of the report)
cello_df = cello_df[cello_df.midi > librosa.note_to_midi('D2')]
guitar_df = ph.dataset.open_dataset(GUITAR_PATH)

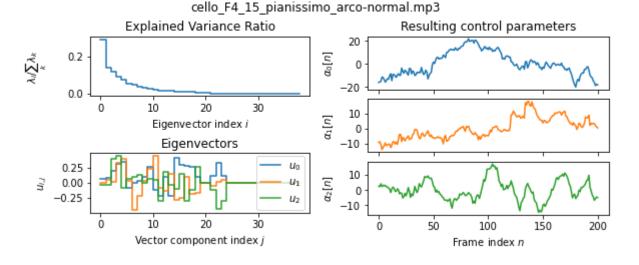
In [6]: if GENERATE_ALL_GRAPHS:
    for filename, row in cello_df.iterrows():
        fig = plt.figure(figsize=(8.2, 3.5), constrained_layout=True)
        plot_single_pca(row.coefs, cello_single_pipeline, fig, 3, filename)
        plt.savefig(CELLO_PATH / (filename + '-SINGLE_PCA.png'))
        plt.close()
```

Let us first look at some randomly chosen samples to get a gauge of what the analysis results will look like:

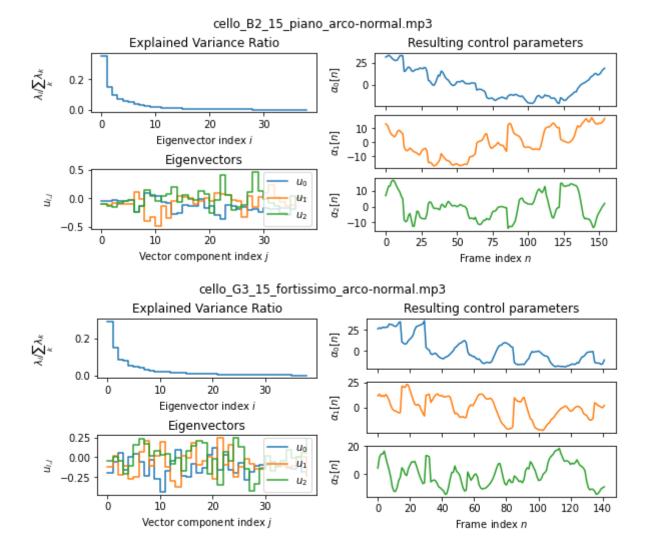
```
for filename, row in cello_df.sample(n=5, random_state=42).iterrows():
    fig = plt.figure(figsize=(8.2, 3.5), constrained_layout=True)
    plot_single_pca(row.coefs, cello_single_pipeline, fig, 3, filename)
```







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Notice that the first control parameter α_0 behaves very differently among the analyses. Let's confirm this by looking at two samples that are perceptually very close to each other:

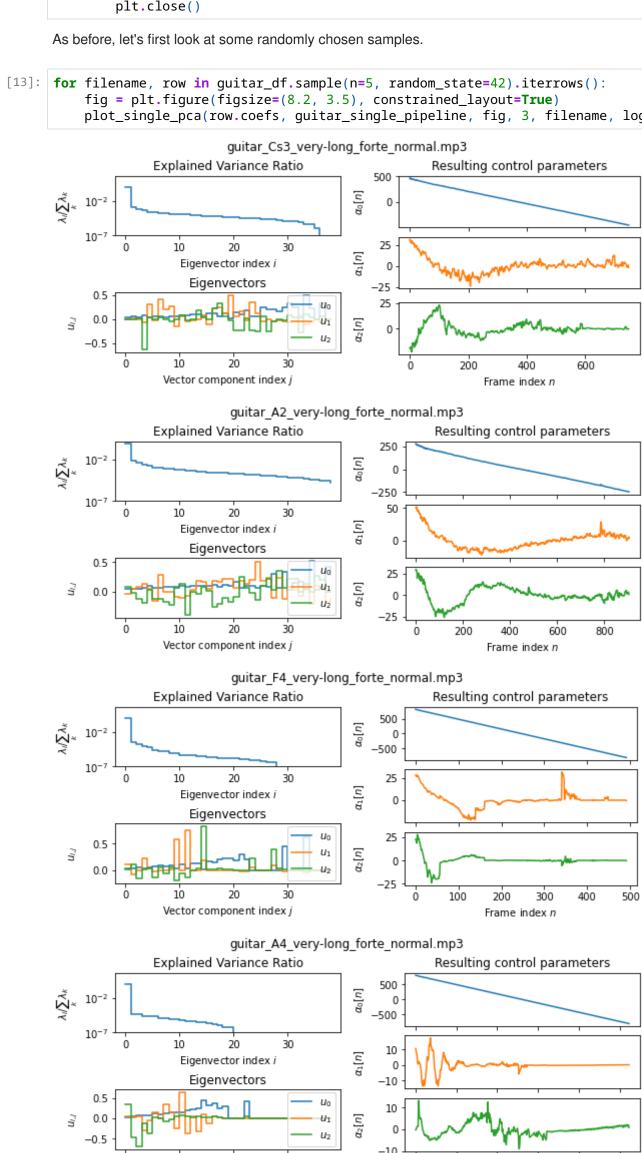
```
In [8]: | %%capture
        fnames = ['cello_G3_15_fortissimo_arco-normal.mp3', 'cello_Gs3_15_fortissimo_arco-normal.mp3']
         for i, fname in enumerate(fnames):
            coefs = cello_df.loc[fname].coefs
            fig = plt.figure(figsize=(8.2,3.5), constrained_layout=True)
            plot_single_pca(coefs, cello_single_pipeline, fig, 3, fname)
            plt.savefig(GFX_PATH / f'3-cello-single-{i}.eps')
In [9]: cello_g3_source_asig = pya.Asig(str(cello_df.loc['cello_G3_15_fortissimo_arco-normal.mp3'].clipped_wav))
        cello_g3_source_asig.save_wavfile(WAVS_PATH / 'ch4_cello_G3_15_fortissimo_arco-normal_clipped.wav')
        cello_gs3_source_asig = pya.Asig(str(cello_df.loc['cello_Gs3_15_fortissimo_arco-normal.mp3'].clipped_wav))
        cello_g3_source_asig.save_wavfile(WAVS_PATH / 'ch4_cello_Gs3_15_fortissimo_arco-normal_clipped.wav')
        # cello_g3_source_asig.play()
         # cello_gs3_source_asig.play()
        Asig('/home/lukas/BA/philharmonia-samples/cello/cello_G3_15_fortissimo_arco-normal_clipped.wav'): 1 x 80384 @ 44100
Out[9]:
        Hz = 1.823s cn=['0']
In [10]: def make_axis_asig_oscillating(mean, ui, scale, note, f=0.5) -> pya.Asig:
            ts = np.linspace(0, 4, 4*int(44100 // 256))
            dbs = mean.reshape(1, -1) + ui.reshape(1, -1) * scale * np.sin(2*np.pi * ts * f).reshape(-1, 1)
            ampls = pya.dbamp(dbs)
             #ampls = ampls / ampls.sum(axis=1).reshape(-1, 1) * 0.1
            return ph.pvoc.additive_resynth(librosa.note_to_hz(note), ampls)
        def make all axes asigs(pipeline, df, fname, note, output prefix):
            trans = pipeline.fit_transform(np.abs(df.loc[fname].coefs))
            pca = pipeline[-1]
            mean = pca.mean_
            asigs = []
            for i in range(3):
                 ui = pca.components_[i]
                 scale = 2*np.std(trans[:, i])
                 asig = make_axis_asig_oscillating(mean, ui, scale, note)
                 asig.save_wavfile(str(WAVS_PATH / f'{output_prefix}_u{i}.wav'), dtype='float32')
                 asigs.append(asig)
            return asigs
        cello_g3_asigs = make_all_axes_asigs(cello_single_pipeline, cello_df, fnames[0], 'G3', 'ch4_cello_single_pca_G3')
        # for easier comparison, we'll use G3 as the pitch for both resyntheses
        cello_gs3_asigs = make_all_axes_asigs(cello_single_pipeline, cello_df, fnames[1], 'G3', 'ch4_cello_single_pca_Gs3')
        (1, 1) (1, 1) (688, 39)
        (1, 1) (1, 1) (688, 39)
        (1, 1) (1, 1) (688, 39)
        (1, 1) (1, 1) (688, 39)
        (1, 1) (1, 1) (688, 39)
        (1, 1) (1, 1) (688, 39)
In [11]: | # cello_g3_asigs[0].play()
```

Moving on to the guitar

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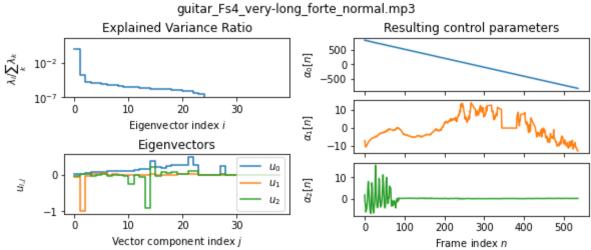
```
In [12]: if GENERATE_ALL_GRAPHS:
             for filename, row in guitar_df.iterrows():
                 fig = plt.figure(figsize=(8.2, 3.5), constrained_layout=True)
                 plot_single_pca(row.coefs, guitar_single_pipeline, fig, 3, filename, logscale_explained_variance=True)
                plt.savefig(GUITAR_PATH / (filename + '-SINGLE_PCA.png'))
                plt.close()
```

```
In [13]: | for filename, row in guitar_df.sample(n=5, random_state=42).iterrows():
             fig = plt.figure(figsize=(8.2, 3.5), constrained_layout=True)
            plot_single_pca(row.coefs, guitar_single_pipeline, fig, 3, filename, logscale_explained_variance=True)
```



-10 10 20 30 100 200 300 400 500 Vector component index j Frame index n

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