In [1]:
```
%matplotlib inline
import os, shutil
import matplotlib.pyplot as plt
import numpy as np
import scipy.io as scio
from scipy.fft import fft, ifft, fftfreq
from scipy.signal import stft, ricker, cwt, butter, iirnotch, lfilter
import scipy.stats as stats
import pywt
from tqdm import tqdm
import pandas as pd
from sklearn.manifold import TSNE
from sklearn.decomposition import PCA
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis

from sklearn.model_selection import train_test_split
from sklearn import datasets
from sklearn.ensemble import RandomForestClassifier
from sklearn.utils import shuffle

from sklearn.inspection import DecisionBoundaryDisplay
from matplotlib.colors import ListedColormap

import torch

import mne

from statsmodels.stats.weightstats import ztest
```

In [ ]:
```
```

In [2]:
```
mode = 'notebook' #notebook, commit, colab

import plotly.offline as pyo
import plotly.graph_objs as go
from plotly.offline import iplot


from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot

if mode == 'colab':
    import cufflinks as cf
    cf.go_offline()
    init_notebook_mode(connected=False)

    def configure_plotly_browser_state():
        import IPython
        display(IPython.core.display.HTML('''
          <script src="/static/components/requirejs/require.js"></script>
          <script>
            requirejs.config({
              paths: {
                base: '/static/base',
                plotly: 'https://cdn.plot.ly/plotly-1.5.1.min.js?noext',
              },
            });
          </script>
          '''))

import plotly.graph_objects as go
import plotly.express as px
from plotly.subplots import make_subplots
import plotly.io as pio

if mode == 'commit':
    pio.renderers.default = "png"
```

In [3]:
```
mne.set_log_level(verbose='ERROR')
```

Dataset Processing

- Source: P300 speller with ALS patients (http://bnci-horizon-2020.eu/database/data-sets)
- Paper: Attention and P300-based BCI performance in people with amyotrophic lateral sclerosis (https://doi.org/10.3389/fnhum.2013.00732)

Extract from the paper (Experimental protocol):

Scalp EEG signals were recorded (g.MOBILAB, g.tec, Austria) from eight channels according to 10–10 standard (Fz, Cz, Pz, Oz, P3, P4, PO7 and PO8; Chatrian et al., 1985; Krusienski et al., 2006) using active electrodes (g.Ladybird, g.tec, Austria). All channels were referenced to the right earlobe and grounded to the left mastoid. The EEG signal was digitized at 256 Hz. Data acquisition and stimuli delivery were managed by the BCI2000 framework (Schalk et al., 2004).

Participants were required to copy spell seven predefined words of five characters each (runs), by controlling a P300 speller (Farwell and Donchin, 1988). The latter consisted of a 6 by 6 matrix containing alphanumeric characters (Figure 1A). Rows and columns on the interface were randomly intensified for 125 ms, with an inter stimulus interval (ISI) of 125 ms, yielding a 250 ms lag between the appearance of two stimuli (stimulus onset asynchrony, SOA). For each character selection (trial) all rows and columns were intensified 10 times (stimuli repetitions) thus each single item on the interface was intensified 20 times. Participants were seated facing a 15” computer screen placed at eye level approximately one meter in front of them. The angular distance subtended by the speller was of 15 degrees. A single flash of a letter at the beginning of each trial cued the target to focus. In the first three runs (15 trials in total) EEG data was stored to perform a calibration of the BCI classifier. Thus no feedback was provided to the participant up to this point. A stepwise linear discriminant analysis (SWLDA) was applied to the data from the three calibration runs (i.e., runs 1–3) to determine the classifier weights (i.e., classifier coefficients) (Krusienski et al., 2006). These weights were then applied during the subsequent four testing runs (i.e., testing set; runs 4–7) when participants were provided with feedback. EEG potentials between 0 and 800 ms after each stimulus onset were decimated by replacing each sequence of 12 samples with their mean value and used for the analysis. The next four runs (20 trials in total) characterized a testing phase in which feedback was provided by showing each spelled character. In cases of error the feedback was represented by a dot (instead of the wrongly typed character) to minimize frustration of the participants.

In [4]:
```
def load_data(filepath):
    """
    Loads EEG signal from the dataset
    """
    sample_matlab_data = scio.loadmat(filepath)  # Structured Matlab Array con
taining all information
    return sample_matlab_data

basedir = 'DataFiles'
```

In [5]:
```
patient_data = []
for file in os.listdir(basedir):
    filepath = os.path.join(basedir, file)
    patient_data.append(load_data(filepath))

print(len(patient_data))
```

```
8
```

In [6]:
```
patient_data[0]
```

Out[6]:

```
{'__header__': b'MATLAB 5.0 MAT-file, Platform: PCWIN, Created on: Tue Nov 25
12:46:00 2014',
 '__version__': '1.0',
 '__globals__': [],
 'data': array([[(array([[array(['Fz'], dtype='<U2'), array(['Cz'], dtype='<U
2'),
                 array(['Pz'], dtype='<U2'), array(['Oz'], dtype='<U2'),
                 array(['P3'], dtype='<U2'), array(['P4'], dtype='<U2'),
                 array(['PO7'], dtype='<U3'), array(['PO8'], dtype='<U3')]],
                dtype=object), array([[ -1.21978372,  -0.32769319,  -1.2199583
1, ...,  -2.65680554,
                   7.37202505,  -0.27890203],
                 [ -1.42616224,  -4.18996393,  -5.65458822, ...,  -9.45534598,
                  -3.67053188,  -5.48506363],
                 [ -1.31524453,  -6.87075831,  -8.55992067, ..., -14.26798757,
                  -11.63200572,  -8.92900433],
                 ...,
                 [ -3.96511643,   5.70748743,   1.11047492, ...,  -5.27998942,
                    9.13724881,  -0.85580654],
                 [ -0.5562302 ,   6.01519786,   3.32213104, ...,  -0.67030739,
                    8.2749988 ,   2.10576813],
                 [  4.22622461,   6.77563943,   6.12924025, ...,   5.20342677,
                    6.29436858,   6.15256883]]), array([[0],
                 [0],
                 [0],
                 ...,
                 [0],
                 [0],
                 [0]], dtype=uint8), array([[0],
                 [0],
                 [0],
                 ...,
                 [0],
                 [0],
                 [0]], dtype=int16), array([[  1801,  11529,  21257,  30985,
40713,  51473,  61201,  70929,
                   80657,  90385, 101145, 110873, 120601, 130329, 140057, 1508
17,
                  160545, 170273, 180001, 189729, 200489, 210217, 219945, 2296
73,
                  239401, 250161, 259889, 269617, 279345, 289073, 299833, 3095
61,
                  319289, 329017, 338745]]), array([[array(['NonTarget'], dtyp
e='<U9'),
                  array(['Target'], dtype='<U6')]], dtype=object), array([[arr
ay(['Row1'], dtype='<U4'), array(['Row2'], dtype='<U4'),
                 array(['Row3'], dtype='<U4'), array(['Row4'], dtype='<U4'),
                 array(['Row5'], dtype='<U4'), array(['Row6'], dtype='<U4'),
                 array(['Col1'], dtype='<U4'), array(['Col2'], dtype='<U4'),
                 array(['Col3'], dtype='<U4'), array(['Col4'], dtype='<U4'),
                 array(['Col5'], dtype='<U4'), array(['Col6'], dtype='<U
4')]],
                dtype=object), array(['male'], dtype='<U4'), array(['55'], dty
pe='<U2'), array(['13'], dtype='<U2'), array(['spinal'], dtype='<U6'))]],
       dtype=[('channels', 'O'), ('X', 'O'), ('y', 'O'), ('y_stim', 'O'), ('t
```

```
rial', 'O'), ('classes', 'O'), ('classes_stim', 'O'), ('gender', 'O'), ('ag
e', 'O'), ('ALSfrs', 'O'), ('onsetALS', 'O')])}
```

In [7]:
```
def get_channel_name(patient, index):
    """
    Returns the name of the EEG channel for the corresponding index
    """
    return patient['data'][0][0]['channels'][0][index]
print(get_channel_name(patient_data[0], 1))
```

```
['Cz']
```

In [8]:
```
def get_channel_index(patient, channel_name):
    """
    Returns the index number of a channel
    """
    indices = [data[0].lower() for data in patient['data'][0][0]['channels']
[0]]
    return indices.index(channel_name.lower())
print(get_channel_index(patient_data[0], 'Fz'))
```

```
0
```

In [9]:
```
print("Data shape")
print(f"Signal: {patient_data[0]['data'][0][0]['X'].shape}")
print(f"Target/Class label: {patient_data[0]['data'][0][0]['y'].shape}")
print(f"Stimulus type: {patient_data[0]['data'][0][0]['y_stim'].shape}")
```

```
Data shape
Signal: (347704, 8)
Target/Class label: (347704, 1)
Stimulus type: (347704, 1)
```

Parameters of the EEG Signal

In [10]:
```
# Functions for EEG data extraction and manipulation

sample_frequency = 256 #Hz
bandpass_filter = (0, 30) # Hz
stimulus_duration = 125 #ms
interstimulus_interval = 125 #ms
total_stimulus = 12 # 6 rows and 6 columns
number_of_times_each_stimulus_appeared_per_trial = 10
total_stimulus_appeared_per_trial = total_stimulus * number_of_times_each_stim
ulus_appeared_per_trial

trial_duration = (stimulus_duration * total_stimulus_appeared_per_trial) + \
(interstimulus_interval * (total_stimulus_appeared_per_trial- 1))

samples_per_trial = (sample_frequency * trial_duration)//1000

print(f"Each trial duration: {trial_duration} ms or {samples_per_trial} sample
s")
```

```
Each trial duration: 29875 ms or 7648 samples
```

In [11]:
```
def get_trials(sample, remove_calibration_data=True):
    """
    Returns all trial data for a patient
    """
    data = sample['data'][0][0]
    signal = data['X']
    stimulus = data['y_stim']
    target = data['y']

    x, y_stimulus, y_target = [], [], []
#     trial_start = 0
    for i in range(data['trial'].shape[1]):
        trial_start = data['trial'][0, i]
        trial_end = trial_start+samples_per_trial


        # Fetch signal
        x.append(signal[trial_start:trial_end])
        # Fetch stimulus
        y_stimulus.append(stimulus[trial_start:trial_end, 0])
        # Fetch target
        y_target.append(target[trial_start:trial_end, 0])

    x, y_stimulus, y_target = np.array(x), np.array(y_stimulus), np.array(y_ta
rget)
    if remove_calibration_data:
        x, y_stimulus, y_target = x[3:], y_stimulus[3:], y_target[3:]
    return x, y_stimulus, y_target

X, y_stim, y_target = get_trials(patient_data[0])
print(X.shape, y_stim.shape, y_target.shape)
print(np.unique(y_stim))
print(np.unique(y_target))
```

```
(32, 7648, 8) (32, 7648) (32, 7648)
[ 0  1  2  3  4  5  6  7  8  9 10 11 12]
[0 1 2]
```

In [12]:
```
number_of_trials_per_run = 5 # each run is a word and each trial is a characte
r of the word
number_of_runs = 7 # total number of words

total_characters_with_calibration = number_of_trials_per_run * number_of_runs
total_characters_without_calibration = number_of_trials_per_run * number_of_ru
ns - 3

def get_dataset(dataset):
    """
    Converts the matlab file of all patients to a single numpy array and retur
ns the dataset
    Returns: Numpy array -> input shape: (patient_id, run, trial, sample, chan
nels),
             stimulus -> (patient_id, run, trial, sample)
             target -> (patient_id, run, trial, sample)
    """
    x, y_stim, y_target = [], [], []
    for i in range(len(dataset)):
        patient = dataset[i]
        x_trial, y_stim_trial, y_target_trial = get_trials(patient, remove_cal
ibration_data=False)

        # Reshape array to group trials by run
        x_trial = x_trial.reshape(-1, number_of_trials_per_run, x_trial.shape
[1], x_trial.shape[2])
        y_stim_trial  = y_stim_trial.reshape(-1, number_of_trials_per_run, y_s
tim_trial.shape[1])
        y_target_trial = y_target_trial.reshape(-1, number_of_trials_per_run,
y_target_trial.shape[1])

        # Add to array
        x.append(x_trial)
        y_stim.append(y_stim_trial)
        y_target.append(y_target_trial)

    return np.array(x), np.array(y_stim), np.array(y_target)


X, y_stim, y_target = get_dataset(patient_data)

print(X.shape, y_stim.shape, y_target.shape)
print(np.unique(y_stim))
print(np.unique(y_target))
```

```
(8, 7, 5, 7648, 8) (8, 7, 5, 7648) (8, 7, 5, 7648)
[ 0  1  2  3  4  5  6  7  8  9 10 11 12]
[0 1 2]
```

Mapping for row/column value to character

In [13]:
```
words =np.array([chr(i) for i in range(ord('A'), ord('Z')+1)] + [str(i) for i
in range(1, 10)] + ['-'])
word_matrix = np.reshape(words, (6, 6))
word_matrix_row = np.arange(7, 13)
word_matrix_column = np.arange(1, 7)
print(word_matrix)
word_to_tup = {}
tup_to_word = {}
for i in range(word_matrix.shape[0]):
    for j in range(word_matrix.shape[1]):
        tup = (word_matrix_row[i], word_matrix_column[j])
        word_to_tup[word_matrix[i, j]] = tup
        tup_to_word[str(tup[0]) + "," + str(tup[1])] = word_matrix[i, j]

print("\nCharacter to indices")
print(word_to_tup)
print("\n Indices to Characters")
print(tup_to_word)
```

```
[['A' 'B' 'C' 'D' 'E' 'F']
 ['G' 'H' 'I' 'J' 'K' 'L']
 ['M' 'N' 'O' 'P' 'Q' 'R']
 ['S' 'T' 'U' 'V' 'W' 'X']
 ['Y' 'Z' '1' '2' '3' '4']
 ['5' '6' '7' '8' '9' '-']]

Character to indices
{'A': (7, 1), 'B': (7, 2), 'C': (7, 3), 'D': (7, 4), 'E': (7, 5), 'F': (7,
6), 'G': (8, 1), 'H': (8, 2), 'I': (8, 3), 'J': (8, 4), 'K': (8, 5), 'L': (8,
6), 'M': (9, 1), 'N': (9, 2), 'O': (9, 3), 'P': (9, 4), 'Q': (9, 5), 'R': (9,
6), 'S': (10, 1), 'T': (10, 2), 'U': (10, 3), 'V': (10, 4), 'W': (10, 5),
'X': (10, 6), 'Y': (11, 1), 'Z': (11, 2), '1': (11, 3), '2': (11, 4), '3': (1
1, 5), '4': (11, 6), '5': (12, 1), '6': (12, 2), '7': (12, 3), '8': (12, 4),
'9': (12, 5), '-': (12, 6)}

 Indices to Characters
{'7,1': 'A', '7,2': 'B', '7,3': 'C', '7,4': 'D', '7,5': 'E', '7,6': 'F', '8,
1': 'G', '8,2': 'H', '8,3': 'I', '8,4': 'J', '8,5': 'K', '8,6': 'L', '9,1':
'M', '9,2': 'N', '9,3': 'O', '9,4': 'P', '9,5': 'Q', '9,6': 'R', '10,1': 'S',
'10,2': 'T', '10,3': 'U', '10,4': 'V', '10,5': 'W', '10,6': 'X', '11,1': 'Y',
'11,2': 'Z', '11,3': '1', '11,4': '2', '11,5': '3', '11,6': '4', '12,1': '5',
'12,2': '6', '12,3': '7', '12,4': '8', '12,5': '9', '12,6': '-'}
```

In [14]:
```
target_class = 2
non_target_class = 1
def convert_stimulus_to_word(y_stim, y_target):
    """
    Takes all consecutive stimulus (row & column number of BCI) and outputs th
e corresponding word that was
    displayed.
    Input shape: (Patients, run, trial, samples)
    Output shape: (Patients, run, trial, character)
    """
    y_stim = y_stim.reshape(-1)
    y_target = y_target.reshape(-1)
    target_stimulus = y_stim[y_target == target_class ]
    vals = []
    for i in range(len(target_stimulus)):
        if len(vals) == 0 or  vals[-1] != target_stimulus[i]:
            vals.append(target_stimulus[i])

    character_indices = []
    characters = []
    for i in range(0, len(vals)-1, 2):
        c = vals[i]
        r = vals[i+1]
        character_indices.append((r, c))
        characters.append(tup_to_word[str(r) + "," + str(c)])

    non_repeating_chars = []
    for c in characters:
        if len(non_repeating_chars) == 0 or non_repeating_chars[-1] != c:
            non_repeating_chars.append(c)

    words = []
    for i in range(0, len(non_repeating_chars), 5):
        words.append(''.join(non_repeating_chars[i:i+5]))
    return words

for i in range(X.shape[0]):
    print(f"Words displayed to patient: {i+1}")
    print(convert_stimulus_to_word(y_stim[0], y_target[0]))
```

```
Words displayed to patient: 1
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 2
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 3
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 4
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 5
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 6
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 7
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
Words displayed to patient: 8
['WGAMN', 'F7ODY', 'KPUAB', 'AJOCY', 'IJYVN', 'O6A7Y', 'GPD']
```

High level overview of the dataset

First we will visualize the EEG signals collected from different patients. We will do a visual inspection to see some of the characteristics of the dataset e.g. what are the minimum and maximum amplitude of the signals for different patients, are there any visible artifacts in the signal, etc.

In [15]:
```
get_channel_index(patient_data[0], 'PO7')
```

Out[15]: 6

In [16]:
```
def view_signal(signal, title='', channels_to_show=[], highpass=None, lowpass=
None, y=None, scalings='auto'):
    signal = signal.reshape(-1, signal.shape[-1]).transpose()
    channels = ['P3', 'PO7', 'Fz', 'Cz', 'Pz', 'Oz', 'P4', 'PO8']
    channel_indices = [get_channel_index(patient_data[0], name) for name in ch
annels]
#     channel_indices = [i for i in range(signal.shape[0])]
#     channels = [get_channel_name(patient_data[0], i)[0] for i in channel_ind
ices]
    if len(channels_to_show) == 0:
        channels_to_show = [i for i in range(len(channels))]
    else:
        channels_to_show = [channels.index(channel) for channel in channels_to
_show]

    info = mne.create_info(channels, sample_frequency, ch_types='eeg')
    data = mne.io.RawArray(signal[channel_indices, :], info)

    target_descriptions = ['No stimulus', 'Non-Target', 'Target']
    target_description_indices = {i:target_descriptions[i] for i in range(len
(target_descriptions))}
    target_description_names = {target_descriptions[i]: i for i in range(len(t
arget_descriptions))}

    if not (y is None):
        y = y.reshape(-1)
        target = np.where(y == target_description_names['Target'])[0]
        non_targets = np.where(y == target_description_names['Non-Target'])[0]
        onsets = []
        duration = []
        description = []

        for i in range(len(target)):
            if i == 0:
                onsets.append(target[i])
                description.append('T')
            else:
                if target[i] != target[i-1]+1:
                    duration.append(target[i-1] - onsets[-1])
                    onsets.append(target[i])
                    description.append('T')
                elif i == len(target) - 1:
                    duration.append(target[i] - onsets[-1])

        for i in range(len(non_targets)):
            if i == 0:
                onsets.append(non_targets[i])
                description.append('N')
            else:
                if non_targets[i] != non_targets[i-1]+1:
                    duration.append(non_targets[i-1] - onsets[-1])
                    onsets.append(non_targets[i])
                    description.append('N')
                elif i == len(non_targets) - 1:
                    duration.append(non_targets[i] - onsets[-1])
```

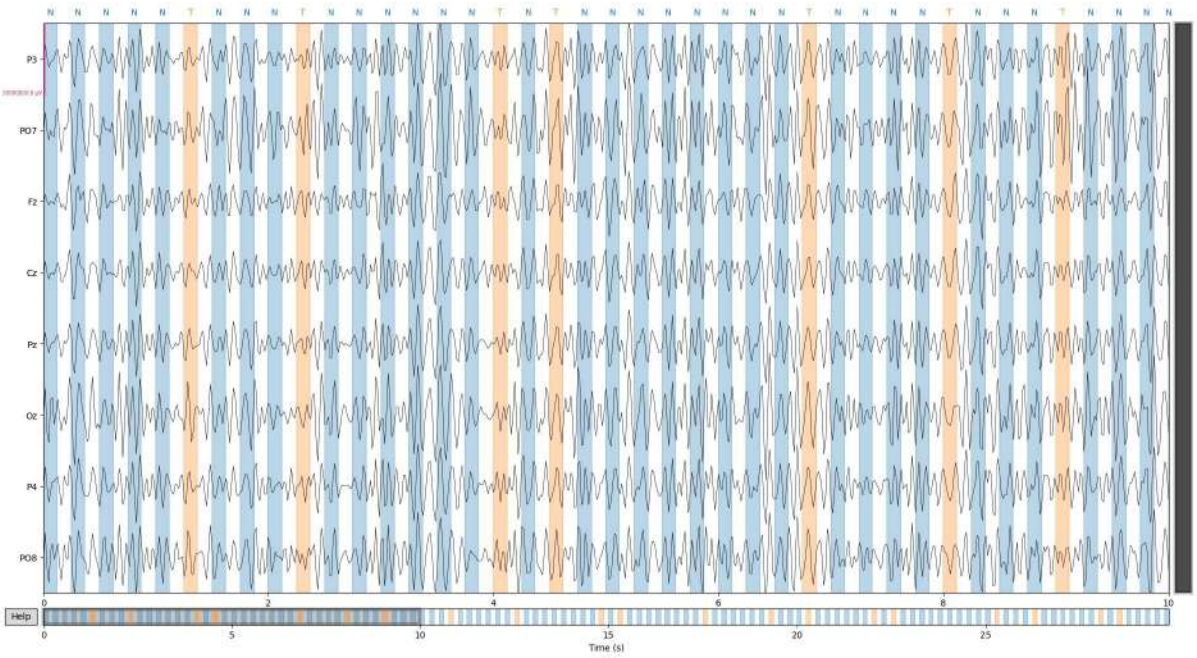
```
        onsets = np.array(onsets)/sample_frequency
        duration = np.array(duration)/sample_frequency

        data.set_annotations(mne.Annotations(onsets, duration, description))


    data.plot(scalings=scalings, title=title, order=channels_to_show, highpass
=highpass, lowpass=lowpass)
```

In [17]:
```
X.shape, y_target.shape
```

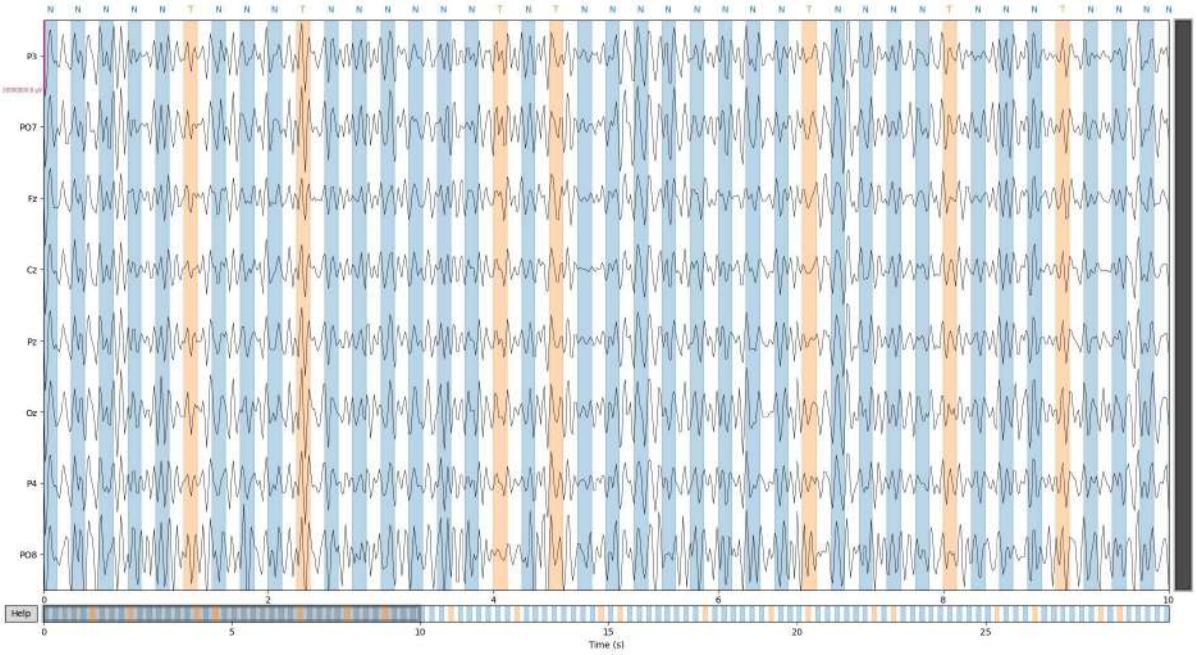
Out[17]:
```
((8, 7, 5, 7648, 8), (8, 7, 5, 7648))
```

In [18]:
```
for i in range(X.shape[0]):
    print(f"Patient {i+1}")
    view_signal(X[i, 0, 0, :, :], title=f'Patient {i+1}', lowpass=20, highpass
=8, y=y_target[i], scalings=dict(eeg=15))
```

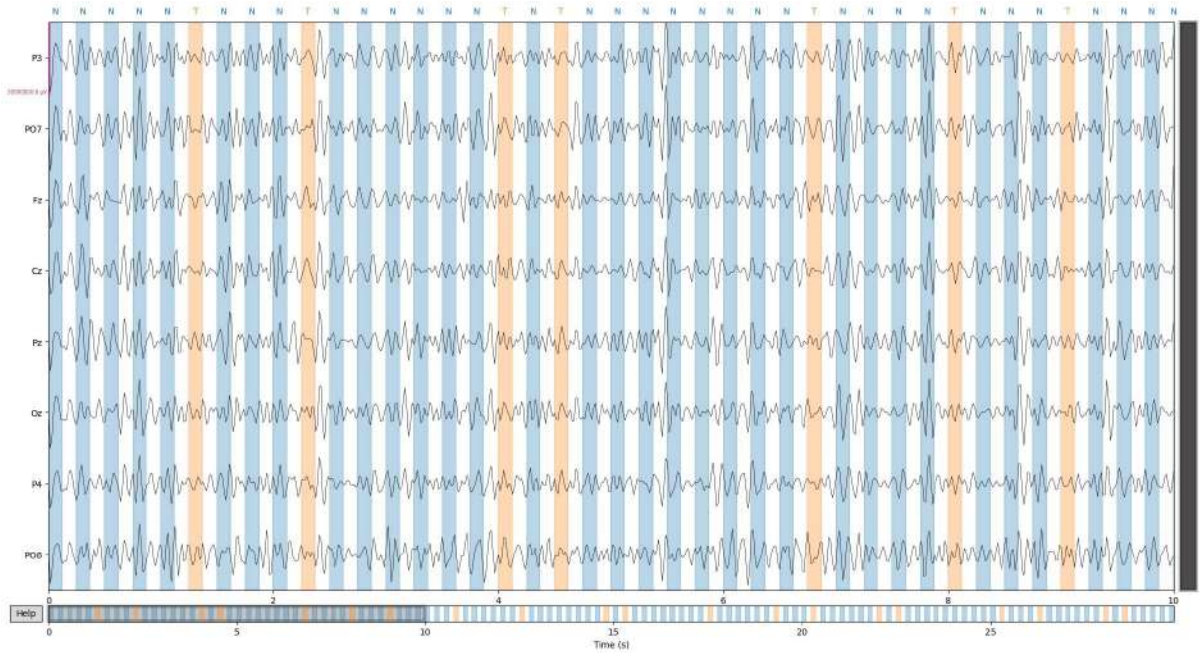
Patient 1



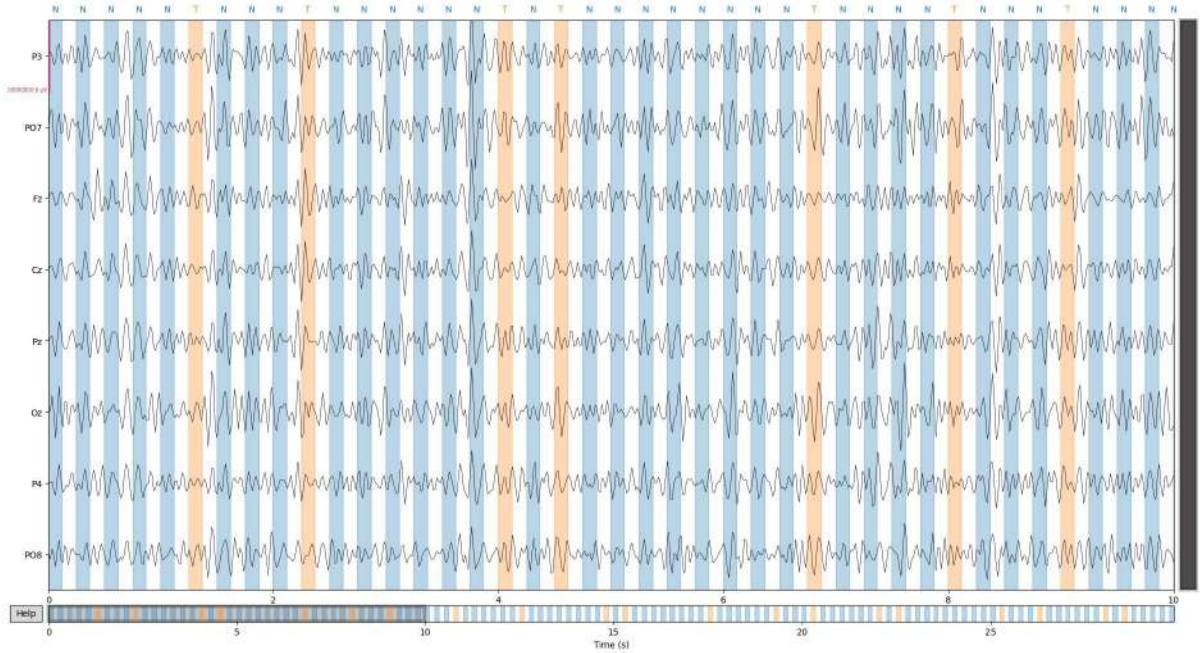
Patient 2



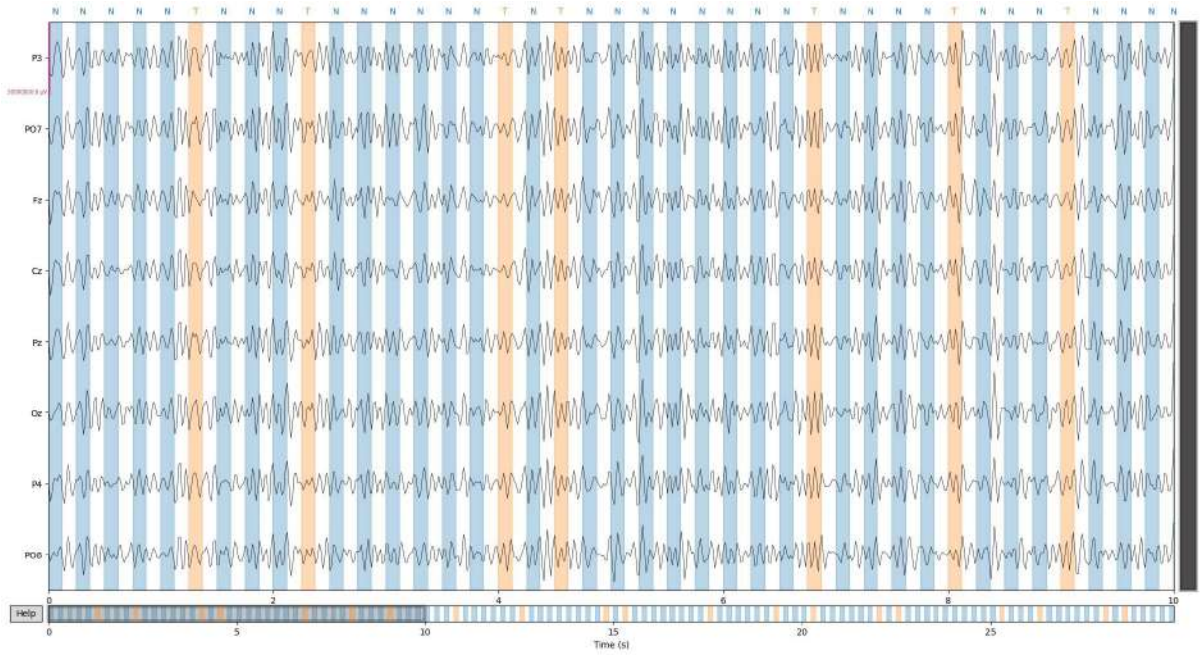
Patient 3



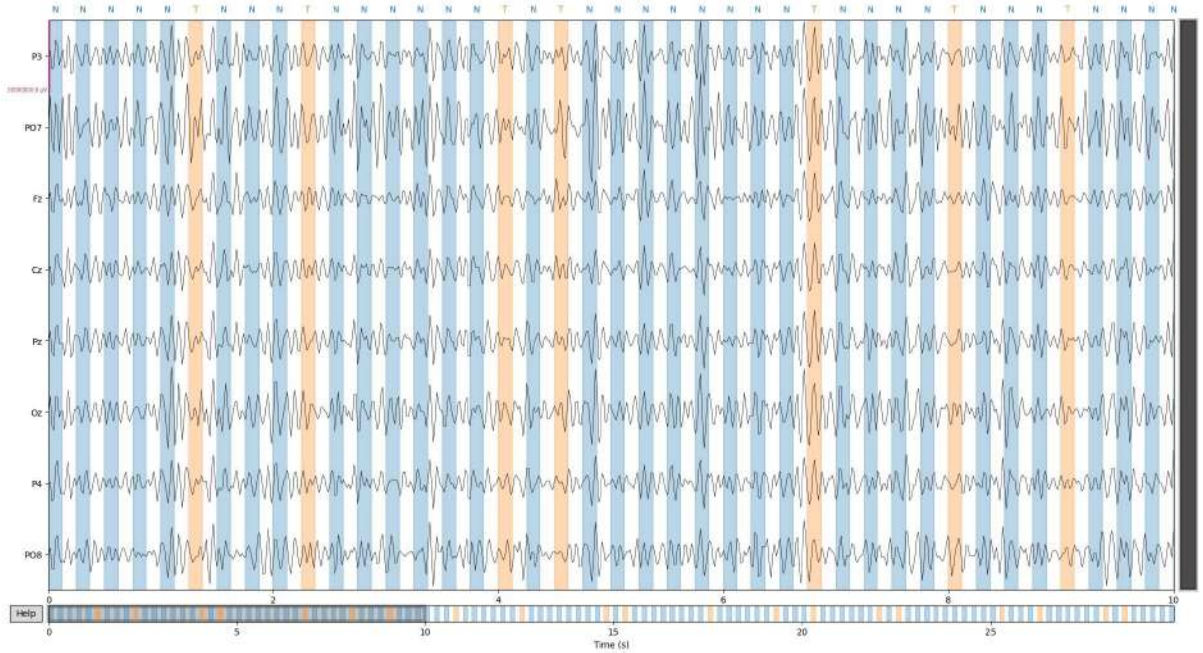
Patient 4



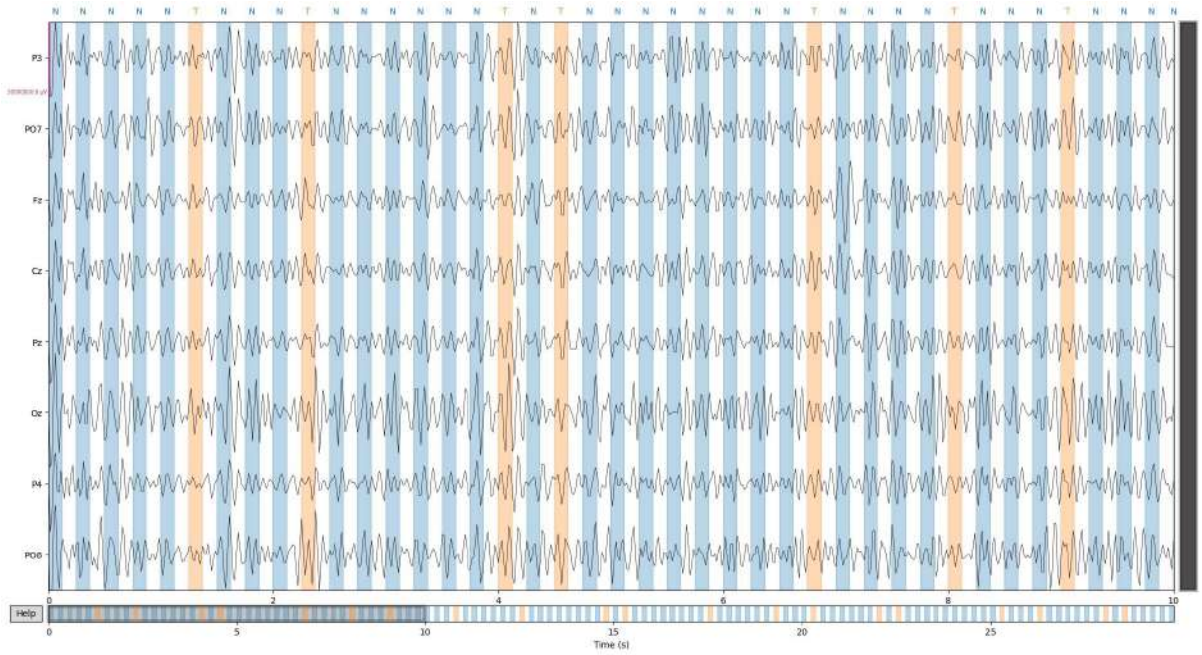
Patient 5



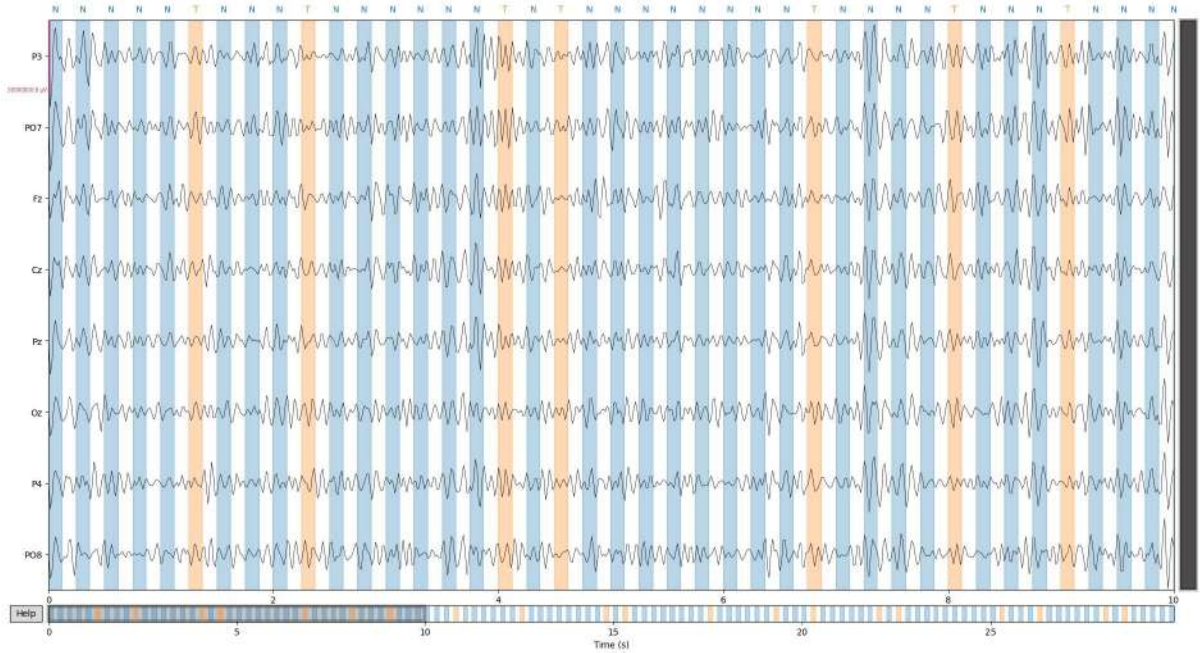
Patient 6



Patient 7



Patient 8



In [19]:
```
# # View in new window
# %matplotlib qt
# patient = 7
# view_signal(X[patient, 0, 0], title='Patient 1', highpass=0.1, lowpass=10, y
=y_target[patient])
```

In [ ]:
```

```

Removing Artifacts - Part I

In this section we will follow the same procedure mentioned in the paper to remove the artifacts and visualize the EEG signal.

Extract from the paper (Data Analysis):

EEG data was high pass and low pass filtered with cut off frequencies of 0.1 Hz and 10 Hz respectively using a 4th order Butterworth filter. In addition, a notch filter was used to remove 50 Hz contamination due to the AC interference. Data was divided into 1000 ms long epochs starting with the onset of each stimulus. Epochs in which peak amplitude was higher than 70 μV or lower than −70 μV were identified as artifacts and removed. A baseline correction was done based on the average EEG activity within 200 ms immediately preceding each epoch. The average waveform for both target and non-target epochs was computed for each trial in order to assess P300 peak amplitude. Particularly, amplitude of the P300 potential in Cz was defined as the highest value of the difference between target and non-target average waveforms in the time interval 250–700 ms

In [20]:
```
def butter_bandpass(lowcut, highcut, fs, order=4):
    return butter(order, [lowcut, highcut], fs=fs, btype='band')

def butter_bandpass_filter(data, lowcut, highcut, fs, order=4, axis=-1):
    b, a = butter_bandpass(lowcut, highcut, fs, order=order)
    y = lfilter(b, a, data, axis=axis)
    return y

def notch_filter(data, frequency, fs, axis=-1, quality_factor=30.0):
    b, a = iirnotch(frequency, quality_factor, fs)
    return lfilter(b, a, data, axis=axis)
```

In [21]:
```
highpass_filter = 0.1 #Hz
lowpass_filter = 10 #Hz
notch_frequency = 50 #Hz
```

Filter the signal

In [22]:
```
X_filtered = butter_bandpass_filter(X, highpass_filter, lowpass_filter, sample
_frequency, order=4, axis=3)
X_filtered = notch_filter(X_filtered, notch_frequency, sample_frequency, axis=
3)
print(X_filtered.shape)
```

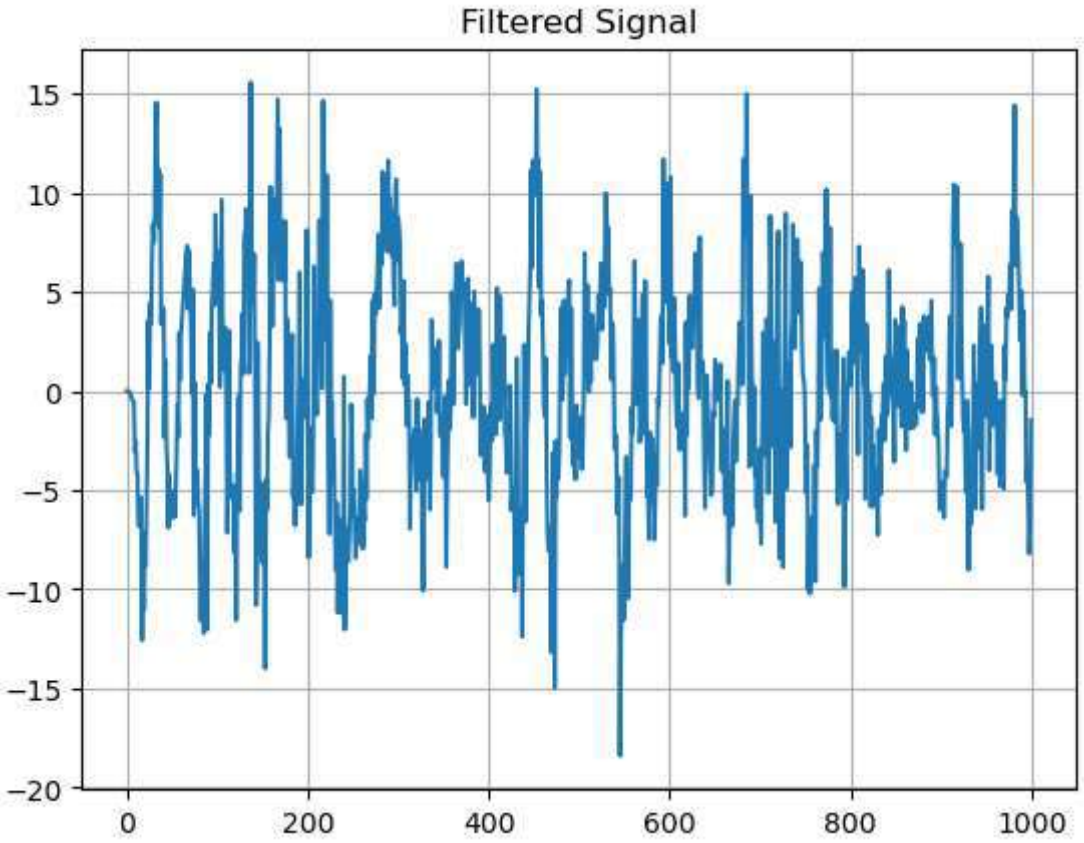
```
(8, 7, 5, 7648, 8)
```

Remove amplitude greater than 70uV or less than -70uv

In [23]:
```
minimum_amplitude = -70
maximum_amplitude = 70

X_filtered[(X_filtered < minimum_amplitude) | (X_filtered > maximum_amplitud
e)] = 0
print(X_filtered.shape)
```

```
(8, 7, 5, 7648, 8)
```

In [24]:
```
plt.figure()
plt.title("Filtered Signal")
plt.plot(X_filtered.reshape((X_filtered.shape[0], -1, X_filtered.shape[1]))[1,
:1000, 0])
plt.grid()
plt.show()
```



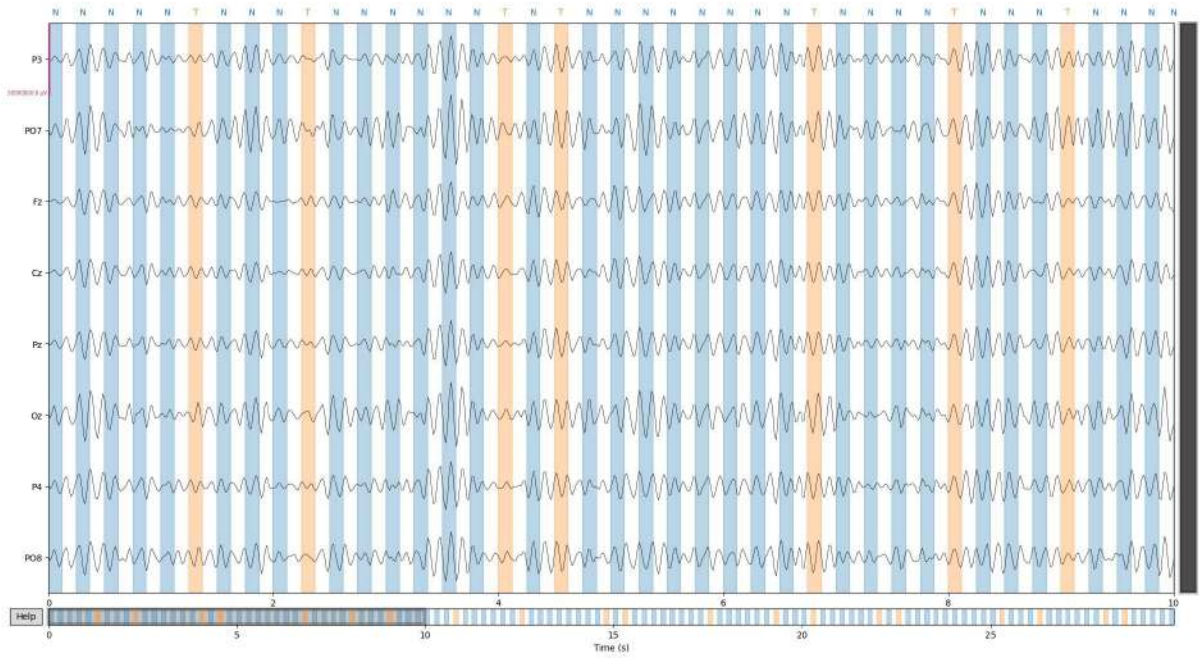
Baseline correction

In [25]:
```
baseline_duration = 200 #ms
baseline_samples = int(sample_frequency*baseline_duration/1000)
epoch_duration = 1000 #ms
epoch_samples = int(sample_frequency*epoch_duration/1000)

X_filtered = X_filtered.reshape((X_filtered.shape[0], -1, X_filtered.shape[-
1]))
y_filtered = y_target.reshape((y_target.shape[0], -1))

for patient in range(X_filtered.shape[0]):
    for channel in range(X_filtered.shape[-1]):
        i = 0
        while i < X_filtered.shape[1]:
            if y_filtered[patient, i] != 0: # Stimulus onset
                average = 0
                if i > baseline_samples:
                    average = np.mean(X_filtered[patient, i-baseline_samples:i
+epoch_samples, channel])
                X_filtered[patient, i:i+epoch_samples, channel] = X_filtered[p
atient, i:i+epoch_samples, channel] - average
                i = i + epoch_samples
            else:
                i += 1
del y_filtered
X_filtered = X_filtered.reshape(X.shape)
print(X_filtered.shape)
```

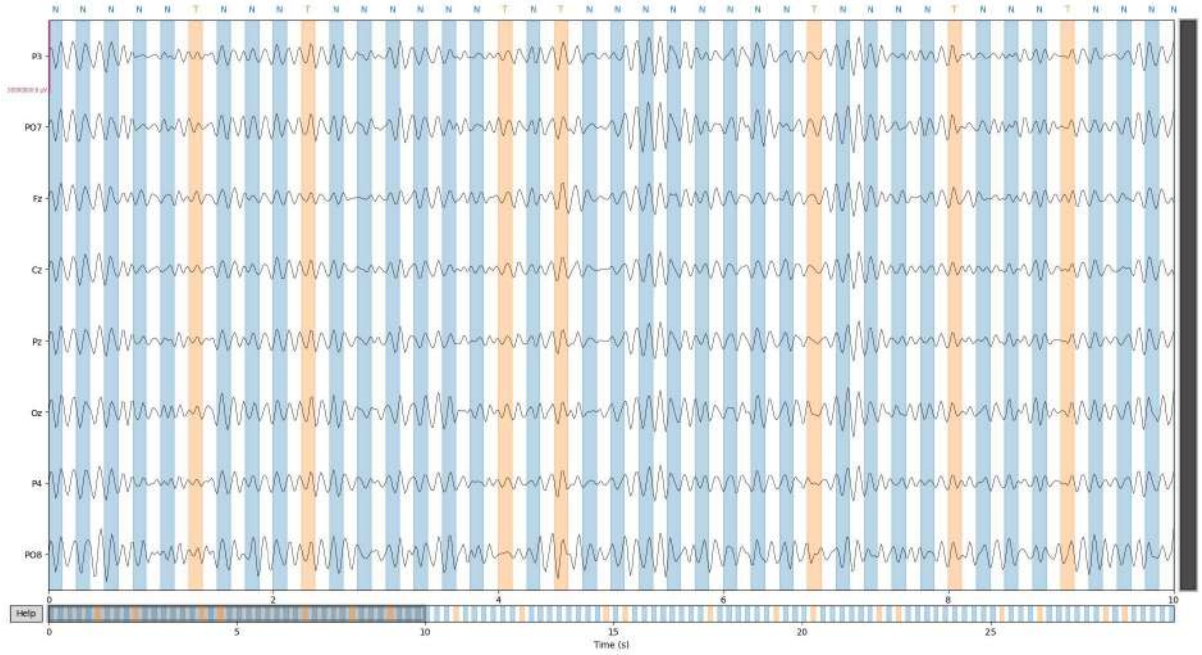
```
(8, 7, 5, 7648, 8)
```

In [26]:
```
%matplotlib inline
for i in range(X.shape[0]):
    print(f"Patient {i+1}")
    view_signal(X_filtered[i, 0, 0, :, :], title=f'Patient {i+1}', lowpass=20,
highpass=8, y=y_target[i],
                scalings=dict(eeg=15))
```

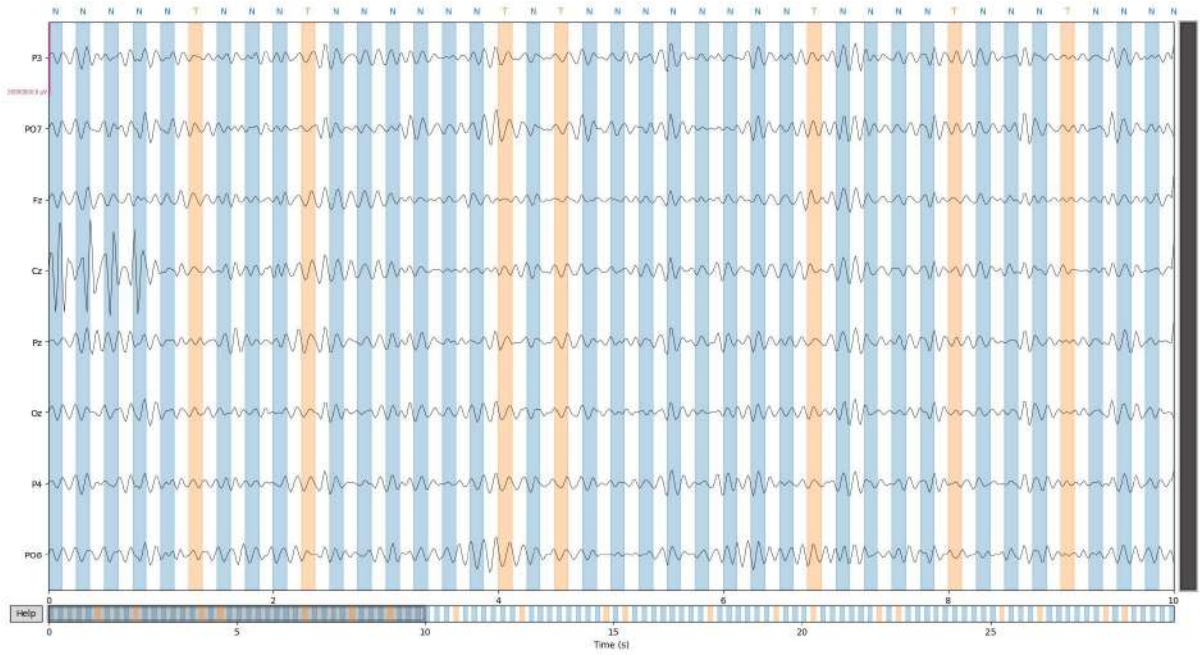
Patient 1



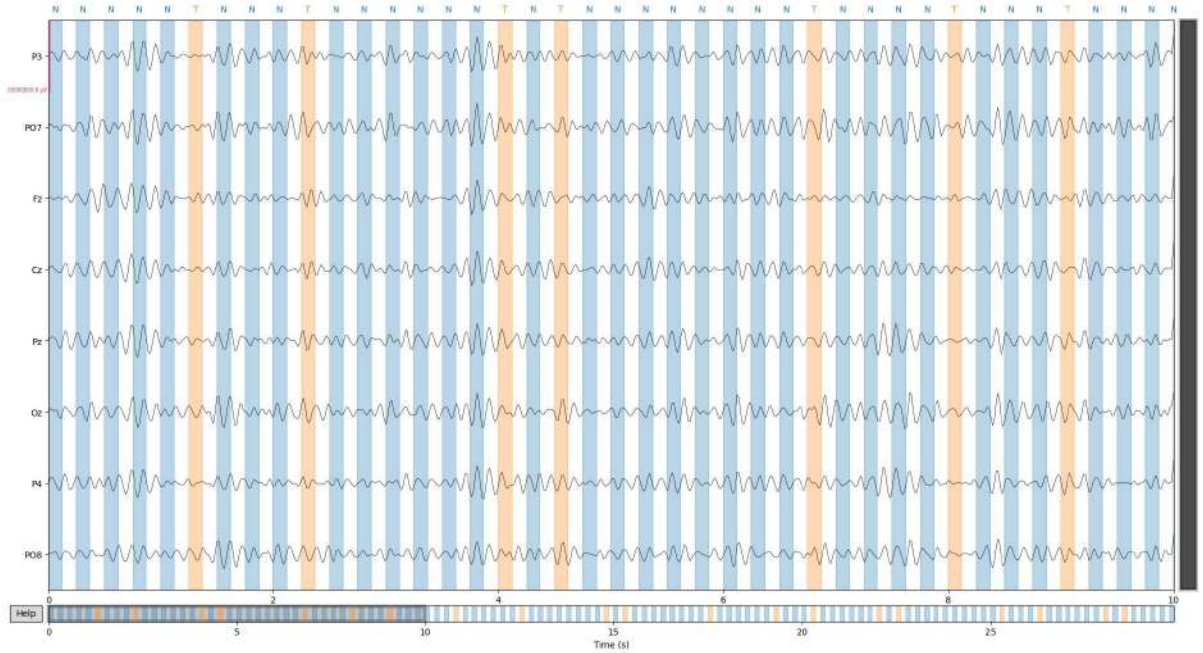
Patient 2



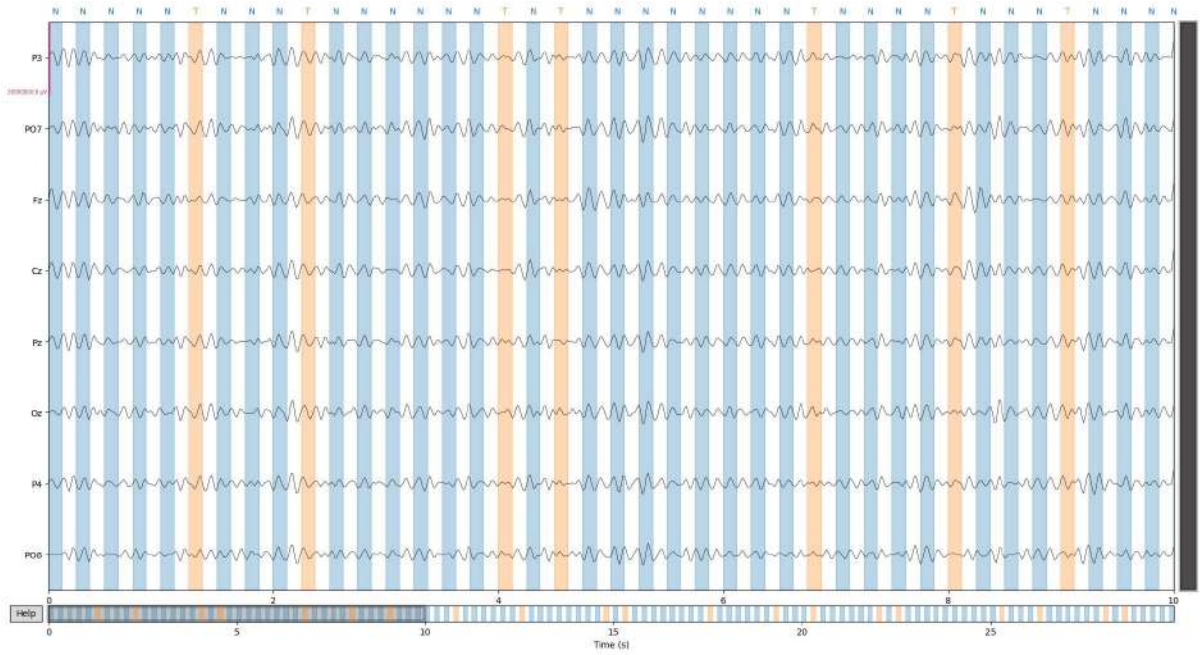
Patient 3



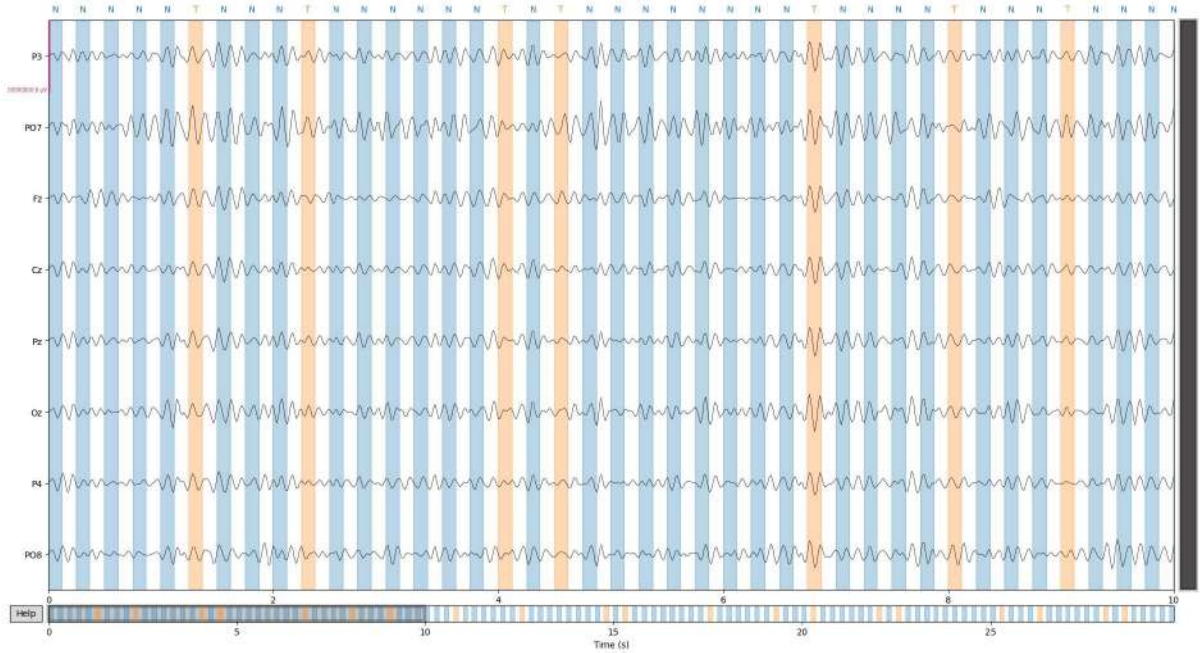
Patient 4



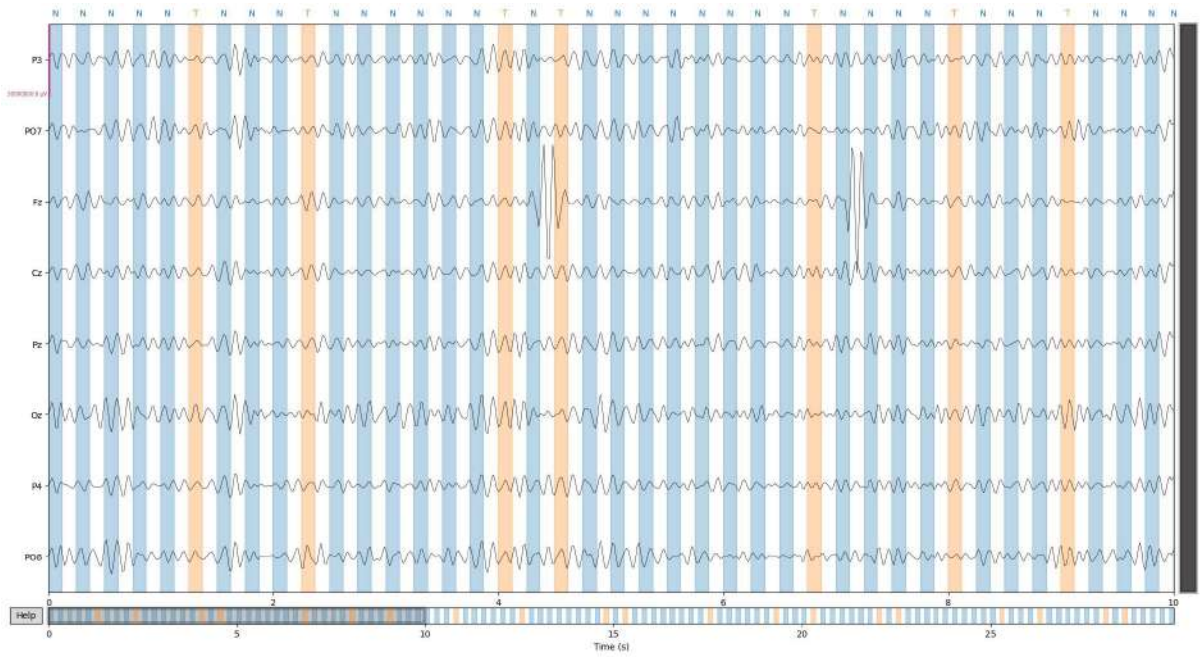
Patient 5



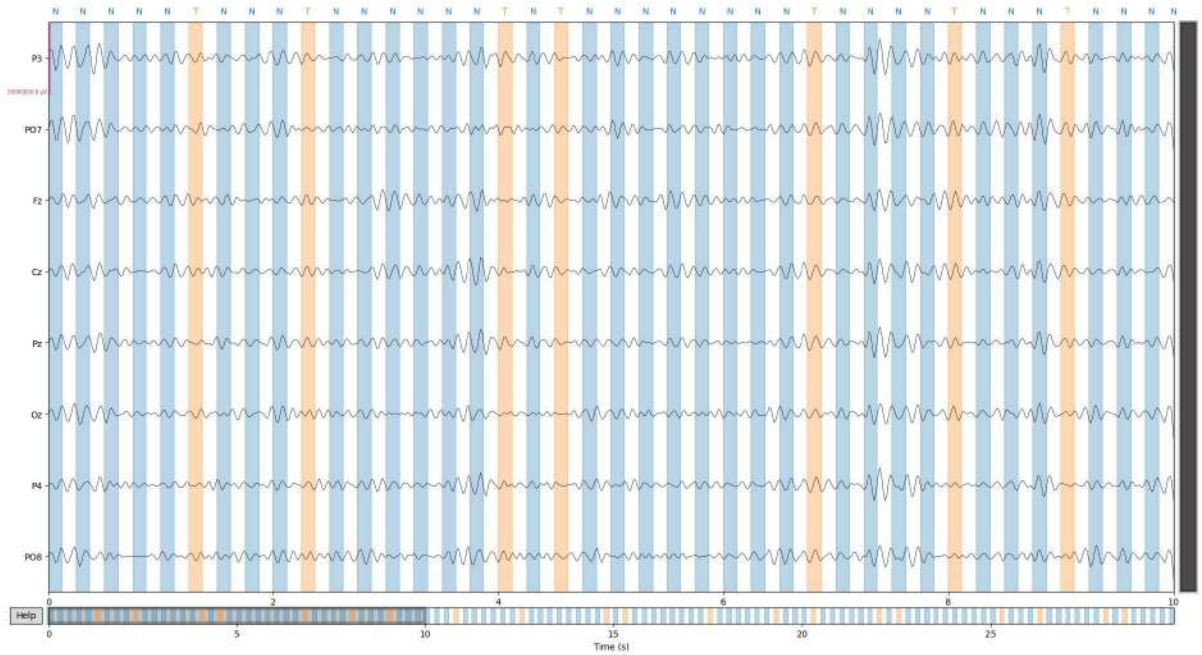
Patient 6



Patient 7



Patient 8



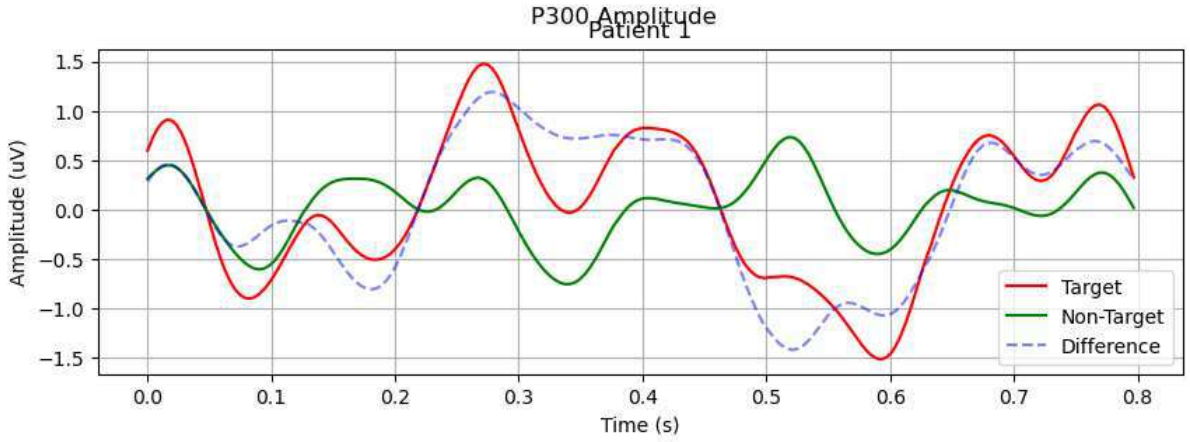
In [27]:
```
# %matplotlib qt
# view_signal(X_filtered[1, 0:2, 0:5, :, :], title=f'Patient {i+1}', y=y_targe
t[i])
```

Calculating average waveform of each onset

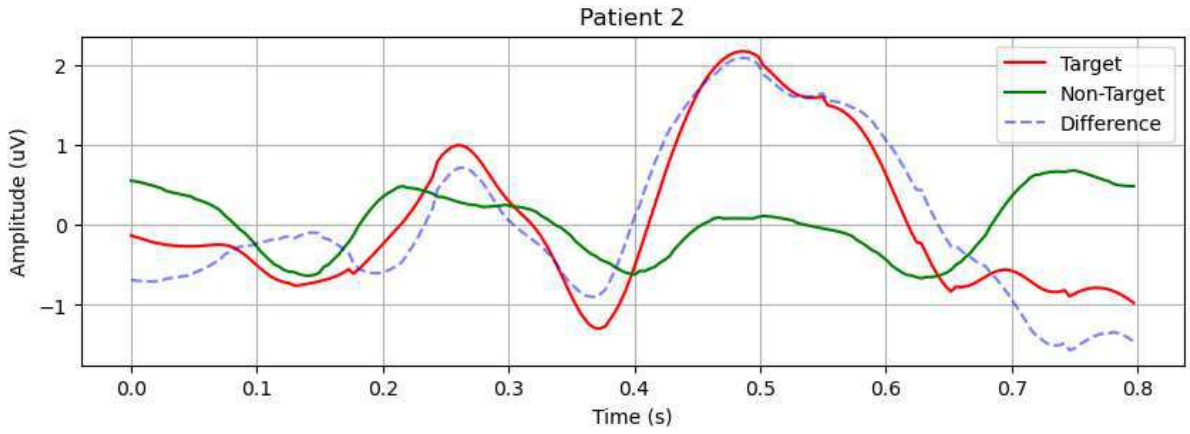
In the paper, the waveform that occured in each trial between 200-700 ms after each onset was collected from 'Cz' channel. The average waveform was calculated for each onset type (Target and Non-target). The highest value of the difference between the average target and non-target waveform was considered as the P300 amplitude.

In [343]:
```
waveform_start_time_after_onset = 0
waveform_end_time_after_onset = 1000
waveform_start_sample_after_onset = int(sample_frequency * waveform_start_time
_after_onset / 1000)
waveform_end_sample_after_onset = 17*12
#waveform_end_sample_after_onset = int(sample_frequency * waveform_end_time_af
ter_onset / 1000)

for i in range(X_filtered.shape[0]):
    target_waveforms = []
    non_target_waveforms = []
    x = X_filtered[i, :, :, :, get_channel_index(patient_data[0], 'Cz')].resha
pe(-1)
    y = y_target[i].reshape(-1)

    for j in range(1, y.size):
        if (y[j] != 0) and  (y[j-1] != y[j]): # start of onset
            if j + waveform_end_sample_after_onset < y.size:
                if y[j] == 1:
                    non_target_waveforms.append(x[j+waveform_start_sample_afte
r_onset:j+waveform_end_sample_after_onset])
                else:
                    target_waveforms.append(x[j+waveform_start_sample_after_on
set:j+waveform_end_sample_after_onset])

    target_waveforms = np.array(target_waveforms)
    non_target_waveforms = np.array(non_target_waveforms)

    x_axis = np.linspace(0, target_waveforms.shape[1]/sample_frequency, target
_waveforms.shape[1])
    print(target_waveforms.shape, non_target_waveforms.shape)
    target_waveforms = np.mean(target_waveforms, axis=0)
    non_target_waveforms = np.mean(non_target_waveforms, axis=0)


    plt.figure(figsize=(10,3))
    if i == 0:
        plt.suptitle("P300 Amplitude")
    plt.title(f"Patient {i+1}")

    plt.plot(x_axis, target_waveforms, 'r-', label='Target')
    plt.plot(x_axis, non_target_waveforms, 'g-', label='Non-Target')
    plt.plot(x_axis, target_waveforms - non_target_waveforms, 'b--', alpha=0.
5, label='Difference')

    plt.xlabel("Time (s)")
    plt.ylabel("Amplitude (uV)")
    plt.legend()
    plt.grid()
    plt.subplots_adjust(hspace=0.5)
    plt.show()
```

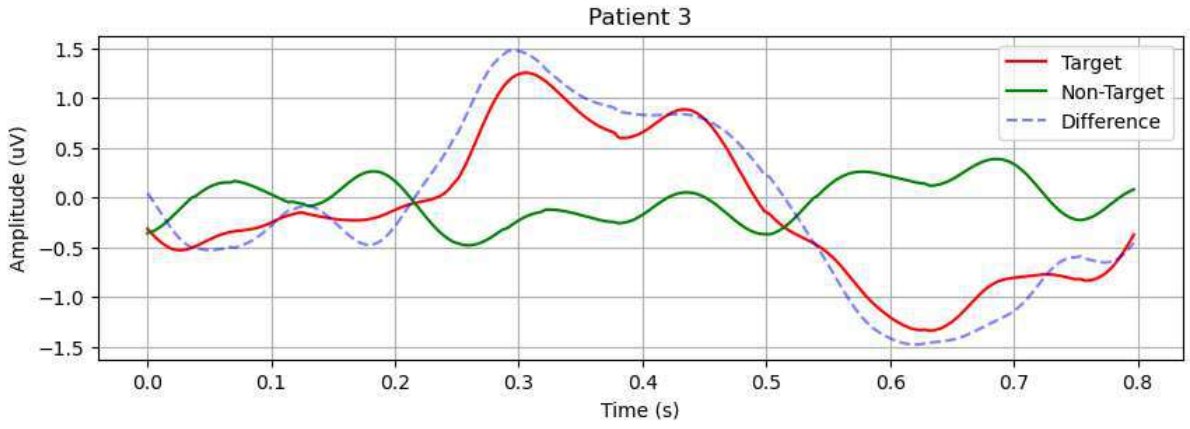
```
(700, 204) (3496, 204)
```



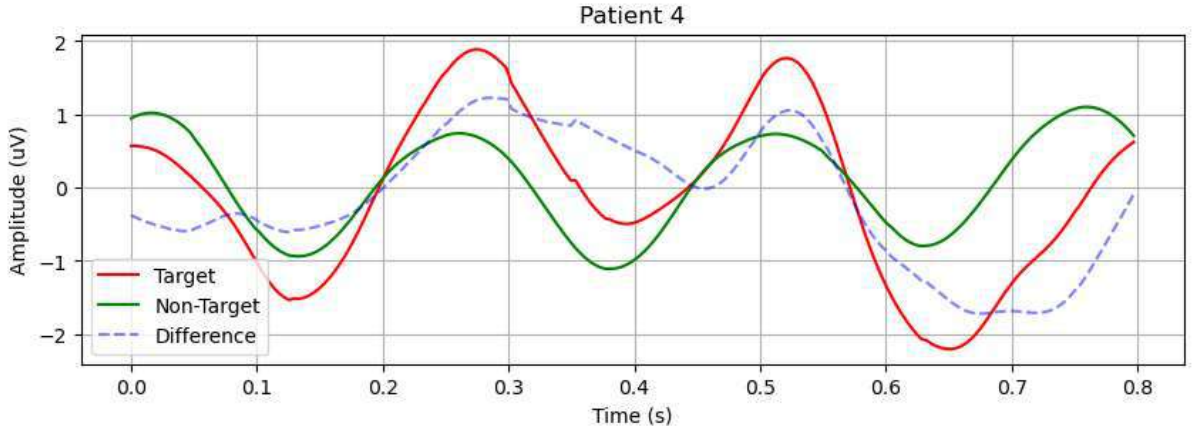

```
(700, 204) (3496, 204)
```



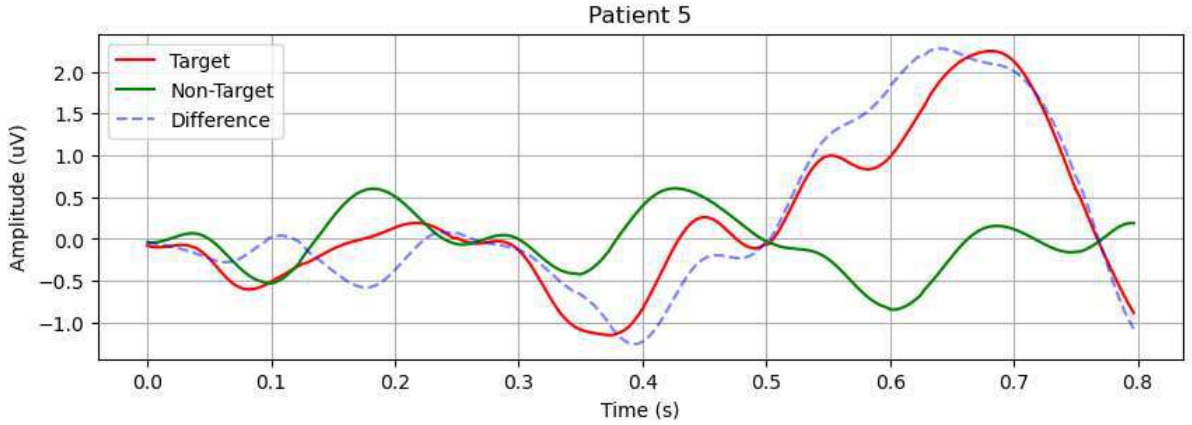

```
(700, 204) (3496, 204)
```



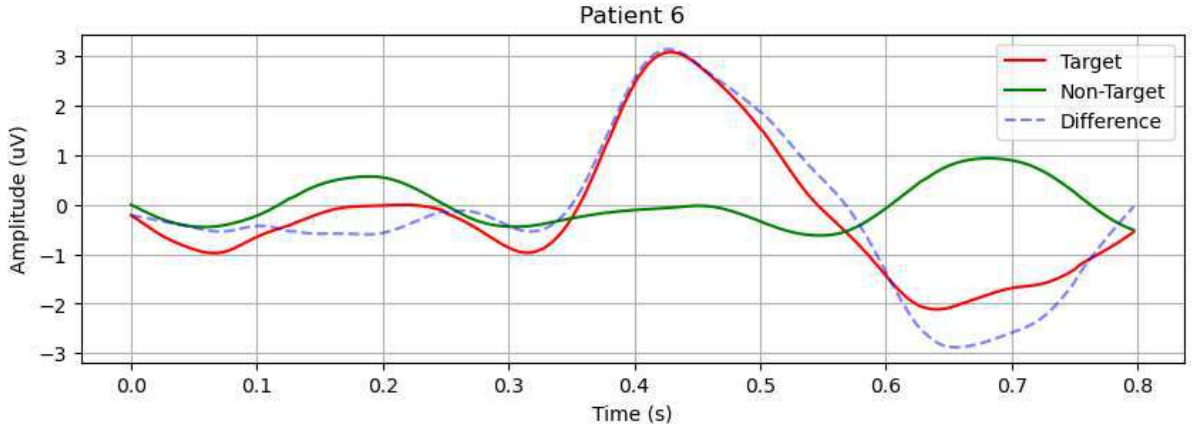

```
(700, 204) (3496, 204)
```



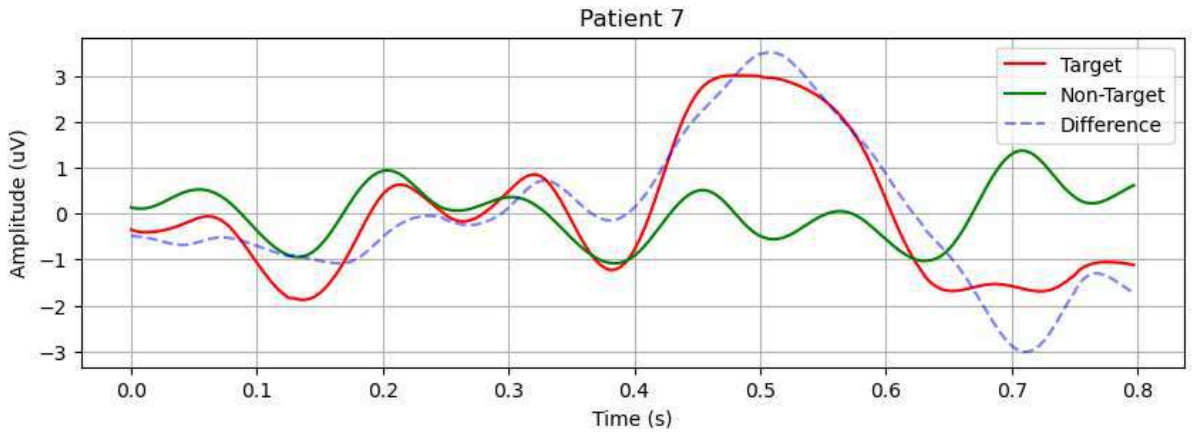

```
(700, 204) (3496, 204)
```



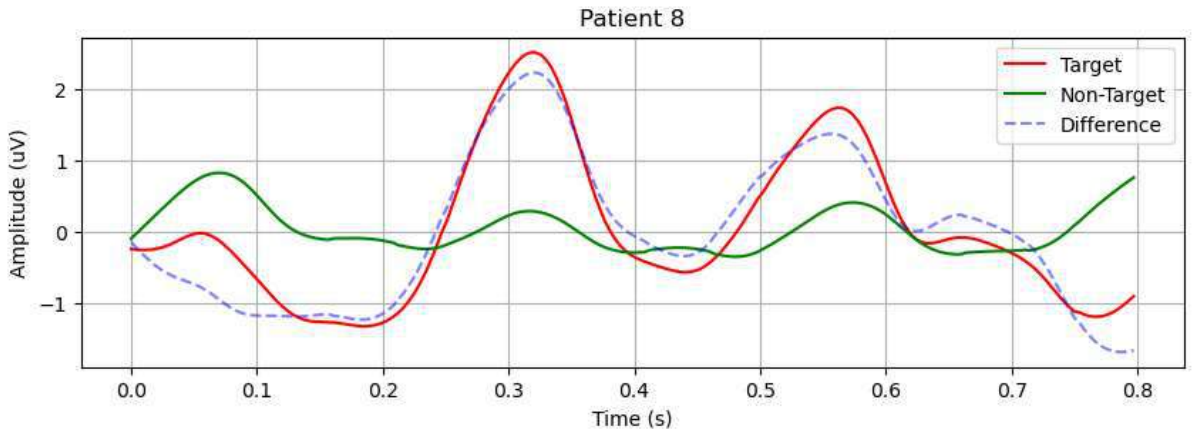

```
(700, 204) (3496, 204)
```




```
(700, 204) (3496, 204)
```




```
(700, 204) (3496, 204)
```



Classification - Part 1

Extract from the paper (Single trial classification)

To provide an estimate of the classifier accuracy we considered the binary classification problem target vs. non-target (Blankertz et al., 2011) that takes into account the correct classification of a target or of a non-target. Frequency filtering, data segmentation and artifact rejection were conducted as in P300 morphology section. EEG data were then resampled by replacing each sequence of 12 samples with their mean value, yielding 17 × 8 samples per epoch (eight being the number of channels), which were concatenated in a feature vector (Krusienski et al., 2006). A seven-fold cross-validation was used to evaluate the binary accuracy (BA) of the classifier on each participant's dataset. For each iteration we applied a SWLDA on the testing dataset (consisting of six words) to extract the 60 most significant control features (Draper and Smith, 1998) and we assessed the BA on the training dataset (the remaining word).

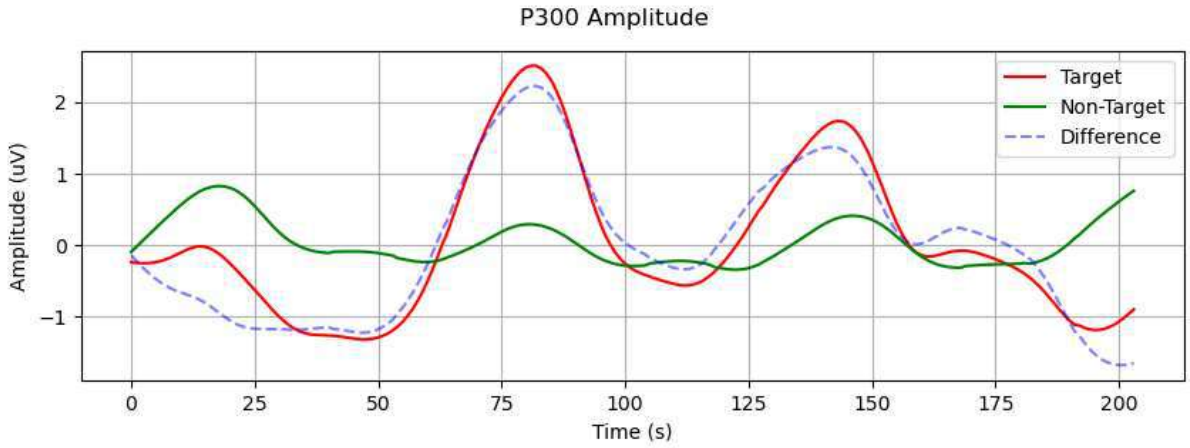
In [347]:
```
def create_dataset(x, y, show_progress=False, get_delayed_samples=0, get_fft=F
alse):
    """
    Input Shape: x: (Patients,Trial, Run, Samples, channels), y: (Patients,Tri
al, Run, Samples)
    Output Shape: (Data, Samples, channels), (Data, Samples)
    """
    waveform_start_time_after_onset = 0
    waveform_start_sample_after_onset = int(sample_frequency * waveform_start_
time_after_onset / 1000)

    stimulus_samples = 256*stimulus_duration//1000
    waveform_end_sample_after_onset = stimulus_samples + get_delayed_samples

    x = x.reshape((x.shape[0], x.shape[1] * x.shape[2] * x.shape[3], x.shape
[4]))
    y = y.reshape((y.shape[0], y.shape[1] * y.shape[2] * y.shape[3]))

    x_result = []
    y_result = []

    for patient in range(x.shape[0]):
        val = range(x.shape[1])
        if show_progress:
            val = tqdm(val)
        for sample in val:
            if (y[patient, sample] != 0) and  (y[patient, sample-1] != y[patie
nt, sample]): # start of onset
                if sample + waveform_end_sample_after_onset < y.shape[-1]:
                    x_result.append(x[i, sample+waveform_start_sample_after_on
set:sample+waveform_end_sample_after_onset, :])
                    y_result.append(y[patient, sample])

    return np.array(x_result), np.array(y_result)
```

In [360]:
```
# As per paper number of samples are 17*12 which and then a running average of
12 samples is calculated to obtain 17 samples
samples = 17*12
additional_samples = samples - (256*stimulus_duration//1000)
x, y = create_dataset(X_filtered, y_target, True, additional_samples)
x.shape
```

```
100%|██████████| 267680/267680 [00:00<00:00, 467139.42it/s]
100%|██████████| 267680/267680 [00:00<00:00, 468765.28it/s]
100%|██████████| 267680/267680 [00:00<00:00, 466326.06it/s]
100%|██████████| 267680/267680 [00:00<00:00, 468775.66it/s]
100%|██████████| 267680/267680 [00:00<00:00, 468776.64it/s]
100%|██████████| 267680/267680 [00:00<00:00, 466274.55it/s]
100%|██████████| 267680/267680 [00:00<00:00, 467139.23it/s]
100%|██████████| 267680/267680 [00:00<00:00, 463097.89it/s]
```

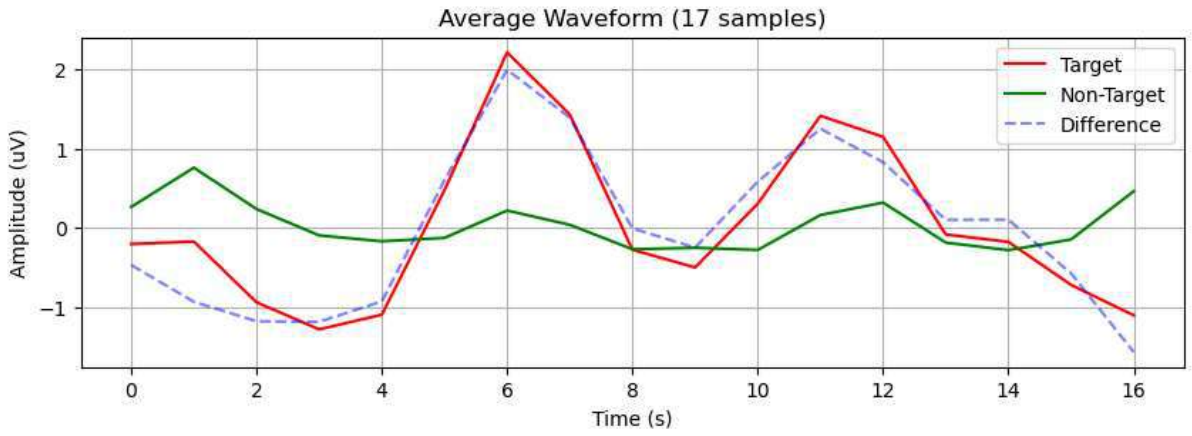
Out[360]: (33576, 204, 8)

In [361]:
```
target_waveforms = np.mean(x[np.where(y == 2)[0], :, get_channel_index(patient
_data[0], 'Cz')], axis=0)

non_target_waveforms = np.mean(x[np.where(y == 1)[0], :, get_channel_index(pat
ient_data[0], 'Cz')], axis=0)

plt.figure(figsize=(10,3))

plt.suptitle("P300 Amplitude")
plt.plot(target_waveforms, 'r-', label='Target')
plt.plot(non_target_waveforms, 'g-', label='Non-Target')
plt.plot(target_waveforms - non_target_waveforms, 'b--', alpha=0.5, label='Dif
ference')

plt.xlabel("Time (s)")
plt.ylabel("Amplitude (uV)")
plt.legend()
plt.grid()
plt.subplots_adjust(hspace=0.5)
plt.show()
```



In [362]:
```
target_waveforms = np.reshape(target_waveforms, (17, 12)).mean(axis=1)
print(target_waveforms.shape)
non_target_waveforms = np.reshape(non_target_waveforms, (17, 12)).mean(axis=1)

plt.figure(figsize=(10, 3))
plt.title("Average Waveform (17 samples)")
plt.plot(target_waveforms, 'r-', label='Target')
plt.plot(non_target_waveforms, 'g-', label='Non-Target')
plt.plot(target_waveforms - non_target_waveforms, 'b--', alpha=0.5, label='Dif
ference')

plt.xlabel("Time (s)")
plt.ylabel("Amplitude (uV)")
plt.legend()
plt.grid()
plt.subplots_adjust(hspace=0.5)
plt.show()
```

```
(17,)
```



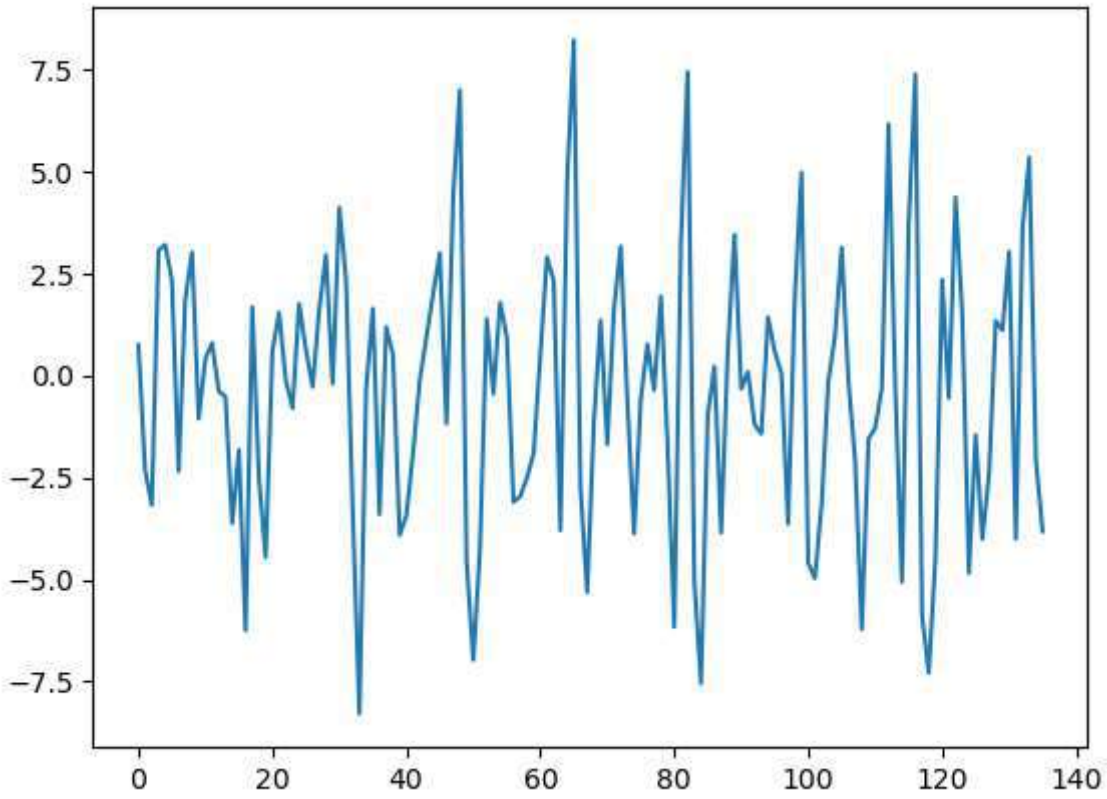
Create Dataset:

1. Labels: Non-Target(1), Target (2)
2. Input Size: 17x8 = 136

In [373]:
```
total_samples_per_class = 17*12 # Number of samples in each waveform
additional_samples = total_samples_per_class - int(256*stimulus_duration/1000)
# Additional sample
x, y = create_dataset(X_filtered, y_target, get_delayed_samples=additional_sam
ples, show_progress=True)
y = y - 1
print(x.shape)

# Bring channel to second axis for ease of visualization
x = x.transpose((0, 2, 1))

# Calculate average of consecutive 12 samples to get a sample of size 17x8
x = x.reshape((x.shape[0], x.shape[1], 17, 12)).mean(axis=-1)
x, y = shuffle(x, y, random_state=12432)
X_data = x.copy()
y_data = y.copy()
x = x.reshape((x.shape[0], -1))
print(x.shape)
```

```
100%|██████████| 267680/267680 [00:00<00:00, 459921.84it/s]
100%|██████████| 267680/267680 [00:00<00:00, 465508.20it/s]
100%|██████████| 267680/267680 [00:00<00:00, 462303.30it/s]
100%|██████████| 267680/267680 [00:00<00:00, 467143.11it/s]
100%|██████████| 267680/267680 [00:00<00:00, 465518.81it/s]
100%|██████████| 267680/267680 [00:00<00:00, 463904.81it/s]
100%|██████████| 267680/267680 [00:00<00:00, 463093.31it/s]
100%|██████████| 267680/267680 [00:00<00:00, 461506.68it/s]

(33576, 204, 8)
(33576, 136)
```

In [374]:
```
plt.figure()
plt.plot(x[2, :])
plt.show()
```



In [375]:
```
np.unique(y)
```

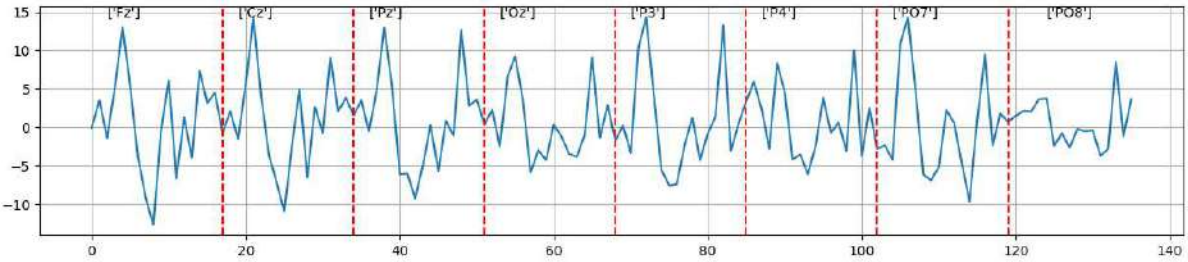
Out[375]:
```
array([0, 1], dtype=uint8)
```

In [376]:
```
# Balancing the dataset
data_per_class = 5600
indices = np.concatenate((np.where(y == 0)[0][:data_per_class], np.where(y ==
1)[0][:data_per_class]))
x = x[indices, :]
y = y[indices]
```

In [377]:
```
X_train, X_test, y_train, y_test = train_test_split(x, y, test_size=0.2, rando
m_state=6150)
print(X_train.shape, y_train.shape, X_test.shape, y_test.shape)
```

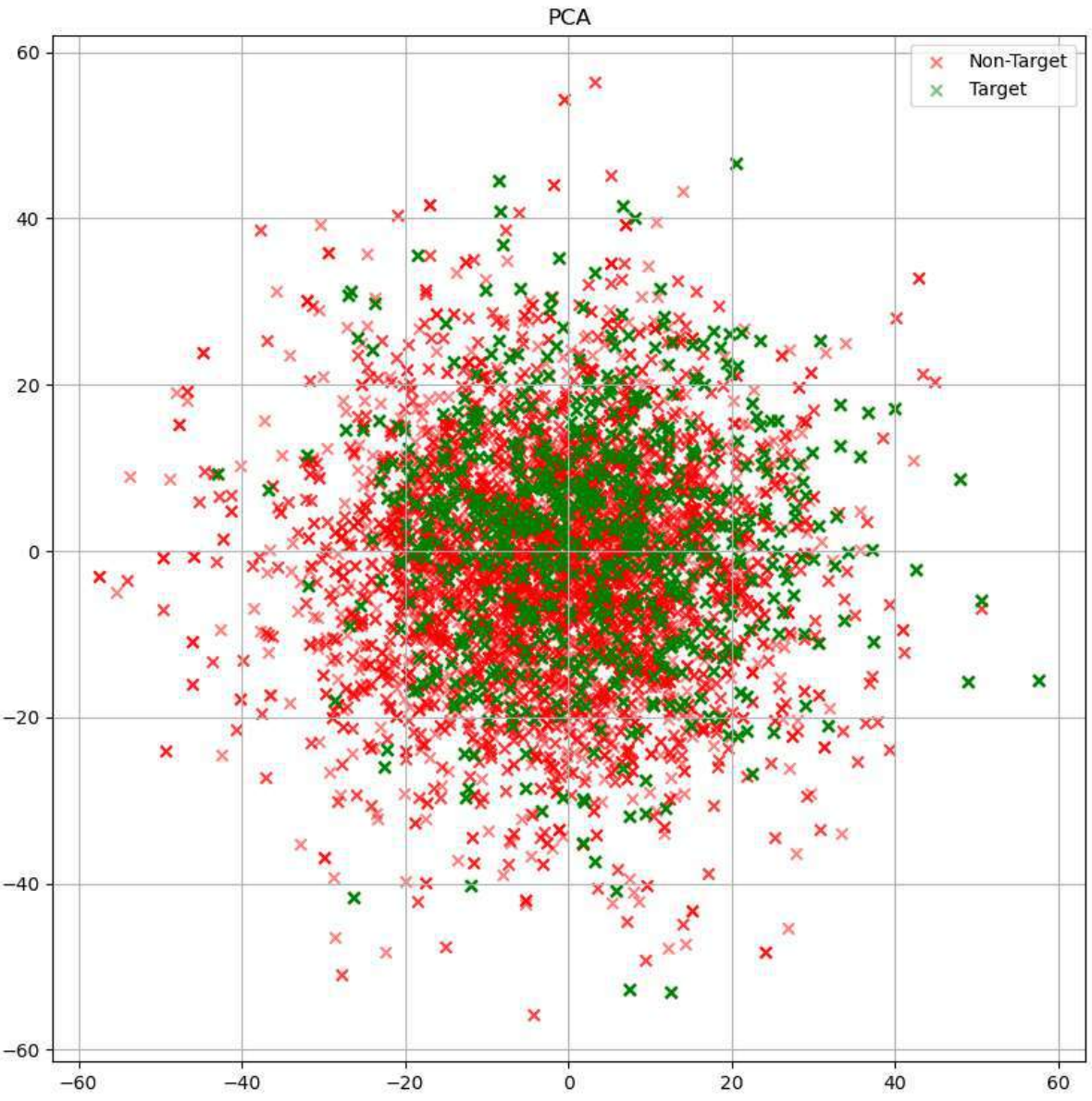
```
(8960, 136) (8960,) (2240, 136) (2240,)
```

In [396]:
```
plt.figure(figsize=(15, 3))
plt.plot(x[0, :])
a = np.max(x[0])
for i in range(1, 8):
    p = x.shape[-1]//8*i
    plt.axvline(x=p, color='red', linestyle='--')
    plt.text(p-15, a, get_channel_name(patient_data[0], i-1))
    if i == 7:
        plt.text(p+5, a, get_channel_name(patient_data[0], i))
plt.grid()
plt.show()
```



PCA for visualization

In [397]:
```
a =  PCA(n_components=2).fit(x).transform(x)
plt.figure(figsize=(10, 10))
plt.title("PCA")
plt.scatter(a[y == 0, 0], a[y == 0, 1], label='Non-Target', color='r', alpha=
0.5, marker='x')
plt.scatter(a[y == 1, 0], a[y == 1, 1], label='Target', color='g', alpha=0.5,
marker='x')
plt.grid()
plt.legend()
plt.show()
```



Stepwise LDA

Source: https://sebastianraschka.com/Articles/2014_python_lda.html (https://sebastianraschka.com/Articles/2014_python_lda.html)

LDA is a supervised machine learning algorithm that reduces the number of dimensions in feature space of a dataset. However, the number of reduced dimension is equal to the minimum value between the number of features in the feature space minus one and total number of classes minus one. Since, this classification algorithm consists of just 2 classes(Target and Non-Target) the reduced number of feature is equal to 1.

Therefore, in order to extract multiple important features using LDA we need to compute Stepwise Linear Discriminant Analysis(SWLDA) which is a form of LDA but calculates multiple important features in order to reduce the dimensionality of the feature space.

Overview

Summarizing the LDA approach in 5 steps:

Listed below are the 5 general steps for performing a linear discriminant analysis; we will explore them in more detail in the following sections.

1. Compute the d-dimensional mean vectors for the different classes from the dataset.
1. Compute the scatter matrices (in-between-class and within-class scatter matrix).
1. Compute the eigenvectors (ee1,ee2,...,eed) and corresponding eigenvalues (λλ1,λλ2,...,λλd) for the scatter matrices.
1. Sort the eigenvectors by decreasing eigenvalues and choose k eigenvectors with the largest eigenvalues to form a d×k dimensional matrix WW (where every column represents an eigenvector).
1. Use this d×k eigenvector matrix to transform the samples onto the new subspace. This can be summarized by the matrix multiplication: YY=XX×WW (where XX is a n×d-dimensional matrix representing the n samples, and yy are the transformed n×k-dimensional samples in the new subspace).

Compute the d-dimensional mean vectors for the different classes from the dataset.

Calculate Mean of feature vector for all signals of each class.

Shape of Mean Vector: MxN where M is no. of classes and N is No. of features

2. Compute the Scatter Matrices

Now, we will compute the two 4x4-dimensional matrices: The within-class and the between-class scatter matrix.

a. Within Class Scatter Matrix, S_W:

The within-class scatter matrix SW is computed by the following equation:

$$S_W = \sum_{i=1}^{c} S_i$$

where 'c' i the no. of available classes and

$$S_i = \sum_{x \in D_i}^{n} (x - m_i)(x - m_i)^T$$

Here,

x = A feature vector that belongs to the i^{th} class

D_i = The set of feature vectors(signals) in the i^{th} class

n = Total no. of feature vectors/signals in the i^{th} class

m_i = Mean vector for the i^{th} class

$$m_i = \frac{1}{n_i} \sum_{x \in D_i}^{n} x_k$$

Here,

x_k = k^{th} feature vector/signal belonging to the i^{th} class

b. Between class Scatter matrix, S_B:

The between-class scatter matrix SB is computed by the following equation:

$$S_B = \sum_{i=1}^{c} N_i (m_i - m)(m_i - m)^T$$

Here,

c = Number of Total Classes available

N_i = Size(Total feature vectors/signals) in i^{th} class

m_i = Mean vector of the i^{th} class

m = Overall Mean(For all classes)

3. Solving the generalized eigenvalue problem for the matrix $S_W^{-1} S_B$

1. Next, we will solve the generalized eigenvalue problem for the matrix $S_W^{-1} S_B$ to obtain the linear discriminants.
2. Then we will perform a quick check that the eigenvector-eigenvalue calculation is correct and satisfy the equation:

$$Av = \lambda v$$

Here,

A = $S_W^{-1} S_B$

v = Eigenvector

λ = eigenvalue

4. Selecting linear discriminants for the new feature subspace

4.1 Sorting the eigenvectors by decreasing eigenvalues

Remember from the introduction that we are not only interested in merely projecting the data into a subspace that improves the class separability, but also reduces the dimensionality of our feature space, (where the eigenvectors will form the axes of this new feature subspace).

However, the eigenvectors only define the directions of the new axis, since they have all the same unit length 1.

So, in order to decide which eigenvector(s) we want to drop for our lower-dimensional subspace, we have to take a look at the corresponding eigenvalues of the eigenvectors. Roughly speaking, the eigenvectors with the lowest eigenvalues bear the least information about the distribution of the data, and those are the ones we want to drop. The common approach is to rank the eigenvectors from highest to lowest corresponding eigenvalue and choose the top k eigenvectors.

4.2 Choosing k eigenvectors with the largest eigenvalues

After sorting the eigenpairs by decreasing eigenvalues, it is now time to construct our k×d-dimensional eigenvector matrix W (here N×2: based on the 2 most informative eigenpairs) and thereby reducing the initial N-dimensional feature space into a 2-dimensional feature subspace.

5. Transforming the samples onto the new subspace

In the last step, we use the 4×2-dimensional matrix WW that we just computed to transform our samples onto the new subspace via the equation:

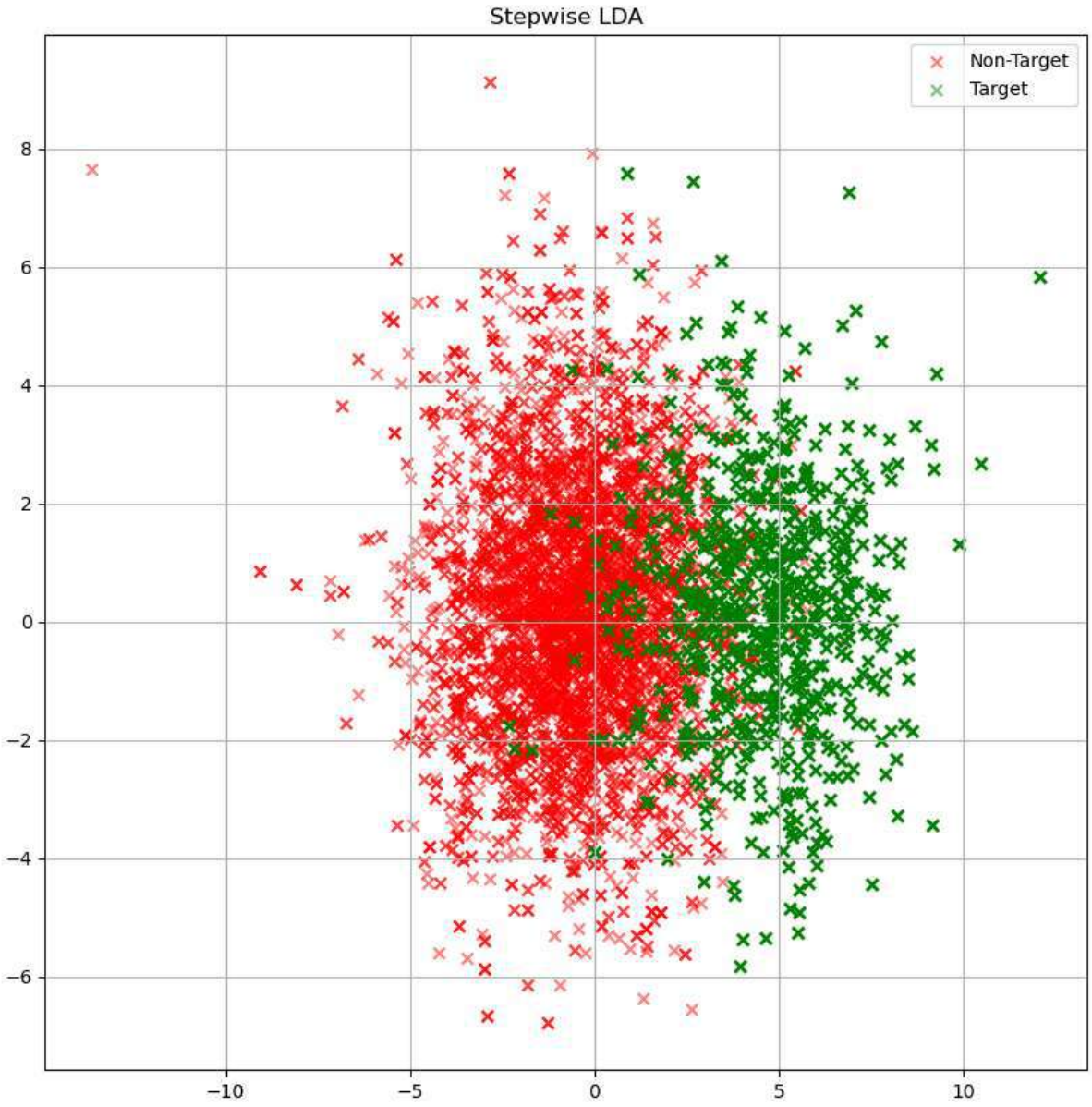
$$Y = XxW$$

(where X is a n×d-dimensional matrix representing the n samples, and Y are the transformed n×k-dimensional samples in the new subspace).

In [295]:
```
class StepwiseLDA:
    def __init__(self, n_components):
        self.n_components = n_components
        self.classes = []
        self.eigenpairs = []
        self.weights = None

    def transform(self, x):
        if self.weights is None:
            raise ValueError("Please fit the model before using it")

        return x.dot(self.weights)



    def fit(self, x, y):
        self.classes = np.unique(y)

        # Calculate mean vectors
        mean_vectors = []
        for c in self.classes:
            mean_vectors.append(np.mean(x[y == c], axis=0))
        mean_vectors = np.array(mean_vectors)



        s_w = np.zeros((x.shape[1],x.shape[1]))  # Create scatter within matri
x for each feature
        s_b = np.zeros((x.shape[1],x.shape[1]))  # Between Class Scatter Matri
x
        overall_mean = np.mean(x, axis=0).reshape(x.shape[1],1)  # Mean for al
l classes

        for cl, mv in zip(self.classes, mean_vectors):  # For each class and i
ts corresponding mean vector
            mv = mv.reshape(x.shape[1],1) # transpose mean vector of the curre
nt class
            x_target = x[y==cl]  # Calculate size/total no. of feature vectors
in the current class
            n = x_target.shape[0]

            # Calculate within-class Scatter matrix
            class_sc_mat = np.zeros((x.shape[1],x.shape[1]))
# scatter matrix for every class
            for row in x_target:
                row = row.reshape(x.shape[1],1) # make column vectors
                class_sc_mat += (row-mv).dot((row-mv).T)

            s_w += class_sc_mat                                 # sum class scatte
r matrices

            # calculate between-class scatter matrix
            s_b += n * (mv - overall_mean).dot((mv - overall_mean).T)  # Calcu
late Between class scatter matrix
```

```
        # Compute Eigen Value and Eigenvector for the dot product between the
two matrices
        eig_vals, eig_vecs = np.linalg.eig(np.linalg.inv(s_w).dot(s_b))


        # Make a list of (eigenvalue, eigenvector) tuples
        self.eigenpairs = [(np.abs(eig_vals[i]), eig_vecs[:,i]) for i in range
(len(eig_vals))]

        # Sort the (eigenvalue, eigenvector) tuples from high to low
        self.eigenpairs = sorted(self.eigenpairs, key=lambda k: k[0], reverse=
True)

        # Calculate weights
        self.weights = self.eigenpairs[0][1].reshape(x.shape[1],1)
        #W = np.hstack((, eig_pairs[1][1].reshape(x_tr_an.shape[1],1)))
        for i in range(1, self.n_components):
            self.weights = np.hstack((self.weights, self.eigenpairs[i][1].resh
ape(x.shape[1],1)))

        return self
```

In [398]:
```
a =  StepwiseLDA(n_components=2).fit(x, y).transform(x)
plt.figure(figsize=(10, 10))
plt.title("Stepwise LDA")
plt.scatter(a[y == 0, 0].real, a[y == 0, 1].real, label='Non-Target', color
='r', alpha=0.5, marker='x')
plt.scatter(a[y == 1, 0].real, a[y == 1, 1].real, label='Target', color='g', a
lpha=0.5, marker='x')
plt.grid()
plt.legend()
plt.show()
```



Random Forest Classification

We will perform Random Forest Classification using the following datasets:

1. **Simple waveform:** Here we will use the individual waveforms as the input data.
2. **PCA Feature:** Here, we will use PCA on each individual waveform to extract important features and perform classification on those feature as inputs.
3. **Stepwise LDA Feature:** Here, we will use Step-Wise LDA on each individual waveform to extract important features and perform classification on those feature as inputs.

1. Simple Waveform

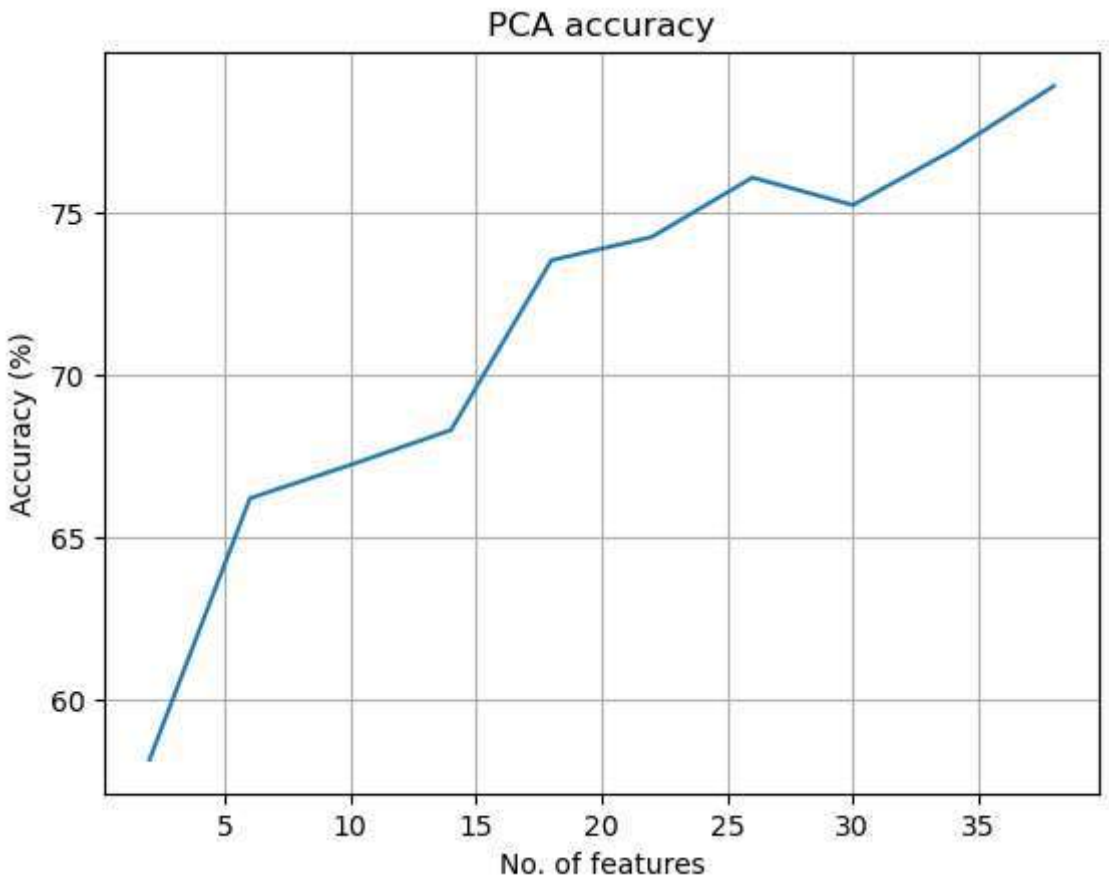
In [399]:
```
clf = RandomForestClassifier(max_depth=2, random_state=26784)
clf.fit(X_train, y_train)
print(f"Accuracy: {clf.score(X_test, y_test)*100:.5f}%")
```

```
Accuracy: 75.66964%
```

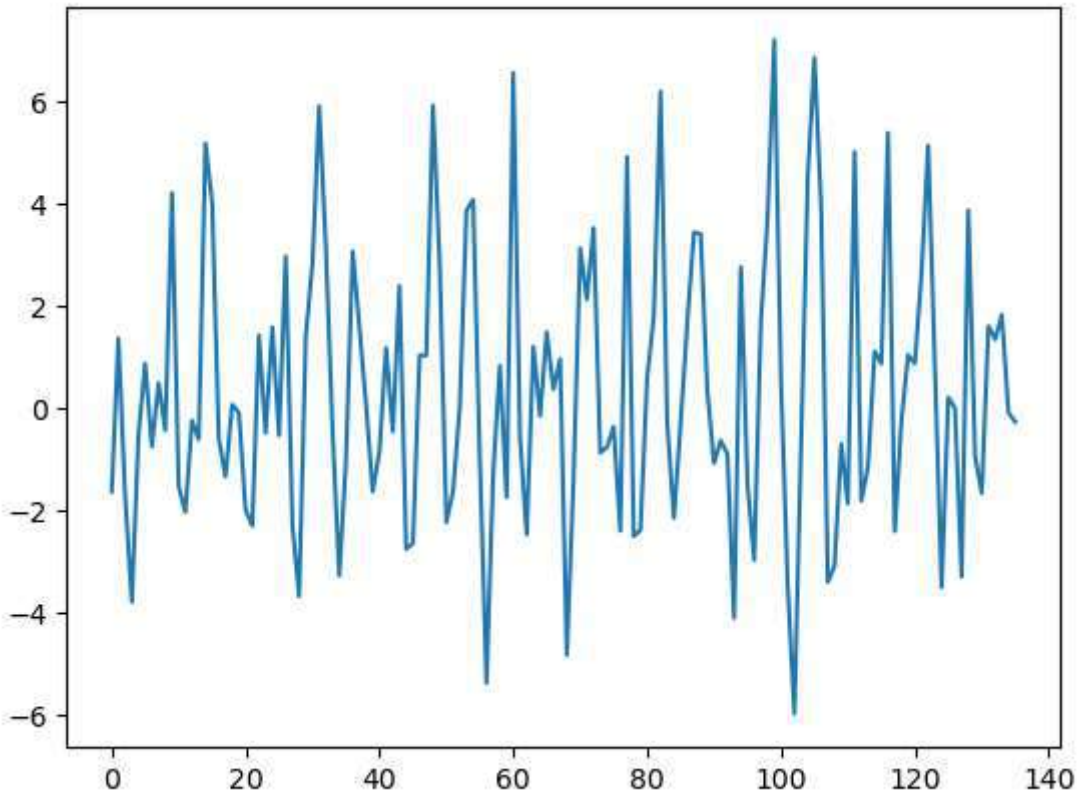
2. PCA

In [400]:
```
input_features = np.arange(2, 42, 4)
accuracies = []

for f in tqdm(input_features):
    pca = PCA(n_components=f)
    pca.fit(X_train, y_train)
    a, b = pca.transform(X_train), pca.transform(X_test)
    clf = RandomForestClassifier(max_depth=2, random_state=26784)
    clf.fit(a, y_train)
    accuracies.append(clf.score(b, y_test)*100)


plt.figure()
plt.title("PCA accuracy")
plt.plot(input_features, accuracies)
plt.grid()
plt.xlabel("No. of features")
plt.ylabel("Accuracy (%)")
plt.show()
```

```
100%|██████████| 10/10 [00:09<00:00,  1.11it/s]
```



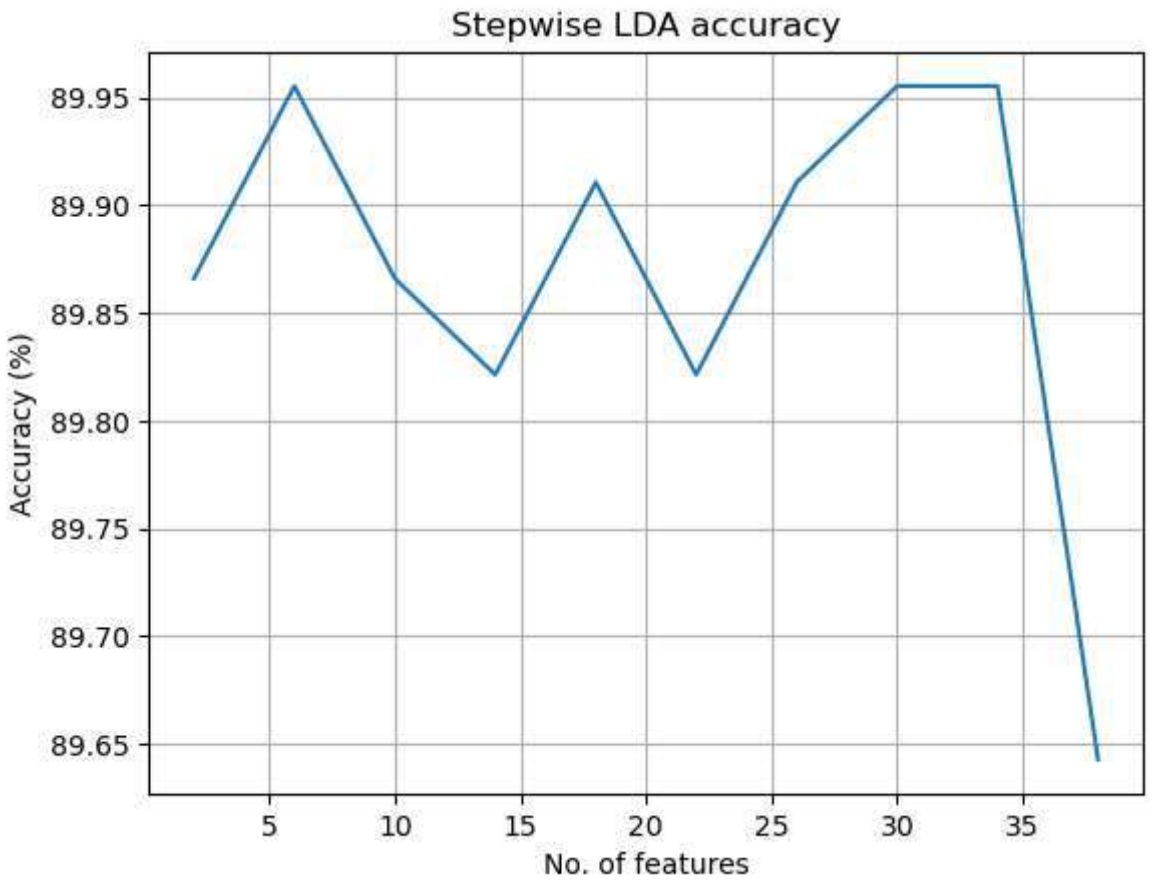
In [401]:
```
plt.figure()
plt.plot(X_train[0, :])
plt.show()
```



3. Stepwise LDA

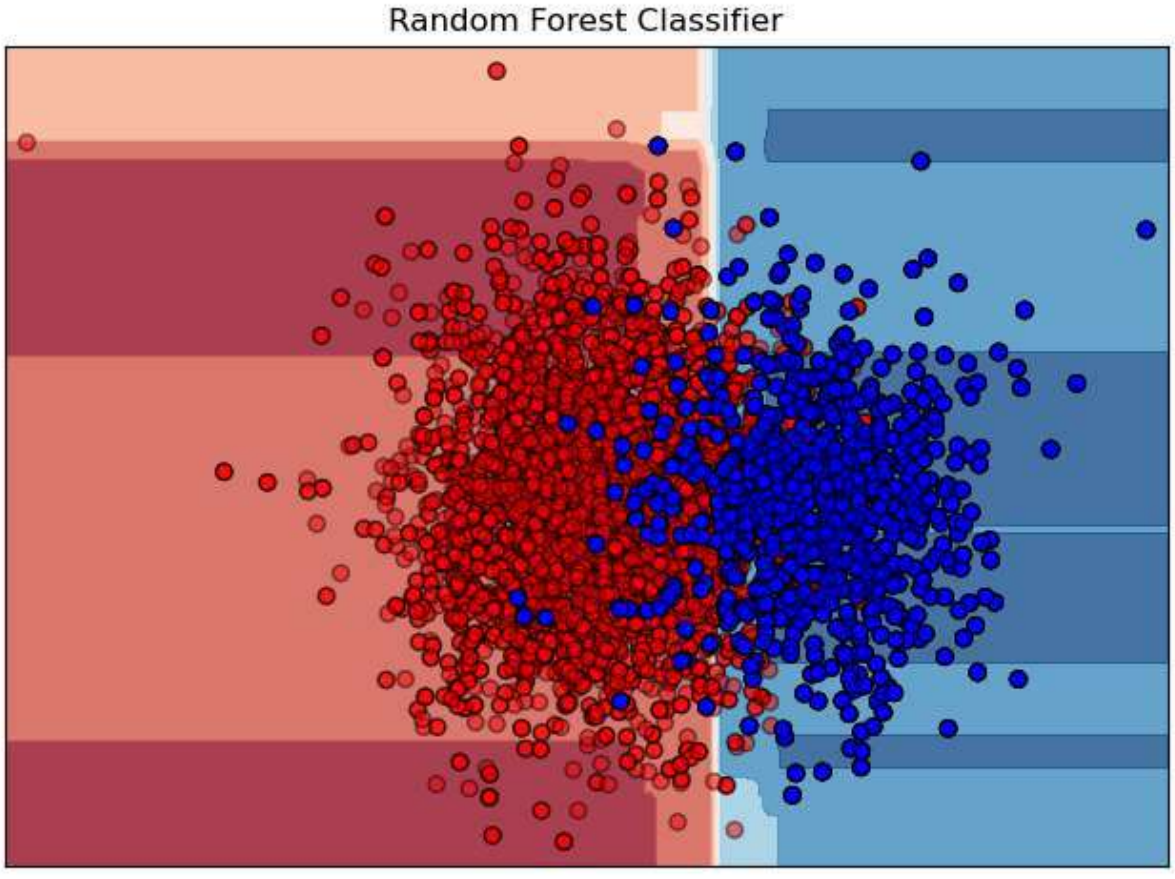
In [402]:
```
input_features = np.arange(2, 42, 4)
accuracies = []

for f in tqdm(input_features):
    lda = StepwiseLDA(f)
    lda.fit(X_train, y_train)
    a, b = lda.transform(X_train), lda.transform(X_test)
    clf = RandomForestClassifier(max_depth=2, random_state=26784)
    clf.fit(a.real, y_train)
    accuracies.append(clf.score(b.real, y_test)*100)


plt.figure()
plt.title("Stepwise LDA accuracy")
plt.plot(input_features, accuracies)
plt.grid()
plt.xlabel("No. of features")
plt.ylabel("Accuracy (%)")
plt.show()
```

```
100%|██████████| 10/10 [00:09<00:00,  1.04it/s]
```



In [ ]:

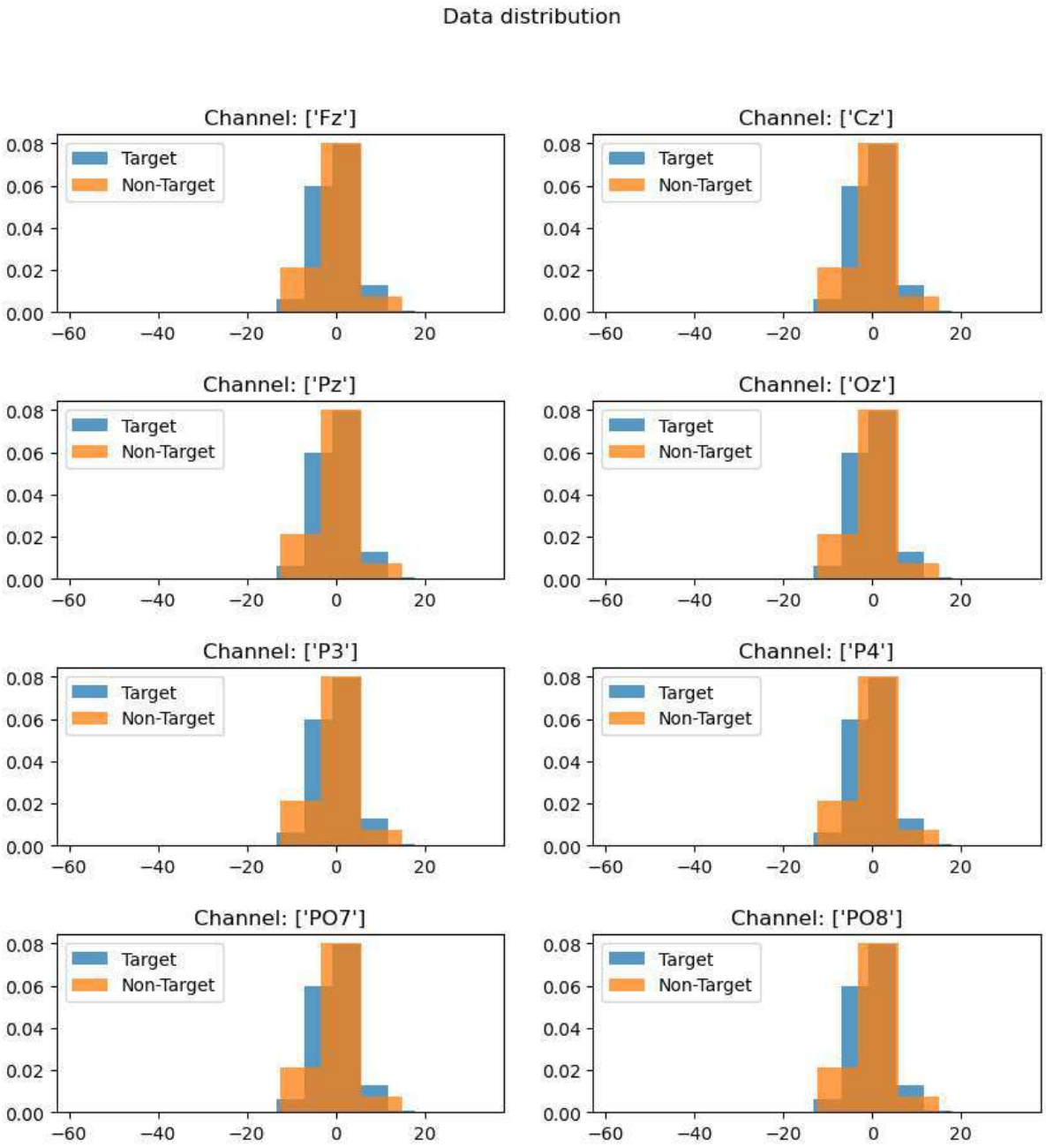
In [403]:
```
a =  StepwiseLDA(n_components=2).fit(x, y).transform(x)
clf = RandomForestClassifier(max_depth=2, random_state=26784)
clf.fit(a.real, y)

plt.figure()

ax = plt.subplot(1, 1, 1)
ax.set_title("Random Forest Classifier")

DecisionBoundaryDisplay.from_estimator(
            clf, a.real, cmap=plt.cm.RdBu, alpha=0.8, ax=ax, eps=0.5
        )

ax.scatter(a[:, 0].real, a[:, 1].real, c=y, alpha=0.5, edgecolors="k", cmap=Li
stedColormap(["#FF0000", "#0000FF"]))

x_min, x_max = a[:, 0].real.min() - 0.5, a[:, 0].real.max() + 0.5
y_min, y_max = a[:, 1].real.min() - 0.5, a[:, 1].real.max() + 0.5

ax.set_xlim(x_min, x_max)
ax.set_xlim(x_min, x_max)
ax.set_ylim(y_min, y_max)
ax.set_xticks(())
ax.set_yticks(())


plt.tight_layout()
plt.show()
```



Stepwise LDA provides the best classification accuracy when the number of features is around 35-40. However, the classification accuracy is around 90\%.

Distribution of the data

In [405]:
```
cols = 2
rows = X_data.shape[1]/cols
if int(rows) != rows:
    rows = int(rows) + 1
else:
    rows = int(rows)




current = 0

fig, ax = plt.subplots(rows, cols, figsize=(10, 10))
plt.suptitle("Data distribution")
for j in range(rows):
    for k in range(cols):
        if current >= X_data.shape[1]:
            break
        ax[j, k].set_title(f"Channel: {get_channel_name(patient_data[0], curre
nt)}")


        ax[j, k].hist(X_data[y_data == 1].reshape(-1)+1e-6, density=True, labe
l='Target', alpha=0.75)
        ax[j, k].hist(X_data[y_data == 0].reshape(-1)+1e-6, density=True, labe
l='Non-Target', alpha=0.75)
        ax[j, k].legend()

        current += 1

plt.subplots_adjust(hspace=0.5)
plt.show()
```


Data distribution
Channel: ['Fz']
Channel: ['Cz']
Channel: ['Pz']
Channel: ['Oz']
Channel: ['P3']
Channel: ['P4']
Channel: ['PO7']
Channel: ['PO8']
Target
Non-Target
0.08
0.06
0.04
0.02
0.00
−60
−40
−20
0
20

Statistical significance of P300

P300 should have a positive deflection in the waveform generated between 200-700 ms after the onset of a stimulus. As seen from the average waveforms calculated above (P300 Amplitude) we do see that the target signal of each channel has a positive peak compared to non-target signal. We would like to check the significance level of this statement.

To calculate whether target waveforms have higher amplitude, we will first calculate the average waveform from a number of sample signals. We will then calculate the average positive peak amplitude of the average waveform. This will provide us the highest peak amplitude of the waveform. We will then test on average, whether the peak amplitude of a target waveform is higher than a non-target waveform.

Therefore, we would like to test the following - Target waveforms have a lower or equal peak amplitude than non-target waveforms. i.e.

$$H_0 : \mu_{target} - \mu_{nontarget} \leq 0$$
$$H_1 : \mu_{target} - \mu_{nontarget} > 0$$

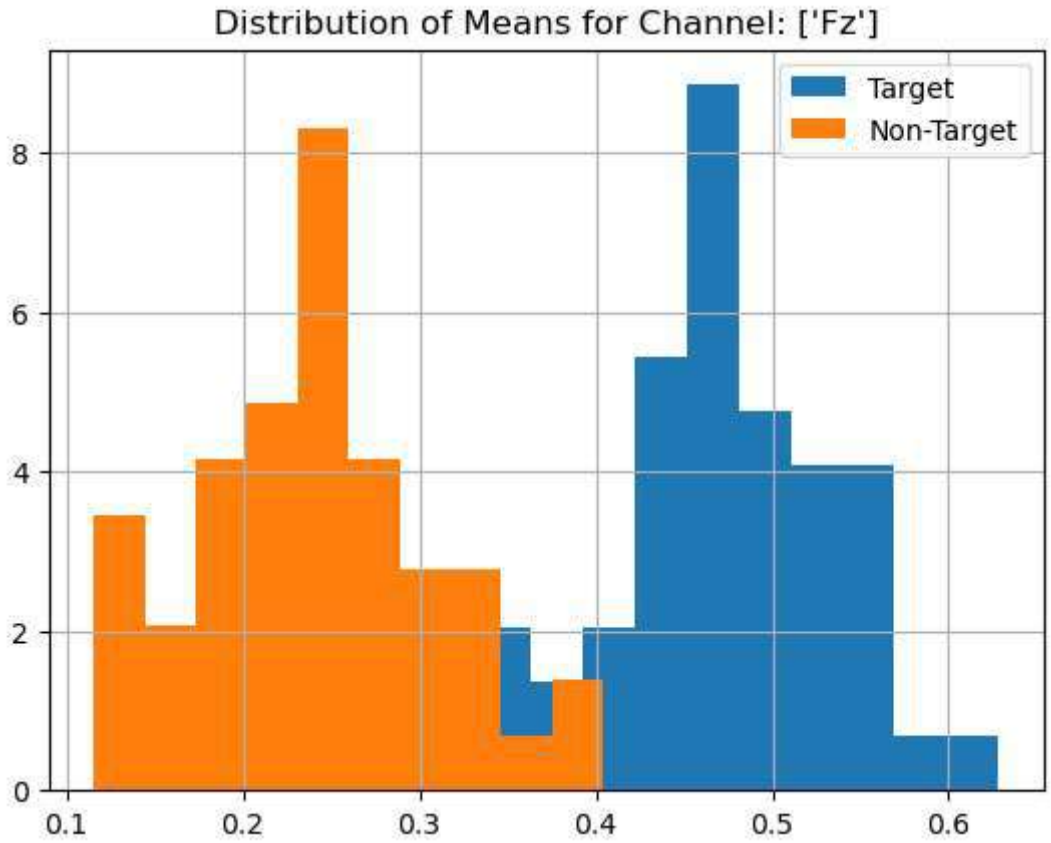
In [406]:
```
x_target = X_data[np.where(y_data == 1)[0]]
x_nontarget = X_data[np.where(y_data == 0)[0]]
print(x_target.shape)
```

```
(5600, 8, 17)
```

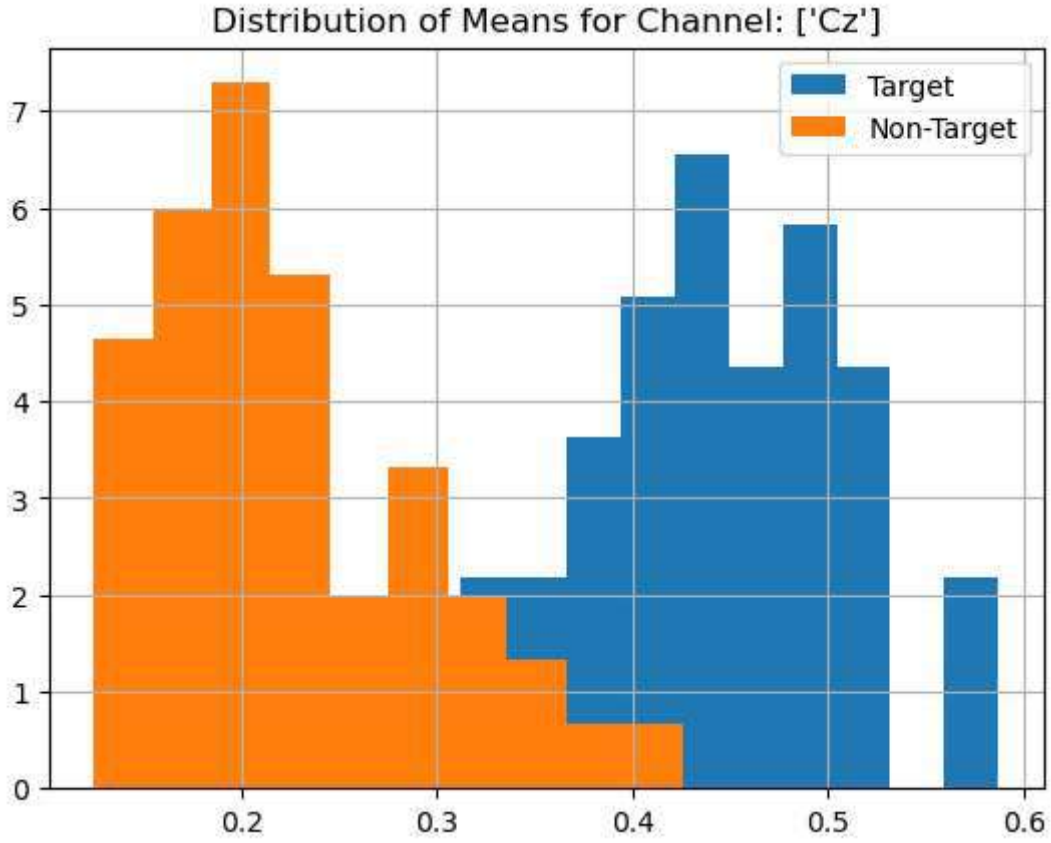
In [408]:
```
mean_calculation_data_size = 100
sample_size = 50



np.random.seed(34324)

def view_distribution():
    for channel in range(x_target.shape[1]):
        ma_t = []
        ma_nt = []
        for _ in range(sample_size):
            # Get average waveform from sample
            t = np.mean(x_target[ np.random.choice(np.arange(x_target.shape
[0]), size=mean_calculation_data_size, replace=False), channel, :], axis=0)
            nt = np.mean(x_nontarget[ np.random.choice(np.arange(x_nontarget.s
hape[0]), size=mean_calculation_data_size, replace=False), channel, :], axis=
0)

            # Remove negative portion of average waveform as P300 deflection i
s positive
            t[t<0] = 0
            nt[nt<0] = 0

            # Calculate the average amplitude of each signal
            ma_nt.append(np.mean(nt))
            ma_t.append(np.mean(t))

        mean_target_amplitude = np.mean(ma_t)
        std_target_amplitude = np.std(ma_t)

        mean_nontarget_amplitude = np.mean(ma_nt)
        std_nontarget_amplitude = np.std(ma_nt)

        print(f"Target Mean: {mean_target_amplitude}, Std: {std_target_amplitu
de}")
        print(f"Non-Target Mean: {mean_nontarget_amplitude}, Std: {std_nontarg
et_amplitude}")

        # T-Statistics
        confidence = 0.95
        d = stats.ttest_ind(ma_t, ma_nt, equal_var=False, alternative='greate
r')
        print(f"Confidence interval: {d.confidence_interval(confidence)}, T-Sc
ore: {d.statistic:.6f}, Degree of freedom: {d.df}, P-Value: {d.pvalue}")
        if d.pvalue > (1-confidence):
            print(f"With a significance level of {1-confidence:.5f}, the hypot
hesis is accepted")
        else:
            print(f"With a significance level of {1-confidence:.5f}, the hypot
hesis is rejected")



        plt.figure()
```

```
        plt.title(f"Distribution of Means for Channel: {get_channel_name(patie
nt_data[0], channel)}")
        plt.hist(ma_t, density=True, label='Target')
        plt.hist(ma_nt, density=True, label='Non-Target')
        plt.grid()
        plt.legend()
        plt.show()


view_distribution()
```

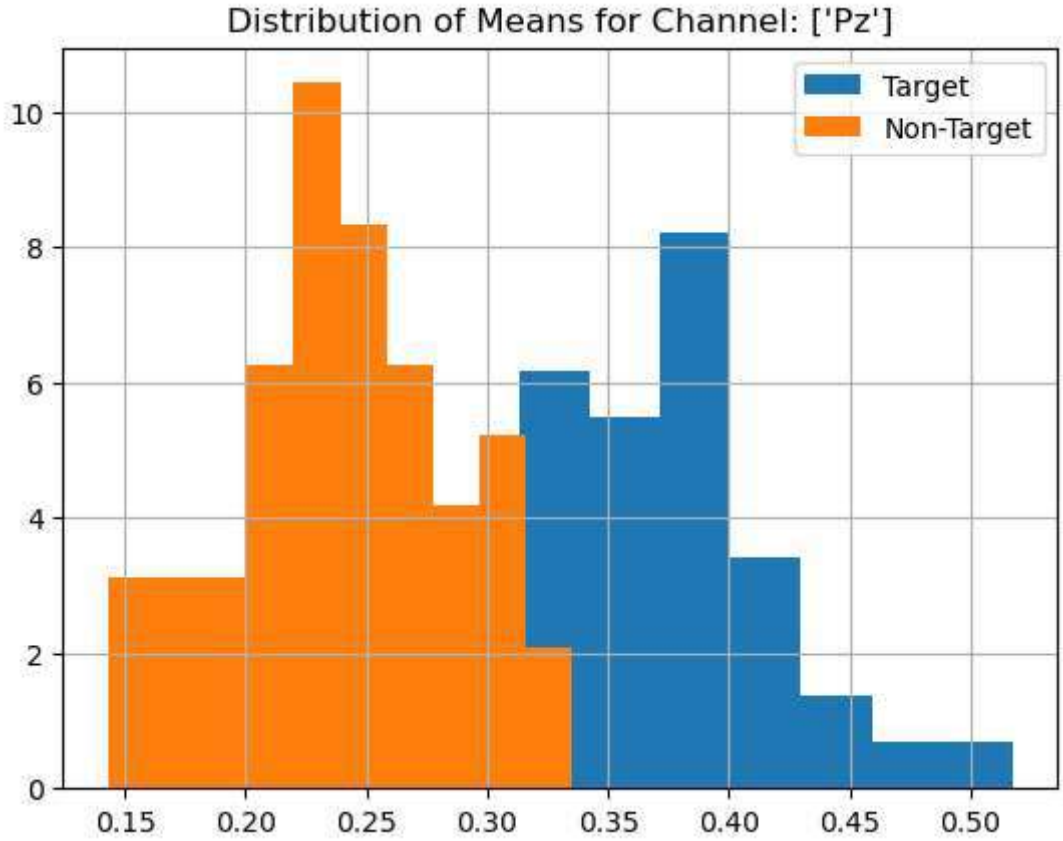
```
Target Mean: 0.4746667094587482, Std: 0.06067926240884431
Non-Target Mean: 0.24015819804121472, Std: 0.06664372629531629
Confidence interval: ConfidenceInterval(low=0.21312602098023875, high=inf), T
-Score: 18.213308, Degree of freedom: 97.15095202987126, P-Value: 2.162793025
238947e-33
With a significance level of 0.05000, the hypothesis is rejected
```



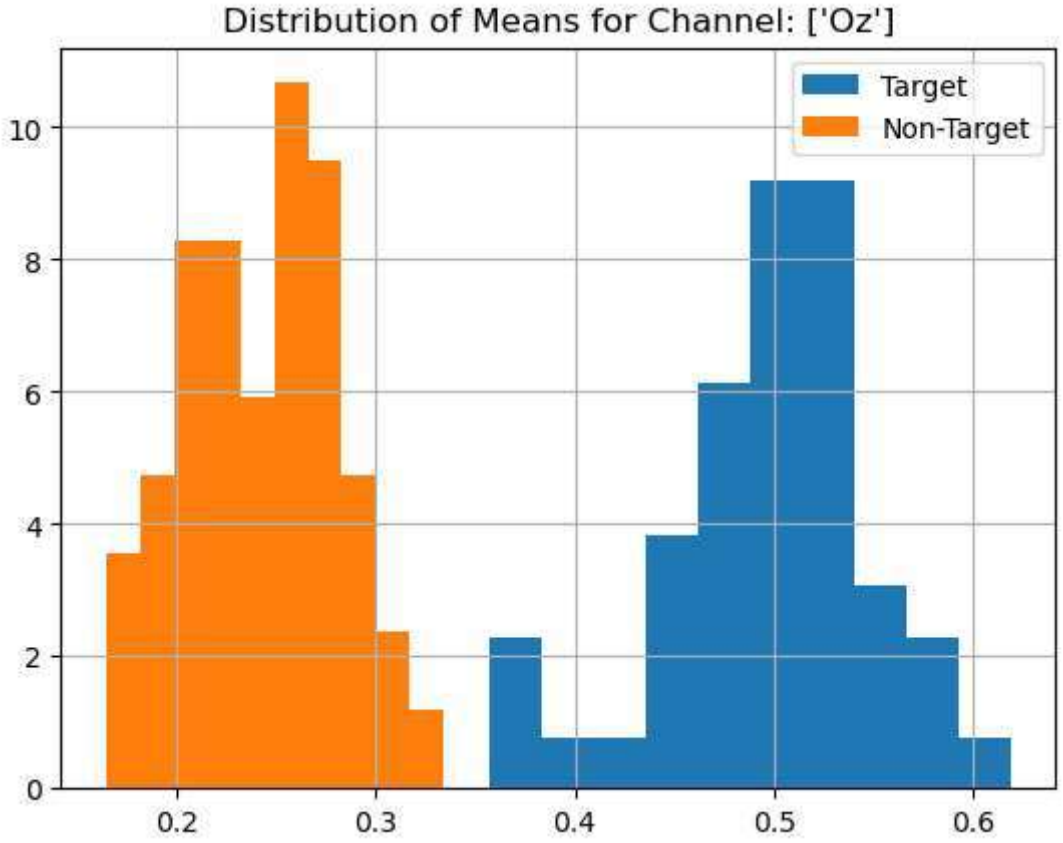

```
Target Mean: 0.4430455069649211, Std: 0.06409750127575528
Non-Target Mean: 0.2240366996275501, Std: 0.06755833438070388
Confidence interval: ConfidenceInterval(low=0.1969165145731703, high=inf), T-
Score: 16.462072, Degree of freedom: 97.73024464785895, P-Value: 3.0944242509
278306e-30
With a significance level of 0.05000, the hypothesis is rejected
```



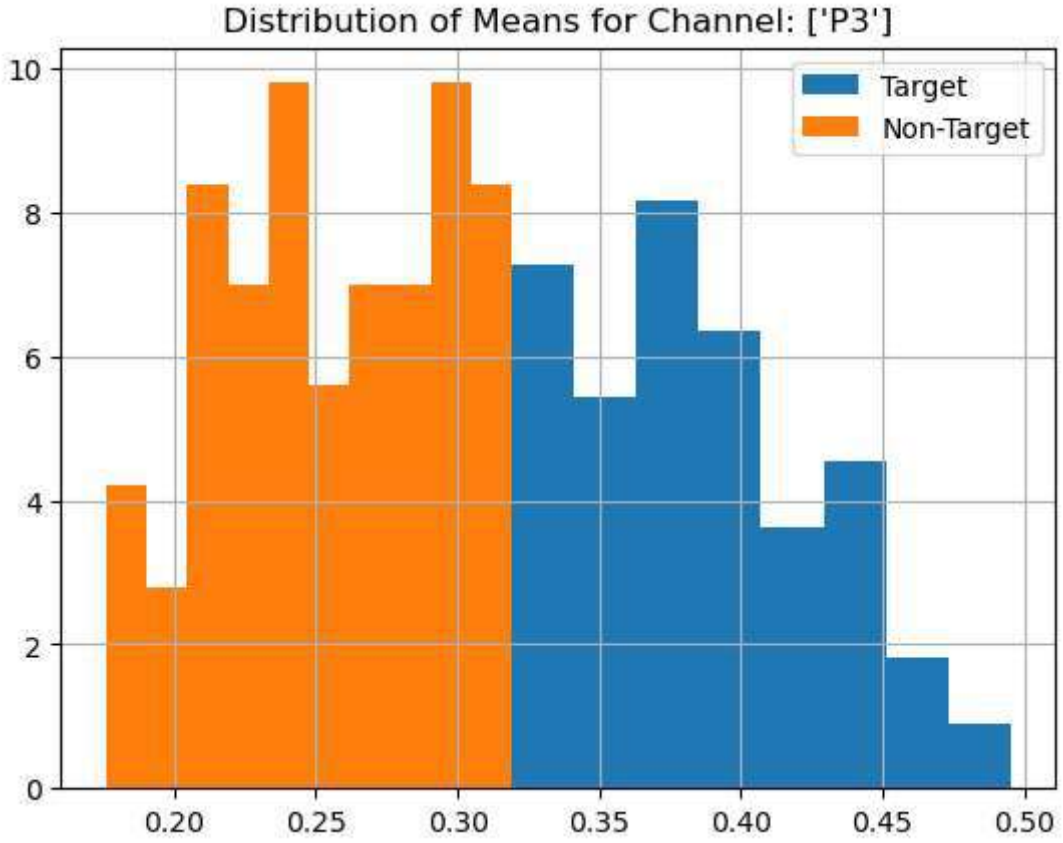

```
Target Mean: 0.35340510703701644, Std: 0.05866412000737728
Non-Target Mean: 0.2407385726597356, Std: 0.04620404466447245
Confidence interval: ConfidenceInterval(low=0.09494282355909965, high=inf), T
-Score: 10.561368, Degree of freedom: 92.89907503939554, P-Value: 6.790690380
754123e-18
With a significance level of 0.05000, the hypothesis is rejected
```



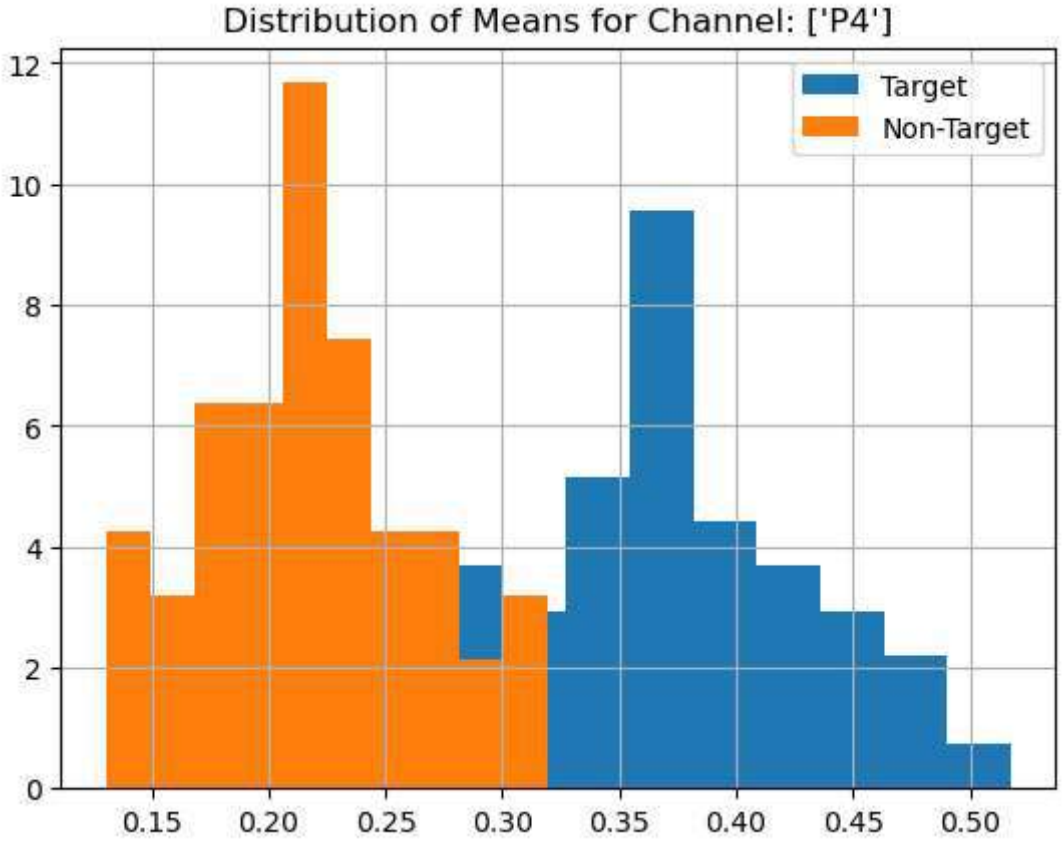

```
Target Mean: 0.49529928174690974, Std: 0.05260673046086157
Non-Target Mean: 0.24200223010514071, Std: 0.03872916141635347
Confidence interval: ConfidenceInterval(low=0.23778738231398838, high=inf), T
-Score: 27.142240, Degree of freedom: 90.05510589000879, P-Value: 1.955583020
1937045e-45
With a significance level of 0.05000, the hypothesis is rejected
```



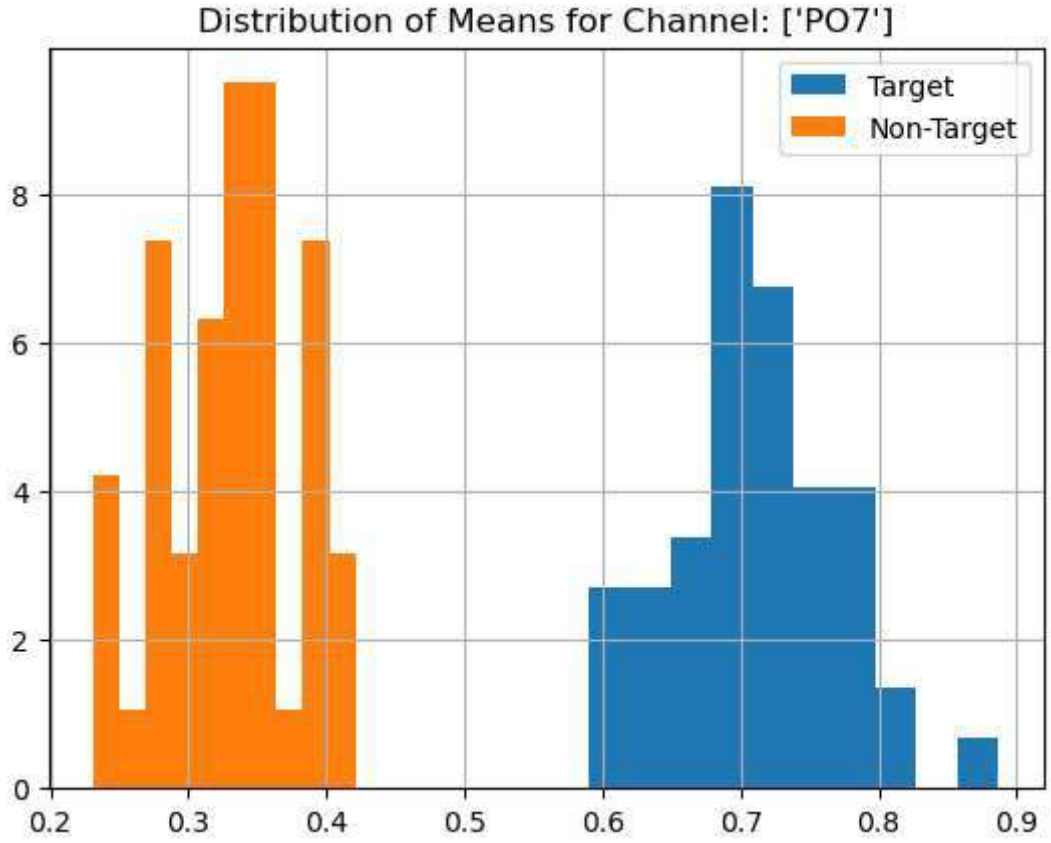

```
Target Mean: 0.3725125640378665, Std: 0.05026233400631502
Non-Target Mean: 0.25610144642838334, Std: 0.03899375926360597
Confidence interval: ConfidenceInterval(low=0.10131146219656093, high=inf), T
-Score: 12.809607, Degree of freedom: 92.29859352311449, P-Value: 1.718673102
0436986e-22
With a significance level of 0.05000, the hypothesis is rejected
```



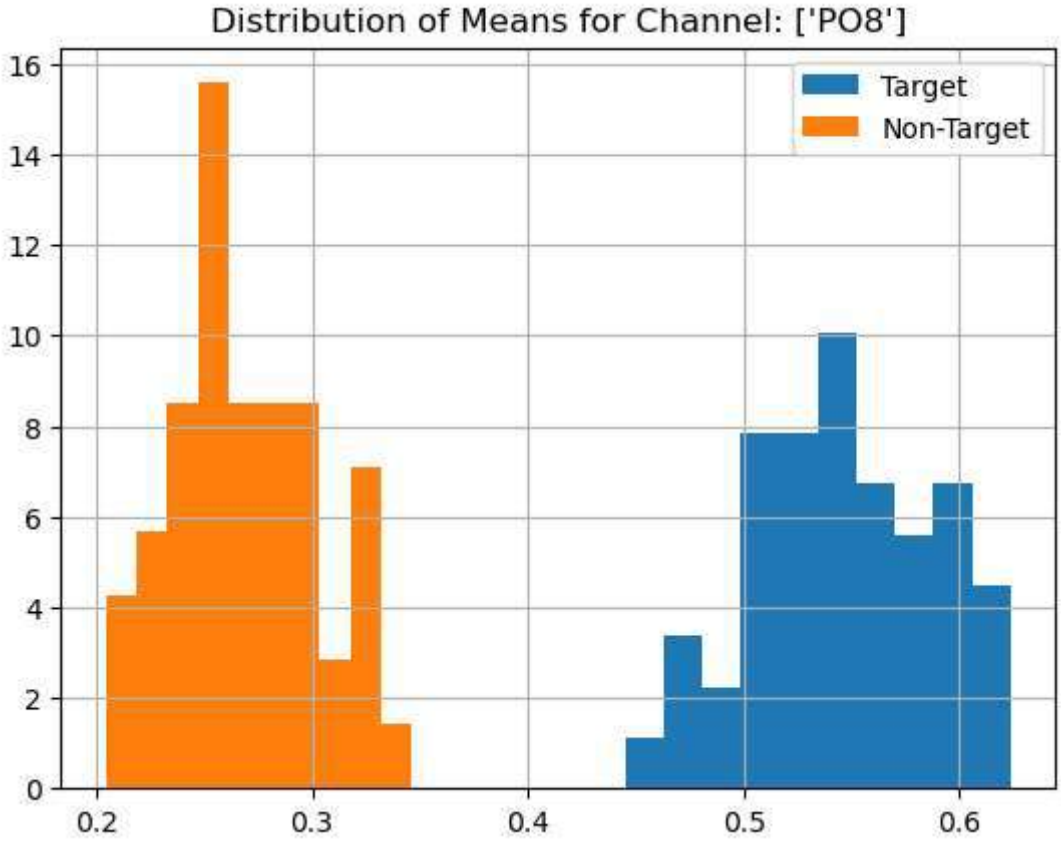

```
Target Mean: 0.3734285999855696, Std: 0.05765315502427675
Non-Target Mean: 0.21836594083244593, Std: 0.044657076692342576
Confidence interval: ConfidenceInterval(low=0.13775280894872133, high=inf), T
-Score: 14.884195, Degree of freedom: 92.23450576280811, P-Value: 1.476920273
1543146e-26
With a significance level of 0.05000, the hypothesis is rejected
```




```
Target Mean: 0.7103176227230938, Std: 0.0615426358446131
Non-Target Mean: 0.33223501553066626, Std: 0.04716664288166952
Confidence interval: ConfidenceInterval(low=0.35967697828337236, high=inf), T
-Score: 34.132528, Degree of freedom: 91.79739465211715, P-Value: 2.972129746
508494e-54
With a significance level of 0.05000, the hypothesis is rejected
```




```
Target Mean: 0.5458552446787204, Std: 0.041959881236350166
Non-Target Mean: 0.26745967183162395, Std: 0.032602831804938254
Confidence interval: ConfidenceInterval(low=0.26578290011561495, high=inf), T
-Score: 36.674196, Degree of freedom: 92.36089310836287, P-Value: 3.805948243
951511e-57
With a significance level of 0.05000, the hypothesis is rejected
```



We can see from the above distribution, that the hypothesis that the P300 amplitude of a target signal is higher in all regions, particularly in Oz (occipital), PO7, and PO8 (Parieto-occipital) regions. So, the null hypothesis is rejected for all channels

Statistical significance of P300 for individual waveform

In the above example, we collected a small sample and extracted the average waveform from the sample. We then used the mean waveform as our sample data. We calculated the mean amplitude of the average waveform to find the significance level. But now we will use individual waveform as our sample and check the significance level of P300.

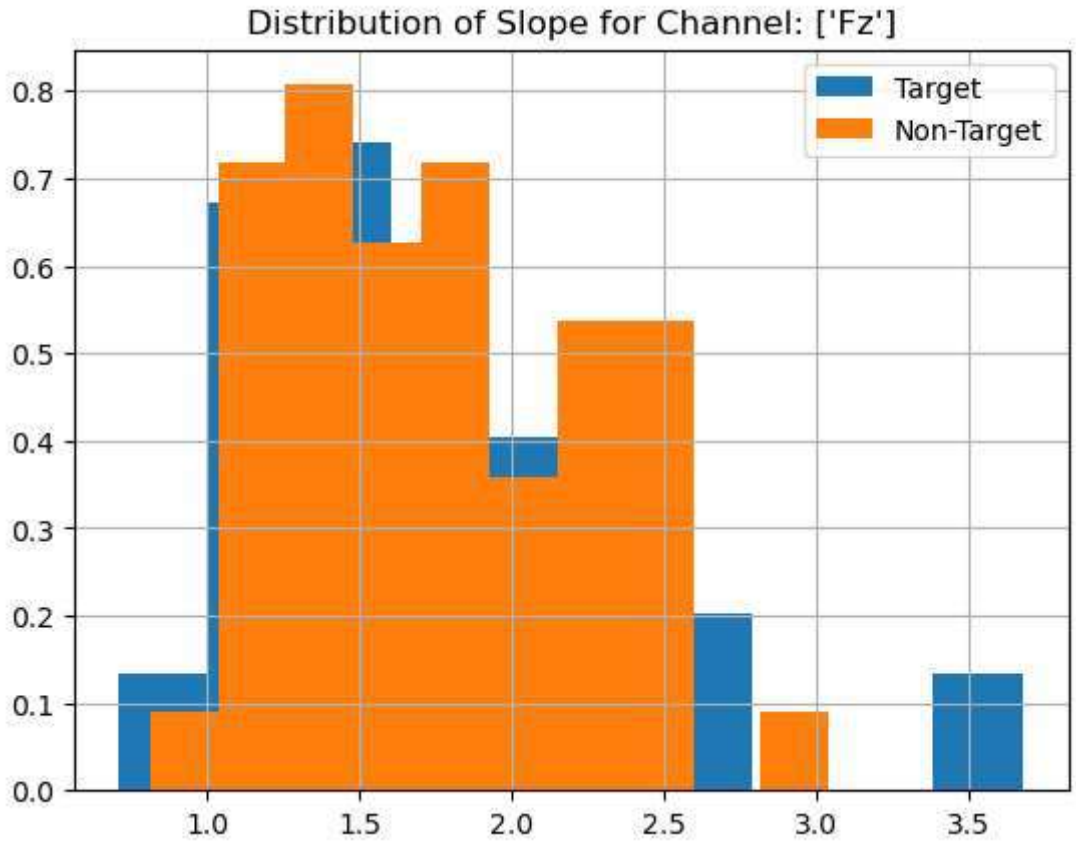
Therefore, we would like to test the following - Target waveforms have a higher peak amplitude than non-target waveforms. i.e.

$$H_0 : \mu_{target} - \mu_{nontarget} \leq 0$$
$$H_1 : \mu_{target} - \mu_{nontarget} > 0$$

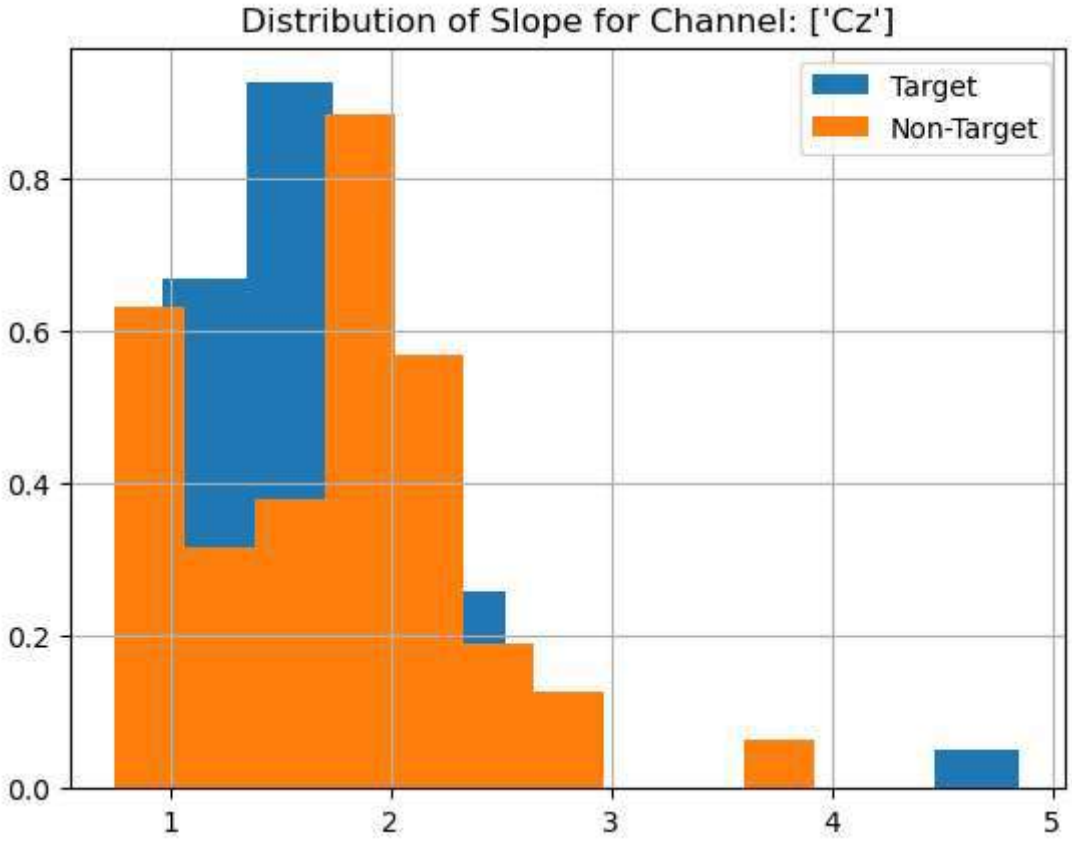
In [409]:
```
sample_size = 50



np.random.seed(34324)

def view_distribution():
    for channel in range(x_target.shape[1]):
        ma_t = []
        ma_nt = []
        for _ in range(sample_size):
            # Get average waveform from sample
            t = x_target[ np.random.choice(np.arange(x_target.shape[0]), size=
1, replace=False), channel, :]
            nt = x_nontarget[ np.random.choice(np.arange(x_nontarget.shape
[0]), size=1, replace=False), channel, :]

            # Remove negative portion of average waveform as P300 deflection i
s positive
            t[t<0] = 0
            nt[nt<0] = 0

            # Calculate the average amplitude of each signal
            ma_nt.append(np.mean(nt))
            ma_t.append(np.mean(t))

        mean_target_amplitude = np.mean(ma_t)
        std_target_amplitude = np.std(ma_t)

        mean_nontarget_amplitude = np.mean(ma_nt)
        std_nontarget_amplitude = np.std(ma_nt)

        print(f"Target Mean: {mean_target_amplitude}, Std: {std_target_amplitu
de}")
        print(f"Non-Target Mean: {mean_nontarget_amplitude}, Std: {std_nontarg
et_amplitude}")

        # T-Statistics
        confidence = 0.95
        d = stats.ttest_ind(ma_t, ma_nt, equal_var=False, alternative='greate
r')
        print(f"Confidence interval: {d.confidence_interval(confidence)}, T-Sc
ore: {d.statistic:.6f}, Degree of freedom: {d.df}, P-Value: {d.pvalue}")
        if d.pvalue > (1-confidence):
            print(f"With a significance level of {1-confidence:.5f}, the hypot
hesis is accepted")
        else:
            print(f"With a significance level of {1-confidence:.5f}, the hypot
hesis is rejected")



        plt.figure()
        plt.title(f"Distribution of Slope for Channel: {get_channel_name(patie
nt_data[0], channel)}")
```

```
        plt.hist(ma_t, density=True, label='Target')
        plt.hist(ma_nt, density=True, label='Non-Target')
        plt.grid()
        plt.legend()
        plt.show()


view_distribution()
```

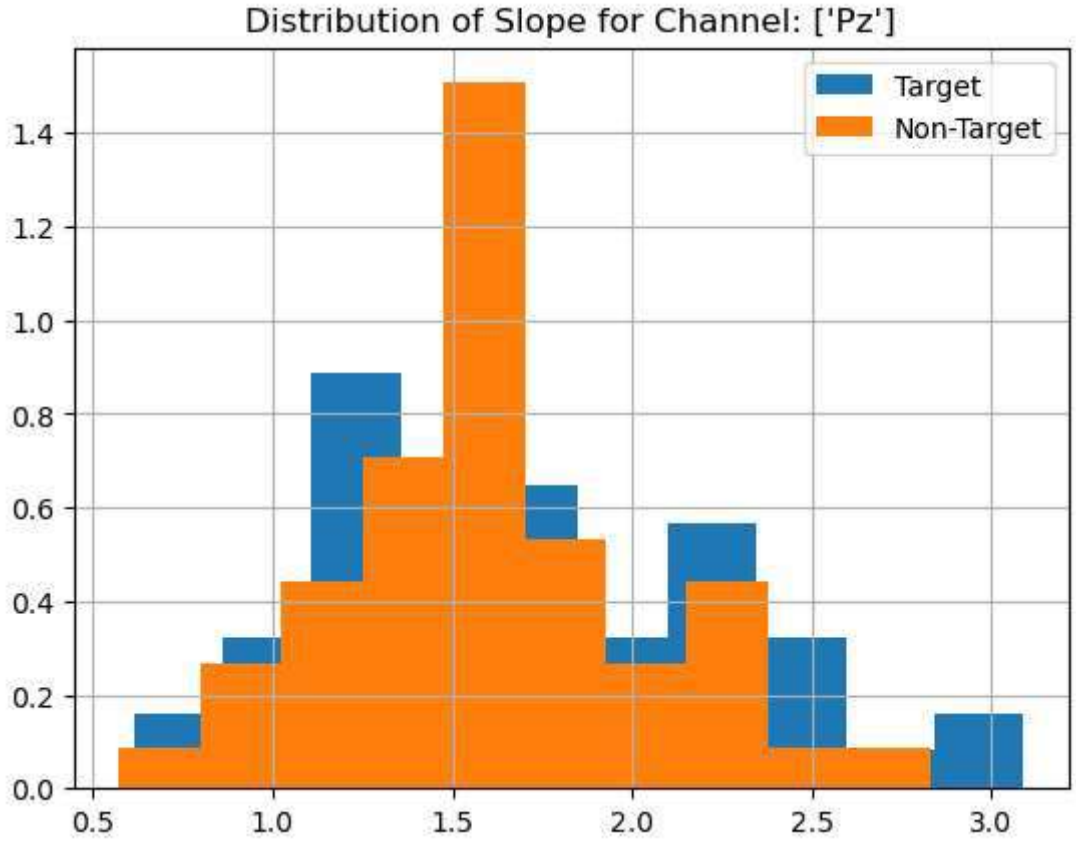
```
Target Mean: 1.7757286746052214, Std: 0.6039467004548362
Non-Target Mean: 1.757631679358547, Std: 0.4876469488151088
Confidence interval: ConfidenceInterval(low=-0.16612234625335642, high=inf),
T-Score: 0.163195, Degree of freedom: 93.83461827019623, P-Value: 0.435357828
5921234
With a significance level of 0.05000, the hypothesis is accepted
```



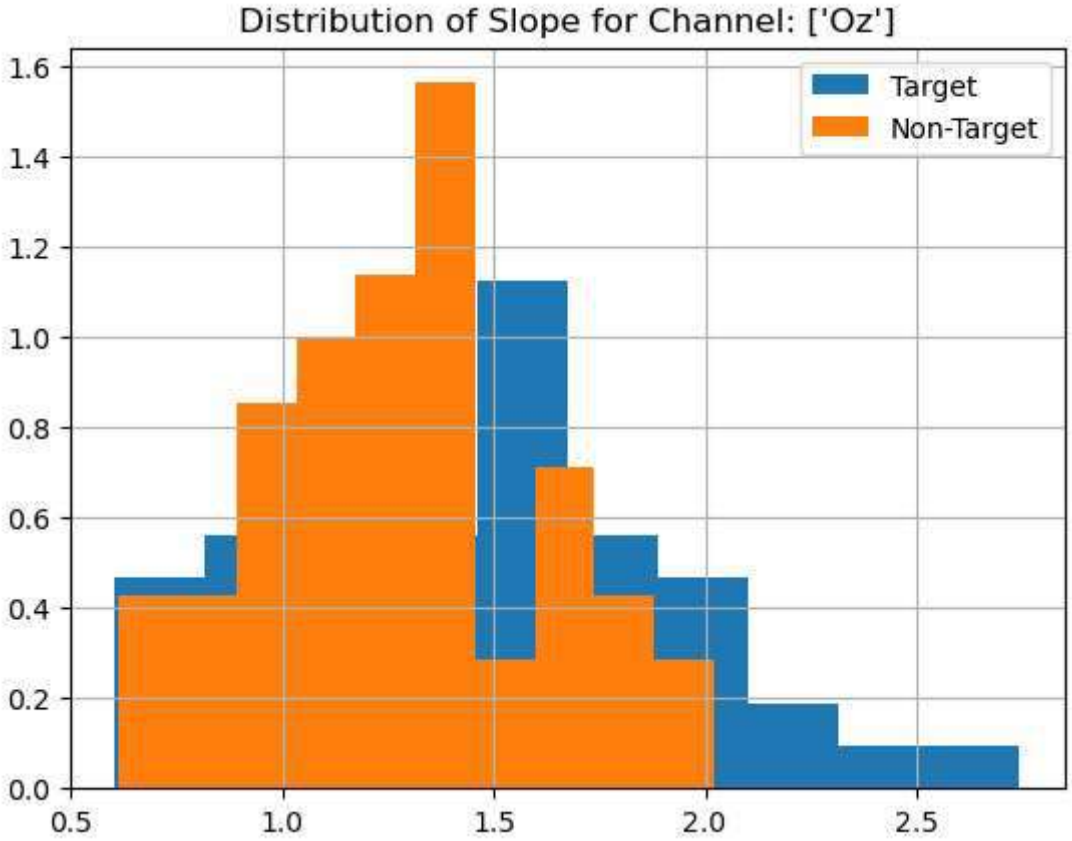

```
Target Mean: 1.7229771446465694, Std: 0.6192546002621162
Non-Target Mean: 1.7469403342880043, Std: 0.6094589246443836
Confidence interval: ConfidenceInterval(low=-0.23007587930674636, high=inf),
T-Score: -0.193060, Degree of freedom: 97.97509491700993, P-Value: 0.57634434
56802365
With a significance level of 0.05000, the hypothesis is accepted
```



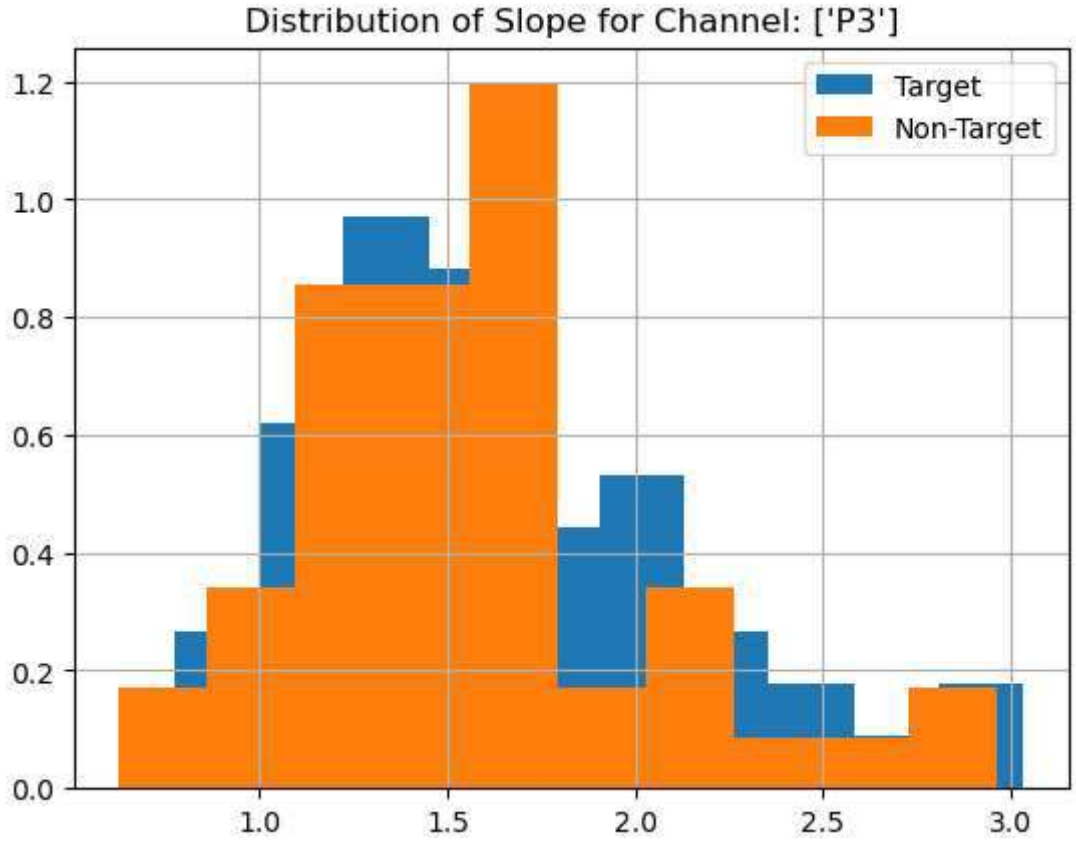

```
Target Mean: 1.703224966352861, Std: 0.5683094164770924
Non-Target Mean: 1.6051949046809277, Std: 0.43781754507998993
Confidence interval: ConfidenceInterval(low=-0.07225798694967697, high=inf),
T-Score: 0.956527, Degree of freedom: 92.0120687949657, P-Value: 0.1706562837
7350206
With a significance level of 0.05000, the hypothesis is accepted
```



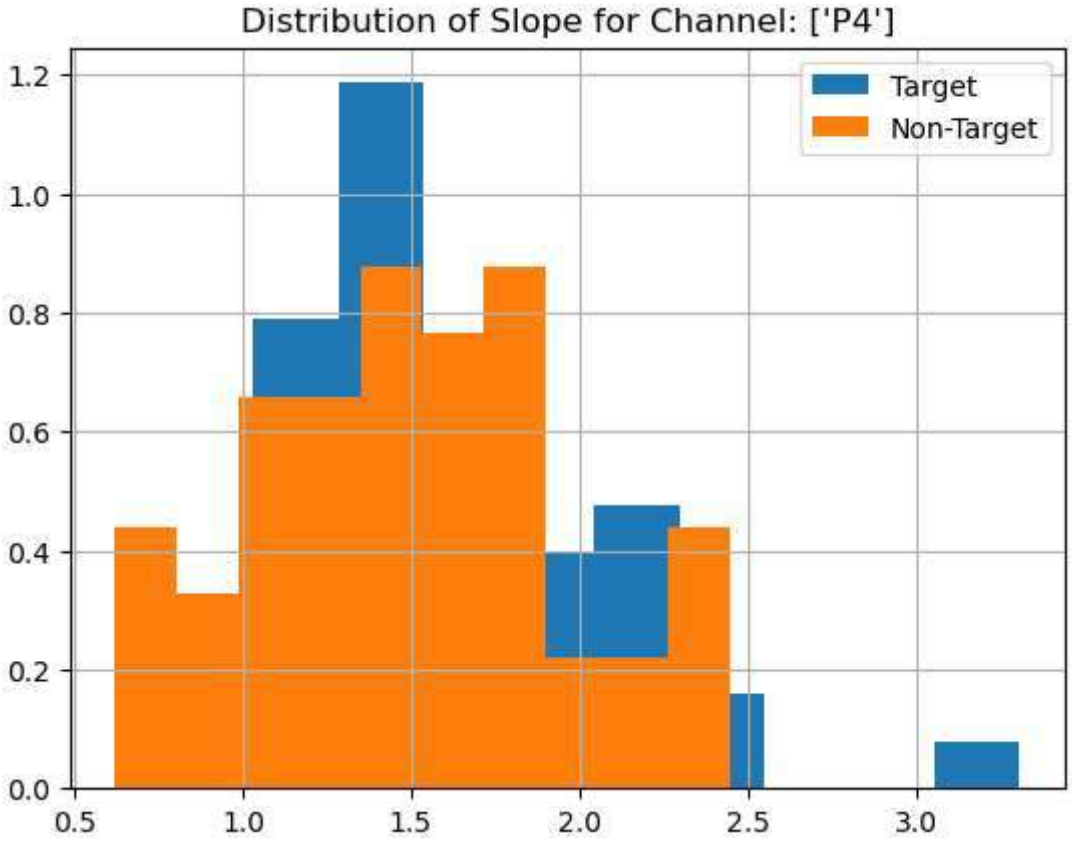

```
Target Mean: 1.4463395989933727, Std: 0.46337513612409925
Non-Target Mean: 1.2734128427544869, Std: 0.3256753918597596
Confidence interval: ConfidenceInterval(low=0.03842303454836368, high=inf), T
-Score: 2.137253, Degree of freedom: 87.91404666185488, P-Value: 0.0176770471
1345975
With a significance level of 0.05000, the hypothesis is rejected
```



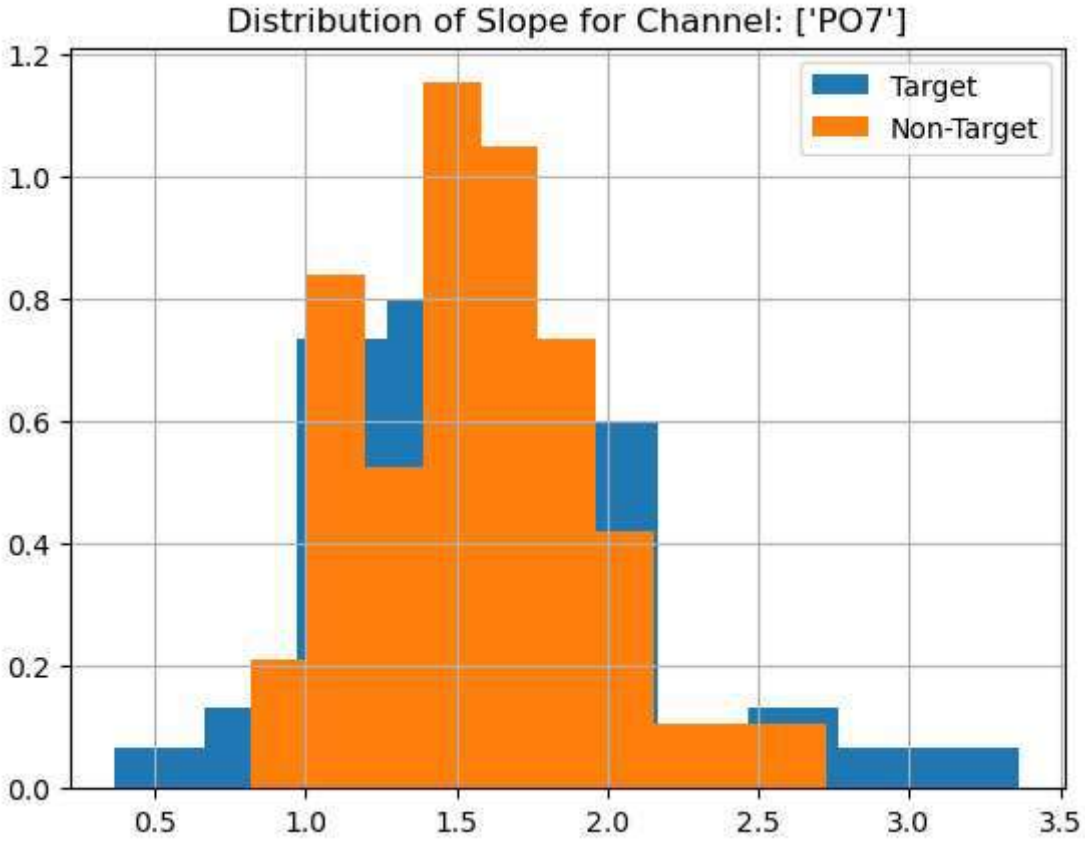

```
Target Mean: 1.6660037054365981, Std: 0.5050721905639041
Non-Target Mean: 1.5636259004868387, Std: 0.47288533361117724
Confidence interval: ConfidenceInterval(low=-0.06176136811145666, high=inf),
T-Score: 1.035771, Degree of freedom: 97.57811971884588, P-Value: 0.151434519
57433365
With a significance level of 0.05000, the hypothesis is accepted
```



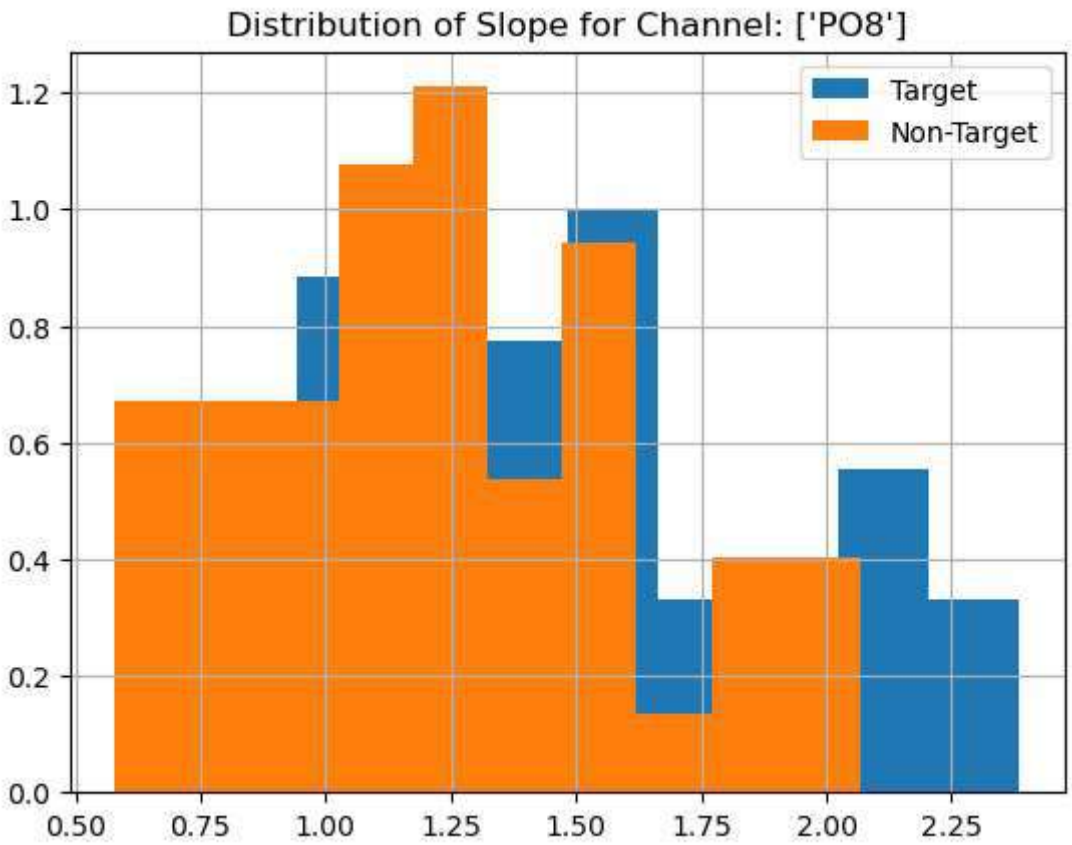

```
Target Mean: 1.5822122994472028, Std: 0.4693581708174683
Non-Target Mean: 1.4957646947093632, Std: 0.4510824364362753
Confidence interval: ConfidenceInterval(low=-0.06798078015472045, high=inf),
T-Score: 0.929575, Degree of freedom: 97.84582354504433, P-Value: 0.177439322
03970747
With a significance level of 0.05000, the hypothesis is accepted
```




```
Target Mean: 1.6066030407183163, Std: 0.5267489352415895
Non-Target Mean: 1.5873330250181223, Std: 0.39253402842968754
Confidence interval: ConfidenceInterval(low=-0.13668789800598746, high=inf),
T-Score: 0.205336, Degree of freedom: 90.59465194575809, P-Value: 0.418885008
82826646
With a significance level of 0.05000, the hypothesis is accepted
```




```
Target Mean: 1.4212659408932398, Std: 0.43980892063267235
Non-Target Mean: 1.2336618203493774, Std: 0.38362088368974845
Confidence interval: ConfidenceInterval(low=0.049135601037613275, high=inf),
T-Score: 2.250195, Degree of freedom: 96.22440138112383, P-Value: 0.013357092
3850459
With a significance level of 0.05000, the hypothesis is rejected
```



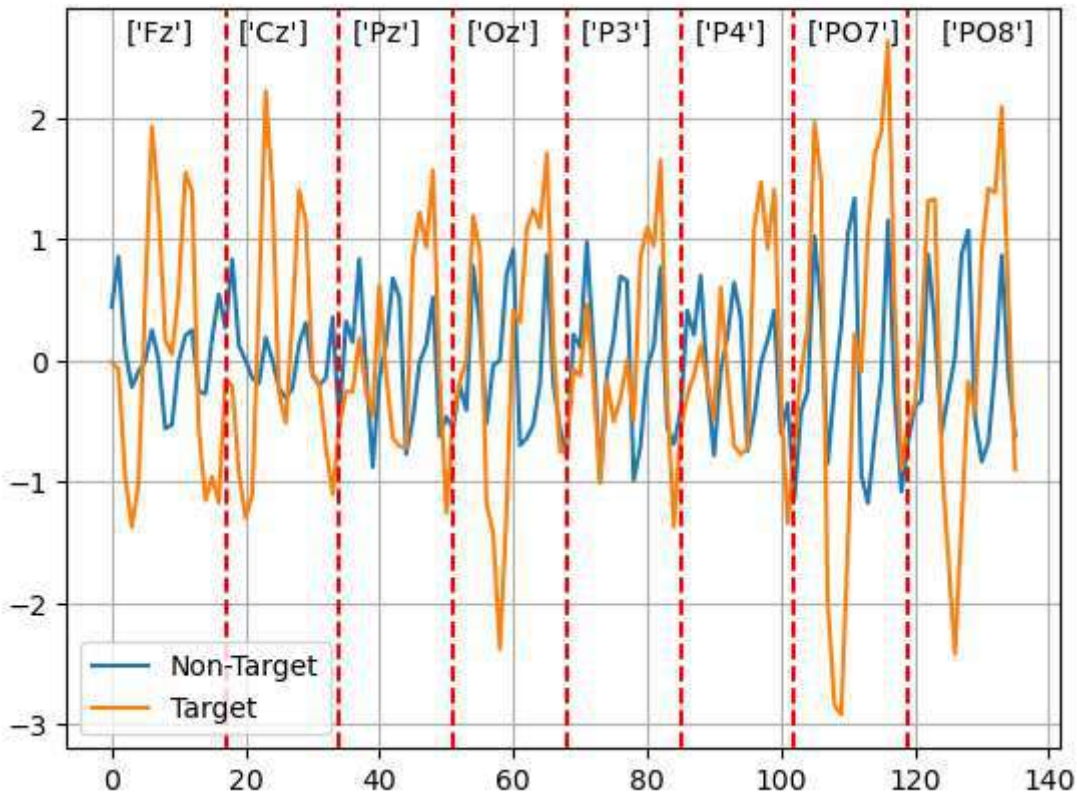
Even though the P300 amplitude was significant when we collected a bunch of samples for each class and calculated their average waveforms, it is not significant when we calculate the P300 amplitude of individual amplitude. However, it is significant in Oz channel. Let us check if deep neural networks can perform a better classification. For input we will use the following datasets:

1. **Simple waveform**
2. **Stepwise LDA**

1. Create Dataset

In [410]:
```
X_train, X_test = torch.tensor(X_train, requires_grad=False).float(), torch.te
nsor(X_test, requires_grad=False).float()
y_train, y_test = torch.tensor(y_train, requires_grad=False).type(torch.LongTe
nsor), torch.tensor(y_test, requires_grad=False).type(torch.LongTensor)
```

In [413]:
```
plt.figure()

plt.plot(torch.mean(X_train[np.where(y_train == 0)[0]], axis=0).numpy(), label
='Non-Target')
plt.plot(torch.mean(X_train[np.where(y_train == 1)[0]], axis=0).numpy(), label
='Target')

a = np.max(torch.mean(X_train[np.where(y_train == 1)[0]], axis=0).numpy())
for i in range(1, 8):
    p = X_train.shape[-1]//8*i
    plt.axvline(x=p, color='red', linestyle='--')
    plt.text(p-15, a, get_channel_name(patient_data[0], i-1))
    if i == 7:
        plt.text(p+5, a, get_channel_name(patient_data[0], i))

plt.grid()
plt.legend()

plt.show()
```



2. Training function

In [48]:
```
@torch.no_grad()
def calculate_accuracy(prediction, true_labels):
    prediction_classes = torch.argmax(prediction, axis=1)
    return (prediction_classes == true_labels).float().mean()

def train(epochs, batch_size, loss_function, optimizer, model, x, y, print_eve
ry=200, learning_rate_decay=None):
    train_accuracy = []
    train_loss = []
    vals = tqdm(range(epochs), desc=f'Epoch: 0, train loss: -, Accuracy: -')

    scheduler = None
    if not (learning_rate_decay is None):
        scheduler = torch.optim.lr_scheduler.ExponentialLR(optimizer, gamma=le
arning_rate_decay)

    for epoch in vals:
        avg_cost = 0

        # Shuffle training data
        dataset = torch.randperm(x.shape[0])

        # For each batch
        for batch in range(0, dataset.size()[0], batch_size):
            model.train()

            range_end = batch+batch_size
            if range_end + batch_size >= dataset.size()[0]:
                range_end = range_end+batch_size
            # Get train and test data
            x_batch = x[dataset[batch:range_end]]
            y_batch = y[dataset[batch:range_end]]

            # Forward pass
            optimizer.zero_grad()
            prediction = model(x_batch)

            # Calculate loss
            loss = loss_function(prediction, y_batch)

            # Backpropagation
            loss.backward() # Calculate gradient
            optimizer.step() # Upgrade gradients


            # Calculate metrics
            train_loss.append(loss.item())
            train_accuracy.append(calculate_accuracy(prediction, y_batch))

            if batch % print_every == 0:
                vals.set_description(f'Epoch: {epoch}, train loss: {train_loss
```

```
[-1]:.5f}, Accuracy: {train_accuracy[-1]*100:3f}')

        if not (scheduler is None):
            scheduler.step() # Learning rate decay

    return train_loss, train_accuracy
```

3. Neural Network Model

In [450]:
```
class ModelDNN(torch.nn.Module):
    def __init__(self, sample_x, total_classes, first_layer_neuron=1024, hidde
n_layers_neurons=[512, ], activation=torch.nn.ReLU):
        super(ModelDNN, self).__init__()

        # Reshape signal so that it has only two dimenstions:
        sample_x = self.get_valid_x(sample_x)
        print(f"Layer 1 input: {sample_x.shape}")

        # Layer 1- Fully Connected layer
        self.fc1 = torch.nn.Linear(sample_x.shape[-1], first_layer_neuron)
        self.act1 = activation()
        self.drop1 = torch.nn.Dropout(0.4)

        self.layer1 = torch.nn.Sequential(self.fc1, self.act1, self.drop1)

        self.layer1.eval()
        with torch.no_grad():
            out = self.layer1(sample_x)
            print(f"Layer 1 output: {out.shape}")
        self.layer1.train()

        self.layers = torch.nn.ModuleList()
        self.layers.append(self.layer1)
        self.activation_layer_name = [type(self.act1).__name__]

        # Add additional hidden layers
        for i in range(len(hidden_layers_neurons)):
            hidden_fc = torch.nn.Linear(out.shape[-1], hidden_layers_neurons
[i])
            hidden_act = activation()
            hidden_drop = torch.nn.Dropout(0.2)
            hidden_layer = torch.nn.Sequential(hidden_fc, hidden_act, hidden_d
rop)

            hidden_layer.eval()
            with torch.no_grad():
                out = hidden_layer(out)
                print(f"Layer {i+2} output: {out.shape}")
            hidden_layer.train()
            self.layers.append(hidden_layer)
            self.activation_layer_name.append(type(hidden_act).__name__)

        # Add output layer
        self.out_fc = torch.nn.Linear(out.shape[1], total_classes, bias=False)

        self.out_fc.eval()
        with torch.no_grad():
            out = self.out_fc(out)
            print(f"Final output: {out.shape}")
        self.out_fc.train()
```

```
    def forward(self, x):
        out = self.get_valid_x(x)

        for layer in self.layers:
            out = layer(out)

        return self.out_fc(out)


    def get_valid_x(self, x):
        if len(x.shape) > 2:
            x = x.reshape((x.shape[0], -1))
        return x

    def show_weight_distribution(self):
        params = []
        for param in self.parameters():
            if len(param.shape) >= 2:
                params.append(param)
        cols = 2
        rows = len(params)/2
        if int(rows) != rows:
            rows = int(rows) + 1
        else:
            rows = int(rows)

        fig, ax = plt.subplots(rows, cols, figsize=(10, 10))
        plt.suptitle("Weight Distribution")

        current = 0
        for i in range(rows):
            for j in range(cols):
                if current >= len(params):
                    break
                ax[i, j].set_title(f"Param: {current+1}")
                ax[i, j].hist(params[current].detach().numpy().reshape(-1))
                ax[i, j].grid()
                current += 1


        plt.subplots_adjust(hspace=0.5)
        plt.show()


    def show_weights(self):
        self.eval()
        with torch.no_grad():
            cols = 2
            rows = len(model.layers)/cols
            if rows == int(rows):
                rows = int(rows)
            else:
                rows = int(rows) + 1

            fig, ax = plt.subplots(rows, cols, figsize=(10, 10))
```

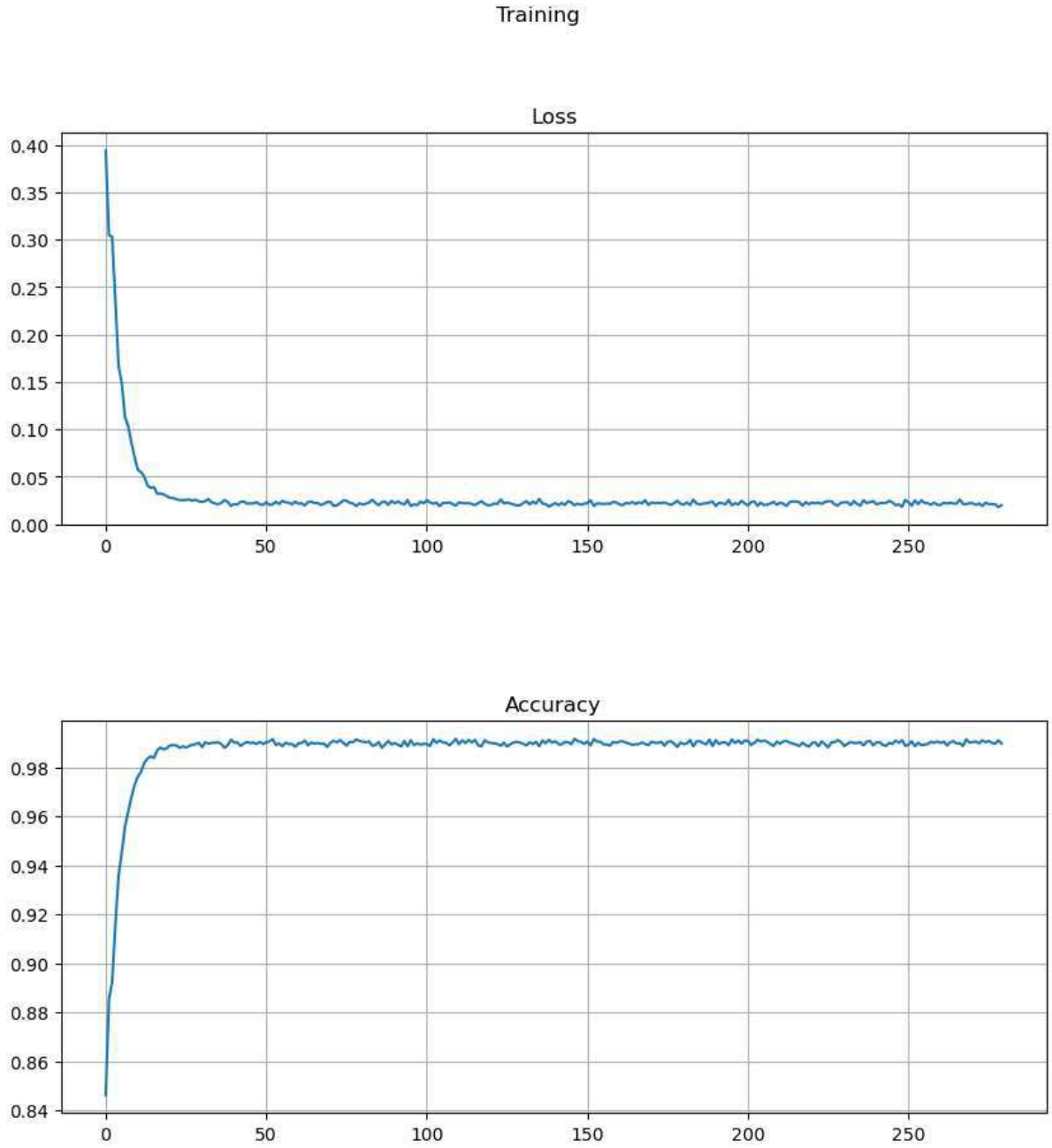
```
            plt.suptitle("Layer Weights")

            current = 0
            current_i = 0
            current_j = 0
            for layer in self.layers:
                if current >= len(model.layers):
                    break
                params = layer.parameters()
                for p in params:
                    if current >= len(model.layers):
                        break
                    if len(p.shape) == 2:
                        weights = p.numpy()
                        ax[current_i, current_j].set_title(f"Weight - Layer {c
urrent+1}")
                        im = ax[current_i, current_j].pcolormesh(weights, cmap
='gray')
                        fig.colorbar(im, ax=ax[current_i, current_j], orientat
ion='vertical')

                        # Draw vertical line where neurons are dead
                        zeros = np.where(np.sum(weights) == 0)[0]
                        for ind in zeros:
                            ax[current_i, current_j].axvline(x=ind, color='b')
                        current += 1
                        if current_j + 1 >= cols:
                            current_j = 0
                            current_i += 1
                        else:
                            current_j += 1


            plt.subplots_adjust(hspace=0.5)
            plt.show()

        self.train()




    def show_output_distribution(self, x):
        self.eval()
        with torch.no_grad():
            out = self.get_valid_x(x)
            activated_outs = []
            for i in range(len(self.layers)):
                module = self.layers[i]
                for layer in module:
                    out = layer(out)
                    if type(layer).__name__ == self.activation_layer_name[i]:
                        activated_outs.append(out)

            cols = 2
            rows = len(activated_outs)/2
```

```
            if int(rows) != rows:
                rows = int(rows) + 1
            else:
                rows = int(rows)

            fig, ax = plt.subplots(rows, cols, figsize=(10, 10))
            plt.suptitle("Activated Output distribution")

            current = 0
            for i in range(rows):
                for j in range(cols):
                    if current >= len(activated_outs):
                        break
                    ax[i, j].set_title(f"Output: {current+1}")
                    ax[i, j].hist(activated_outs[current].detach().numpy().res
hape(-1))
                    ax[i, j].grid()
                    current += 1


            plt.subplots_adjust(hspace=0.5)
            plt.show()


        self.train()
```

4. Classification - Simple Waveform

In [414]:
```
model = ModelDNN(X_test, np.unique(y_test).size, first_layer_neuron=512, hidde
n_layers_neurons=[128, 64, 32, 16])
epochs = 500
batch_size = 32
learning_rate = 1e-2

loss, accuracy = train(
    epochs=epochs,
    batch_size=batch_size,
    loss_function=torch.nn.CrossEntropyLoss(),
    optimizer=torch.optim.Adam(params=model.parameters(), lr=learning_rate),
    model=model,
    x=X_train,
    y=y_train,
    print_every=200,
    learning_rate_decay=0.9
)

running_mean = epochs
plt.figure(figsize=(10, 10))
plt.suptitle("Training")

plt.subplot(2, 1, 1)
plt.title("Loss")
plt.plot(np.array(loss).reshape(-1, running_mean).mean(axis=1))
plt.grid()

plt.subplot(2, 1, 2)
plt.title("Accuracy")
plt.plot(np.array(accuracy).reshape(-1, running_mean).mean(axis=1))

plt.grid()

plt.subplots_adjust(hspace=0.5)

plt.show()
```

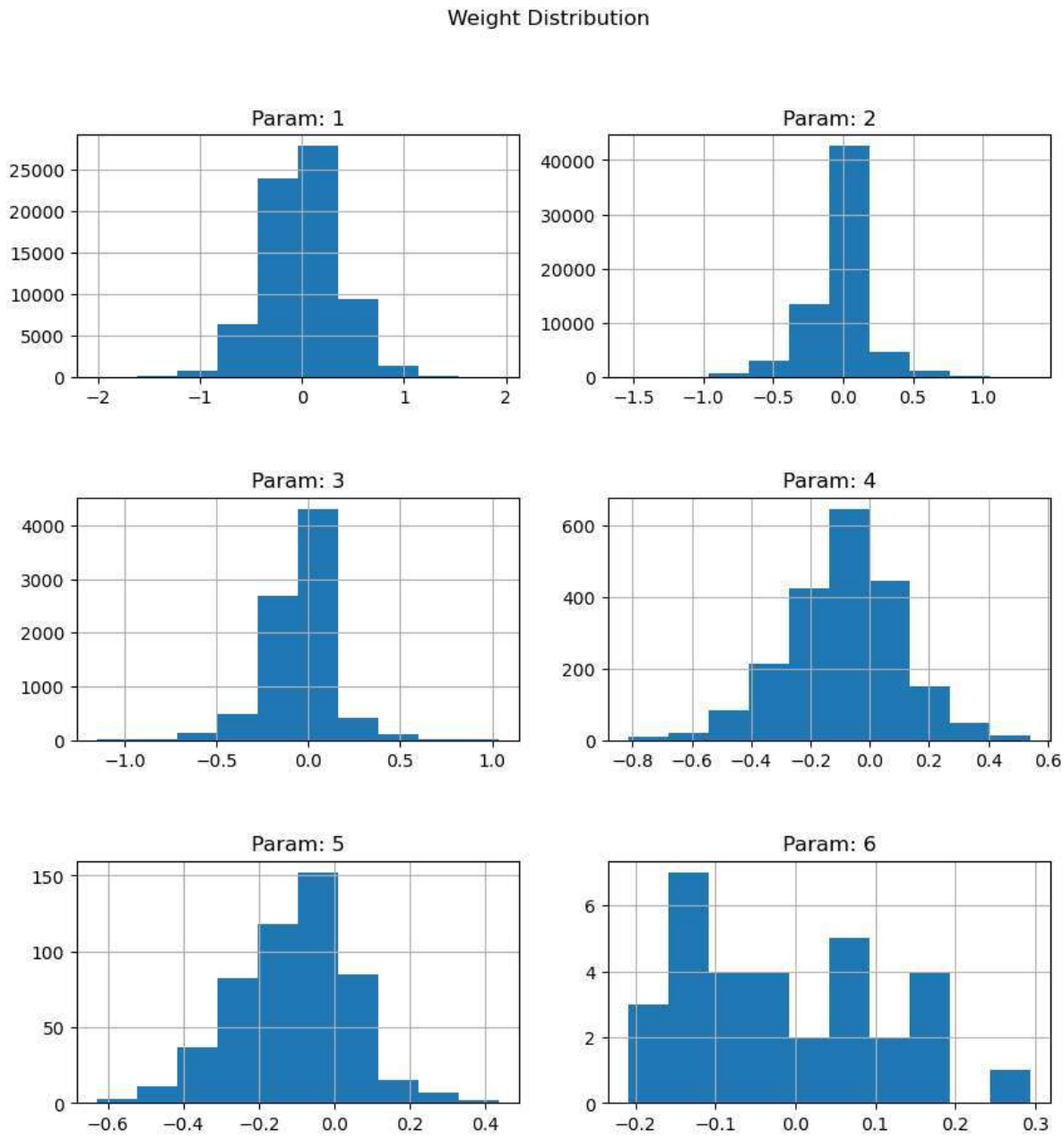
```
Layer 1 input: torch.Size([2240, 136])
Layer 1 output: torch.Size([2240, 512])
Layer 2 output: torch.Size([2240, 128])
Layer 3 output: torch.Size([2240, 64])
Layer 4 output: torch.Size([2240, 32])
Layer 5 output: torch.Size([2240, 16])
Final output: torch.Size([2240, 2])

Epoch: 499, train loss: 0.06286, Accuracy: 93.750000: 100%|[redacted]| 500/500 [08:14<00:00,  1.01it/s]
```



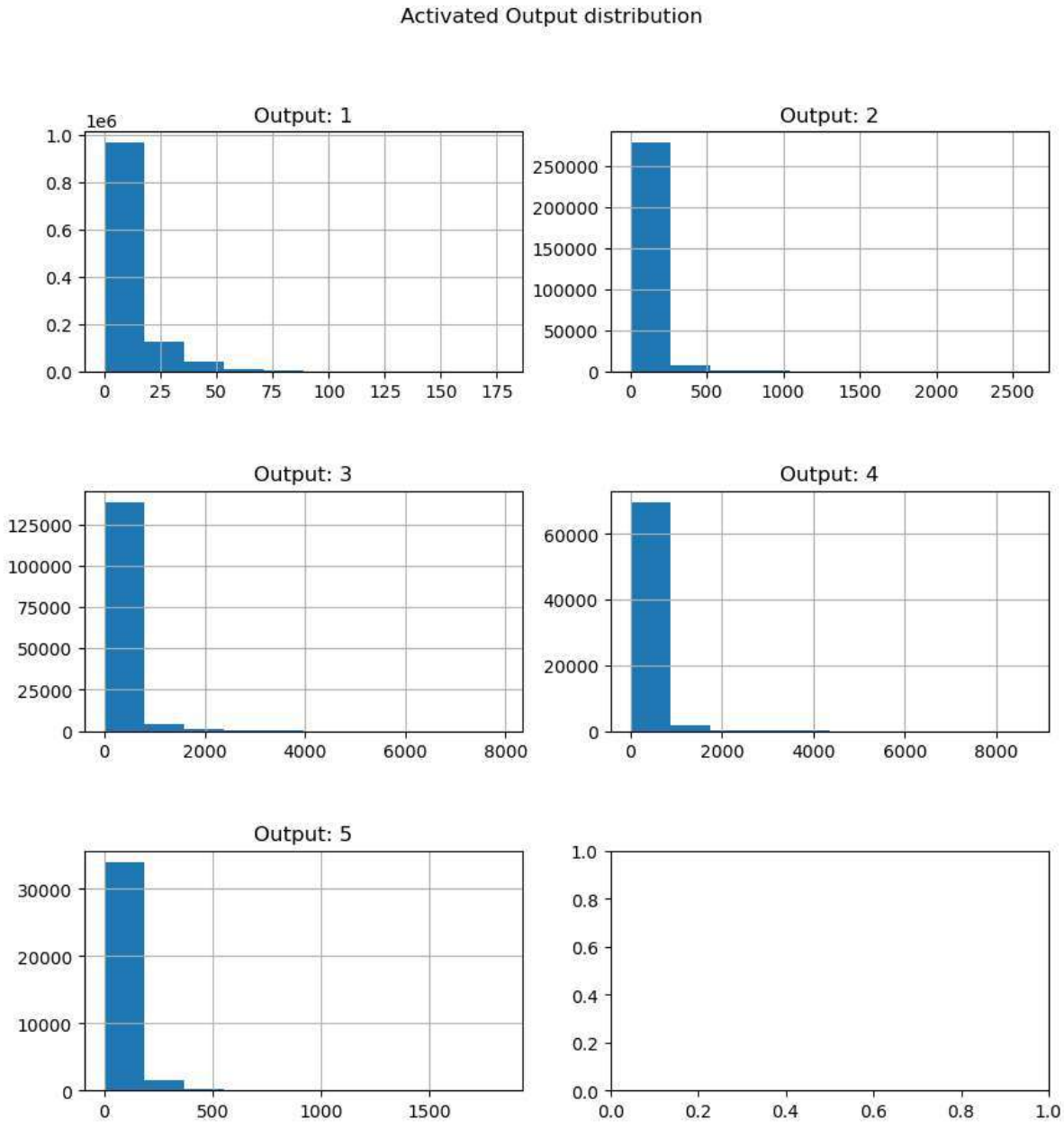
In [415]:
```
with torch.no_grad():
    print(f"Accuracy: {calculate_accuracy(model(X_test), y_test)*100:.3f}%")
```

```
Accuracy: 97.946%
```

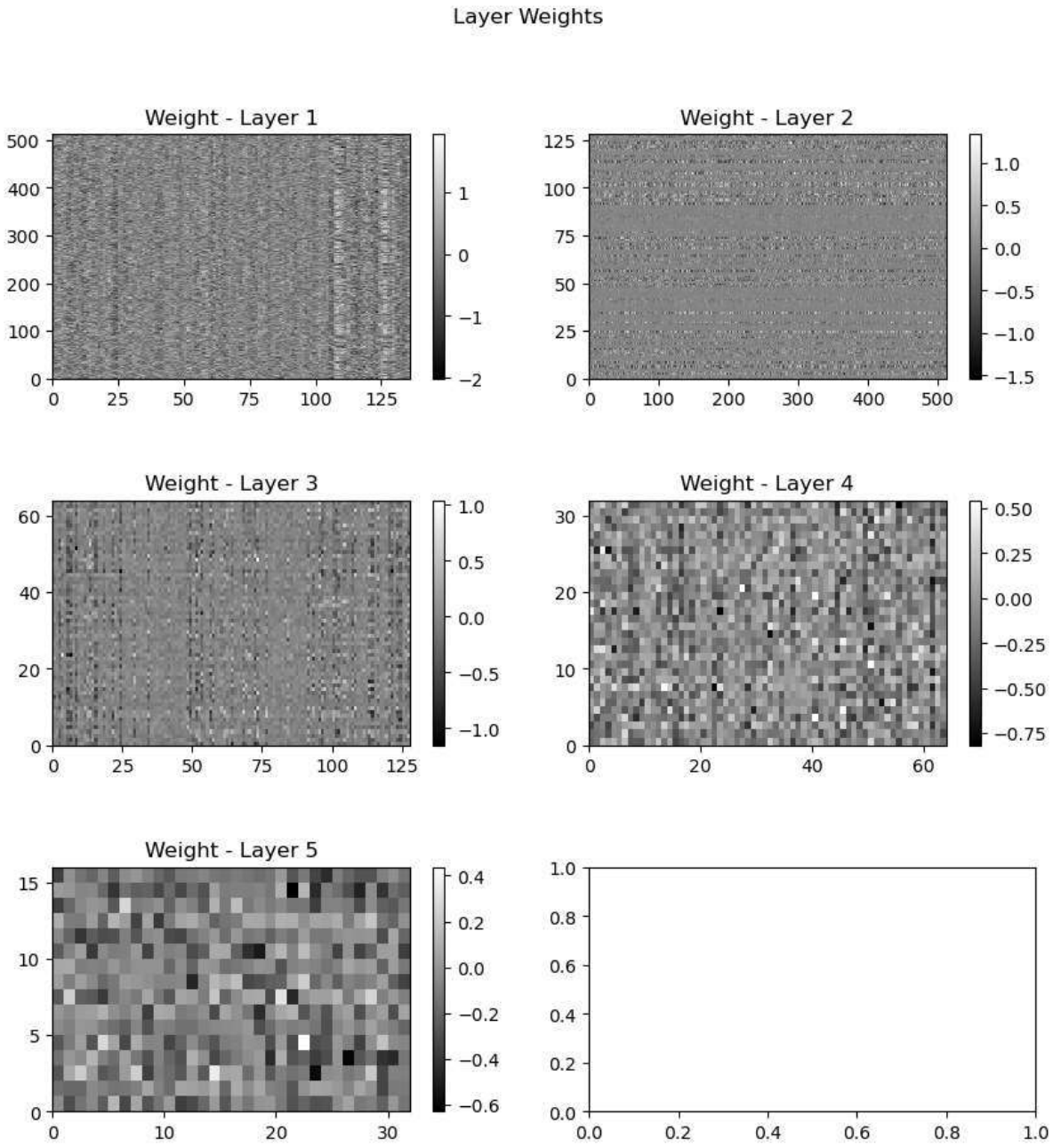
In [418]:
```
model.show_weight_distribution()
```



In [419]:
```
model.show_output_distribution(X_test)
```



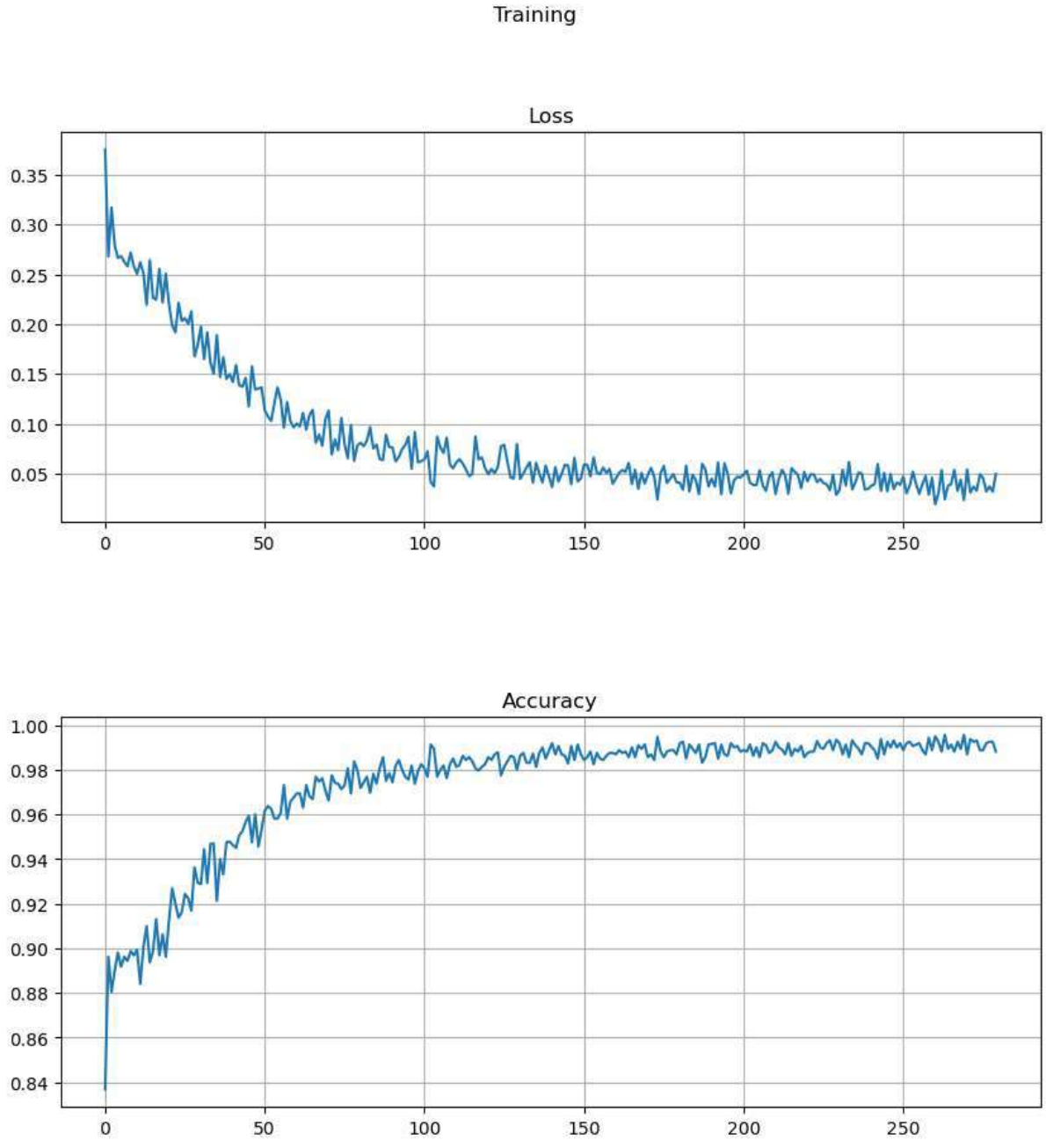
In [420]:
```
model.show_weights()
```



5. Classification - Stepwise LDA (35 features)

In [421]:
```
lda = StepwiseLDA(n_components=35)
lda.fit(X_train.numpy(), y_train.numpy())
model = ModelDNN(
    torch.tensor(lda.transform(X_test.numpy()).real).float(),
    np.unique(y_test.numpy()).size,
    first_layer_neuron=512,
    hidden_layers_neurons=[128, 64, 32, 16],
    activation=torch.nn.Tanh
)
epochs = 50
batch_size = 32
learning_rate = 1e-3

loss, accuracy = train(
    epochs=epochs,
    batch_size=batch_size,
    loss_function=torch.nn.CrossEntropyLoss(),
    optimizer=torch.optim.Adam(params=model.parameters(), lr=learning_rate),
    model=model,
    x=torch.tensor(lda.transform(X_train.numpy()).real).float(),
    y=y_train,
    print_every=200,
    learning_rate_decay=0.95
)

running_mean = epochs
plt.figure(figsize=(10, 10))
plt.suptitle("Training")

plt.subplot(2, 1, 1)
plt.title("Loss")
plt.plot(np.array(loss).reshape(-1, running_mean).mean(axis=1))
plt.grid()

plt.subplot(2, 1, 2)
plt.title("Accuracy")
plt.plot(np.array(accuracy).reshape(-1, running_mean).mean(axis=1))

plt.grid()

plt.subplots_adjust(hspace=0.5)

plt.show()
```

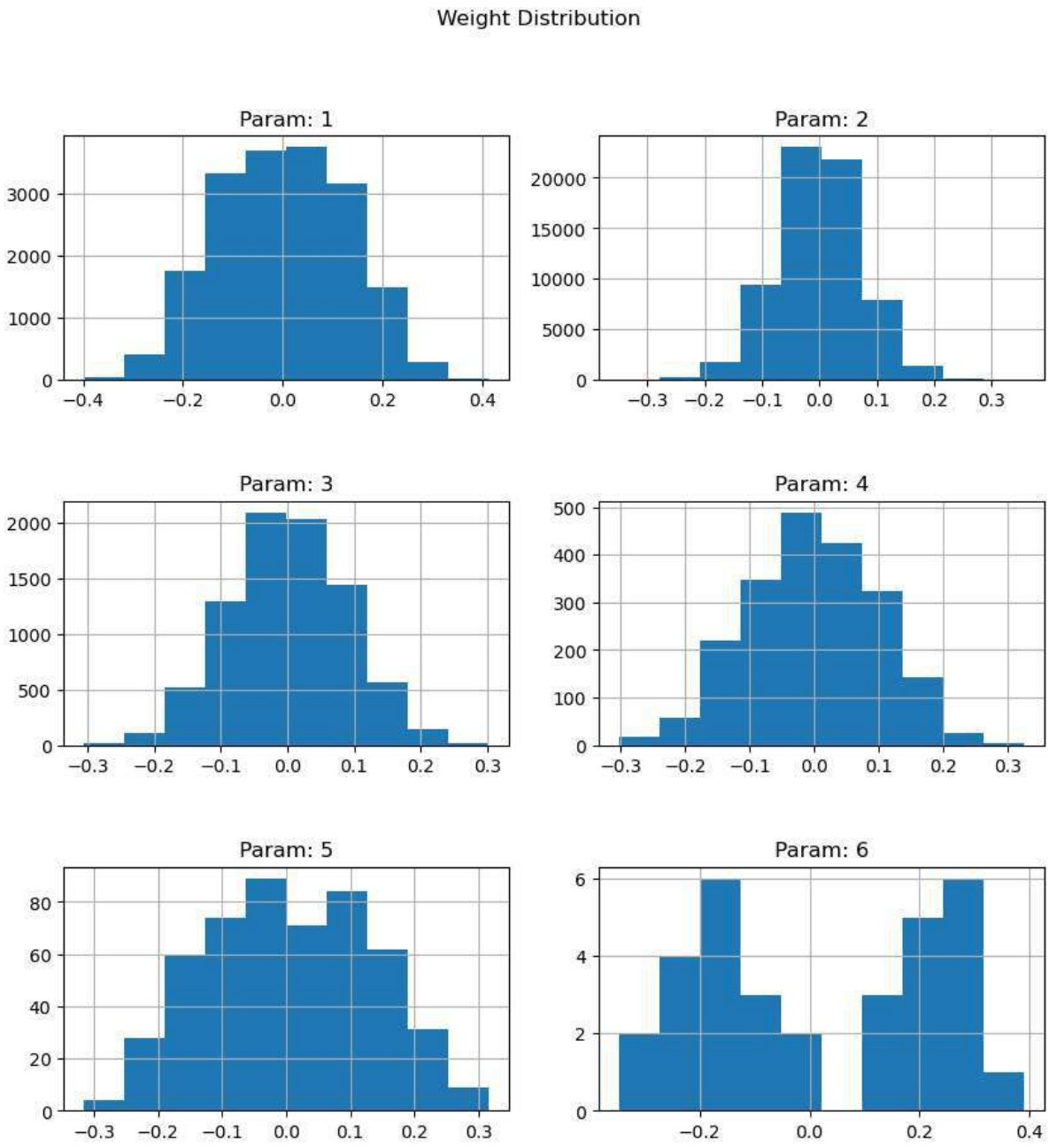
```
Layer 1 input: torch.Size([2240, 35])
Layer 1 output: torch.Size([2240, 512])
Layer 2 output: torch.Size([2240, 128])
Layer 3 output: torch.Size([2240, 64])
Layer 4 output: torch.Size([2240, 32])
Layer 5 output: torch.Size([2240, 16])
Final output: torch.Size([2240, 2])

Epoch: 49, train loss: 0.00611, Accuracy: 100.000000: 100%|[redacted]| 50/50 [00:42<00:00,  1.17it/s]
```



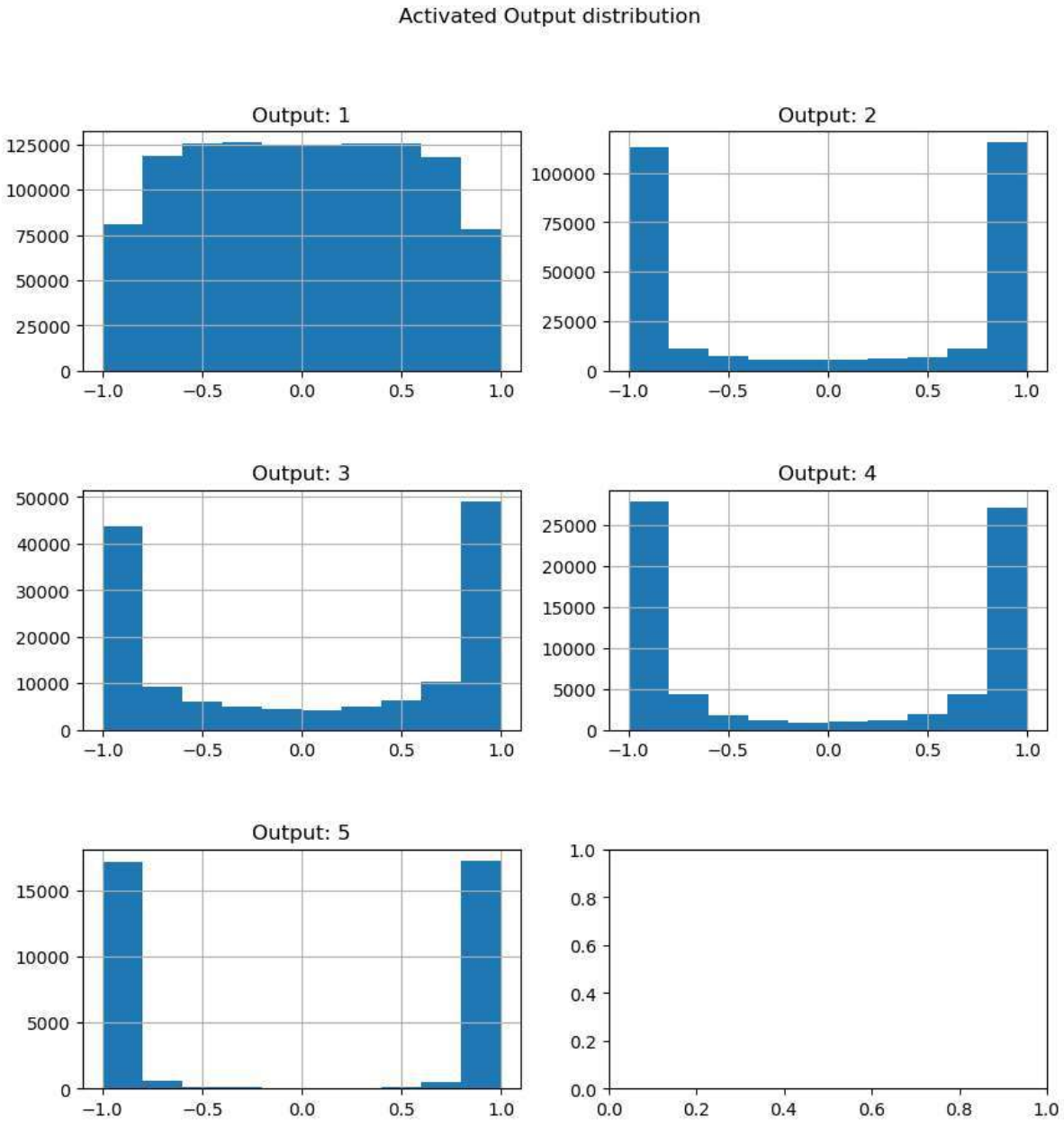
In [422]:
```
with torch.no_grad():
    print(f"Accuracy: {calculate_accuracy(model(torch.tensor(lda.transform(X_test.numpy()).real).float()), y_test)*100:.3f}%")
```

```
Accuracy: 97.634%
```

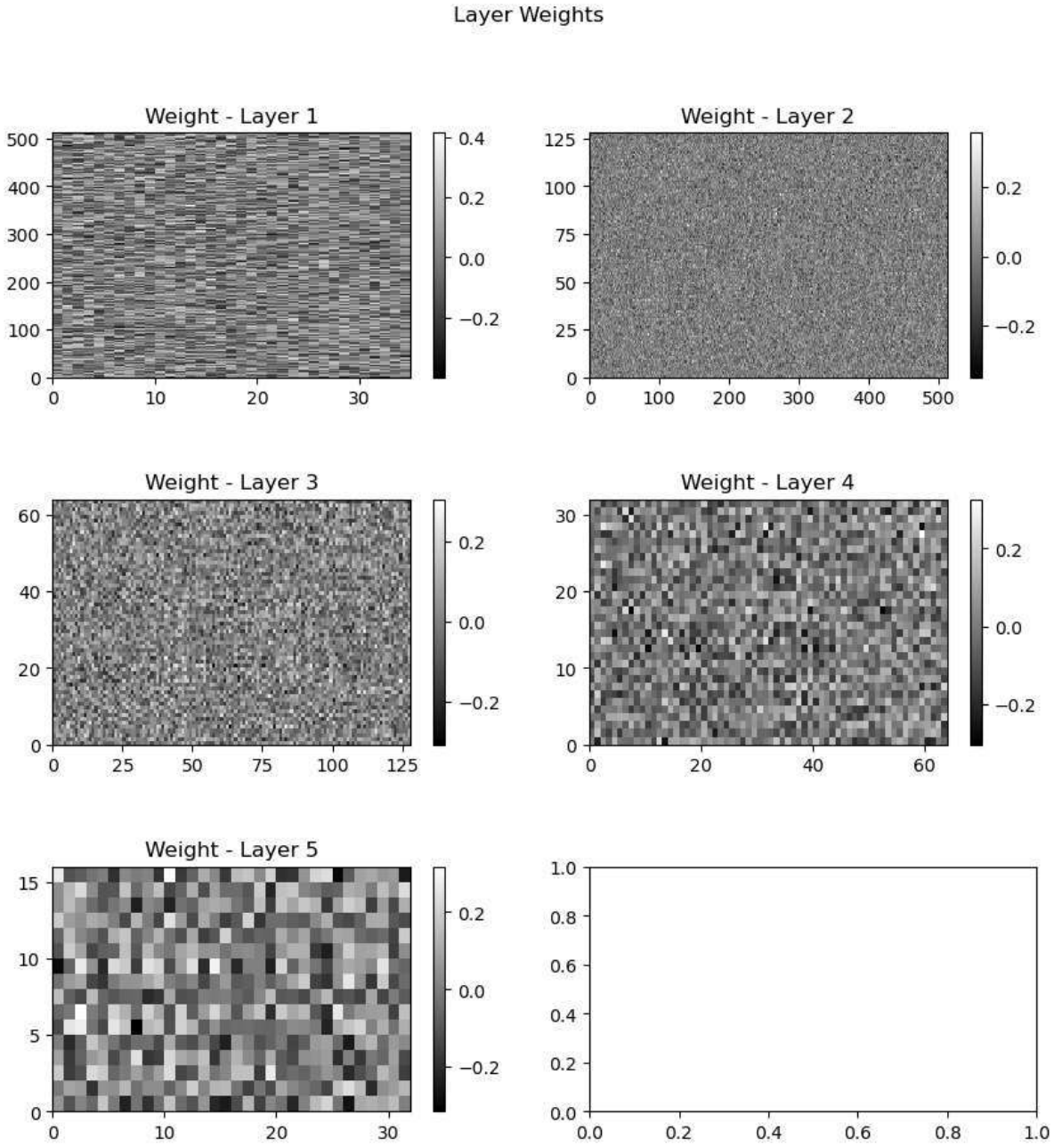
In [423]:
```
model.show_weight_distribution()
```



In [424]:
```
model.show_output_distribution(torch.tensor(lda.transform(X_test.numpy()).rea
l).float())
```



In [425]:
```
model.show_weights()
```



Deep Neural Networks also provide a classification accuracy over 97\%. DNNs perform much better than RFC. However, if we reduce the dimensionality using Stepwise LDA, we obtain similar accuracy as the raw signal but we gain an increase in speed of classification.

Classification using Pz, Oz, PO7, and PO8

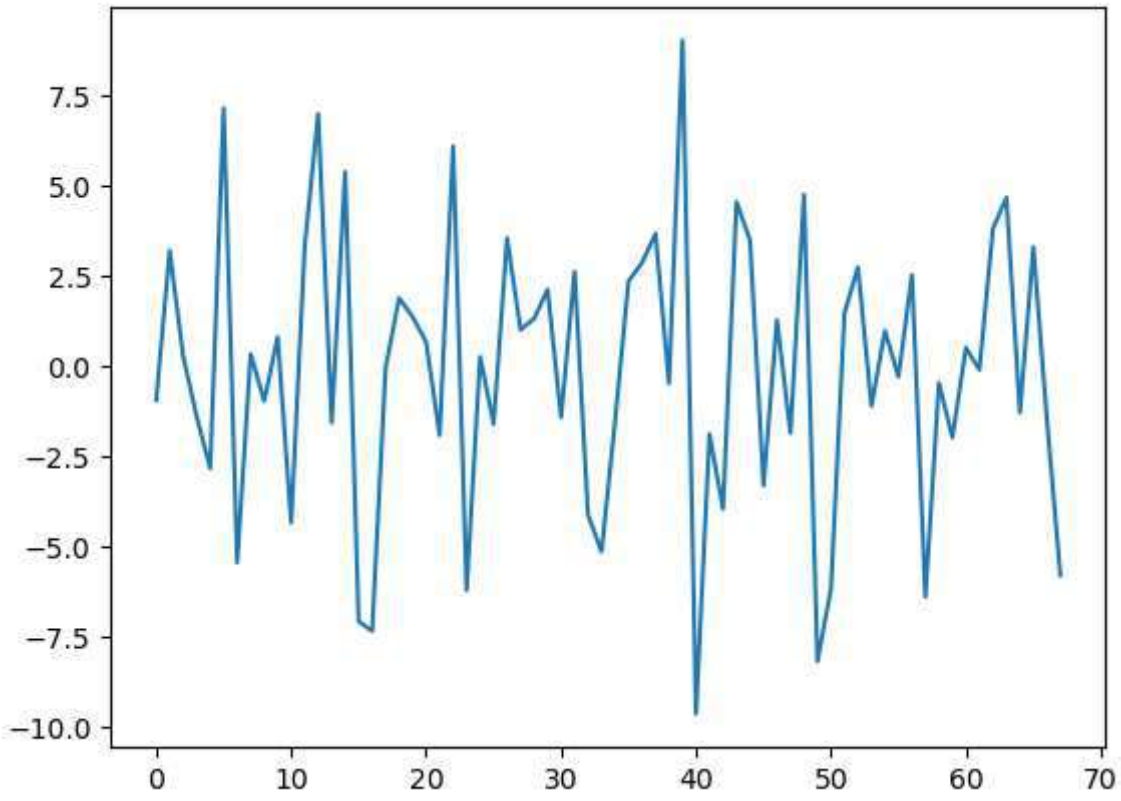
Earlier we saw that the statistical significance of P300 amplitude was prominent in parietal and occipital region. Therefore, we will now use the data of these channels only to perform classification using Neural Networks and Stepwise LDA.

Create Dataset

In [478]:
```
total_samples_per_class = 17*12 # Number of samples in each waveform
additional_samples = total_samples_per_class - int(256*stimulus_duration/1000)
# Additional sample
x, y = create_dataset(X_filtered, y_target, get_delayed_samples=additional_sam
ples, show_progress=True)
y = y - 1
print(x.shape)

# Bring channel to second axis for ease of visualization
x = x.transpose((0, 2, 1))

cnames = ['Pz', 'Oz', 'PO7', 'PO8']
c = []
for n in cnames:
    c.append(get_channel_index(patient_data[0], n))

x = x[:, c, :] # Only use Oz, PO7, and PO8 channel

# Calculate average of consecutive 12 samples to get a sample of size 17x8
x = x.reshape((x.shape[0], x.shape[1], 17, 12)).mean(axis=-1)
x, y = shuffle(x, y, random_state=12432)
X_data = x.copy()
y_data = y.copy()
x = x.reshape((x.shape[0], -1))
print(x.shape)
```

```
100%|██████████| 267680/267680 [00:00<00:00, 460721.50it/s]
100%|██████████| 267680/267680 [00:00<00:00, 462313.01it/s]
100%|██████████| 267680/267680 [00:00<00:00, 456010.38it/s]
100%|██████████| 267680/267680 [00:00<00:00, 466337.88it/s]
100%|██████████| 267680/267680 [00:00<00:00, 452925.90it/s]
100%|██████████| 267680/267680 [00:00<00:00, 459930.32it/s]
100%|██████████| 267680/267680 [00:00<00:00, 467152.83it/s]
100%|██████████| 267680/267680 [00:00<00:00, 467152.25it/s]

(33576, 204, 8)
(33576, 68)
```

In [479]:
```
plt.figure()
plt.plot(x[2, :])
plt.show()
```



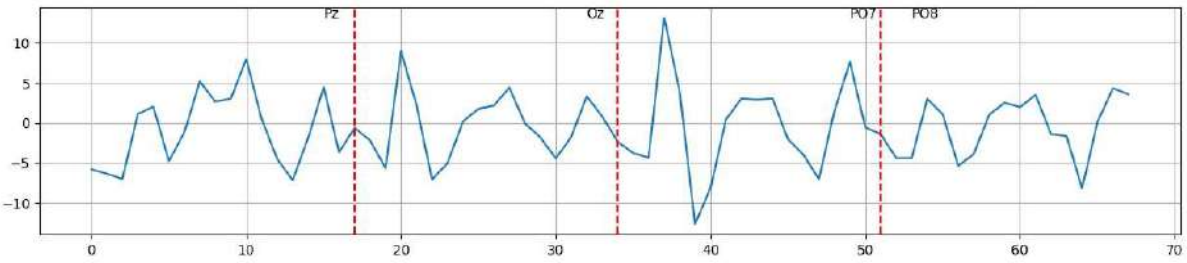
In [480]:
```
np.unique(y)
```

Out[480]:
```
array([0, 1], dtype=uint8)
```

In [481]:
```
# Balancing the dataset
data_per_class = 5600
indices = np.concatenate((np.where(y == 0)[0][:data_per_class], np.where(y ==
1)[0][:data_per_class]))
x = x[indices, :]
y = y[indices]


X_train, X_test, y_train, y_test = train_test_split(x, y, test_size=0.2, rando
m_state=6150)
print(X_train.shape, y_train.shape, X_test.shape, y_test.shape)
```

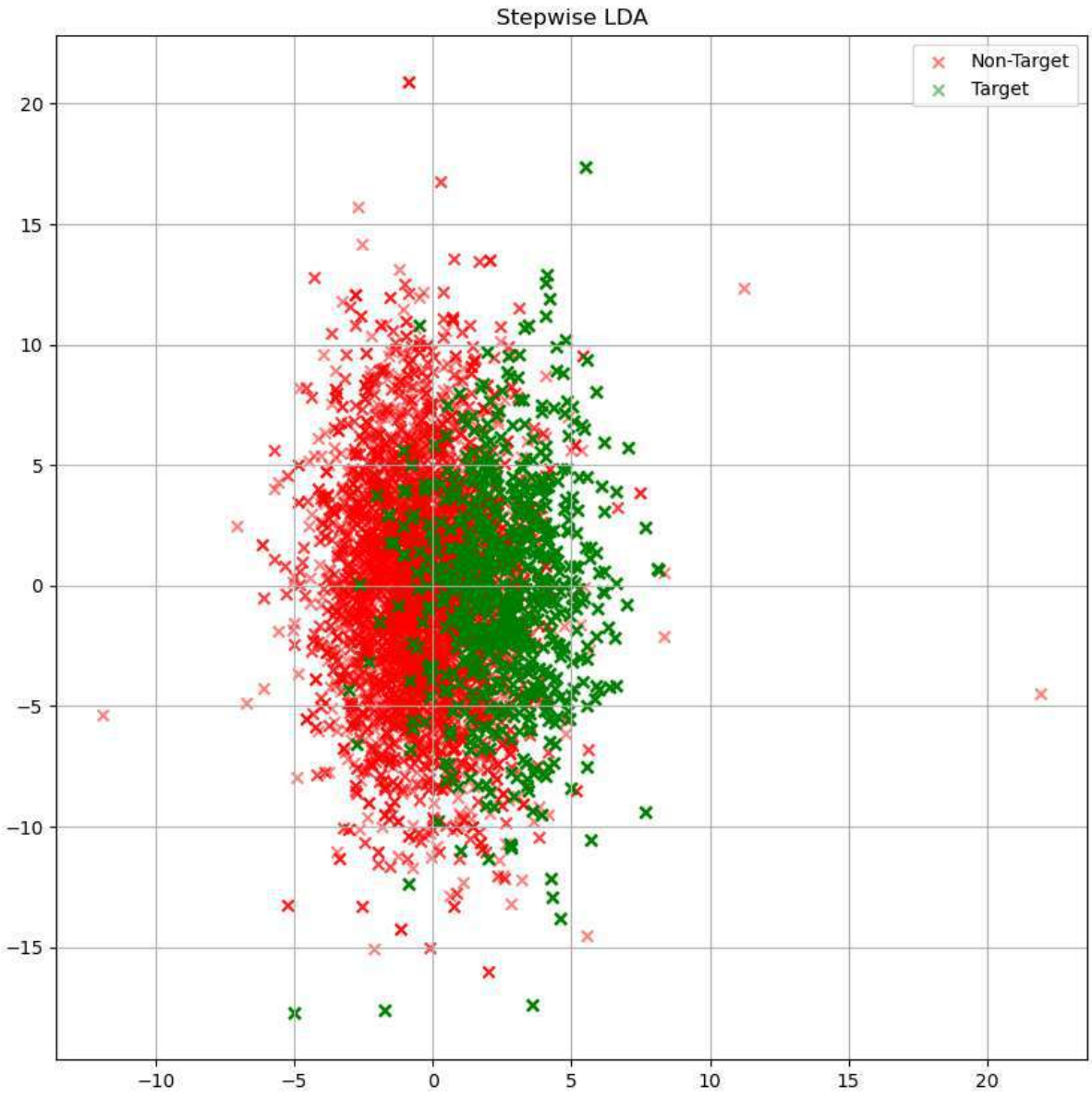
```
(8960, 68) (8960,) (2240, 68) (2240,)
```

In [482]:
```
plt.figure(figsize=(15, 3))
plt.plot(x[0, :])
a = np.max(x[0])
for i in range(1, X_data.shape[1]):
    p = x.shape[-1]//X_data.shape[1]*i
    plt.axvline(x=p, color='red', linestyle='--')
    plt.text(p-2, a, cnames[i-1])
    if i == X_data.shape[1]-1:
        plt.text(p+2, a, cnames[i])
plt.grid()
plt.show()
```



Stepwise LDA Visualization

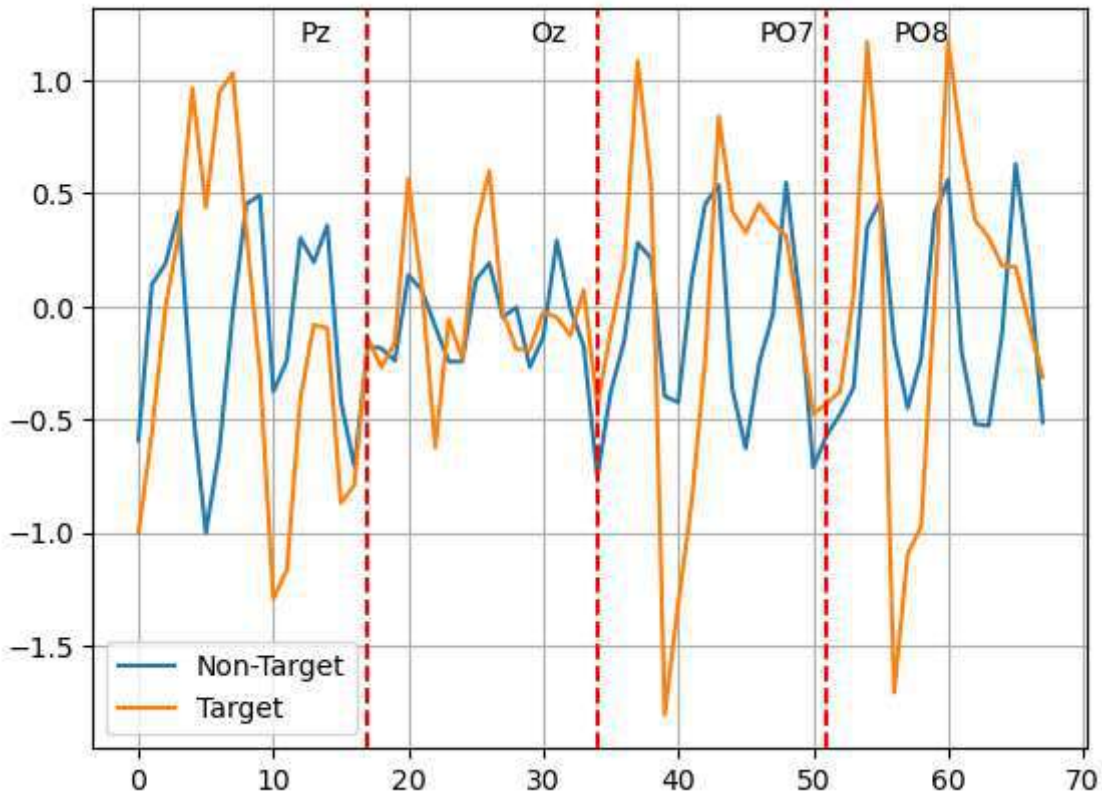
In [483]:
```
a =  StepwiseLDA(n_components=2).fit(x, y).transform(x)
plt.figure(figsize=(10, 10))
plt.title("Stepwise LDA")
plt.scatter(a[y == 0, 0].real, a[y == 0, 1].real, label='Non-Target', color
='r', alpha=0.5, marker='x')
plt.scatter(a[y == 1, 0].real, a[y == 1, 1].real, label='Target', color='g', a
lpha=0.5, marker='x')
plt.grid()
plt.legend()
plt.show()
```



Classification

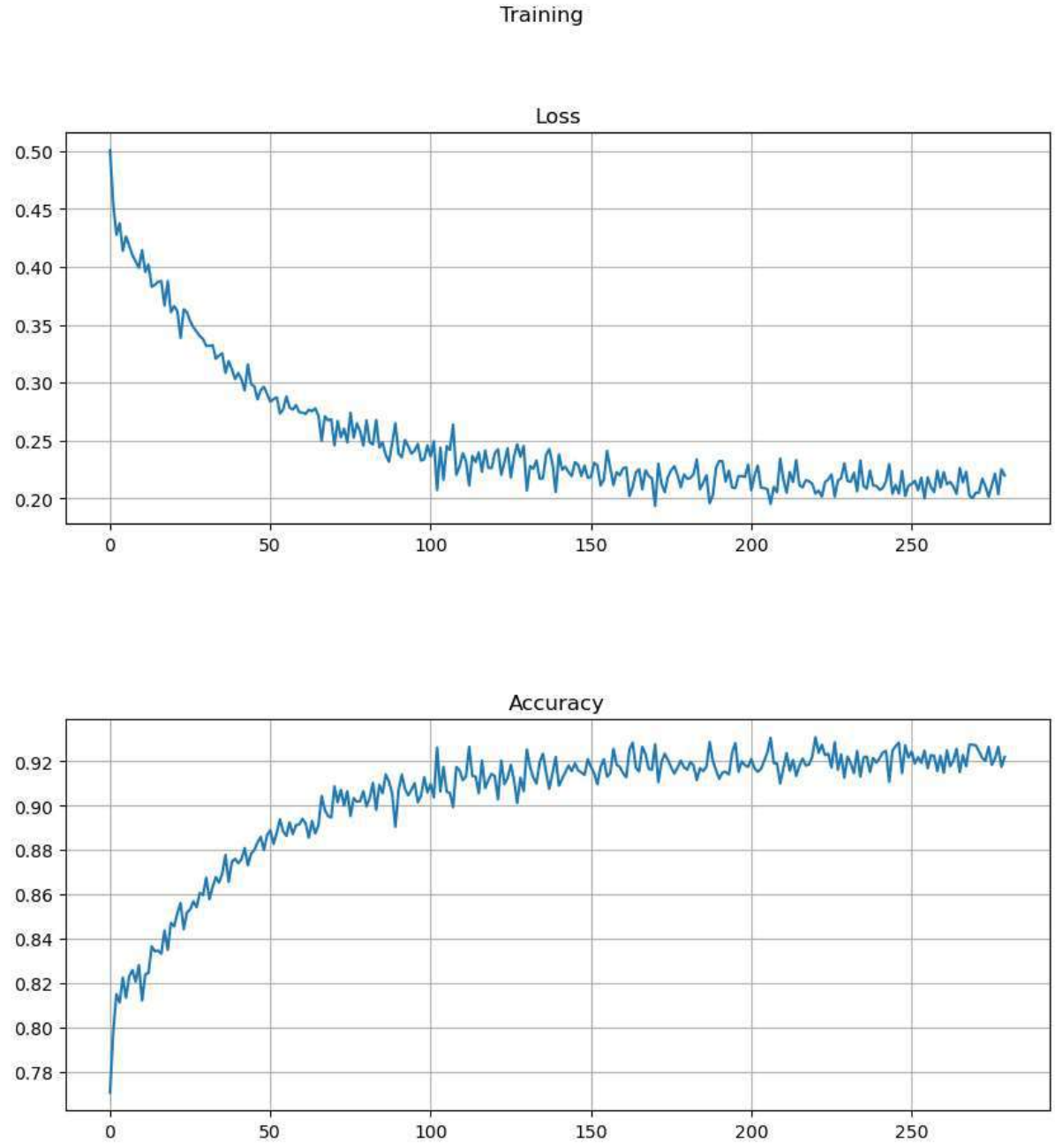
In [484]:
```
X_train, X_test = torch.tensor(X_train, requires_grad=False).float(), torch.te
nsor(X_test, requires_grad=False).float()
y_train, y_test = torch.tensor(y_train, requires_grad=False).type(torch.LongTe
nsor), torch.tensor(y_test, requires_grad=False).type(torch.LongTensor)
```

In [485]:
```
plt.figure()

plt.plot(torch.mean(X_train[np.where(y_train == 0)[0]], axis=0).numpy(), label
='Non-Target')
plt.plot(torch.mean(X_train[np.where(y_train == 1)[0]], axis=0).numpy(), label
='Target')

a = np.max(torch.mean(X_train[np.where(y_train == 1)[0]], axis=0).numpy())
for i in range(1, X_data.shape[1]):
    p = X_train.shape[-1]//X_data.shape[1]*i
    plt.axvline(x=p, color='red', linestyle='--')
    plt.text(p-5, a, cnames[i-1])
    if i == X_data.shape[1]-1:
        plt.text(p+5, a, cnames[i])

plt.grid()
plt.legend()

plt.show()
```



In [486]:
```
lda = StepwiseLDA(n_components=35)
lda.fit(X_train.numpy(), y_train.numpy())
model = ModelDNN(
    torch.tensor(lda.transform(X_test.numpy()).real).float(),
    np.unique(y_test.numpy()).size,
    first_layer_neuron=128,
    hidden_layers_neurons=[64, 32, 16],
    activation=torch.nn.Tanh
)
epochs = 100
batch_size = 32
learning_rate = 1e-3

loss, accuracy = train(
    epochs=epochs,
    batch_size=batch_size,
    loss_function=torch.nn.CrossEntropyLoss(),
    optimizer=torch.optim.Adam(params=model.parameters(), lr=learning_rate),
    model=model,
    x=torch.tensor(lda.transform(X_train.numpy()).real).float(),
    y=y_train,
    print_every=200,
    learning_rate_decay=0.95
)

running_mean = epochs
plt.figure(figsize=(10, 10))
plt.suptitle("Training")

plt.subplot(2, 1, 1)
plt.title("Loss")
plt.plot(np.array(loss).reshape(-1, running_mean).mean(axis=1))
plt.grid()

plt.subplot(2, 1, 2)
plt.title("Accuracy")
plt.plot(np.array(accuracy).reshape(-1, running_mean).mean(axis=1))

plt.grid()

plt.subplots_adjust(hspace=0.5)

plt.show()
```

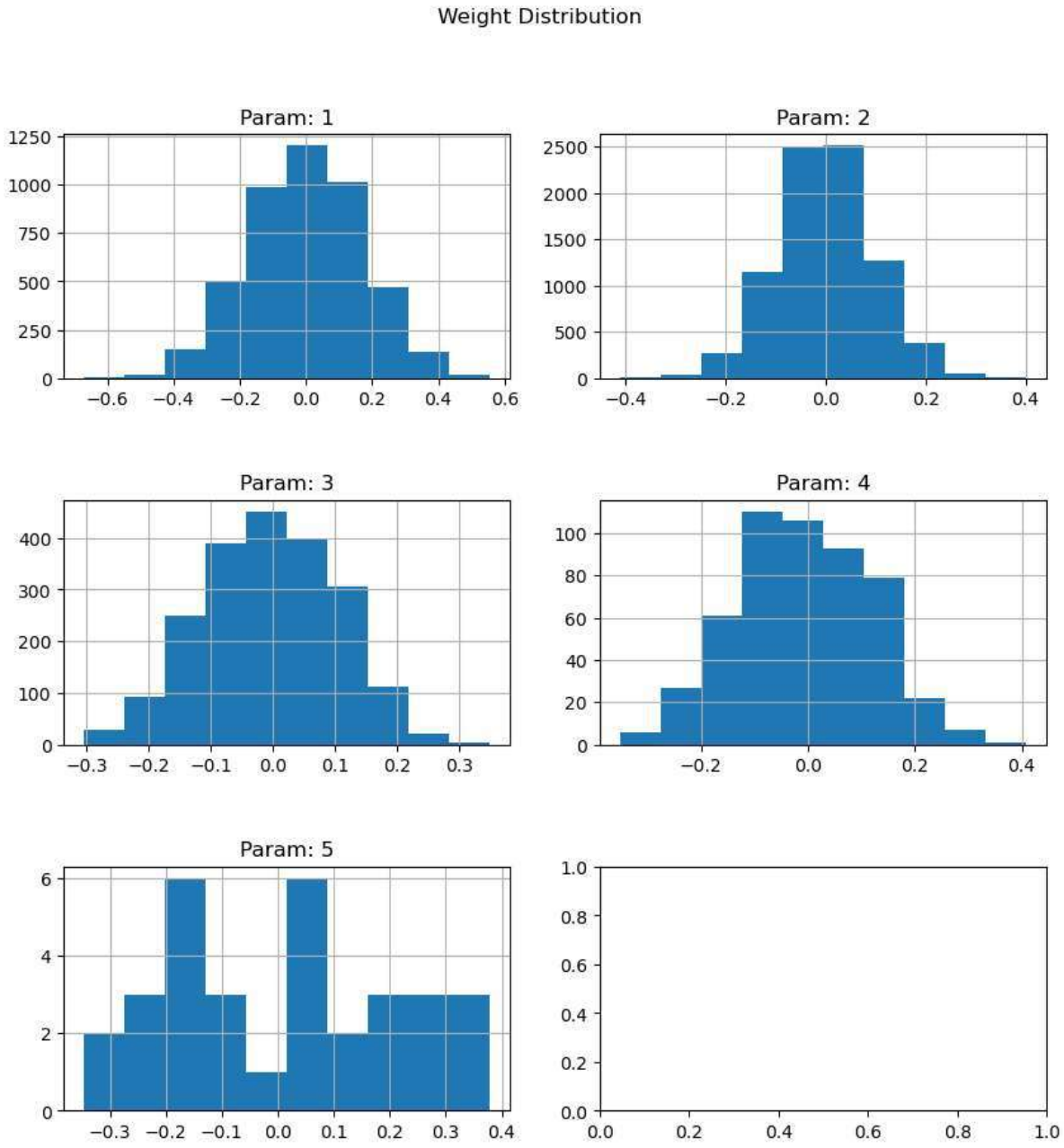
```
Layer 1 input: torch.Size([2240, 35])
Layer 1 output: torch.Size([2240, 128])
Layer 2 output: torch.Size([2240, 64])
Layer 3 output: torch.Size([2240, 32])
Layer 4 output: torch.Size([2240, 16])
Final output: torch.Size([2240, 2])

Epoch: 99, train loss: 0.13805, Accuracy: 96.875000: 100%|[redacted]| 100/100 [00:53<00:00,  1.86it/s]
```



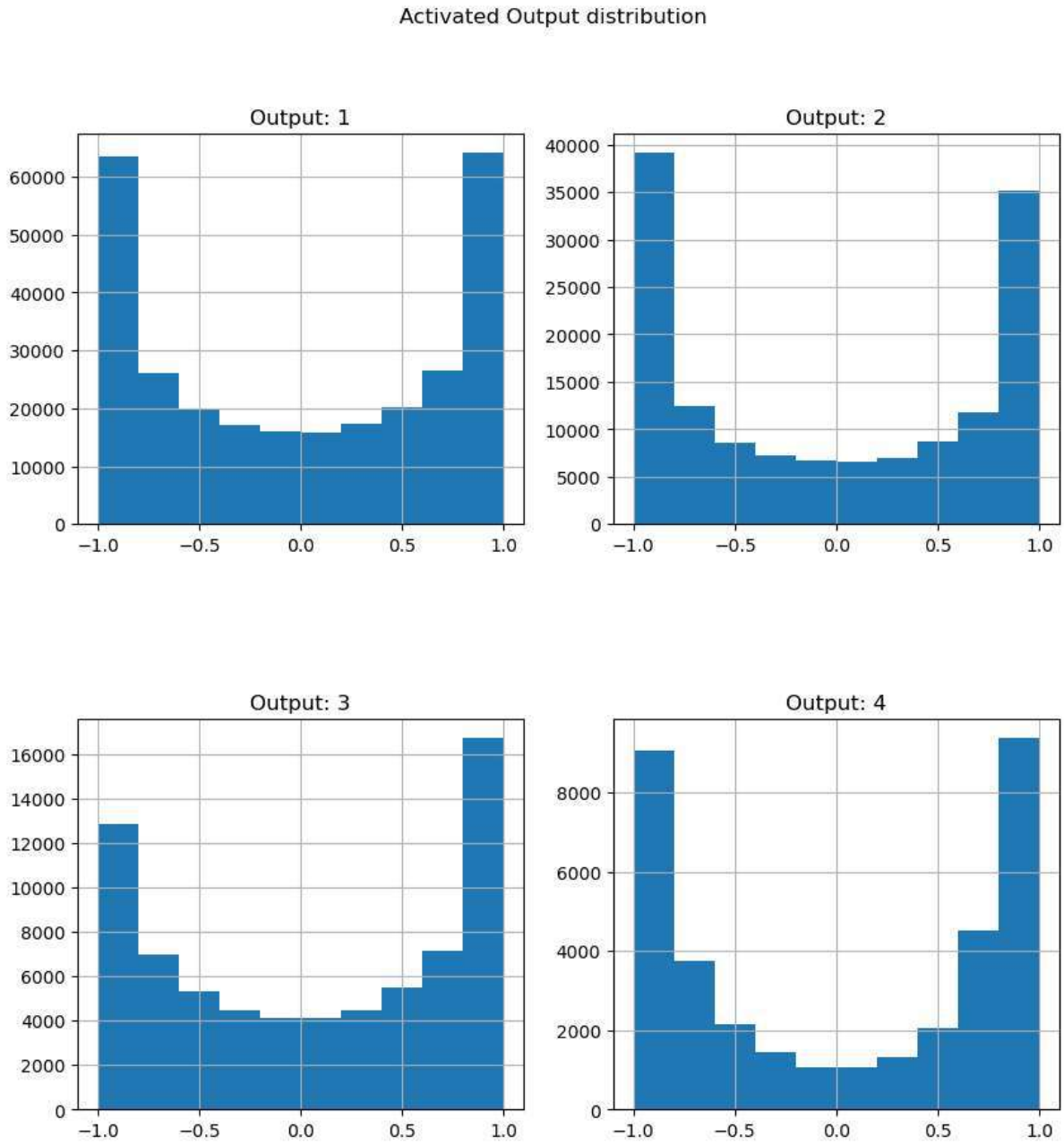
In [487]:
```
with torch.no_grad():
    print(f"Accuracy: {calculate_accuracy(model(torch.tensor(lda.transform(X_test.numpy()).real).float()), y_test)*100:.3f}%")
```

```
Accuracy: 89.955%
```

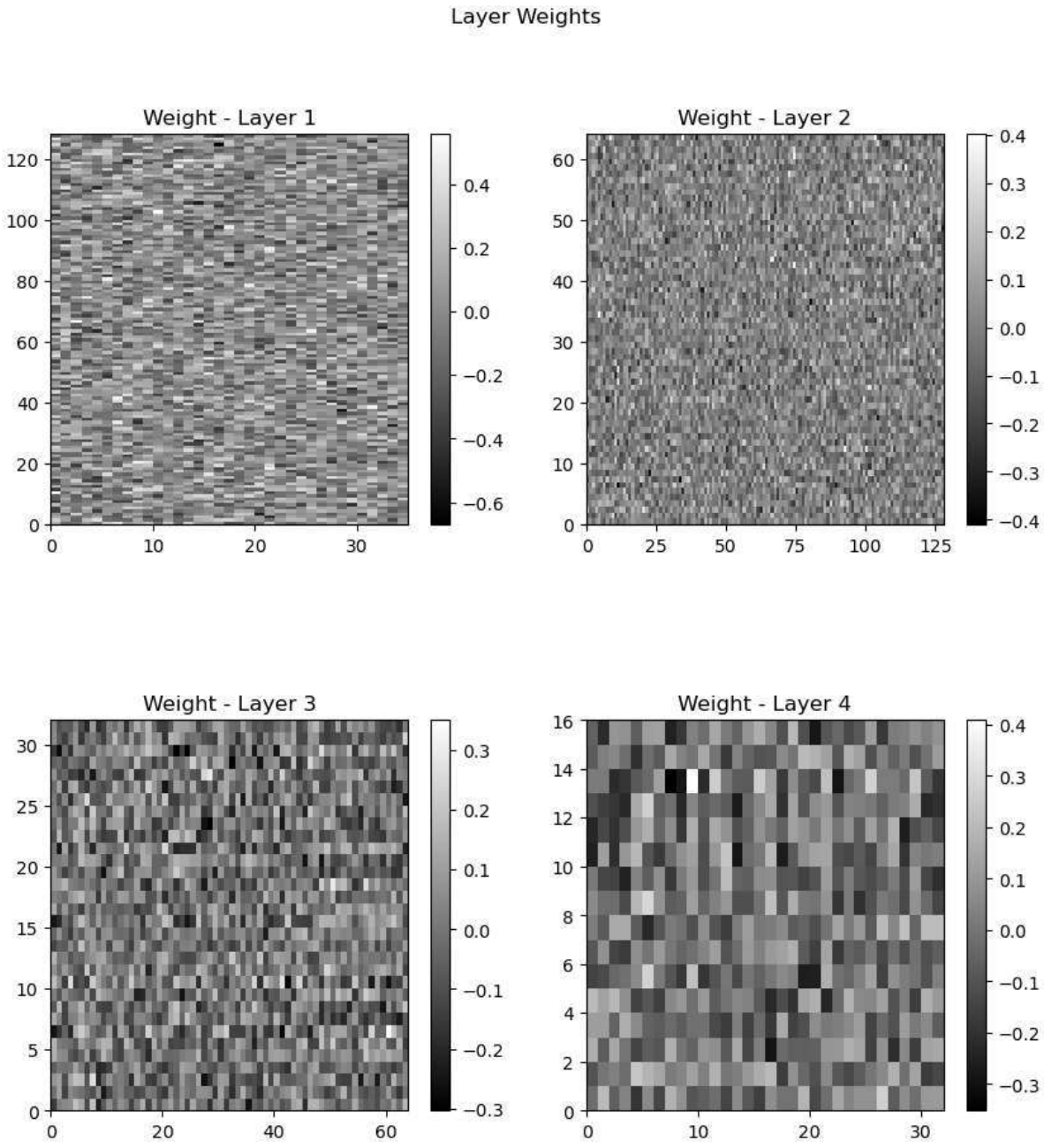
In [488]:
```
model.show_weight_distribution()
```



In [489]:
```
model.show_output_distribution(torch.tensor(lda.transform(X_test.numpy()).rea
l).float())
```



In [490]:
```
model.show_weights()
```



In [ ]:
```

```