```
        squeezeFiles.append(file.replace('\n', ''))
```

Remove the .txt files (not necessary unless you want to re-run entire notebook again in future)

[5]:
```
rm hold.txt
```

[6]:
```
rm squeeze.txt
```

Extracting the total number of files along with how many epochs there are per certain condition.

[7]:
```
sumHoldTrials = 0
sumSqueezeTrials = 0

for file in holdFiles:
    data = scipy.io.loadmat(file)
    sumHoldTrials += data["EEG"][0][0]["trials"][0][0]

for file in squeezeFiles:
    data = scipy.io.loadmat(file)
    sumSqueezeTrials += data["EEG"][0][0]["trials"][0][0]
```

Testing stft4EegChannel functionality, also useful to determine shape of data by having f (frequency) and t (time). To understand how stft4EegChannel works, I suggest looking at https://isaacmenchaca.github.io/2020/02/07/EegTF.html.

[8]:
```
# 103 trials total
f, t, Zxx = EegTF.stft4EegChannel(fileName = file, channel = 'Cz',
            timeStep = 10,  startTime = -1500, endTime = 3500, windowSize =␣
 ↪1000,
            desiredStartTime = -1000, desiredEndTime = 3000,
            trial_epoch =1,
            frequencyStop = 40,
            windowTaper = 'hann', plot_data=None)
```

2 Perform STFT TF Decomp., Adjust Data into Matrices, and Create Identity Labels

Setting up and concatenating data per condition (hold and squeeze).

[9]:
```
x_TF_hold = np.zeros([sumHoldTrials, len(f), len(t), 1])
x_TF_squeeze = np.zeros([sumSqueezeTrials, len(f), len(t), 1])

totalHoldTrials = 0
for fileindex, file in enumerate(holdFiles):
    data = scipy.io.loadmat(file)
    EEGtrials = data["EEG"][0][0]["trials"][0][0]
    for epoch in range(EEGtrials):
```