

# Running the Equiluminance Data Files to Extract Eye Position

Our dataset is generated using the code in <https://github.com/iandol/equiluminance> -- this repo contains both the experiment code and analysis code from the paper: <https://www.nature.com/articles/s41598-024-51982-z>

You need to add the equiluminance github to the MATLAB path and it depends on Opticka <https://github.com/iandol/opticka> as opticka contains the edfmex loading functions, base classes and other analysis code.

The experiment generates an EDF and MAT file with the same filename. The MAT file specifies all the experiment settings. To load data and run the pupilPower analysis use the `pupilPower` class; the `run` method will ask for an EDF file, there should be a matching MAT file in the same folder which specified the trial data:

```
p = pupilPower;
```

```
----> pupilPower#13097F5FD: You should REPARSE the data to fully enable this change  
calibrateLuminance<1AACF535A> Deleting: 1AACF535A | DELETE Method
```

```
p.run;
```

```
----> stimulusSequence loadobj: Rebuilding structure...
```

```
---->>> LOADING raw EDF data:
```

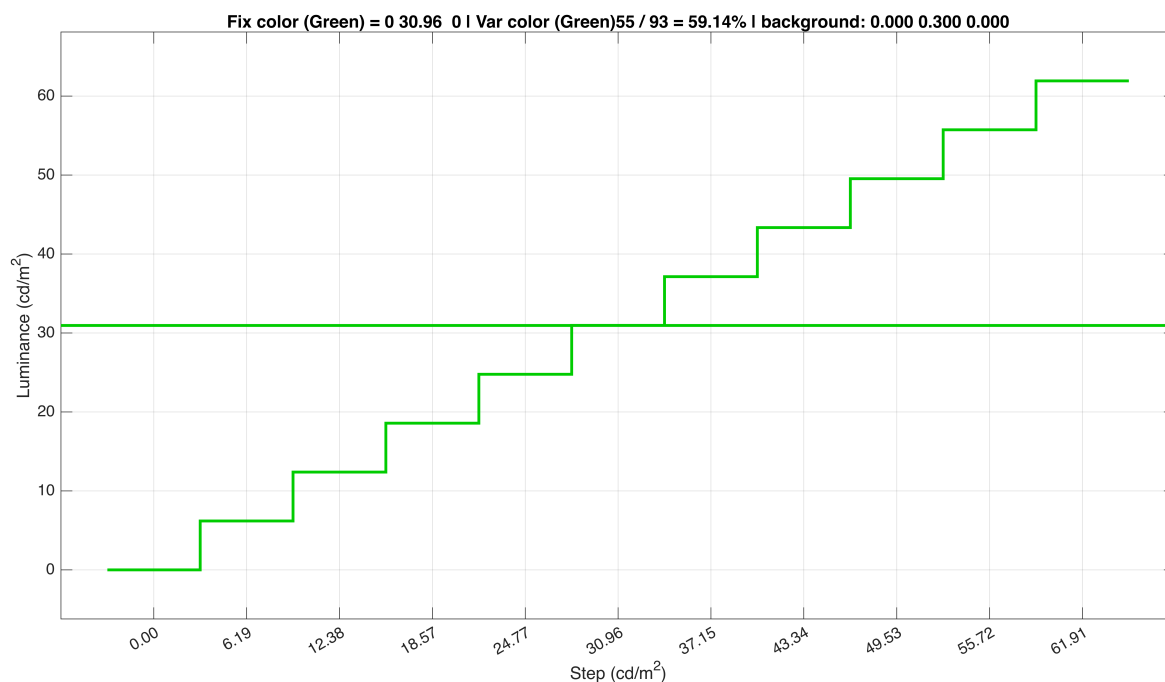
```
Loading:100%
```

```
:#: Loading Raw EDF Data took 2.92 secs
```

```
Parsing Eyelink Events: [=====] Done. [1 seconds]
```

```
Simple Parsing of EDF Trials took 1.04 secs
```

```
----> pupilPower FFT calculation took 0.217 secs
```

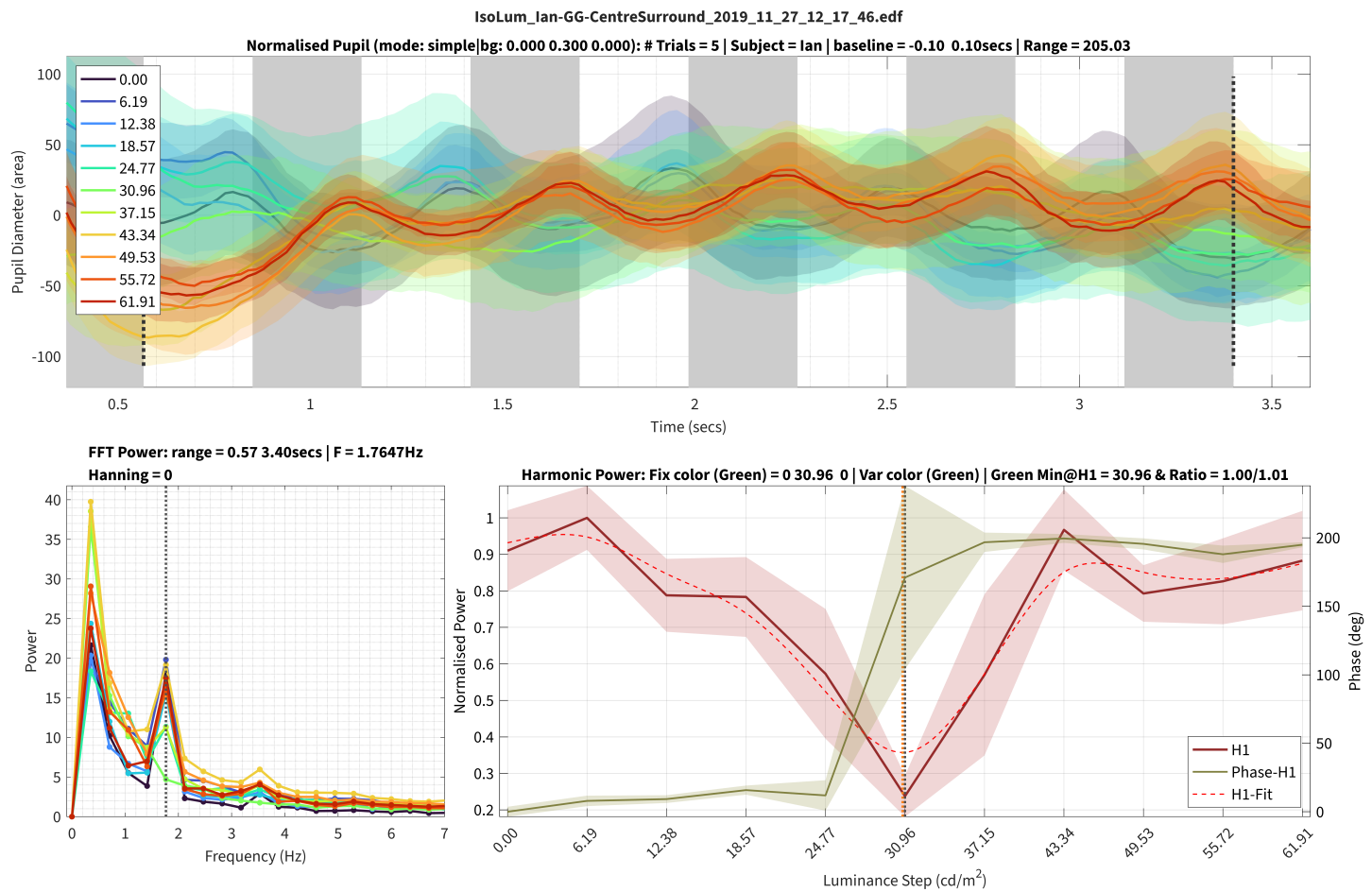


```
sse: 0.0424  
rsquare: 0.9132
```

```

dfe: 3.7221
adjrsquare: 0.7668
rmse: 0.1068

```



This code loads the EDF and parses it into trials.

## Finding the raw data

You should see the result of the pupilPower analysis as a plot segmented into averaged trials for each luminance used. Each luminance variable has a different oscillation amplitude, choose one with the biggest amplitude. Now pupilPower extracts only the pupil signal locked to stimulus onset, yet the parsed EDF is available in the pupilData property:

```
data = p.pupilData; % raw and parsed eyelink data
```

---> : You should REPARSE the data to fully enable this change

```
disp(data)
```

eyelinkAnalysis with properties:

```

file: 'IsoLum_Ian-GG-CentreSurround_2019_11_27_12_17_46.edf'
dir: '/Users/ian/'
trialStartMessageName: 'TRIALID'
variableMessageName: 'TRIALID'

```

```

rtStartMessage: 'END_FIX'
rtEndMessage: 'END_RT'
trialEndMessage: 'TRIAL_RESULT'
rtOverrideMessage: 'SYNCTIME'
minSaccadeDistance: 1
    VFAC: 5
    MINDUR: 2
    tS: [0x0 struct]
excludeIncorrect: 0
    ROI: []
    TOI: []
    verbose: 0
pixelsPerCm: 27
distance: 68
useDiameter: {[0] [9250] [8]}
isParsed: 1
sampleRate: 1000
    raw: [0x0 struct]
    trials: [1x93 struct]
    vars: [1x11 struct]
    trialList: [-10 10 6 3 9 11 7 8 5 2 1 4 3 11 1 6 9 10 7 4 -2 -2 2 8 5 3 4 5 11 -10 -10]
    correct: [1x1 struct]
    breakFix: [1x1 struct]
    incorrect: [1x1 struct]
    unknown: [1x1 struct]
    display: [1919 1079]
    otherinfo: [1x1 struct]
needOverride: 0
    ROIInfo: []
    TOIInfo: []
validation: [0x0 struct]
    ppd: 32
    doPlots: 1
baselineWindow: [-0.2000 0]
measureRange: [0.5667 3.4002]
plotRange: [-1.1010 6.5260]
rootDirectory: ''
    gd: [0x0 getDensity]
    options: [1x1 struct]
    openUI: 0
    name: 'eyelinkAnal'
    comment: '** DATE: Wed Nov 27 14:06:05 2019** TYPE: EDF_FILE BINARY EVENT SAMPLE TA
dateStamp: 02-Oct-2024 12:15:52
    uuid: '130983459'
    paths: [1x1 struct]
    fullName: 'eyelinkAnal<eyelinkAnalysis#130983459>'

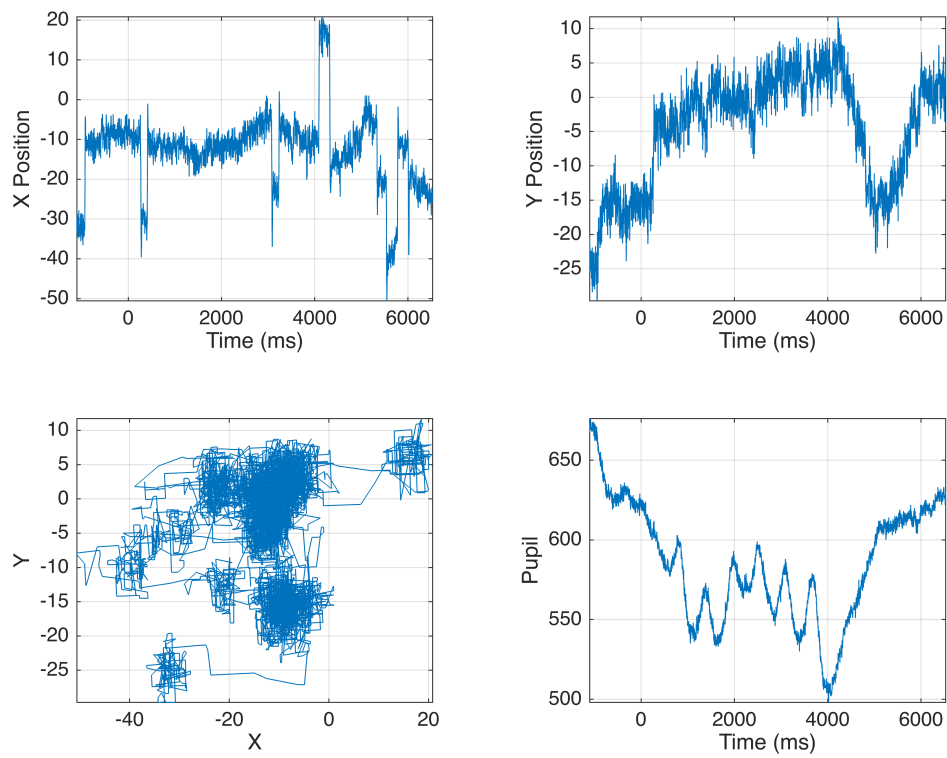
```

```
var1 = data.vars(1); % first variable (in this case luminance)
```

```

figure;
t=tiledlayout(2,2);
nexttile(t);
plot(var1.trial(1).times,var1.trial(1).gx);
xlabel('Time (ms)'); ylabel('X Position');grid on;axis tight;
nexttile(t);
plot(var1.trial(1).times,var1.trial(1).gy);
xlabel('Time (ms)'); ylabel('Y Position');grid on; axis tight;
nexttile
plot(var1.trial(1).gx,var1.trial(1).gy);
xlabel('X'); ylabel('Y');grid on; axis tight;
nexttile
plot(var1.trial(1).times,var1.trial(1).pa);
xlabel('Time (ms)'); ylabel('Pupil');grid on; axis tight;

```



This plots the X and Y data linked to stimulus onset for the first trial of the first variable. The raw trials are in `data.trials` which include all variables and both correct and incorrect trials. `data.vars` should include only correct trials for that variable.