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startup_analyse_tennessee

```
Running startup file Tennessee...
Warning: Objects of edu/ucsc/neurobiology/vision/io/PhysiologicalImagingFi
class exist - not clearing java
Warning: Objects of edu/ucsc/neurobiology/vision/io/chunk/GlobalsFile clas
exist - not clearing java
Warning: Objects of edu/ucsc/neurobiology/vision/io/STAFile class exist -
clearing java
```

```
datafile = '2012-08-09-3/data002';
% type_name= cell(1,1);
% type_name{1}='On Parasol';

datarun=load_data(datafile)
datarun=load_sta(datarun)
datarun=load_params(datarun)
datarun=load_ei(datarun,'all','array_type',519);
```

```
datarun =

    names: [1x1 struct]
```

```
Stimulus information synchronized.
```

```
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!!! WARNING! STIMULUS PARAMETERS WERE GUESSED! !!!
```

```
given parameters:
```

```
    interval: 1
    field_height: 40
    field_width: 80
    independent: 't'
    refresh_period: 8.3274
    stixel_height: 8
```

```

        stixel_width: 8

guessed parameters:

        interval: 1
        field_height: 40
        field_width: 80
        independent: 't'
        refresh_period: 8.3274
        stixel_height: 8
        stixel_width: 8
        x_start: 0
        x_end: 640
        y_start: 80
        y_end: 400
        monitor_x: 640
        monitor_y: 480
        monitor_refresh: 120

!!! WARNING! STIMULUS PARAMETERS WERE GUESSED! !!!
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

Cell ids synchronized.

datarun =

        names: [1x1 struct]
        stas: [1x1 struct]
        globals: [1x1 edu.ucsc.neurobiology.vision.io.chunk.GlobalsFile]
        stimulus: [1x1 struct]
        cell_ids: [1x253 int32]

datarun =

        names: [1x1 struct]
        stas: [1x1 struct]
        globals: [1x1 edu.ucsc.neurobiology.vision.io.chunk.GlobalsFile]
        stimulus: [1x1 struct]
        cell_ids: [1x253 int32]
        vision: [1x1 struct]
        cell_types: {1x10 cell}

vision_id=3676;
idx=[1:length(datarun.cell_ids)];
matlab_id=idx(datarun.cell_ids==vision_id);
cell_ei=datarun.ei.eis{matlab_id};

cell_ei_mag=sum(cell_ei.^2,2);
[v,center_elec]=max(cell_ei_mag);

```

```

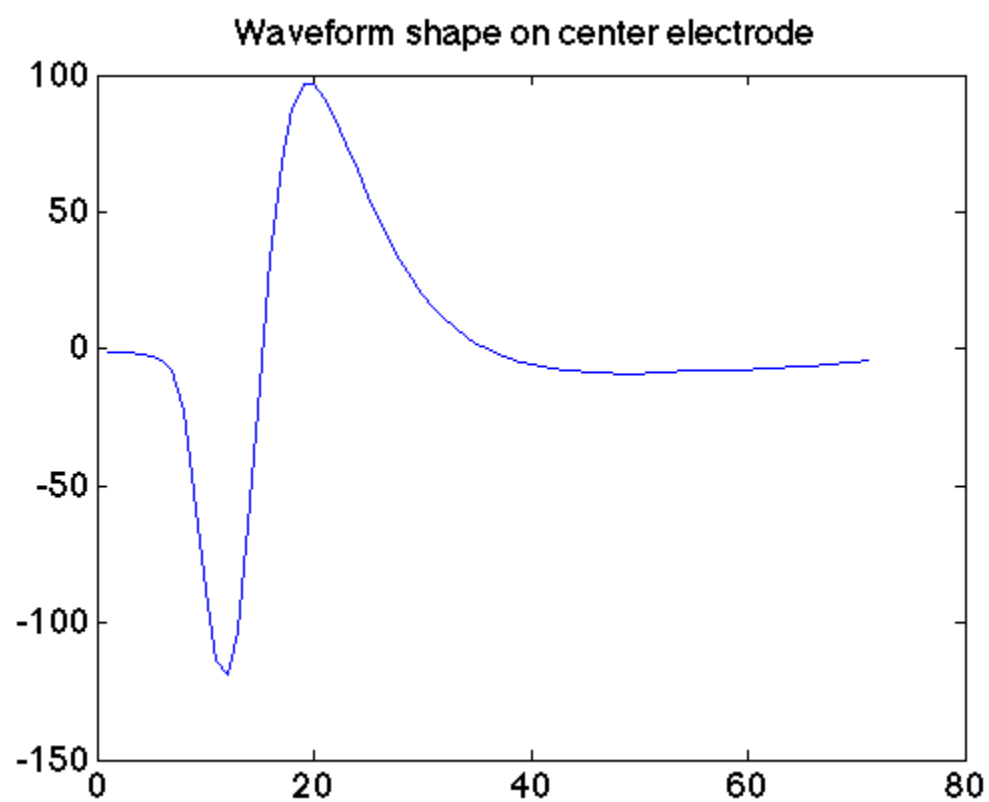
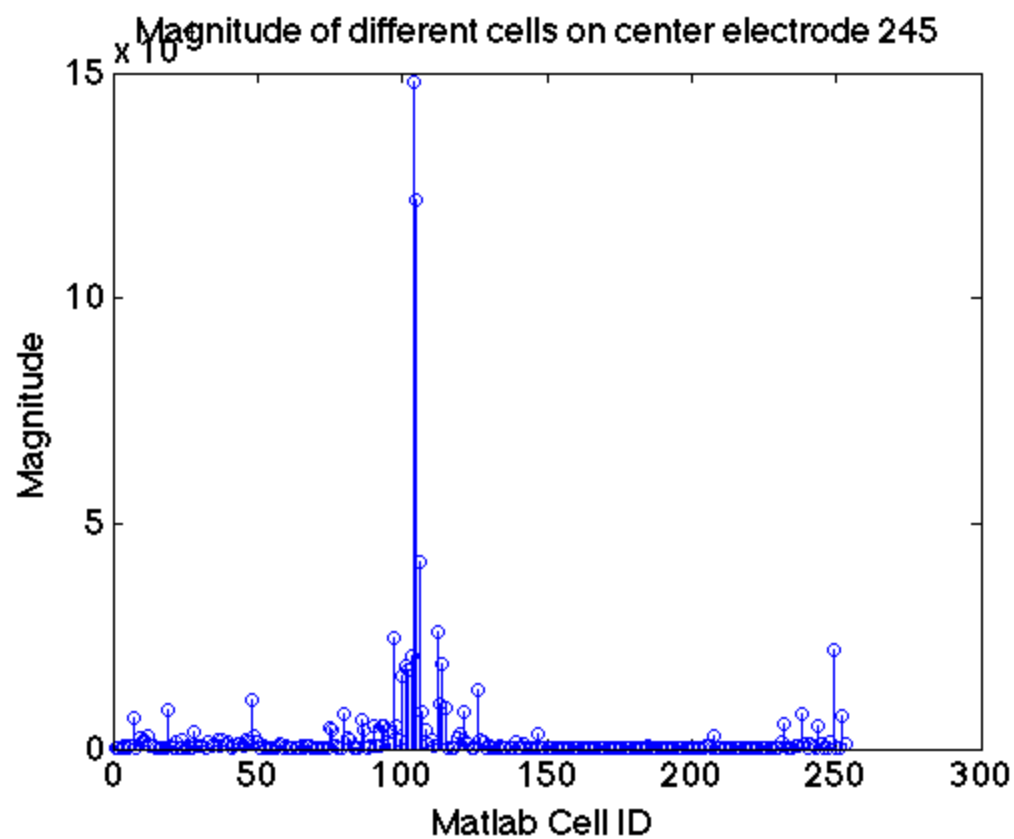
% Get all cells which are strong at calculated center electrode
% otherCellsMatlabID;
magCenterElec=[];
for icell=1:length(datarun.ei.eis)
    x=datarun.ei.eis{icell}(center_elec,:);
    magCenterElec=[magCenterElec;sum(x.^2)];
end
figure;stem(magCenterElec);
xlabel('Matlab Cell ID');
ylabel('Magnitude');
title(sprintf('Magnitude of different cells on center electrode %d',center_elec));

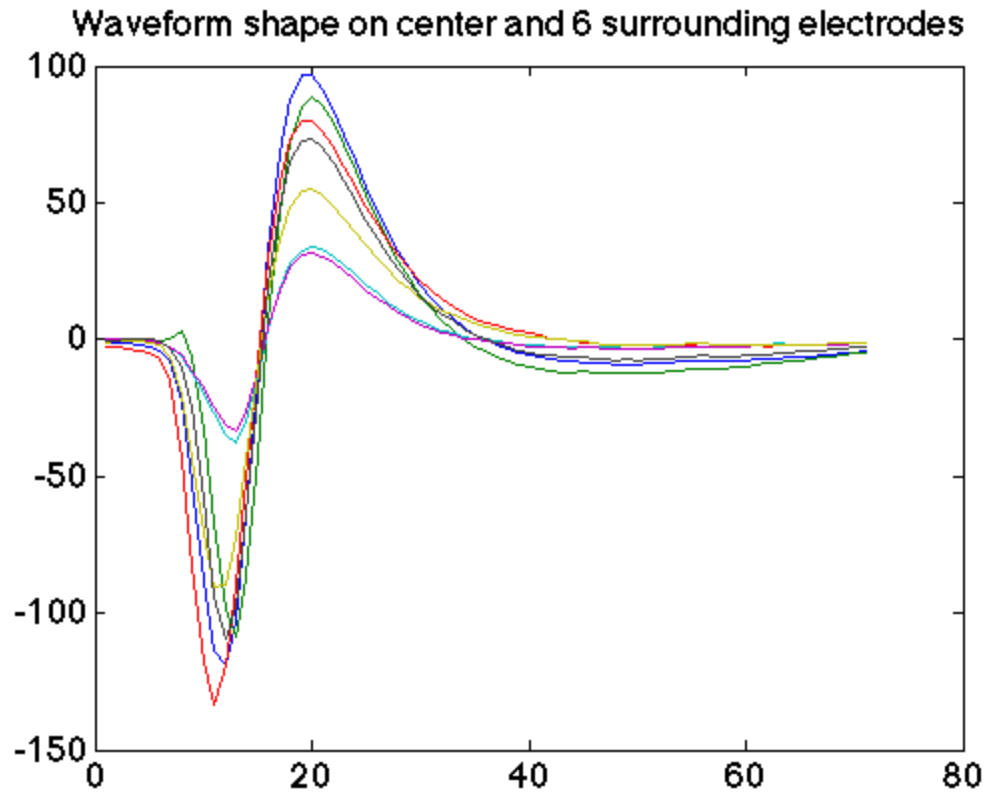
% get surround electrodes
centerElecPos=datarun.ei.position(center_elec,:);
distCenterElec = datarun.ei.position-repmat(centerElecPos,[size(datarun.ei.position,1),1]);
distCenterElec=sum(distCenterElec.^2,2);
[sortedDist,nearestChannels]=sort(distCenterElec,'ascend');
elecList=nearestChannels(1:7);

% Get Initial waveform estimates
% For center electrode
init_waveform=datarun.ei.eis{matlab_id}(center_elec,:);
figure;plot(init_waveform);
title('Waveform shape on center electrode');

init_waveform_all_channels=datarun.ei.eis{matlab_id}(elecList,:);
figure;
plot(init_waveform_all_channels');
title('Waveform shape on center and 6 surrounding electrodes');

```





Load more data

```
% raster of data
dataTrials=cell(9,1);
allElecData=cell(9,1);
trialStartIndices=cell(9,1);

for imov=[3]
    imov
    %dataTrials{imov}=getTrialData(sprintf('/Volumes/Data/2014-08-20-0/data00%d',imov))
    [dataTrials{imov},allElecData{imov},trialStartIndices{imov}]=getTrialDataMultipleE
end

    imov =

        3

    Analysing Data

    figure;
    plot(dataTrials{3}(1,800:8000));
    spikeLowerThreshold=input('Spike Lower Threshold');

    binSize=40;
```

```

for imov=3:3
    imov
    [~,dataTrialsSpike{imov}]=getTrialSpikes(dataTrials{imov}(:,1:200000),spikeLower
end

figure;
for imov=3:3
    subplot(1,1,imov-2);
    plotSpikeRaster(logical(dataTrialsSpike{imov}));
    title(sprintf('Movie %d',imov));
end

```

```

Error using input
Cannot call INPUT from EVALC.

```

```

Error in analyse (line 70)
    spikeLowerThreshold=input('Spike Lower Threshold');

```

PSTH

```

psthBinSize=20;      psthData=cell(9,1);      timeLog=cell(9,1);      for      imov=3:3
[timeLog{imov},psthData{imov}]=      psth_calc(dataTrialsSpike{imov},psthBinSize,'nonoverlap');
%mean(dataTrialsSpike{imov},1); end

figure; for imov=3:3 subplot(1,1,imov-2); plot(timeLog{imov}*binSize/(20000),psthData{imov});
ylim([0,200]); title(sprintf('Movie %d .. %0.4f',imov,var(psthData{imov}))); end

pltIdx=[1:length(psthData{3})]; figure; plot(timeLog{3}*binSize/(20000),psthData{3}(pltIdx),'b')

```

Do CBP spike sorting?

```

%spike_sort_CBP
%

```

Load previous result?

```

load('/Volumes/Analysis/nishal/NSEM_cell3676_2.mat');
% have spike_times, spike_amps, etc

```

Take spiking information found from vision

```

neuronFile=edu.ucsc.neurobiology.vision.io.NeuronFile('/Volumes/Analysis/2012-08-0
vision_spk_times= neuronFile.getSpikeTimes(vision_id);

```

Make raster

```

figure;
imov=3;
n_cell=no_cells
for icell=1:n_cell
    subplot(3,2,icell);

```

```

        plot(waveforms{3}{icell});
        title(sprintf('Cell : %d',icell));
    end

    subplot(3,2,5);
    plot(init_waveform_all_channels');

    correct_cell=-50;%input('What is the correct cell?');
    cbp_spk_times=spike_times{imov}{correct_cell};

    vision_spk_train =zeros(20000*1100,1);
    vision_spk_train(vision_spk_times)=1;

    cbp_spk_train=zeros(20000*1100,1);
    cbp_spk_train(round(cbp_spk_times))=1;

    dummyTrain=cbp_spk_train;
    %   trialStartIndices=trialStartIndices{3};
    trialIntervalSamples = 11*20000;
    numTrials=100;

    % NOTE: use only 29 samples
    dataTrials=zeros(numTrials,trialIntervalSamples);
    for iTrial=1:numTrials-1 % 30th sample less data?
        dataTrials(iTrial,:)=dummyTrain(trialStartIndices(iTrial):trialStartIndices(iT
    end

    dataTrials_cbp = dataTrials;

    dummyTrain=vision_spk_train;

    % NOTE: use only 29 samples
    dataTrials=zeros(numTrials,trialIntervalSamples);
    for iTrial=1:numTrials-1 % 30th sample less data?
        dataTrials(iTrial,:)=dummyTrain(trialStartIndices(iTrial):trialStartIndices(iT
    end

    dataTrials_vision = dataTrials;

    binSize=20;

    spikesBinnedcbp=getTrialSpikes( dataTrials_cbp,0.01,'max',binSize);
    spikesBinnedvision=getTrialSpikes( dataTrials_vision,0.01,'max',binSize);

    LineFormat = struct();
    LineFormat.Color = [0.3 0.3 0.3];
    LineFormat.LineWidth = 0.35;
    LineFormat.LineStyle = ':';
    %   plotSpikeRaster(spikes,'LineFormat',LineFormat)
    figure;
    subplot(3,1,1);
    plotSpikeRaster(logical(spikesBinnedvision),'LineFormat',LineFormat);

```

```

title('Vision');
xlabel('Time');
ylabel('Trial');

subplot(3,1,2);
LineFormat.Color = [1 0 0];
plotSpikeRaster(logical(spikesBinnedcbp), 'LineFormat', LineFormat);
title('CBP');
xlabel('Time');
ylabel('Trial');

```

Better Raster

```

numTrials=100;
dummyTimes=vision_spk_times;
dummyTrialTimes=cell(numTrials-1,1);
for iTrial=1:numTrials-1
    dummyTrialTimes{iTrial}=dummyTimes(dummyTimes>=trialStartIndices(iTrial)& dummyTimes<trialStartIndices(iTrial+1))/20000;
end
vision_spks=dummyTrialTimes;

numTrials=100;
dummyTimes=cbp_spk_times;
dummyTrialTimes=cell(numTrials-1,1);
for iTrial=1:numTrials-1
    dummyTrialTimes{iTrial}=dummyTimes(dummyTimes>=trialStartIndices(iTrial)& dummyTimes<trialStartIndices(iTrial+1))/20000;
end
cbp_spks=dummyTrialTimes;

figure;
subplot(2,1,1);
plotSpikeRaster(vision_spks);

title('Vision');
xlabel('Time');
ylabel('Trial');

subplot(2,1,2);
plotSpikeRaster(cbp_spks);
title('CBP');
xlabel('Time');
ylabel('Trial');

```

PSTH

```

psthBinSize=40%20;

[timeLog,psthData]= psth_calc(spikesBinnedcbp,psthBinSize, 'nonoverlap');%mean(data)

figure;

```

```
subplot(2,1,1);  
plot(timeLog/(20000),psthData);  
  
[timeLog,psthData]= psth_calc(spikesBinnedvision,psthBinSize,'nonoverlap');%mean(  
hold on;  
plot(timeLog/(20000),psthData,'r');
```

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