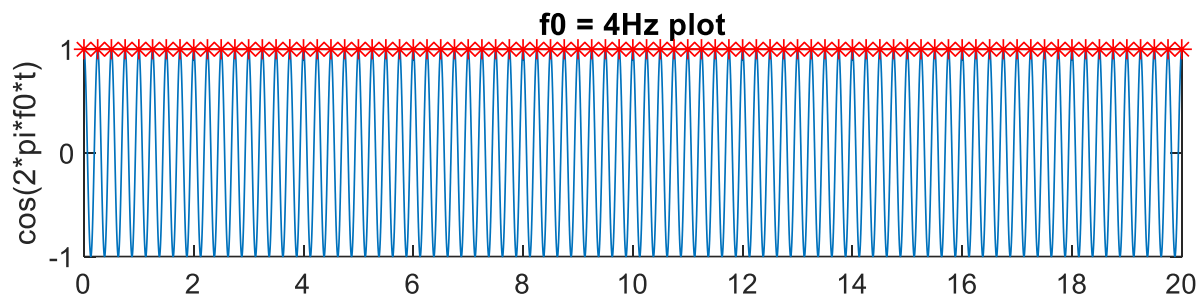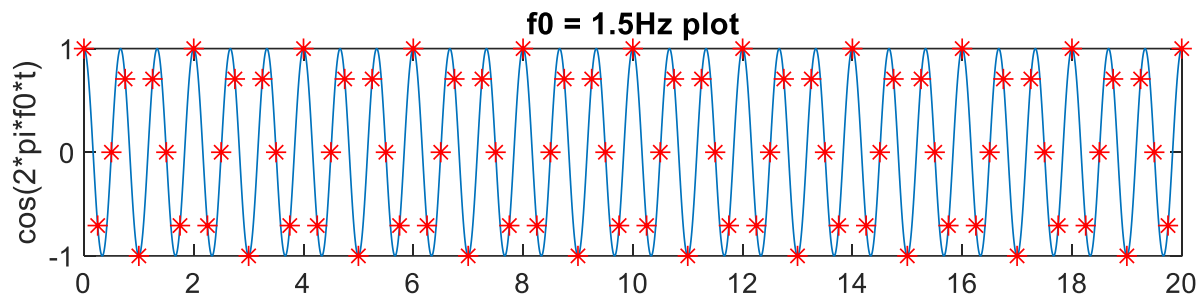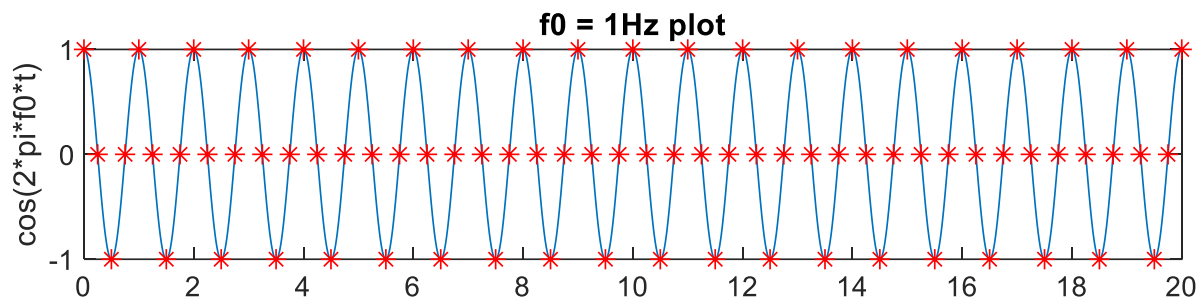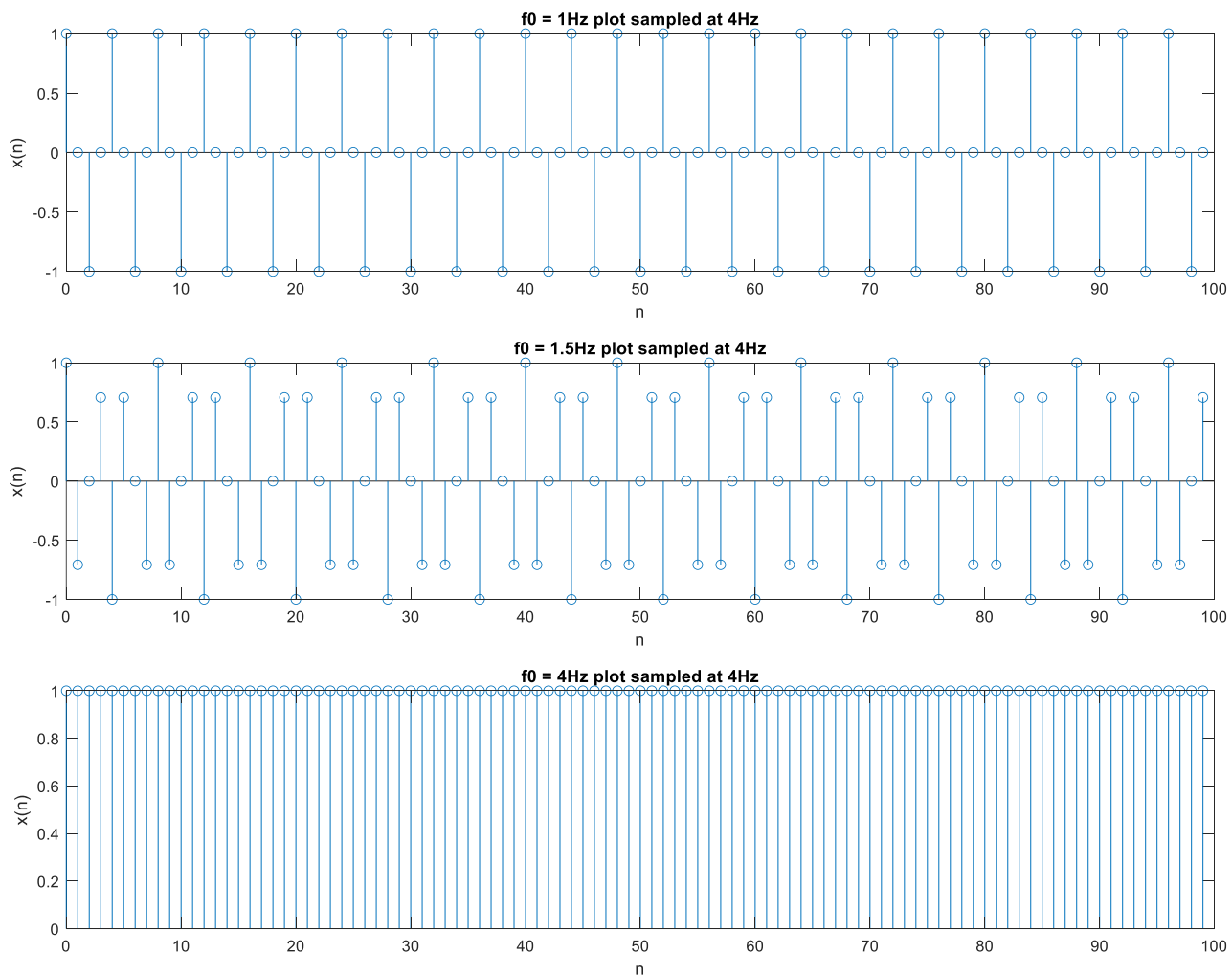1. (Digital signal) Consider the following analog sinusoidal signal xa(t)=cos(2p f0 t).

(a) Sketch (plot) the signal xa(t) for 0≤t≤20 for f0=1, 1.5, and 4 Hz respectively.

*Red dots are data points of the signal sampled at 4Hz

(b) For the sample rate Fs = 4Hz, plot the digital signal x(n) for 0≤n≤99. Explain the

similarities and differences among the various plots (for f0=1, 1.5, and 4 Hz respectively).

For the 1Hz plot the signal is getting sampled every 1/4th of the signals period since the signal is a sinusoid that means we are sampling on every peak and valley and nowhere in between.

For the 1.5Hz signal we are sampling 8 times / 3 periods of the signal. Because we aren't sampling the signal only on the peaks and valleys it looks a little odd at first glance, we see the in-between points as the signal goes from one extreme to another. We are seeing an example of leakage, the signal being sampled is offset from the discrete sampling points.

For the 4Hz signal we are sampling at the same frequency of the signal. Therefore, we are only sampling 1 point per period, and we are getting the same point every period meaning we will only see a straight line of data. In this case we sampled the peak every time.

Similarities between the 3 plots are in the data points we see, in all of them we see the positive peaks, in the 1st 2 plots we see the positive and negative peaks as well as the 0 crossing valleys.

For differences, the 3rd plot shows nothing but the positive peaks, the 2nd plot shows intermediary points between peaks and valleys, and the 1st plot only shows what it needs to show.

(c) Suppose that f0 =5Hz and Fs=20Hz. Plot the signal x(n). What is the frequency of the signal x(n)?

f0 = 5Hz plot

x(n) sampled at 20Hz
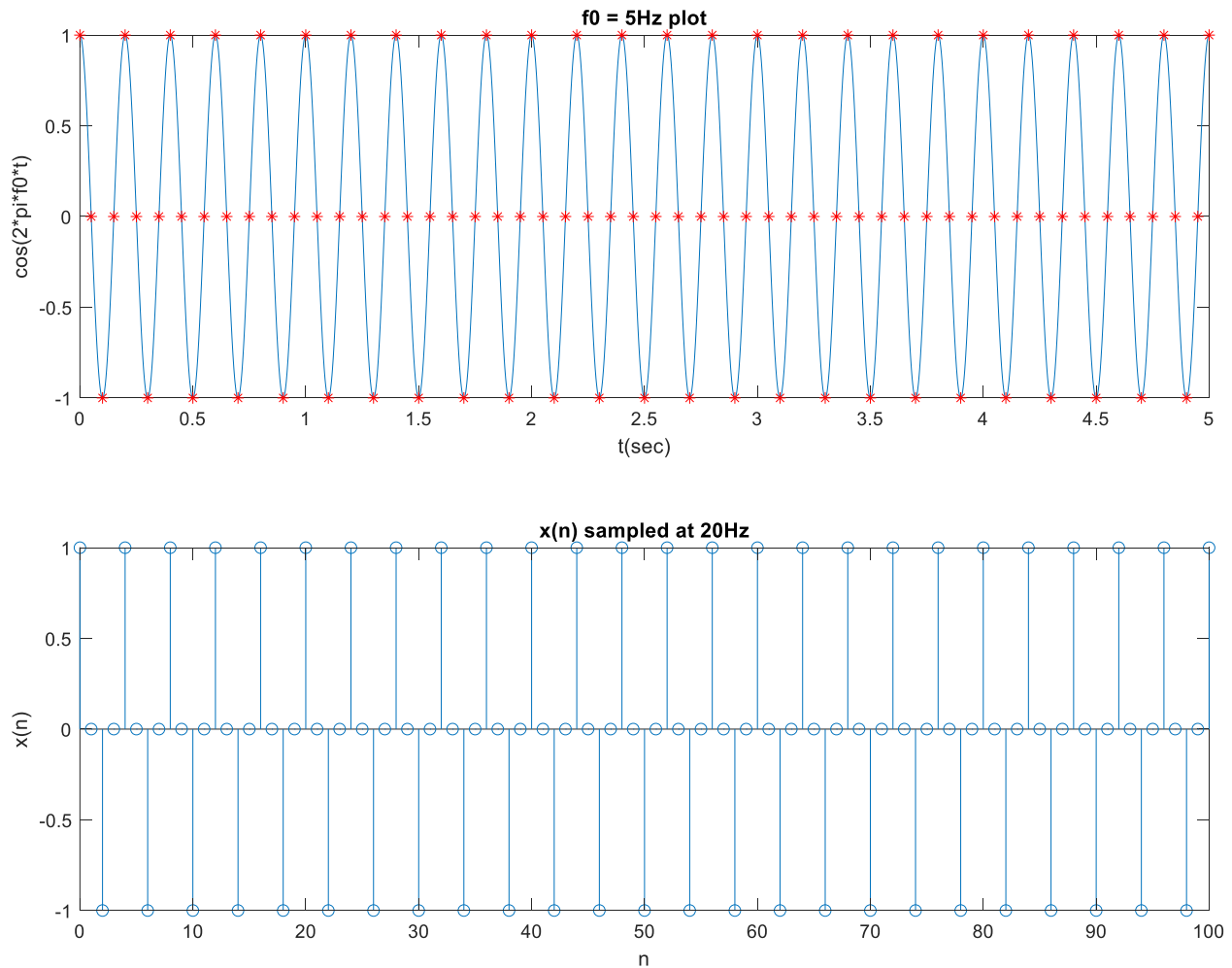
The frequency of the sampled signal is still 5Hz because we sampled at more than double the signals frequency.

(d) Same as in (c), let y(n)=x(2n-1), i.e. by taking the even-numbered samples of x(n), is this a sinusoidal signal? Why? If so, what is its frequency?

f0 = 5Hz plot

y(n) sampled at 20Hz
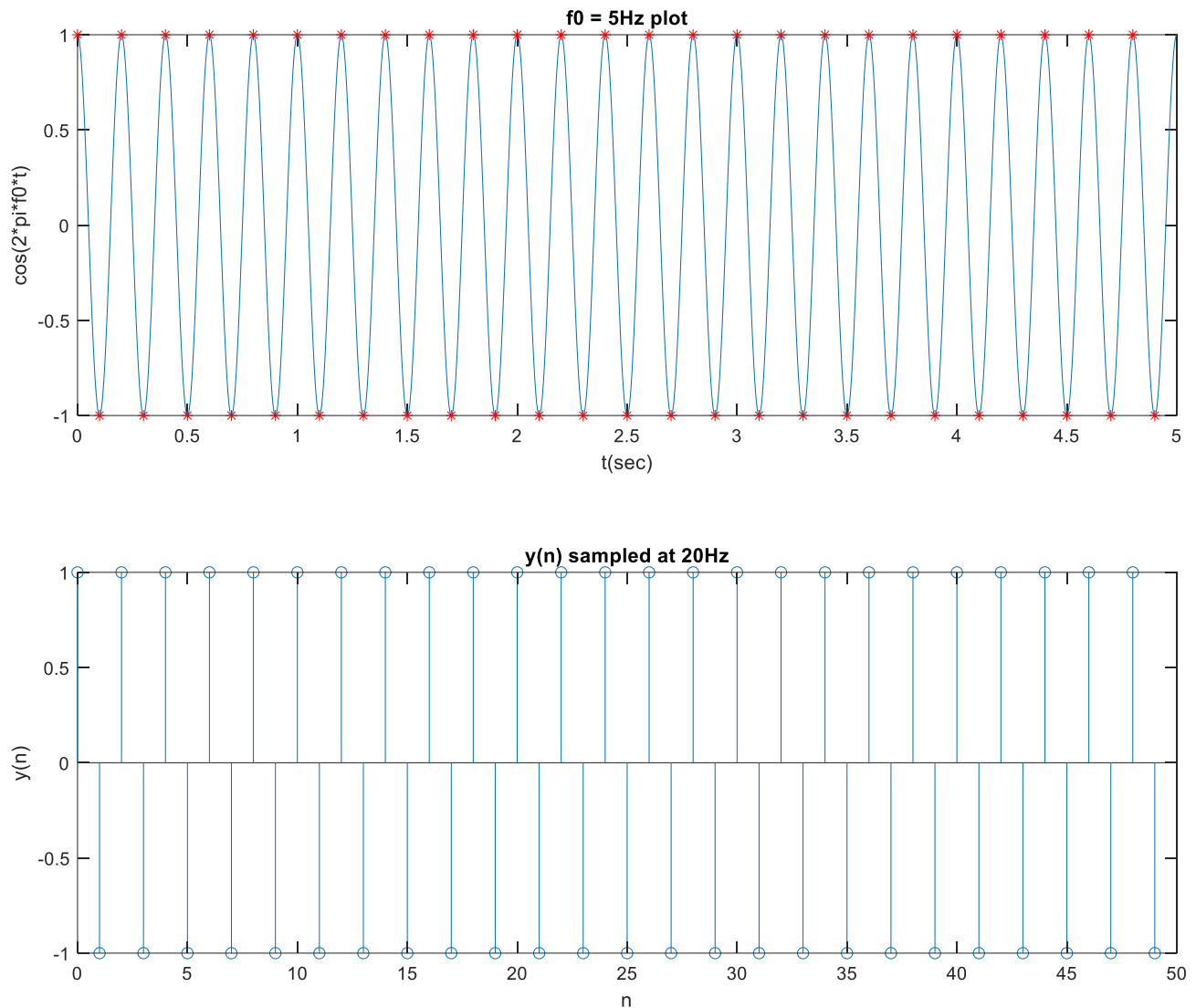
Taking samples on every even value of n ie n=0,2,4…. Is essentially the same as sampling at a frequency of 10Hz which is still 2 times the frequency of our signal so we continue to see a sinusoidal signal with a frequency of 5Hz. This is because we are sampling the signal on every positive and negative peak of the sinusoid. However, if we were to sample the signal on every odd n ie n=1,3,5… we would have just seen a line at 0 because our signal is a cos function.

2. (Correlation analysis of EEG channels)

Figure 1. Bulb-squeezing Task

EEG data description: During the experiment, subjects were seated 2 m away from a large computer screen. They were asked to squeeze a pressure responsive bulb with their right hand in order to match vertical target bars on the screen that represented 25 % of maximum voluntary contraction (MVC). The

task consisted of 7 squeezing trials, where each trial contained 10 seconds of rest period followed by 2 seconds of squeezing (see Figure 1). EEG signals are sampled at 250 Hz.

Please download both 'pdData.mat' (the EEG data for a subject with Parkinson's disease) and 'normalData.mat' (the EEG data for a normal subject). Each data file contains three variables:

• data (number of channels x number of timepoints)

• ampVec (1 x number of timepoints); ampVec(t)=1 during squeezing, amp(t)=0 during rest

• channel_name (1xnumber of channels)

Sub-problems:

(a) Plot the second EEG node, plot the data.
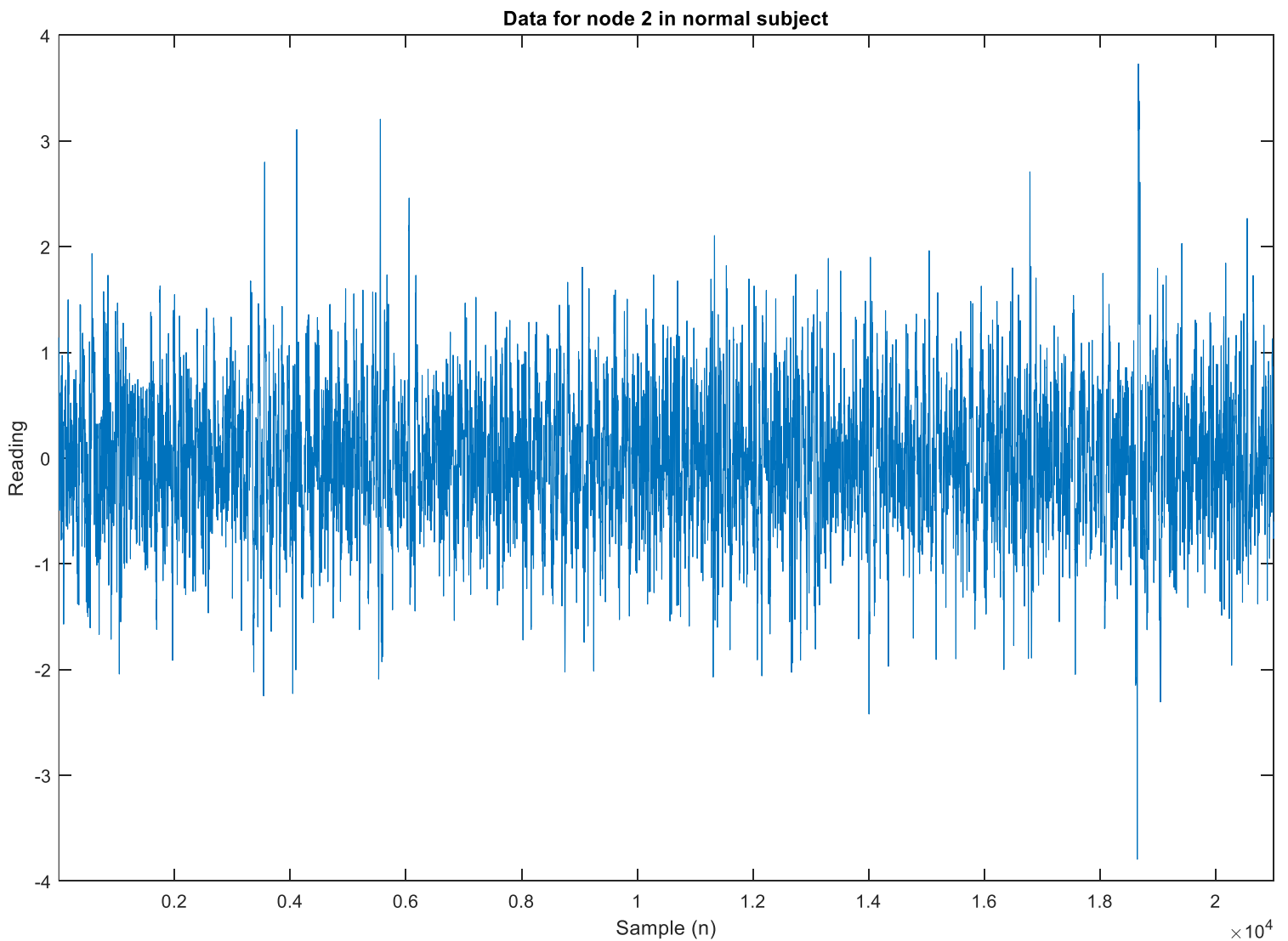
Data for node 2 in normal subject

(b) Separate the data into the rest part and the squeezing part based on the vector ampVec.

squeeze data

rest data
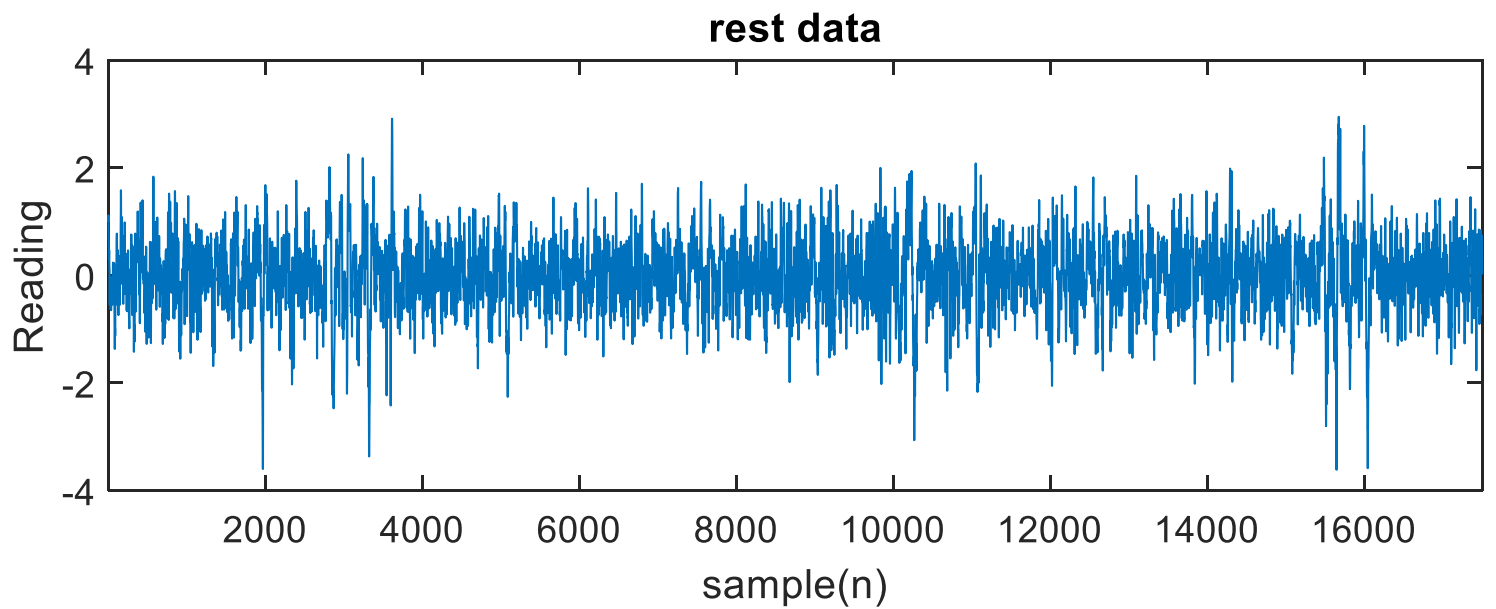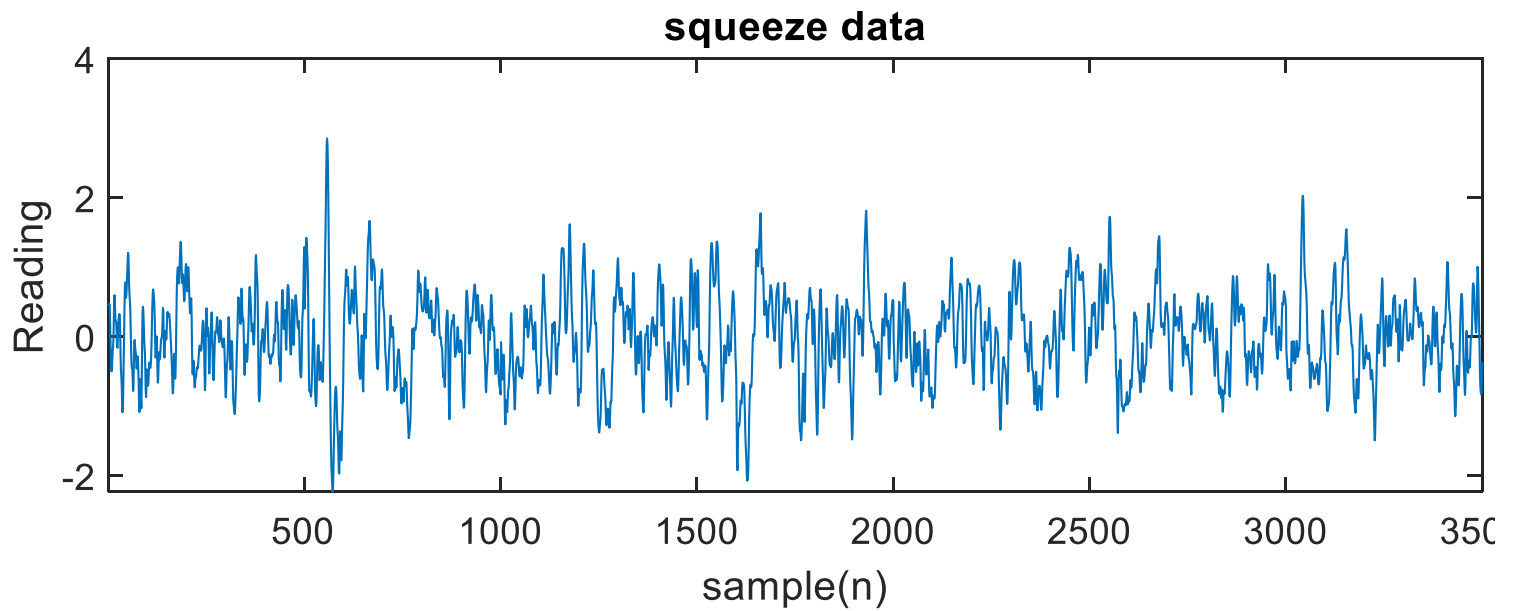
(c) Based on the EEG data of the 'rest' state, calculate the covariance matrix C_r; Based on the EEG data of the 'squeezing' state, calculate the covariance matrix C_s.

C_r:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.43	0.33	0.34	0.26	0.22	0.33	0.32	0.32	0.16	0.08	0.08	0.23	0.12	-0.02	-0.29	-0.10	0.04	0.03	-0.01
2	0.33	0.43	0.30	0.28	0.33	0.45	0.48	0.25	0.12	0.08	0.32	0.39	0.14	0.02	-0.12	0.06	0.02	0.10	0.11
3	0.34	0.30	0.73	0.54	0.28	0.28	0.28	0.75	0.56	-0.03	0.10	0.21	0.50	0.32	-0.01	0.07	0.02	0.31	0.23
4	0.26	0.28	0.54	0.76	0.56	0.41	0.30	0.59	0.59	0.12	0.22	0.17	0.37	0.25	0.03	0.07	0.07	0.22	0.17
5	0.22	0.33	0.28	0.56	0.72	0.59	0.47	0.29	0.29	0.26	0.41	0.33	0.17	0.04	-0.05	0.06	0.07	0.09	0.09
6	0.33	0.45	0.28	0.41	0.59	0.77	0.65	0.21	0.11	0.24	0.58	0.54	0.13	-0.01	-0.07	0.13	0.04	0.09	0.14
7	0.32	0.48	0.28	0.30	0.47	0.65	0.90	0.25	0.08	0.08	0.74	0.84	0.32	0.17	0.19	0.37	-0.04	0.31	0.38
8	0.32	0.25	0.75	0.59	0.29	0.21	0.25	0.98	0.77	-0.02	0.12	0.24	0.79	0.64	0.27	0.27	0.05	0.57	0.44
9	0.16	0.12	0.56	0.59	0.29	0.11	0.08	0.77	1.06	-0.02	0.07	0.04	0.69	0.72	0.39	0.22	0.12	0.50	0.36
10	0.08	0.08	-0.03	0.12	0.26	0.24	0.08	-0.02	-0.02	0.31	0.03	0.03	0.01	-0.12	-0.20	-0.16	0.08	-0.11	-0.13
11	0.08	0.32	0.10	0.22	0.41	0.58	0.74	0.12	0.07	0.03	1.05	0.86	0.32	0.22	0.43	0.64	-0.01	0.33	0.48
12	0.23	0.39	0.21	0.17	0.33	0.54	0.84	0.24	0.04	0.03	0.86	1.01	0.39	0.23	0.31	0.56	-0.05	0.39	0.52
13	0.12	0.14	0.50	0.37	0.17	0.13	0.32	0.79	0.69	0.01	0.32	0.39	1.04	0.91	0.64	0.57	0.02	0.91	0.74
14	-0.02	0.02	0.32	0.25	0.04	-0.01	0.17	0.64	0.72	-0.12	0.22	0.23	0.91	1.04	0.82	0.61	0.00	0.90	0.74
15	-0.29	-0.12	-0.01	0.03	-0.05	-0.07	0.19	0.27	0.39	-0.20	0.43	0.31	0.64	0.82	1.10	0.86	-0.07	0.78	0.81
16	-0.10	0.06	0.07	0.07	0.06	0.13	0.37	0.27	0.22	-0.16	0.64	0.56	0.57	0.61	0.86	1.00	-0.08	0.72	0.89
17	0.04	0.02	0.02	0.07	0.07	0.04	-0.04	0.05	0.12	0.08	-0.01	-0.05	0.02	0.00	-0.07	-0.08	0.61	-0.04	-0.05
18	0.03	0.10	0.31	0.22	0.09	0.09	0.31	0.57	0.50	-0.11	0.33	0.39	0.91	0.90	0.78	0.72	-0.04	1.03	0.91
19	-0.01	0.11	0.23	0.17	0.09	0.14	0.38	0.44	0.36	-0.13	0.48	0.52	0.74	0.74	0.81	0.89	-0.05	0.91	1.02

C_s:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.38	0.31	0.40	0.29	0.21	0.32	0.43	0.40	0.21	0.00	0.24	0.39	0.21	0.04	-0.11	0.05	0.05	0.10	0.10
2	0.31	0.41	0.37	0.29	0.29	0.42	0.51	0.36	0.19	0.03	0.38	0.47	0.23	0.08	0.01	0.15	0.05	0.16	0.19
3	0.40	0.37	0.72	0.52	0.30	0.36	0.48	0.70	0.46	-0.06	0.26	0.39	0.41	0.20	-0.03	0.08	0.10	0.20	0.17
4	0.29	0.29	0.52	0.71	0.55	0.46	0.44	0.54	0.47	0.09	0.35	0.34	0.31	0.16	0.02	0.10	-0.01	0.16	0.14
5	0.21	0.29	0.30	0.55	0.71	0.58	0.45	0.34	0.31	0.25	0.40	0.35	0.20	0.07	-0.04	0.10	-0.08	0.09	0.09
6	0.32	0.42	0.36	0.46	0.58	0.75	0.62	0.37	0.24	0.22	0.59	0.57	0.26	0.12	0.05	0.23	-0.01	0.18	0.21
7	0.43	0.51	0.48	0.44	0.45	0.62	0.80	0.50	0.26	0.04	0.60	0.72	0.39	0.21	0.14	0.33	0.04	0.32	0.36
8	0.40	0.36	0.70	0.54	0.34	0.37	0.50	0.88	0.60	-0.03	0.35	0.48	0.65	0.47	0.22	0.29	0.12	0.43	0.37
9	0.21	0.19	0.46	0.47	0.31	0.24	0.26	0.60	0.82	0.01	0.21	0.21	0.50	0.48	0.28	0.20	0.08	0.33	0.25
10	0.00	0.03	-0.06	0.09	0.25	0.22	0.04	-0.03	0.01	0.29	0.04	0.05	0.03	-0.05	-0.09	-0.08	-0.04	-0.05	-0.06
11	0.24	0.38	0.26	0.35	0.40	0.59	0.60	0.35	0.21	0.04	0.83	0.68	0.38	0.29	0.31	0.56	-0.03	0.37	0.42
12	0.39	0.47	0.39	0.34	0.35	0.57	0.72	0.48	0.21	0.05	0.68	0.86	0.43	0.26	0.18	0.46	-0.02	0.38	0.45
13	0.21	0.23	0.41	0.31	0.20	0.26	0.39	0.65	0.50	0.03	0.38	0.43	0.80	0.68	0.49	0.51	0.11	0.68	0.57
14	0.04	0.08	0.20	0.16	0.07	0.12	0.21	0.47	0.48	-0.05	0.29	0.26	0.68	0.79	0.64	0.55	0.08	0.68	0.57
15	-0.11	0.01	-0.03	0.02	-0.04	0.05	0.14	0.22	0.28	-0.09	0.31	0.18	0.49	0.64	0.77	0.64	0.08	0.60	0.57
16	0.05	0.15	0.08	0.10	0.10	0.23	0.33	0.29	0.20	-0.08	0.56	0.46	0.51	0.55	0.64	0.82	-0.01	0.62	0.68
17	0.05	0.05	0.10	-0.01	-0.08	-0.01	0.04	0.12	0.08	-0.04	-0.03	-0.02	0.11	0.08	0.08	-0.01	0.58	0.08	0.06
18	0.10	0.16	0.20	0.16	0.09	0.18	0.32	0.43	0.33	-0.05	0.37	0.38	0.68	0.68	0.60	0.62	0.08	0.77	0.68
19	0.10	0.19	0.17	0.14	0.09	0.21	0.36	0.37	0.25	-0.06	0.42	0.45	0.57	0.57	0.57	0.68	0.06	0.68	0.73

(d) Based on the EEG data of the 'rest' state, calculate the matrix R of correlation coefficients, and comment on the dependencies between the EEG nodes. (You can use 'mesh' commend to display the matrix R.) Compare the differences between the Pakinson's disease subject the normal subject (e.g. based on features such as the eigenvalues of R; For each EEG node k, calculate the summation of R(k,j) over j and use such summations as features for comparison) and comment on your results.

Based on the following data taken at rest we can make multiple observations.

From the summation of correlation data for each node we can see how interdependent a particular node is, i.e., how correlated the signals are to other nodes. In healthy patient we see an average correlation of about 6.7. In a patient suffering from Parkinson's disease, we see a much lower average correlation of about 0.09.

Looking at the data in the table as well as the 3d mesh plot of the data we can see that the average correlation closer to 0 in the sick patient is due to a larger number of negative correlations between nodes. A negative correlation between nodes would signify that there is an inverse relationship between those nodes and therefore there is an inverse relationship between those regions of the brain where they should instead be working together. From the correlation matrix and mesh we can also see that there are is a much lower correlation between nodes that are farther apart. This makes sense as we would expect brain regions located farther apart would have more trouble communicating, than regions closer together. We can see that in our sick patient that the regions that are farther apart actually end up having negative correlations meaning that the brain is miscommunicating between those distant regions.

The eigenvalues of our correlation matrix give us variance along the principal axes of our datapoints for each node. A larger eigenvalue corresponds to a greater variance and thus a larger spread of datapoints. In both cases we see the largest eigenvalues for the last node in our dataset. Relatively the eigenvalues stay between 0-1 until the last 3 nodes where they effectively double between nodes.

2 nodes standout as outliers in our correlation matrix for having particularly low correlations values. Node 10 (CZ) and node 17 (P8) these nodes only really stand out in the healthy patient data as in the sick patient data all other nodes drop to similar correlation values.

R_rest:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1.00	0.77	0.60	0.46	0.39	0.57	0.51	0.50	0.23	0.21	0.12	0.35	0.19	-0.02	-0.43	-0.16	0.08	0.05	-0.01
2	0.77	1.00	0.54	0.49	0.59	0.79	0.77	0.39	0.17	0.23	0.48	0.60	0.21	0.03	-0.17	0.09	0.04	0.15	0.17
3	0.60	0.54	1.00	0.72	0.39	0.37	0.34	0.88	0.63	-0.07	0.11	0.24	0.57	0.37	-0.02	0.08	0.03	0.36	0.26
4	0.46	0.49	0.72	1.00	0.76	0.54	0.36	0.68	0.66	0.25	0.24	0.20	0.42	0.28	0.03	0.08	0.11	0.25	0.19
5	0.39	0.59	0.39	0.76	1.00	0.80	0.58	0.35	0.33	0.56	0.47	0.39	0.20	0.04	-0.06	0.08	0.11	0.10	0.10
6	0.57	0.79	0.37	0.54	0.80	1.00	0.78	0.24	0.12	0.49	0.64	0.61	0.15	-0.01	-0.08	0.15	0.06	0.11	0.16
7	0.51	0.77	0.34	0.36	0.58	0.78	1.00	0.27	0.08	0.14	0.76	0.88	0.33	0.17	0.19	0.39	-0.05	0.32	0.40
8	0.50	0.39	0.88	0.68	0.35	0.24	0.27	1.00	0.76	-0.05	0.12	0.24	0.78	0.64	0.26	0.27	0.06	0.57	0.44
9	0.23	0.17	0.63	0.66	0.33	0.12	0.08	0.76	1.00	-0.04	0.07	0.04	0.65	0.69	0.36	0.22	0.15	0.48	0.35
10	0.21	0.23	-0.07	0.25	0.56	0.49	0.14	-0.05	-0.04	1.00	0.06	0.06	0.01	-0.21	-0.35	-0.29	0.19	-0.19	-0.24
11	0.12	0.48	0.11	0.24	0.47	0.64	0.76	0.12	0.07	0.06	1.00	0.84	0.30	0.21	0.40	0.63	-0.01	0.32	0.46
12	0.35	0.60	0.24	0.20	0.39	0.61	0.88	0.24	0.04	0.06	0.84	1.00	0.38	0.23	0.29	0.55	-0.07	0.39	0.51
13	0.19	0.21	0.57	0.42	0.20	0.15	0.33	0.78	0.65	0.01	0.30	0.38	1.00	0.87	0.60	0.56	0.02	0.88	0.72
14	-0.02	0.03	0.37	0.28	0.04	-0.01	0.17	0.64	0.69	-0.21	0.21	0.23	0.87	1.00	0.76	0.60	-0.01	0.87	0.71
15	-0.43	-0.17	-0.02	0.03	-0.06	-0.08	0.19	0.26	0.36	-0.35	0.40	0.29	0.60	0.76	1.00	0.82	-0.09	0.73	0.76
16	-0.16	0.09	0.08	0.08	0.08	0.15	0.39	0.27	0.22	-0.29	0.63	0.55	0.56	0.60	0.82	1.00	-0.11	0.71	0.87
17	0.08	0.04	0.03	0.11	0.11	0.06	-0.05	0.06	0.15	0.19	-0.01	-0.07	0.02	-0.01	-0.09	-0.11	1.00	-0.05	-0.06
18	0.05	0.15	0.36	0.25	0.10	0.11	0.32	0.57	0.48	-0.19	0.32	0.39	0.88	0.87	0.73	0.71	-0.05	1.00	0.89
19	-0.01	0.17	0.26	0.19	0.10	0.16	0.40	0.44	0.35	-0.24	0.46	0.51	0.72	0.71	0.76	0.87	-0.06	0.89	1.00

Eigenvalues:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.000	0.000	0.026	0.050	0.061	0.091	0.104	0.122	0.130	0.167	0.218	0.311	0.376	0.717	0.904	1.314	2.739	4.274	7.395

Sum of columns:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
5.382	7.326	7.415	7.713	7.177	7.479	8.233	8.396	6.954	1.750	7.210	7.721	8.835	7.222	5.021	6.535	1.404	7.932	7.675

Sum of matrix =   127.3781, average correlation between nodes =   6.7041

R_rest_parkinsons:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1.00	0.39	0.28	0.42	0.53	0.39	0.29	0.08	0.01	0.16	-0.12	-0.05	-0.25	-0.50	0.11	-0.51	-0.38	-0.51	-0.45
2	0.39	1.00	0.01	0.35	0.68	0.81	0.74	-0.20	-0.28	0.12	0.13	0.27	-0.51	-0.73	0.12	-0.47	-0.39	-0.61	-0.50
3	0.28	0.01	1.00	0.56	0.16	-0.09	0.02	0.70	0.27	-0.26	-0.63	-0.17	0.15	-0.06	-0.41	-0.54	-0.37	-0.21	-0.30
4	0.42	0.35	0.56	1.00	0.77	0.47	0.25	0.15	0.35	0.26	-0.18	-0.22	-0.35	-0.39	-0.35	-0.59	-0.63	-0.62	-0.64
5	0.53	0.68	0.16	0.77	1.00	0.86	0.47	-0.27	0.01	0.52	0.20	-0.11	-0.67	-0.66	-0.01	-0.48	-0.64	-0.73	-0.67
6	0.39	0.81	-0.09	0.47	0.86	1.00	0.71	-0.44	-0.24	0.41	0.39	0.12	-0.73	-0.73	0.11	-0.32	-0.48	-0.69	-0.58
7	0.29	0.74	0.02	0.25	0.47	0.71	1.00	-0.22	-0.40	-0.01	0.21	0.57	-0.51	-0.71	0.05	-0.36	-0.25	-0.56	-0.44
8	0.08	-0.20	0.70	0.15	-0.27	-0.44	-0.22	1.00	0.27	-0.50	-0.75	-0.14	0.61	0.30	-0.39	-0.44	-0.15	0.13	-0.04
9	0.01	-0.28	0.27	0.35	0.01	-0.24	-0.40	0.27	1.00	0.30	-0.20	-0.50	0.16	0.48	0.00	-0.26	-0.46	-0.16	-0.37
10	0.16	0.12	-0.26	0.26	0.52	0.41	-0.01	-0.50	0.30	1.00	0.57	-0.30	-0.56	-0.15	0.42	0.03	-0.47	-0.48	-0.47
11	-0.12	0.13	-0.63	-0.18	0.20	0.39	0.21	-0.75	-0.20	0.57	1.00	0.23	-0.61	-0.27	0.41	0.52	0.01	-0.34	-0.20
12	-0.05	0.27	-0.17	-0.22	-0.11	0.12	0.57	-0.14	-0.50	-0.30	0.23	1.00	-0.20	-0.42	-0.06	0.06	0.34	-0.18	-0.01
13	-0.25	-0.51	0.15	-0.35	-0.67	-0.73	-0.51	0.61	0.16	-0.56	-0.61	-0.20	1.00	0.70	-0.24	-0.11	0.22	0.67	0.38
14	-0.50	-0.73	-0.06	-0.39	-0.66	-0.73	-0.71	0.30	0.48	-0.15	-0.27	-0.42	0.70	1.00	0.03	0.20	0.10	0.63	0.30
15	0.11	0.12	-0.41	-0.35	-0.01	0.11	0.05	-0.39	0.00	0.42	0.41	-0.06	-0.24	0.03	1.00	0.23	-0.15	-0.13	-0.15
16	-0.51	-0.47	-0.54	-0.59	-0.48	-0.32	-0.36	-0.44	-0.26	0.03	0.52	0.06	-0.11	0.20	0.23	1.00	0.61	0.34	0.54
17	-0.38	-0.39	-0.37	-0.63	-0.64	-0.48	-0.25	-0.15	-0.46	-0.47	0.01	0.34	0.22	0.10	-0.15	0.61	1.00	0.54	0.78
18	-0.51	-0.61	-0.21	-0.62	-0.73	-0.69	-0.56	0.13	-0.16	-0.48	-0.34	-0.18	0.67	0.63	-0.13	0.34	0.54	1.00	0.83
19	-0.45	-0.50	-0.30	-0.64	-0.67	-0.58	-0.44	-0.04	-0.37	-0.47	-0.20	-0.01	0.38	0.30	-0.15	0.54	0.78	0.83	1.00

Eigenvalues:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.000	0.017	0.037	0.053	0.068	0.103	0.116	0.126	0.172	0.243	0.276	0.344	0.475	0.769	0.940	1.121	2.718	4.239	7.184

Sum of columns:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.892	0.944	0.132	0.611	0.962	0.959	0.841	-0.298	-0.027	0.580	0.361	0.225	-0.831	-0.867	0.573	-0.571	-0.772	-1.077	-0.982

Sum of matrix = 1.6553, average correlation between nodes = 0.0871

Correlation of normal rest data

Correlation of parkinsons disease rest data
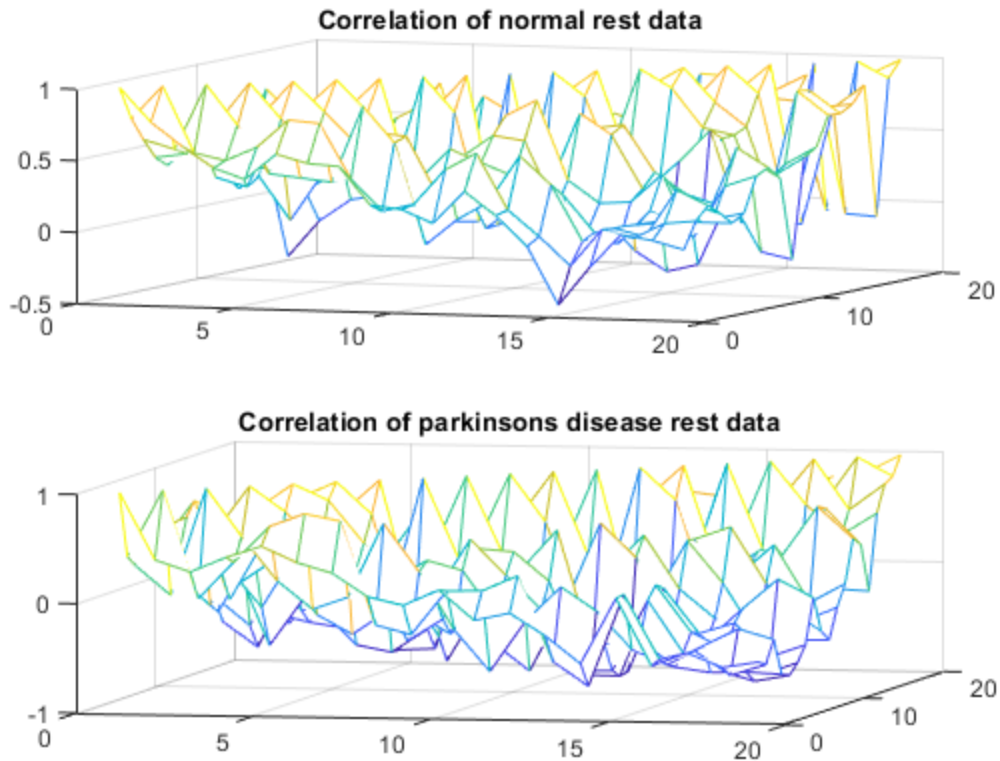
(e) Repeat (d) for the 'squeezing' state.

Much like the data above we can reassert most of the observations we saw before but for the squeezing data.

From the summation of correlation data for each node we can see how interdependent a particular node is. In healthy patient we see an average correlation of about 7.9. In a patient suffering from Parkinson's disease, we see a much lower average correlation of about 0.05.

Looking at the data in the table as well as the 3d mesh plot of the data we can see that the average correlation closer to 0 in the sick patient is due to a larger number of negative correlations between nodes signifying an inverse relationship between those nodes and an inverse relationship between those regions of the brain. From the correlation matrix and mesh we can again see that there are is a much lower correlation between nodes that are farther apart. We can see that in our sick patient that the regions that are farther apart actually end up having negative correlations meaning that the brain is miscommunicating between those distant regions.

The eigenvalues of our correlation matrix give us variance along the principal axes of our datapoints for each node. A larger eigenvalue corresponds to a greater variance and thus a larger spread of datapoints. In both cases we see the largest eigenvalues for the last node in our dataset. Relatively the eigenvalues stay between 0-1 until the last 3 nodes where they effectively double between nodes.

Again, the same 2 nodes standout as outliers in our correlation matrix for having particularly low correlations values. Node 10 (CZ) and node 17 (P8) these nodes only really stand out in the healthy patient data as in the sick patient data all other nodes drop to similar correlation values.

Overall, we can see a much higher average correlation value in the healthy patient when they are squeezing rather than when they are at rest, this is expected as we would assume that the brain would be more active when we are actively trying to use our motorskills.

R_squeeze:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1.00	0.79	0.76	0.56	0.42	0.60	0.78	0.70	0.38	-0.01	0.43	0.68	0.38	0.08	-0.20	0.08	0.11	0.18	0.20
2	0.79	1.00	0.68	0.54	0.54	0.77	0.89	0.60	0.33	0.09	0.65	0.80	0.40	0.14	0.01	0.26	0.10	0.28	0.34
3	0.76	0.68	1.00	0.72	0.43	0.49	0.63	0.88	0.60	-0.14	0.34	0.49	0.54	0.27	-0.04	0.10	0.15	0.27	0.24
4	0.56	0.54	0.72	1.00	0.77	0.63	0.58	0.68	0.61	0.19	0.45	0.43	0.41	0.22	0.02	0.13	-0.02	0.21	0.19
5	0.42	0.54	0.43	0.77	1.00	0.79	0.59	0.44	0.41	0.55	0.53	0.46	0.26	0.09	-0.05	0.13	-0.13	0.13	0.13
6	0.60	0.77	0.49	0.63	0.79	1.00	0.80	0.45	0.31	0.46	0.75	0.71	0.34	0.15	0.06	0.30	-0.01	0.24	0.28
7	0.78	0.89	0.63	0.58	0.59	0.80	1.00	0.59	0.32	0.09	0.74	0.88	0.50	0.27	0.18	0.40	0.06	0.41	0.47
8	0.70	0.60	0.88	0.68	0.44	0.45	0.59	1.00	0.71	-0.06	0.41	0.55	0.78	0.56	0.27	0.34	0.17	0.53	0.46
9	0.38	0.33	0.60	0.61	0.41	0.31	0.32	0.71	1.00	0.02	0.25	0.25	0.62	0.60	0.36	0.25	0.11	0.41	0.32
10	-0.01	0.09	-0.14	0.19	0.55	0.46	0.09	-0.06	0.02	1.00	0.09	0.09	0.07	-0.11	-0.19	-0.15	-0.09	-0.11	-0.13
11	0.43	0.65	0.34	0.45	0.53	0.75	0.74	0.41	0.25	0.09	1.00	0.81	0.47	0.36	0.39	0.68	-0.05	0.46	0.54
12	0.68	0.80	0.49	0.43	0.46	0.71	0.88	0.55	0.25	0.09	0.81	1.00	0.53	0.32	0.22	0.55	-0.02	0.47	0.57
13	0.38	0.40	0.54	0.41	0.26	0.34	0.50	0.78	0.62	0.07	0.47	0.53	1.00	0.86	0.63	0.63	0.16	0.87	0.75
14	0.08	0.14	0.27	0.22	0.09	0.15	0.27	0.56	0.60	-0.11	0.36	0.32	0.86	1.00	0.82	0.69	0.12	0.87	0.75
15	-0.20	0.01	-0.04	0.02	-0.05	0.06	0.18	0.27	0.36	-0.19	0.39	0.22	0.63	0.82	1.00	0.81	0.12	0.79	0.76
16	0.08	0.26	0.10	0.13	0.13	0.30	0.40	0.34	0.25	-0.15	0.68	0.55	0.63	0.69	0.81	1.00	-0.01	0.78	0.88
17	0.11	0.10	0.15	-0.02	-0.13	-0.01	0.06	0.17	0.11	-0.09	-0.05	-0.02	0.16	0.12	0.12	-0.01	1.00	0.13	0.09
18	0.18	0.28	0.27	0.21	0.13	0.24	0.41	0.53	0.41	-0.11	0.46	0.47	0.87	0.87	0.79	0.78	0.13	1.00	0.91
19	0.20	0.34	0.24	0.19	0.13	0.28	0.47	0.46	0.32	-0.13	0.54	0.57	0.75	0.75	0.76	0.88	0.09	0.91	1.00

Eigenvalues:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.000	0.000	0.030	0.052	0.065	0.078	0.106	0.118	0.138	0.154	0.207	0.244	0.334	0.603	0.954	1.482	1.900	3.824	8.710

Sum of columns:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
7.938	9.231	8.410	8.337	7.484	9.112	10.170	10.061	7.863	1.645	9.303	9.788	10.178	8.048	5.957	7.848	1.992	8.821	8.746

Sum of matrix =   150.9328, average correlation between nodes = 7.9438

R_squeeze_Parkinsons:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1.00	0.14	0.23	0.31	0.47	0.31	0.12	0.04	-0.04	0.18	-0.11	-0.14	-0.21	-0.40	0.09	-0.39	-0.27	-0.42	-0.37
2	0.14	1.00	-0.08	0.31	0.62	0.71	0.61	-0.17	-0.23	0.09	0.12	0.17	-0.47	-0.65	0.01	-0.38	-0.32	-0.52	-0.42
3	0.23	-0.08	1.00	0.48	0.09	-0.16	-0.01	0.70	0.31	-0.27	-0.64	-0.15	0.18	-0.01	-0.40	-0.55	-0.32	-0.21	-0.29
4	0.31	0.31	0.48	1.00	0.77	0.50	0.16	0.17	0.37	0.20	-0.27	-0.29	-0.28	-0.36	-0.42	-0.63	-0.62	-0.55	-0.56
5	0.47	0.62	0.09	0.77	1.00	0.86	0.37	-0.23	0.06	0.49	0.14	-0.21	-0.61	-0.61	-0.11	-0.51	-0.64	-0.68	-0.62
6	0.31	0.71	-0.16	0.50	0.86	1.00	0.62	-0.41	-0.16	0.43	0.37	0.02	-0.68	-0.66	-0.02	-0.33	-0.50	-0.66	-0.56
7	0.12	0.61	-0.01	0.16	0.37	0.62	1.00	-0.23	-0.36	0.00	0.23	0.53	-0.48	-0.64	0.02	-0.30	-0.20	-0.50	-0.40
8	0.04	-0.17	0.70	0.17	-0.23	-0.41	-0.23	1.00	0.36	-0.42	-0.70	-0.17	0.54	0.31	-0.33	-0.46	-0.20	0.01	-0.14
9	-0.04	-0.23	0.31	0.37	0.06	-0.16	-0.36	0.36	1.00	0.30	-0.24	-0.43	0.16	0.47	-0.06	-0.33	-0.53	-0.21	-0.42
10	0.18	0.09	-0.27	0.20	0.49	0.43	0.00	-0.42	0.30	1.00	0.57	-0.26	-0.53	-0.16	0.33	-0.01	-0.50	-0.45	-0.47
11	-0.11	0.12	-0.64	-0.27	0.14	0.37	0.23	-0.70	-0.24	0.57	1.00	0.26	-0.60	-0.26	0.41	0.53	0.03	-0.27	-0.16
12	-0.14	0.17	-0.15	-0.29	-0.21	0.02	0.53	-0.17	-0.43	-0.26	0.26	1.00	-0.23	-0.38	0.00	0.14	0.37	-0.12	0.03
13	-0.21	-0.47	0.18	-0.28	-0.61	-0.68	-0.48	0.54	0.16	-0.53	-0.60	-0.23	1.00	0.71	-0.20	-0.11	0.19	0.62	0.35
14	-0.40	-0.65	-0.01	-0.36	-0.61	-0.66	-0.64	0.31	0.47	-0.16	-0.26	-0.38	0.71	1.00	0.05	0.19	0.06	0.54	0.25
15	0.09	0.01	-0.40	-0.42	-0.11	-0.02	0.02	-0.33	-0.06	0.33	0.41	0.00	-0.20	0.05	1.00	0.31	0.00	-0.08	-0.06
16	-0.39	-0.38	-0.55	-0.63	-0.51	-0.33	-0.30	-0.46	-0.33	-0.01	0.53	0.14	-0.11	0.19	0.31	1.00	0.64	0.36	0.55
17	-0.27	-0.32	-0.32	-0.62	-0.64	-0.50	-0.20	-0.20	-0.53	-0.50	0.03	0.37	0.19	0.06	0.00	0.64	1.00	0.54	0.78
18	-0.42	-0.52	-0.21	-0.55	-0.68	-0.66	-0.50	0.01	-0.21	-0.45	-0.27	-0.12	0.62	0.54	-0.08	0.36	0.54	1.00	0.83
19	-0.37	-0.42	-0.29	-0.56	-0.62	-0.56	-0.40	-0.14	-0.42	-0.47	-0.16	0.03	0.35	0.25	-0.06	0.55	0.78	0.83	1.00

Eigenvalues:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.000	0.016	0.052	0.067	0.073	0.109	0.146	0.154	0.194	0.285	0.372	0.378	0.503	0.884	1.047	1.253	2.485	4.379	6.602

Sum of columns:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
0.535	0.556	-0.123	0.282	0.636	0.674	0.553	-0.336	0.010	0.534	0.415	0.138	-0.633	-0.546	0.533	-0.283	-0.506	-0.760	-0.696

Sum of matrix =   0.9834, average correlation between nodes = 0.0518

Correlation of normal squeeze data

Correlation of parkinsons disease squeeze data
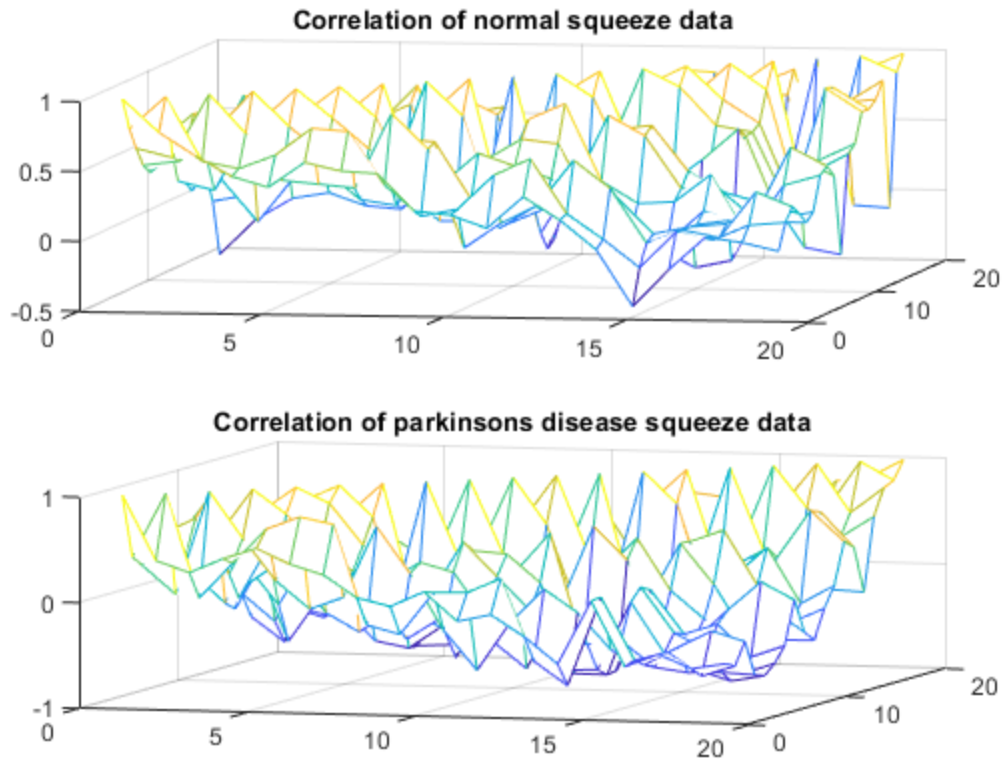
Matlab code:

```
clear; close all;
% Assignment 1 q1
% Andrew Munro-West 18363572
% 1. (Digital signal) Consider the following analog sinusoidal signal
xa(t)=cos(2p f0 t).
% (a) Sketch (plot) the signal xa(t) for 0?t?20 for f0=1, 1.5, and 4 Hz
respectively.

Fs = 4;
t = 0:0.001:20;ts = 0:1/Fs:25; f1 = 1; f2 = 1.5; f3 = 4;
x1= cos(2*pi*f1*t);
x2= cos(2*pi*f2*t);
x3= cos(2*pi*f3*t);
x1s= cos(2*pi*f1*ts);
x2s= cos(2*pi*f2*ts);
x3s= cos(2*pi*f3*ts);
figure
tiledlayout(3,1)

ax1 = nexttile;
plot(ax1,t,x1,ts(1,1:81),x1s(1,1:81),'r*')
title(ax1,'f0 = 1Hz plot')
ylabel(ax1,'cos(2*pi*f0*t)')
xlabel(ax1,'t(sec)')
```

```matlab
ax3 = nexttile;
plot(ax3,t,x2,ts(1,1:81),x2s(1,1:81),'r*')
title(ax3,'f0 = 1.5Hz plot')
ylabel(ax3,'cos(2*pi*f0*t)')
xlabel(ax3,'t(sec)')

ax5 = nexttile;
plot(ax5,t,x3,ts(1,1:81),x3s(1,1:81),'r*')
title(ax5,'f0 = 4Hz plot')
ylabel(ax5,'cos(2*pi*f0*t)')
xlabel(ax5,'t(sec)')

% (b) For the sample rate Fs = 4Hz, plot the digital signal x(n) for 0?n?99. Explain the
% similarities and differences among the various plots (for f0=1, 1.5, and 4 Hz respectively).

figure
tiledlayout(3,1)

ax2 = nexttile;
stem(ax2,ts(1,1:100),x1s(1,1:100))
xticks(0:10/4:25)
xticklabels(0:10:100)
title(ax2,'f0 = 1Hz plot sampled at 4Hz')
ylabel(ax2,'x(n)')
xlabel(ax2,'n')

ax4 = nexttile;
stem(ax4,ts(1,1:100),x2s(1,1:100))
xticks(0:10/4:25)
xticklabels(0:10:100)
title(ax4,'f0 = 1.5Hz plot sampled at 4Hz')
ylabel(ax4,'x(n)')
xlabel(ax4,'n')

ax6 = nexttile;
stem(ax6,ts(1,1:100),x3s(1,1:100))
xticks(0:10/4:25)
xticklabels(0:10:100)
title(ax6,'f0 = 4Hz plot sampled at 4Hz')
ylabel(ax6,'x(n)')
xlabel(ax6,'n')


%same plots but only to t=2 instead of 20 for better clarity of the shape
% Fs = 4;
% t = 0:0.001:2;ts = 0:1/Fs:2; f1 = 1; f2 = 1.5; f3 = 4;
% x1= cos(2*pi*f1*t);
% x2= cos(2*pi*f2*t);
% x3= cos(2*pi*f3*t);
% x1s= cos(2*pi*f1*ts);
% x2s= cos(2*pi*f2*ts);
% x3s= cos(2*pi*f3*ts);
```

```matlab
% figure
% tiledlayout(3,2)
%
% ax1 = nexttile;
% plot(ax1,t,x1,ts,x1s,'r*')
% title(ax1,'f0 = 1Hz plot')
% ylabel(ax1,'cos(2*pi*f0*t)')
%
% ax2 = nexttile;
% stem(ax2,ts,x1s,'r')
% title(ax2,'f0 = 1Hz plot sampled at 4Hz')
% ylabel(ax2,'cos(2*pi*f0*t)')
%
% ax3 = nexttile;
% plot(ax3,t,x2,ts,x2s,'r*')
% title(ax3,'f0 = 1.5Hz plot')
% ylabel(ax3,'cos(2*pi*f0*t)')
%
% ax4 = nexttile;
% stem(ax4,ts,x2s,'r')
% title(ax4,'f0 = 1.5Hz plot sampled at 4Hz')
% ylabel(ax4,'cos(2*pi*f0*t)')
%
% ax5 = nexttile;
% plot(ax5,t,x3,ts,x3s,'r*')
% title(ax5,'f0 = 4Hz plot')
% ylabel(ax5,'cos(2*pi*f0*t)')
%
% ax6 = nexttile;
% stem(ax6,ts,x3s,'r')
% title(ax6,'f0 = 4Hz plot sampled at 4Hz')
% ylabel(ax6,'cos(2*pi*f0*t)')

% (c) Suppose that f0 =5Hz and Fs=20Hz. Plot the signal x(n). What is the
frequency of the
% signal x(n)?

Fs = 20;
t = 0:0.001:5;ts = 0:1/Fs:5; f1 = 5;
x1= cos(2*pi*f1*t);
x1s= cos(2*pi*f1*ts);
figure
tiledlayout(2,1)
ax1 = nexttile;
plot(ax1,t,x1,ts,x1s,'r*')
title(ax1,'f0 = 5Hz plot')
ylabel(ax1,'cos(2*pi*f0*t)')
xlabel(ax1,'t(sec)')

ax2= nexttile;
stem(ax2,ts,x1s)
xticks(0:10/Fs:5)
xticklabels(0:10:100)
title(ax2,'x(n) sampled at 20Hz')
ylabel(ax2,'x(n)')
xlabel(ax2,'n')
```

```matlab
% % (d) Same as in (c), let y(n)=x(2n-1), i.e. by taking the even-numbered
samples of x(n), is this
% % a sinusoidal signal? Why? If so, what is its frequency?

% Fs = 10;
% t = 0:0.001:20;ts = 0:1/Fs:20; f1 = 5;
% x1= cos(2*pi*f1*t);
% x1s= cos(2*pi*f1*ts);
figure
tiledlayout(2,1)

ax1 = nexttile;
plot(ax1,t,x1,ts(2:2:100),x1s(2:2:100),'r*')
title(ax1,'f0 = 5Hz plot')
ylabel(ax1,'cos(2*pi*f0*t)')
xlabel(ax1,'t(sec)')

ax2= nexttile;
stem(ax2,ts(2:2:100),x1s(2:2:100))
xticks(0:10/Fs:5)
xticklabels(0:5:50)
title(ax2,'y(n) sampled at 20Hz')
ylabel(ax2,'y(n)')
xlabel(ax2,'n')
ylim(ax2,[-1,1])




clear; close all;
% Assignment 1 q2
% Andrew Munro-West 18363572
%
% (a) Plot the second EEG node, plot the data.

A = importdata('normalData.mat');
B = importdata('pdData.mat');
len = size(A.data,2);
wid = size(A.data,1);

figure
plot([1:1:len],A.data(2,1:len))
xlim([1,len])
title('Data for node 2 in normal subject')
ylabel('Reading')
xlabel('Sample (n)')
%
% (b) Separate the data into the rest part and the squeezing part based on
the vector ampVec.
% squeeze = A.data.*A.ampVec;
% rest = A.data.*~A.ampVec;
squeeze = A.data(:,~~A.ampVec);
squeezeP = B.data(:,~~B.ampVec);
rest = A.data(:,~A.ampVec);
restP = B.data(:,~B.ampVec);
```

```matlab
sl = size(squeeze,2);
rl = size(rest,2);

figure
tiledlayout(2,1)

ax1 = nexttile;
plot(ax1,[1:1:sl],squeeze(1,1:sl))
title(ax1,'squeeze data')
ylabel(ax1,'Reading')
xlabel(ax1,'sample(n)')
xlim([1,sl])
ax2 = nexttile;
plot(ax2,[1:1:rl],rest(1,1:rl))
xlim([1,rl])
title(ax2,'rest data')
ylabel(ax2,'Reading')
xlabel(ax2,'sample(n)')




% (c) Based on the EEG data of the 'rest' state, calculate the covariance
matrix C_r; Based on the EEG data of the 'squeezing' state, calculate the
covariance matrix C_s.
squeeze = transpose(squeeze);
squeezeP =transpose(squeezeP);
rest = transpose(rest);
restP = transpose(restP);

C_r = cov(rest);
C_s = cov(squeeze);
C_rp = cov(restP);
C_sp = cov(squeezeP);

% (d) Based on the EEG data of the 'rest' state, calculate the matrix R of
correlation coefficients, and comment on the dependencies between the EEG
nodes. (You can use 'mesh' commend to display the matrix R.) Compare the
differences between the Pakinson's disease subject the normal subject (e.g.
based on features such as the eigenvalues of R; For each EEG node k,
calculate the summation of R(k,j) over j and use such summations as features
for comparison) and comment on your results.
R_rest = corrcoef(rest);
R_restP = corrcoef(restP);
e_rest = transpose(eig(R_rest));
e_restP = transpose(eig(R_restP));
s_rest = sum(R_rest);
s_restP = sum(R_restP);

figure
tiledlayout(2,1)
ax1 = nexttile;
mesh(ax1,R_rest)
title(ax1,'Correlation of normal rest data')

ax2 = nexttile;
```

```matlab
mesh(ax2,R_restP)
title(ax2,'Correlation of parkinsons disease rest data')

% (e) Repeat (d) for the 'squeezing' state.
R_squeeze = corrcoef(squeeze);
R_squeezeP = corrcoef(squeezeP);
e_squeeze = transpose(eig(R_squeeze));
e_squeezeP = transpose(eig(R_squeezeP));
s_squeeze = sum(R_squeeze);
s_squeezeP = sum(R_squeezeP);

figure
tiledlayout(2,1)
ax1 = nexttile;
mesh(ax1,R_rest)
title(ax1,'Correlation of normal squeeze data')

ax2 = nexttile;
mesh(ax2,R_restP)
title(ax2,'Correlation of parkinsons disease squeeze data')
```