**Things I have tried:**

1. Use the 32 nodes dataframe (each contains patients from the corresponding control group), and calculate the mean response curve for each node.
2. For each patient, analyze the all nodes by applying “Wave” function and plot varince on the 1st PC.
3. Use original time-series, grouped by node, across different patients where each corresponding to 1 of the 4 control groups (PD-placebo, PD-Ldopa, HC-placebo, HC-Ldopa). Apply fpca on each node dataframe, and analyze whether there is a common pattern where most variance happens for each group of patients.
4. Analyzing the result from step 3, pick a subset of nodes according to the fpca plots (variance pattern).
5. Repeat step 2, and use only a subset of nodes according to the result from step 4.

­­­PD-placebo HC-placebo

Chart, histogram

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PD-Ldopa HC-Ldopa

­Chart, histogram

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1. A short list (biased) of PC1 variance plot of patients

PD-placebo. HC-placebo

Chart, radar chart

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Chart

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A picture containing graphical user interface

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Chart, line chart

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Some data itself just looks weird and suspicious.

Chart

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Chart

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