Current implementation –

1. Load all traces one by one as columns into a single data frame called df
2. Filter the data frame and make a copy df\_filtered
3. Create peak analysis dataframe which has cropped peaks, peak\_x, peak\_y, etc
4. Make plot of raw and filtered trace and show only a small region
5. Wait for user to click on graph which calls pt\_on\_peak\_pick.

Pass df, df\_filtered, peak\_analysis.

Functions

1. pt\_on\_peak\_pick uses df, df\_filtered to generate new plots.
2. pt\_make\_plot uses data1d and data1d\_filtered
3. pt\_gaussian\_filter uses df and returns df\_filtered
4. pt\_get\_all\_peaks uses df\_filtered

New implementation so that we can handle a lot more data. Main idea is not to load too much data into the memory at the same time.

1. To create peak analysis dataframe, load 1 wave at a time and filter it.
2. For plotting raw and filtered data, load the wave and filter it one at a time.