Instant Gas Exchange Analysis (IGEA) package

I am from Dr. Andrew Leakey’s lab and part of the traits I measure in my project are photosynthesis, stomata conductance and Ci.Ca in a maize population, using Licor 6400. Instead of conducting measurements in the field, this year we used a protocol that allows us to measure these plant physiology parameters in lab. In the early morning our team went to the field and harvested leaves marked specific for analysis. Then we took the leaves back to lab and incubated them in growth chamber in the same high light condition. Every leave had absorbed half an hour of light before they were taken out and measured in Licor. Measurements were taken for 4 minutes for each leaf and we had 4 machines running at the same time. My job in this R package is to combine the data generated at that time, clean them, take average and find best way to present them.

The input of data would be the raw data generated from Licor 6400. Due to the different versions of the machine, the output formats have slightly difference. We marked the info of the leave before the beginning of measurements. So, the data would have a time series of 4 minutes of recording beneath the name “remark” for each leaf. The values I want to extract from each measurement is: 1. the photosynthesis, stomata conductance and Ci/Ca values when the leaf has maximum stomata conductance value in the first minute. 2. The mean value of photosynthesis, stomata conductance and Ci/Ca in the last minute. Currently we don’t know which value is more representative of true physiology of the leaf, but they are all reasonable so we decide to calculate both and decide later when we correlate those with other traits.

Three functions included in my package are:

1. Measurement data sorting and cleaning. Raw data are pretty dirty. Even though each machine does the same job recording measurements, some of them have their unique way of formatting. This function will combine the multiple input raw data, sort them, find bizarre measurements and clean them.
2. Graphing. Each measurement shall be plotted out and be put together with measurements from the same genotype to see if there are outliers.
3. Calculate plot means and genotype means. Since I was using a RCBD design, in 2 blocks there were 2 plants sampled. I want to calculate how much variation there are both within the plots and within the genotype and finally get the mean all at once.

Combine and Screen

Find