Yellow highlighted code must be edited

|  |
| --- |
| %% Main function for My\_Micromet data processing |
| % Created by <author> on <date> |
| % |
| % ============================ |
| % Setup the project and siteID |
| projectPath = '/Users/<username>/Project/My\_Micromet/'; |
| structProject=set\_TAB\_project(projectPath); |
| siteID = 'SITEID1'; |
|  |
| % Create database from raw data |
| %% Flux data from EddyPro output files |
| % |
| % Input file name |
| fileName = fullfile(structProject.sitesPath,siteID,'Flux','MY\_EDDYPRO\_OUTPUT.csv'); |
|  |
| % Read the file |
| optionsFileRead.flagFileType = 'fulloutput'; % select fulloutput, biomet, or summary |
| [~, ~,tv,outStruct] = fr\_read\_EddyPro\_file(fileName,[],[],optionsFileRead); |
|  |
| % set database path |
| databasePath = fullfile(db\_pth\_root,'yyyy',siteID,'Flux'); |
|  |
| % Convert outStruct into database |
| missingPointValue = NaN; |
| timeUnit= '30MIN'; |
| structType = 1; |
| db\_struct2database(outStruct,databasePath,0,[],timeUnit,missingPointValue,structType,1); |
|  |
| %% Met data from Campbell Scientific TOA5 output files |
| % |
| % Input file name |
| fileName = fullfile(structProject.sitesPath,siteID,'Met','MY\_CS\_TOA5\_OUTPUT.dat'); |
|  |
| % Read the file |
| [~,~,~,outStruct] = fr\_read\_TOA5\_file(fileName); |
|  |
| % set database path |
| databasePath = fullfile(db\_pth\_root,'yyyy',siteID,'Met'); |
|  |
| % Convert outStruct into database |
| missingPointValue = NaN; |
| timeUnit= '30MIN'; |
| structType = 1; |
| db\_struct2database(outStruct,databasePath,0,[],timeUnit,missingPointValue,structType,1); |
|  |