5/17/2024

**Analyze IMS Standard Operating Procedures**

* **Installation**
  + The latest version of AIMS can be found on GitHub
    - <https://github.com/BioMEMS/AnalyzeIMS>
  + Clone the GitHub repository using GitHub desktop (or whichever process you prefer)
  + Several packages are necessary to utilize all the functions of AIMS:
    - Computer Vision Toolbox
    - Deep Learning Toolbox
    - Curve Fitting Toolbox
    - Image Processing Toolbox
  + If any of the above packages are not installed, some functions of AIMS will not work
    - All of these packages should be available with the standard MATLAB license
  + Installing MATLAB packages
    - If you are not familiar with installing packages in MATLAB, follow the steps below
    - Under the “Apps” tab, clock on the “Get More Apps” button to open the add-on explorer
      * A screenshot of a computer

        Description automatically generated
    - In the add-on explorer, simply open and install all necessary packages
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* **Loading Data**
  + Run AnalyzeIMS.m in MATLAB. A figure should appear like the one below:
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  + Click the “Add Files” or “Add Folder”. A pop-up window should appear:
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  + Select the files or folder full of files that you would like to load in.
  + Several errors can occur that prevent loading files
    - Files must follow the correct naming convention
      * They must end in \_Pos.xls, \_Neg.xls, or \_Hdr.xls.
      * Each file must have a \_Pos, \_Neg, and a \_Hdr file associated with it for AIMS to load it in.
        + E.g. file1\_Pos.xls, file1\_Neg.xls, *and* file1\_Hdr.xls
        + The \_Pos and \_Neg files contain the positive and negative spectra, respectively, and the \_Hdr file contains metadata.
    - Files must be of the correct format as well
      * AIMS can only load tab-delimited text files that are saved with a .xls extension. They must also have a specific header format.
      * If issues with file format are encountered, I would suggest comparing the affected files to known good files that can be loaded into AIMS
  + If files are loaded successfully, they will appear in the sample window and their spectra can be viewed
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* **Preprocessing**
  + Smoothing and baseline removal can be performed in the preprocessing tab
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  + Simply press the “Apply” button to pre-process the data with the shown parameters
  + For most purposes, the default parameters for smoothing and baseline removal work well
    - It is recommended to learn about Savitzky-Golay filtering and ALS baseline removal before altering these parameters
    - Using inappropriate values for these parameters may give strange or unhelpful results