

Notes on using **enzalyze**

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1 Introduction

My idea for the workflow for this package is:

1. **Read** in the export file using the appropriate read function. Right now the only function I have is `read_biotek`. Note that I have no real idea what the Biotek raw format actually looks like - this is basically a guess. Melt it by well location.
2. **Preprocess** the data:
 - (a) Read & parse the ‘legend file’ that contains the name of each sample in each well. Reading is done by `read_plate_setup()` and parsing is done by `sample_name_parser()`.
 - (b) Merge the raw data object and the ‘legend’ object.
 - (c) *I thought I was going to put something else there*
3. **Calculate** calibration curves.
 - (a) Pull out the standards from the parsed, merged data frame
 - (b) For each standard name (& sample/buffer?) calculate a calibration curve. Return the slopes etc. To somewhere.
4. **Calibrate** the data.