Agenda 18 Feb. 2022

Deliverables from the last meeting:

- Noah:
  - Created shared Google Drive folder Tripoli_DocumentsForPIs
  - Draft letter announcing project (partially completed in Google Drive)
  - List of contacts/email addresses (TIMS done, ICPMS still to do, in Google Drive)
  - Submitted overdue annual reports, which have been accepted. I touched base with Raleigh that we're in the clear.
  - Solicit mass spectrometer example files - not started. Start with KU TIMS files form Isotopx
- Scott:
  - Start discussion thread about input data standard, link to Google Sheet
- Jim:
  - Continued preparatory work on architecture and look and feel.

Discussion:

- Branding/logo design
- Webpage/splash screen design

Where to locate example mass spectrometer files? Put them onto GitHub. Jim will make a folder to put them inside of productDocs, there is a folder is now called dataFormatDocs. Jim will strip out metadata and put it into Scott's scratch pad of data to include in the data standard.

While we're on data subject – the model that we use for tracers – is this a good starting point? Noah: yes. Noah, will need to add some more 'reference materials' models for e.g., synthetic reference materials. See new discussion group on "Reference Materials"

Logo: Orange/yellow and gradients for colors, rounded edges. Schematized mass spec and histogram/gaussian inside ok-ed by committee vote.

Have a stats course included in the documents – standard deviation vs. error all the way to MCMC. Scott will be in charge, adapting existing course materials.

Jim: back to architecture. How do we get data in? Noah: Might be one or multiple files, could be placed in different paths by mass spec software. But will be predictable, headers may be informative. Will need to integrate with laboratory workflow. Jim: how to identify data elements? Noah: will need to be flexible, many labels are human-generated. May not be able to automatically match with data dictionary. Will likely need an input screen. Jim: this is analogous to 'Project' idea in SQUID. Noah: we should be able to map to masses, but might need user's help (list of elements is small, but list of polyatomic species larger, less predictable).