**Editorial comments:**  
  
1. For steps that involve software (for example, 2.1.2, 2.1.3, 2.1.4, 2.1.5, 2.1.6, 2.1.7, 2.2.1.2, 2.2.1.3, 2.2.1.4, 2.2.2.3) please make sure to provide all the details such as “click this”, “select that”, “observe this”, etc. Please mention all the steps that are necessary to execute the action item. Please provide details so a reader may replicate your, this is the level of detail we’re looking for. Please keep in mind that software steps without a graphical user interface cannot be filmed.

The following text has been modified such that they are more detailed and thus easier to execute. (Page 5-6, line 192-266) and (Page 6, line 266-282)

“2.1. Data treatment:

NOTE: Matlab has the capability of performing MVDA without the addition of a graphical user interface (GUI). However, we recommend the purchase of GUI, PLS-Toolbox, Mathworks, Inc. (Natick, Massachusetts, USA). The following instructions when referring to Matlab will assume that is in conjunction with PLS-toolbox, and example data treatment script has been attached.

2.1.1. Open the appropriate multivariate data analysis software, such as The Unscrambler X®, CAMO, (Oslo, Norway) and Matlab, Mathworks, Inc. (Natick, Massachusetts, USA), click “import data” and select the type of file for analysis. E.g Select Bruker Opus files for files collected on a Bruker Alpha ATR FTIR spectrometer

2.1.1.1. In Matlab, input “analysis” into the command window to open the GUI. Right click the ‘X’ box to find “import data”

2.1.1.2. In Unscrambler, click the tab “file” to find “import”

2.1.2. Import sample, water and baseline spectra as data sets into the workspace by selecting all spectra in each set separately and clicking “open” and give each set a short name. E.g. ‘wat’ for dataset of water spectra.

2.1.3. Select new table/matrix by clicking “new matrix/vector” and generate a n×1 vector, where n is the number of samples. Input the parasitemia of each sample and give the vector the name “Parasitemia”.

2.1.3.1. In Matlab, this is done in the command window by clicking “new variable”

2.1.3.2. In Unscrambler, this is done by clicking the icon “new matrix”

2.1.4. Plot data by clicking the “plot data icon” and inspect the spectra for water vapour effects by clicking “zoom” and zooming in on 1800-1400 cm-1; most clearly observed as short, sharp, narrow peaks along the slopes of the amide I and amide II bands.

2.1.5. In cases of extreme water vapour, open edit/pre-process data tab, and select “smoothing”. Reduce noise and/or strong water vapour contributions by smoothing the sample and water spectra using up to 25 points of smoothing or use a water vapour correction method.

2.1.6. Correct non-horizontal baseline by using the baseline correction algorithm if appropriate, under the same edit/pre-process data tab in step 2.1.4.

2.1.7. Average water spectra and copy the rows into an n×m matrix equivalent to the sample dataset and reduce it to 70% intensity by multiplying it by 0.7.

2.1.7.1. In programs like Matlab, this is done in the command window by inputting the following script “AverageWater=mean(WaterDataset)”. Then copy-pasting the rows to match the sample data set. To reduce the intensity, input “AverageWater70= AverageWater\*0.70”

2.1.8. Subtract average water spectra from each sample spectrum.

2.1.8.1. In programs like Matlab, this is done in the command window by inputting the following script “WaterCorrectedData=SampleDataset-AverageWater70”.

2.1.9. Open edit/pre-process data tab apply a second derivative function, normalise data by selecting single normal variate (SNV) function and mean centre data.

2.1.9.1. In programs like Matlab, this can be done in one go. First select “derivative”, and input 25 points of smoothing, polynomial order of 3 and derivative order on the sample set using 25 points of smoothing and a Savitzky-Golay function. Then select “SNV” and “mean center”. Click “okay/apply” .

2.1.10. Open edit/pre-process data tab and in “column variables”, select 2980-2800 cm-1 and 1750-850 cm-1 by making sure only their boxes are ticked.

2.2. Data analysis:

2.2.1. Principal Component Analysis (PCA):

2.2.1.1. Click “Analysis”, then “Decomposition” and select PCA.

2.2.1.1.1. In programs like Matlab, click “build model”

2.2.1.1.2. In programs like Unscrambler, you must input the PCA methods. Input the optimal number of Principal Components (PCs) -in this work, 7- and a maximum of 100 iterations, and select cross-validation for the validation method. Click “Run”.

2.2.1.2. Observe the 95% confidence limit, the dashed ring, on the scores plot between PC1 and PC2”

(Page 5-6, line 192-266)

“2.2.2.1. Click “Analysis”, then “Regression” and select PLS-R.

2.2.2.1.1. In programs like Matlab, right click “Y” block and select the vector “Parasitemia” then click “Build model”

2.2.2.1.2. In programs like Unscrambler, you must input the PLS-R methods. Select the vector “Parasitemia” as the “Y reference” and the sample dataset as “X data set” and select”

(Page 6, line 266-282)  
  
2. Figure 1: Please add (A) and (B) labels to the figure. Please add the proper unit (if it is intensity, indicate it) to the Y axis of panel (B). Please upload the figure a .png, .pdf, or a .tiff file (not .psd). Please combine all panels of one figure into a single image file.

This has been amended so that the file is now .png  
  
3. Please provide the “Supplementary material” for the “script for executing the data treatment”.

An example of a script for Matlab has been added as supplementary material   
  
4. Please revise the table of the essential supplies, reagents, and equipment. The table should include the name, company, and catalog number of all relevant materials in separate columns in an xls/xlsx file. Please list all the materials, equipment, instrument, and software used in your work.

This has been amended so that all products have the name, company, and catalog number.